ANTIBODIES THAT ARE CAPABLE OF SPECIFICALLY BINDING TISSUE FACTOR PATHWAY INHIBITOR

The invention relates to antibodies that are capable of specifically binding tissue factor pathway inhibitor (TFPI), neutralising free TFPI and reducing the clotting time of blood. Furthermore, the invention relates to polynucleotides that encode such antibodies and to cells that comprise the polynucleotides or that express the antibodies of the invention. Such antibodies have utility in the treatment of subjects with a coagulopathy, alone as well as in combination with a second agent.
Antibodies that are capable of specifically binding tissue factor pathway inhibitor.

FIELD OF THE INVENTION

The present invention relates to antibodies that are capable of specifically binding the C-terminal of tissue factor pathway inhibitor (TFPI) and which are thus capable of neutralising the free pool of TFPI. The invention also relates to uses for such antibodies, such as therapeutic and pharmaceutical uses.

BACKGROUND OF THE INVENTION

In subjects 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 cascade results in insufficient blood coagulation and potentially life-threatening bleeding, or damage to internal organs, such as the joints. Subjects such as human beings with haemophilia A and B may receive coagulation factor replacement therapy such as exogenous Factor VIII or Factor IX, respectively. However, such patients are at risk of developing "inhibitors" (antibodies) to such exogenous factors, rendering formerly efficient therapy ineffective. 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 infections and thrombotic complications. Subjects with a coagulopathy may only receive therapy after a bleed has commenced, rather than as a precautionary measure, which often impinges upon their general quality of life. Thus, there are still many unmet medical needs in the haemophilia community, in particular, and in subjects with coagulopathies, in general.

The coagulation cascade is normally set into motion upon vessel wall injury, which exposes sub-endothelial tissue factor (TF) to the components of circulating blood. In brief, TF forms a complex with Factor VII/Factor Vila (FVII/FVIIa) on the surface of TF-expressing cells. This complex activates Factor X (FX) to Factor Xa (FXa) which, with Factor Va (FVa) as cofactor, leads to the generation of a limited amount of thrombin (FIIa). Small amounts of thrombin activate platelets, which results in surface exposure of phospholipids that support the binding of the tenase complex, Factor Vila/Factor IXa (FVIIa/FIXa). The tenase complex activates large amounts of FX to FXa, which subsequently results in the generation of a large amount of thrombin. A full thrombin burst is needed for the formation of a mechanically strong fibrin structure and stabilization of the haemostatic plug.

In individuals with haemophilia, FVIII or FIX is present at low levels, or may be entirely absent. Due to the lack of tenase activity, the capacity to generate FXa is low and insufficient to support the propagation phase of coagulation. In contrast, the TF-mediated initiation phase of coagulation is not dependent on the formation of the tenase complex. Initiation of coagulation via
the TF-pathway will, however, be blocked by plasma inhibitors shortly after the initial FXa generation. One such inhibitor is tissue factor pathway inhibitor (TFPI), which inhibits both FXa and TF/FVIIa and plays a key role as a feed-back inhibitor of on-going coagulation. TFPI is a strong inhibitor of the TF-FVIIa complex only in the presence of FXa. Thus, efficient inhibition of TF/FVIIa requires generation of FXa, formation of the FXa/TFPI complex, and a subsequent formation of the ternary TF/FVIIa/FXa/TFPI complex.

Several pools of TFPI exist in vivo. A major fraction is bound to the vascular endothelium, a minor fraction is associated with lipoproteins in the blood, a small fraction is present in platelets and, finally, a small amount exists as free, circulating TFPI. Furthermore, TFPI exists as TFPIalpha, TFPIbeta and TFPlgamma forms. Neutralization of the inhibitory activity of certain fractions of TFPI may prove efficient in treatment of undesired bleedings.

Antibodies that are capable of binding TFPI are known in the art. Several documents disclose antibodies that are capable of binding to the K3 domain of TFPI, namely:


JP6153981A.

These references do not disclose TFPI antibodies for the treatment of subjects with a coagulopathy.

There is still a need in the art of medicine for pharmaceuticals which may be used to enhance coagulation. There is a need for pharmaceuticals which may be administered not only intravenously but also by other routes of administration, such as subcutaneously. Thus, there is a need for pharmaceuticals, such as antibodies, which are pro-coagulant even when administered in low doses and/or which have a high bioavailability. Furthermore, there is a need for pharmaceuticals, such as antibodies, which are suitable for the prophylactic treatment of individuals with a congenital or acquired coagulopathy such as haemophilia A, haemophilia B, haemophilia A with inhibitors or haemophilia B with inhibitors. More specifically, there is a need for pharmaceuticals, such as antibodies, that lower the threshold for FVIII or FIX activity in individuals with haemophilia A and haemophilia B, respectively. Within the particular realm of antibodies that are capable of binding TFPI, there is a need for antibodies which do not bind to all pools of TFPI, such as antibodies which do not affect the function of endothelial cell-bound TFPI, such as the GPI-anchored pool of TFPI. More specifically, there is a need for TFPI antibodies that demonstrate dose linearity with respect to their half-life in plasma.

Disclosed herein are antibodies which are suitable for use as pharmaceuticals. Such antibodies may have a substantial impact upon the quality of life of - not least - individuals with haemophilia A or B, with or without inhibitors.

SUMMARY OF THE INVENTION

The inventors have developed monoclonal antibodies that are capable of specifically binding to the C-terminal of full length tissue factor pathway inhibitor (TFPI), wherein "C-terminal" is herein defined as that portion of TFPI which is, or which corresponds to, amino acid residues 186-276 of
The present invention relates to these antibodies and to other antibodies that are derived from these antibodies and/or that have similar binding properties and that are capable of modulating the activity of free TFPI.


Another particular antibody comprises the heavy chain variable region of SEQ ID NO: 7 and the light chain variable region of SEQ ID NO: 5. Another particular antibody comprises the heavy chain variable region of SEQ ID NO: 9 and the light chain variable region of SEQ ID NO: 11. A third particular antibody comprises the heavy chain variable region of SEQ ID NO: 13 and the light chain variable region of SEQ ID NO: 15.

The invention also provides polynucleotides which encode an antibody of the invention, such as polynucleotides which encode an antibody light chain and/or an antibody heavy chain of the invention.

The invention also provides pharmaceutical compositions comprising an antibody or polynucleotide of the invention and a pharmaceutically acceptable carrier or diluent.

The antibodies, polynucleotides and compositions of the invention are also provided for use in the treatment or prevention of a coagulopathy or the stimulation of blood clotting. That is, the invention provides a method for the treatment or prevention of a coagulopathy, or the stimulation of blood clotting, said method comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an antibody, polynucleotide or composition of the invention.

**BRIEF DESCRIPTION OF THE SEQUENCE LISTING**

SEQ ID NO: 1 provides the amino acid sequence of full length human TFPI (signal peptide sequence omitted).

SEQ ID NO: 2 provides the amino acid sequence of truncated TFPI (1-239).

SEQ ID NO: 3 provides the amino acid sequence of truncated TFPI (1-245).
SEQ ID NO: 4 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI4F1 10 (also designated mAb 4F1 10).

SEQ ID NO: 5 provides the amino acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI4F1 10.

SEQ ID NO: 6 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI4F1 10.

SEQ ID NO: 7 provides the amino acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI4F1 10.

SEQ ID NO: 8 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI22F66.

SEQ ID NO: 9 provides the amino acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI22F66.

SEQ ID NO: 10 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI22F66.

SEQ ID NO: 11 provides the amino acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI22F66.

SEQ ID NO: 12 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI22F71.

SEQ ID NO: 13 provides the amino acid sequence (signal peptide sequence omitted) of the variable heavy (VH) domain of anti-TFPI22F71.

SEQ ID NO: 14 provides the nucleic acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI22F71.

SEQ ID NO: 15 provides the amino acid sequence (signal peptide sequence omitted) of the variable light (VL) domain of anti-TFPI22F71.

SEQ ID NO: 16 provides the nucleic acid sequence of the reverse primer that was used for HC (VH domain) amplification.

SEQ ID NO: 17 provides the nucleic acid sequence of the reverse primer that was used for TFPI22F66 and TFPI22F71 LC (VL domain) amplification.

SEQ ID NO: 18 provides the nucleic acid sequence of the reverse primer that was used for TFPI4F1 10 LC amplification.

SEQ ID NO: 19 provides the amino acid sequence of Factor VII/Factor Vila.

SEQ ID NO: 20 provides the amino acid sequence of Factor VIII.

SEQ ID NO: 21 provides the amino acid sequence of Factor IX.

SEQ ID NO: 22 provides the amino acid sequence of truncated TFPI (1-240).

SEQ ID NO: 23 provides the amino acid sequence of truncated TFPI (1-241).

SEQ ID NO: 24 provides the amino acid sequence of truncated TFPI (1-242).

SEQ ID NO: 25 provides the amino acid sequence of truncated TFPI (1-243).

SEQ ID NO: 26 provides the amino acid sequence of truncated TFPI (1-244).
DESCRIPTION OF THE DRAWINGS

Figure 1 shows the effect of the 4F110 TFPI antibody on TF-induced clot formation. Clotting time was measured with a dilute PT assay at various fixed concentrations of TF (Innovin® diluted 1:7,500; 1:15,000; 1:30,000) and antibody (0.005 - 1 nM).

Figure 2 shows the effect of 4F110 anti-TFPI on TF-induced thrombin generation in FVIII-depleted plasma. Clotting was initiated by calcification and addition of Innovin® (TF source) to citrated FVIII-depleted plasma supplemented with 10 µM PS/PC in the absence and presence of 10 nM 4F110.

Figure 3 shows the effect of 4F110 anti-TFPI on TF-induced thrombin generation in FVIII-depleted plasma replenished with various levels of rFVIII. Clotting was initiated by calcification and addition of Innovin® (TF source) to citrated FVIII-depleted plasma supplemented with 10 µM PS/PC in the absence and presence of 10 nM 4F110. Bars show the corresponding lag times calculated based on a thrombin threshold level of 1 nM (means ± SD, n = x).

Figure 4 shows the effect of 4F110 anti-TFPI and rFVIII on TF-induced clot formation in FVIII-depleted plasma supplemented with 150,000 platelets/µl measured by thromboelastography (TEG) analysis. A. TEG curves show the effect of adding 0.005, 0.05 and 1.0 U/ml rFVIII to FVIII-depleted plasma in the absence of anti-TFPI. B. TEG curves show the effect of adding 0.005, 0.05 and 1.0 U/ml rFVIII to FVIII depleted plasma in the presence of 10 nM 4F110 anti-TFPI.

C. R values (clot times) for the curves without AB shown in A (open bars) and with AB shown in B (closed bars). D. K (speed of clot kinetics) values for the curves without AB shown in A (open bars) and with AB shown in B (closed bars). E. Angle values for the curves without AB shown in A (open bars) and with AB shown in B (closed bars). F. MA (maximal amplitude) values for the curves without AB shown in A (open bars) and with AB shown in B (closed bars).

Figure 5 shows the fluorescence-activated cell sorter (FACS) analysis of a TFPI-expressing cell line. As also illustrated in figure 6, the two C-terminal monoclonal antibodies were not able to bind to TFPI on a cellular surface.

Figure 6 shows that the C-terminal TFPI antibodies named 4F110, 22F66, 22F71, 22F74, 22F79 and 22F132 do not bind or bind very poorly to truncated TFPI(l-239) (middle five bars).

Figure 7 shows that six TFPI antibodies (4F110, 22F66, 22F71, 22F132, 22F79, 22F74) bind to different truncated forms of TFPI, listed at the right. Binding is relative to the binding to wild type (wt) TFPI (1.0).

Figure 8 shows the neutralization of TFPI inhibition of FVIIa/TF/FXa activity in the presence of phospholipid (PS/PC) vesicles. Open circle: 4F110; filled circle 22F66; square: 22F71; grey triangle: 22F79; open triangle: 22F74; grey rhombus: 22F132.

Figure 9 is a cartoon of the structure of TFPI and the various pools of TFPI.
DESCRIPTION OF THE INVENTION

The invention relates to antibodies that are capable of specifically binding full-length tissue factor pathway inhibitor (TFPI), such as antibodies that bind to the "C-terminal" of TFPI. Such antibodies may specifically bind the C-terminal domain and/or the Kunitz 3 (K3) domain of TFPI; that is, they may bind to the "C-terminal" but may not bind to the Kunitz 1 (K1) domain of TFPI, the Kunitz 2 (K2) domain of TFPI, or to other similar molecules. Antibodies of the invention may not bind to a TFPI molecule that comprise the K1 and/or K2 domain but that lack that portion of TFPI which is C-terminal to the K2 domain. Antibodies of the invention may be incapable of binding truncated TFPI, such as C-terminal truncated TFPI. Truncated forms of TFPI that may not be bound by the antibodies of the invention include the polypeptide of SEQ ID NO: 2 and a polypeptide having the sequence of amino acids 1 to 161 of SEQ ID NO: 1. Alternatively, the antibodies may bind the K1 domain of TFPI, the K2 domain of TFPI, or other molecules such as truncated TFPI molecules with a low affinity compared to that with which they bind the C-terminal of TFPI.

The term "TFPI", as used herein, encompasses any naturally occurring form of TFPI which may be derived from any suitable organism. For example, TFPI for use as described herein may be vertebrate TFPI, such as mammalian TFPI, such as TFPI from a primate (such as a human); a rodent (such as a mouse or a rat), a lagomorph (such as a rabbit), or an artiodactyl (such as a cow, sheep, pig or camel). Preferably, the TFPI is human TFPI. The TFPI may be a mature form of TFPI such as a TFPI protein that has undergone post-translational processing within a suitable cell. Such a mature TFPI protein may, for example, be glycosylated. The TFPI may be a full length TFPI protein. The term TFPI also encompasses variants, isoforms and other homologs of such TFPI molecules. Variant TFPI molecules may have the same type of activity as naturally occurring TFPI, such as the ability to neutralize the catalytic activity of FXa, or the ability to inhibit a complex of TF-FVIIa/FXa.

The term "C-terminal", as used herein, refers to any part of TFPI that is C-terminal to the amino acid residue which corresponds to amino acid 187 of human TFPI (SEQ ID NO: 1). The term "C-terminal" specifically excludes the Kunitz 1 (K1) and Kunitz 2 (K2) domains of TFPI. On the other hand, the term "C-terminal" includes parts of TFPI that are within the Kunitz 3 (K3) domain of TFPI (amino acids 188-238) and/or parts of TFPI that include amino acids 240-276.

"Free TFPI" is the in vivo pool of TFPI that contains an available "C-terminal". The term "free TFPI" refers to the soluble pool of TFPI in plasma. Other pools of TFPI, that are not "free TFPI", are GPI-anchored TFPI and lipoprotein bound TFPI. In contrast to free TFPI, these pools of TFPI do not have a C-terminal that is available for binding to, e.g., an antibody. Antibodies of the invention may be capable of specifically binding free TFPI, but may not be capable of specifically binding GPI-anchored TFPI. Antibodies of the invention may be capable of specifically binding free TFPI, but may not be capable of specifically binding lipoprotein bound TFPI.

Thus, the invention relates to antibodies that may be capable of modulating the activity of free TFPI, only. Such antibodies may possess the ability to shorten clotting time. For example, an antibody of the invention may have the ability to shorten clotting time in human FVIII-deficient
plasma or human FIX-deficient plasma, or to reduce time to clot as measured in a thromboelastography (TEG) analysis of human whole blood.

Antibodies of the invention may be monoclonal antibodies in the sense that they are made by identical immune cells that are all clones of the same parent cell. Antibodies of the invention may be produced, screened and purified using the methods described in the Examples. Antibodies of the invention may also be produced by means of other methods known to the person skilled in the art, such as a phage display or a yeast display. Once produced, antibodies may be screened for binding to, for example, full length TFPI, truncated TFPI (1-161), truncated TFPI (1-239), truncated TFPI (1-240), truncated TFPI (1-241), truncated TFPI (1-242), truncated TFPI (1-243), truncated TFPI (1-244), truncated TFPI (1-245) and truncated TFPI (1-246) using the methods described in the Examples.

The term "antibody" herein refers to a protein, derived from a germline immunoglobulin sequence, that is capable of specifically binding to an antigen or a portion thereof. The term includes full length antibodies of any isotype (that is, IgA, IgE, IgG, IgM and/or IgY) and any single chain thereof.

The term "antibody", as referred to herein, includes whole antibodies and any antigen binding fragment (i.e., "antigen-binding portion") or single chains thereof. An antibody refers to a glycoprotein comprising at least two heavy chains (HC) and two light chains (LC) that are inter-connected by disulfide bonds; or an antigen binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (VH) and a heavy chain constant region (CH). Each light chain is comprised of a light chain variable region (VL) and a light chain constant region (CL). The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system.

Examples of antigen-binding fragments of the invention include Fab, Fab', F(ab')2, F(ab)2, Fv (scFv; see e.g., Bird et al., Science 1988; 242:425-426; and Huston et al. PNAS 1988; 85:5879-5883); dsFv, Fd (typically the VH and CH1 domain), and dAb (typically a VH domain) fragments; VH, VL, VhH, and V-NAR domains; monovalent molecules comprising a single VH and a single VL chain; minibodies, diabodies, triabodies, tetrabodies, and kappa bodies (see, e.g., Ill et al.. Protein Eng 1997; 10:949-57); camel IgG; IgNAR; as well as one or more isolated CDRs or a functional paratope, where the isolated CDRs or antigen-binding residues or polypeptides can be associated or linked together so as to form a functional antibody fragment. Various types of antibody fragments have been described or reviewed in, e.g., Holliger and Hudson, Nat Biotechnol 2005; 23:1126-1136; WO2005040219, and published U.S. Patent Applications 20050238646 and 20020161201.
"Fab fragments", including "Fab" and "Fab(ab')2" fragments, of an antibody are derived from said antibody by cleavage of the heavy chain in the hinge region on the N-terminal or C-terminal side 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 the first constant domain (CH1) of the heavy chain. "F(ab')2" fragments comprise a pair of "Fab" fragments that are generally covalently linked by their hinge cysteines. A Fab' is formally derived from a F(ab')2 fragment by cleavage of the hinge disulfide bonds connecting the heavy chains in the F(ab')2. 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. F(ab')2 fragments are capable of divalent binding, whereas Fab and Fab' fragments can bind monovalently. Generally, Fab fragments lack the constant CH2 and CH3 domains, i.e. the Fc part, where interaction with the Fc receptors would occur. Thus, 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 F(ab')2, or Fab fragments may be produced recombinantly using techniques that are well known to the person skilled in the art.

An "Fv" fragment is an antibody fragment that contains a complete antigen 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 VH-VL dimer. Collectively, the six hypervariable regions or a subset thereof confer antigen binding specificity to the antibody. However, even a single variable domain comprising only three hypervariable regions specific for an antigen has the ability to recognize and bind antigen, although usually at a lower affinity than the entire binding site (Cai & Garen, Proc. Natl. Acad. Sci. USA, 93: 6280-6285, 1996). For example, naturally occurring camelid antibodies that only have a heavy chain variable domain (VHH) can bind antigen (Desmyter et al., J. Biol. Chem., 277: 23645-23650, 2002; Bond et al., J. Mol. Biol. 2003; 332 : 643-655).

"Single-chain Fv" or "scFv" antibody fragments comprise the VH and VL domains of antibody, where these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the VH and VL 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, Rosenberg and Moore eds. Springer-Verlag, New York, pp. 269-315.

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, in which fragments comprise a heavy chain variable domain (VH) connected to a light chain variable domain (VL) in the same polypeptide chain (VH and VL). 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. Diabodies
are described more fully, for example, in EP 404,097; WO 93/1 1161; and Hollinger et al., 1993, Proc. Natl. Acad. Sci. USA, 90:6444-6448.

The expression "linear antibodies" refers to antibodies as described in Zapata et al., 1995, Protein Eng., 8(10) :1057-1062. Briefly, these antibodies contain a pair of tandem Fd segments (VH-CH1-VH-CH1) that, together with complementary light chain polypeptides, form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

The term "monobody" as used herein, refers to an antigen binding molecule with a heavy chain variable domain and no light chain variable domain. A monobody can bind to an antigen in the absence of light chains and typically has three hypervariable regions, for example CDRs designated CDRH1, CDRH2, and CDRH3. A heavy chain IgG monobody has two heavy chain antigen binding molecules connected by a disulfide bond. The heavy chain variable domain comprises one or more hypervariable regions, preferably a CDRH3 or HVL-H3 region.

Antibody fragments may be obtained using conventional recombinant or protein engineering techniques, and the fragments may be screened for binding to full length TFPI, truncated TFPI (1-161), truncated TFPI (1-239), truncated TFPI (1-240), truncated TFPI (1-241), truncated TFPI (1-242), truncated TFPI (1-243), truncated TFPI (1-244), truncated TFPI (1-245) and truncated TFPI (1-246) 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 MuTFPI4F110 antibody, the MuTFPI22F66 antibody, the MuTFPI22F71 antibody, the MuTFPI 22F74 antibody, the MuTFPI 22F79 antibody, the MuTFPI 22F132 antibody, or a variant of any one of these antibodies. An antibody of the invention may be, or may comprise, an antigen binding portion of one of these antibodies, or variants thereof. For example, the 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.

The MuTFPI4F110 antibody has a variable heavy chain sequence as shown in SEQ ID NO: 5 and a variable light chain sequence as shown in SEQ ID NO: 7. An antibody of the invention may comprise this variable heavy chain sequence and/or this variable light chain sequence. The MuTFPI4F110 antibody has the CDR sequences shown at amino acid residues 31 to 35, 50 to 66 and 99 to 107 of SEQ ID NO: 5 and amino acid residues 24 to 34, 50 to 56 and 89 to 97 of SEQ ID NO: 7. An antibody of the invention may comprise 1, 2, 3, 4, 5 or all 6 of these CDR sequences. An antibody of the invention may comprise amino acid residues 99 to 107 of SEQ ID NO: 5.

The MuTFPI22F66 antibody has a variable heavy chain sequence as shown in SEQ ID NO: 9 and a variable light chain sequence as shown in SEQ ID NO: 11. An antibody of the invention may comprise this variable heavy chain sequence and/or this variable light chain sequence. The MuTFPI22F66 antibody has the CDR sequences shown at amino acid residues 31 to 35, 50 to 66 and 99 to 106 of SEQ ID NO: 9 and amino acid residues 24 to 33, 49 to 55 and 88 to 96 of SEQ ID
An antibody of the invention may comprise 1, 2, 3, 4, 5 or all 6 of these CDR sequences. An antibody of the invention may comprise amino acid residues 99 to 106 of SEQ ID NO: 9.

The mTFPI22F71 antibody has a variable heavy chain sequence as shown in SEQ ID NO: 13 and a variable light chain sequence as shown in SEQ ID NO: 15. An antibody of the invention may comprise this variable heavy chain sequence and/or this variable light chain sequence. The mTFPI22F71 antibody has the CDR sequences shown at amino acid residues 31 to 35, 50 to 66 and 99 to 111 of SEQ ID NO: 13 and amino acid residues 24 to 38, 54 to 60 and 93 to 101 of SEQ ID NO: 15. An antibody of the invention may comprise 1, 2, 3, 4, 5 or all 6 of these CDR sequences. An antibody of the invention may comprise amino acid residues 99 to 111 of SEQ ID NO: 13.

An antibody of the invention may be a human antibody or a humanised antibody. The term "human antibody", as used herein, is intended to include antibodies having variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is 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). However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

Such a human antibody may be a human monoclonal antibody. Such a human monoclonal antibody may be produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, e.g., a transgenic mouse, rat or rabbit, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell.

Human antibodies may be isolated from sequence libraries built on selections of human germline sequences, further diversified with natural and synthetic sequence diversity.

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 derivatives" refers to any modified form of the human antibody, e.g., a conjugate of the antibody and another agent or antibody.

The term "humanised antibody" is intended to refer to a human/non-human chimeric antibody that contains a minimal sequence (CDR regions) derived from non-human immunoglobulin. Humanized antibodies are thus human immunoglobulins (recipient antibody) in which residues from a hyper-variable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as from a mouse, rat, rabbit, or non-human primate, having the desired specificity, affinity, and capacity. In some instances, 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.

The term "humanized antibody derivative" refers to any modified form of the humanized antibody, such as a conjugate of the antibody and another agent or antibody.
Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FR residues are those of a human immunoglobulin sequence. The humanized antibody can optionally also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

The "fragment crystallizable" region ("Fc region"/"Fc domain") of an antibody is the N-terminal region of an antibody, which comprises the constant CH2 and CH3 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 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. Preferably, a modified Fc domain comprises one or more, and perhaps all of the following mutations that will result in decreased affinity to certain Fc receptors (L234A, L235E, and G237A) and in reduced Clq-mediated complement fixation (A330S and P331S), respectively (residue numbering according to the EU index).

In one aspect, antibodies of the invention may be engineered to include modifications within the Fc region, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, protein stability and/or antigen-dependent cellular cytotoxicity, or lack thereof. 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.

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, 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 CH1 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 further be modified to stabilize the antibody, e.g., to reduce the risk of a bivalent antibody separating into two monovalent VH-VL fragments. For example, in an
IgG4 constant region, residue S241 may be mutated to a proline (P) residue to allow complete disulphide bridge formation at the hinge (see, e.g., Angal et al., Mol Immunol. 1995; 30:105-8).

An antibody of the invention will have the ability to bind to TFPI. An antibody of the invention is, preferably, capable of specifically binding the C-terminal of TFPI. That is, it is capable of binding the C-terminal of TFPI with a greater binding affinity than that with which it binds to the K1 domain of TFPI, the K2 domain of TFPI, or another molecule.

The target molecule of an antibody of the invention may be any TFPI molecule as described herein, such as a naturally occurring TFPI molecule, a fully mature TFPI molecule or a full-length TFPI molecule. The TFPI molecule may be in a form that is present in plasma in vivo. The target molecule may be TFPI in a form that is present in plasma in vivo. The antibody of the invention may be able to discriminate between the various naturally occurring forms of TFPI, binding to some but not to others. For example, antibodies of the invention may not be capable of binding naturally occurring, truncated forms of TFPI that do not comprise a K3 domain and/or a carboxy terminal domain. However, the target molecule may be a truncated TFPI molecule that comprises a K3 domain and/or a carboxy terminal. The target molecule may be a variant or a fragment of a TFPI molecule. The target molecule may consist of, or may comprise, the amino acid sequence of SEQ ID NO: 1, or a fragment or other variant thereof. Target molecules comprise a suitable epitope for antibody binding, such as the epitope described herein.

The target molecule may comprise five or more, ten or more, fifteen or more, twenty or more, twenty five or more, or thirty or more surface accessible residues of TFPI or of a particular region of TFPI, such as the K3 domain or the C-terminal of TFPI. A surface accessible residue is a residue having more than 40% relative accessibility.

Methods of measuring surface accessibility are well known in the art, having first been described by Lee & Richards in 1971 [B. Lee and F.M. Richards, "The Interpretation of Protein Structures: Estimation of Static Accessibility" J. Mol. Biol. 55, 379-400 (1971)]. Surface accessibilities may be calculated using the computer program Quanta 2005, from Accelrys Inc., using the atomic coordinates originating from, for example, X-ray structures or homology built structures.

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 (intrinsic activity).

Binding affinity between two molecules, e.g. an antibody, or fragment thereof, and an antigen, through a monovalent interaction may be quantified by determination of the dissociation, or binding, constant ($K_d$). In turn, $K_d$ can be determined by measurement of the kinetics of complex formation and dissociation, e.g. by the SPR method (Biacore). 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, e.g. comparison of the binding affinity of different antibodies for a given antigen, may be compared by comparison of the $K_0$ values for the individual antibody/antigen complexes.

Similarly, the specificity of an interaction may be assessed by determination and comparison of the $K_0$ value for the interaction of interest, e.g. a specific interaction between an antibody and an antigen, with the $K_0$ value of an interaction not of interest.

Typically, the $K_0$ for the antibody with respect to the target will be 2-fold, preferably 5-fold, more preferably 10-fold less than $K_0$ with respect to the other, non-target molecule such as unrelated material or accompanying material in the environment. More preferably, the $K_0$ will be 50-fold less, such as 100-fold less, or 200-fold less; even more preferably 500-fold less, such as 1,000-fold less, or 10,000-fold less.

The value of this binding constant can be determined directly by well-known methods, and can be computed even for complex mixtures by methods such as those, for example, set forth in Caceci et al. (Byte 9:340-362, 1984). For example, the $K_0$ may be established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong & Lohman (Proc. Natl. Acad. Sci. USA 90, 5428-5432, 1993). Other standard assays to evaluate the binding ability of ligands such as antibodies towards targets are known in the art, including 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 Surface Plasmon Resonance (SPR), e.g. by using a Biacore™ system.

A competitive binding assay can be conducted in which the binding of the antibody to the target is compared to the binding of the target by another ligand of that target, such as another antibody. The concentration at which 50% inhibition occurs is known as the $K_i$. Under ideal conditions, the $K_i$ is equivalent to $K_0$. The $K_i$ value will never be less than the $K_0$, so measurement of $K_i$ can conveniently be substituted to provide an upper limit for $K_0$.

An antibody of the invention may have a $K_0$ for its target of $1 \times 10^{-7}$ M or less, $1 \times 10^{-6}$ M or less, or $1 \times 10^{-5}$ M or less, or $1 \times 10^{-4}$ M or less, $1 \times 10^{-3}$ M or less, or $1 \times 10^{-2}$ M or less. The $K_0$ of an antibody of the current invention may be less than 0.8 nM, such as less than 0.7 nM, such as less than 0.6 nM, such as less than 0.5 nM, such as less than 0.4 nM, such as less than 0.3 nM, such as less than 0.2 nM, such as less than 0.1 nM, such as less than 0.05 nM, such as less than 0.025 nM, such as less than 0.015 nM, such as less than 0.10 nM.

An antibody that specifically binds its target may bind its target with a high affinity, that is, exhibiting a low $K_0$ as discussed above, and may bind to other, non-target molecules with a lower affinity. For example, the antibody may bind to non-target molecules with a $K_0$ of $1 \times 10^{-6}$ M or more, more preferably $1 \times 10^{-5}$ M or more, more preferably $1 \times 10^{-4}$ M or more, more preferably $1 \times 10^{-3}$ M or more, even more preferably $1 \times 10^{-2}$ M or more. An antibody of the invention is preferably capable of binding to its target with an affinity that is at least two-fold, 10-fold, 50-fold, 100-fold 200-fold, 500-fold, 1,000-fold or 10,000-fold or greater than its affinity for binding to another non-target molecule.
The antibody of the current invention may be capable of neutralising TFPI inhibition of the FVIIa/TF/FX complex.

The antibody of the current invention may be capable of binding TFPI such that the percentage of free TFPI in a subject is reduced to less than 50%, such as less than 30%, such as less than 29%, such as less than 28%, such as less than 27%, such as less than 26%, such as less than 25%, such as less than 24%, such as less than 23%, such as less than 22%, such as less than 21%, such as less than 20%, such as less than 19%, such as less than 18%, such as less than 17%, such as less than 16%, such as less than 15%, such as less than 14%, such as less than 13%, such as less than 12%, such as less than 11%, such as less than 10%, such as less than 9%, such as less than 8%, such as less than 7%, such as less than 6%, such as less than 5%, such as less than 4%, such as less than 3%, such as less than 2%, such as less than 1%, such as between 1% and 0%.

The term "complementarity-determining region" ("CDR") or "hypervariable region", when used herein, refers to the amino acid residues of an antibody that are responsible for antigen binding. The CDRs are generally comprised of amino acid residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in 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) and/or those residues from a "hypervariable loop" (residues 26-32 (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 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 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 term "framework region" or "FR" residues refer to those VH or VL amino acid residues that are not within the CDRs, as defined herein.

An antibody of the invention may comprise a CDR region from one or more of the specific antibodies disclosed herein, such as a CDR region from within SEQ ID NOs: 5, 7, 9, 11, 13 or 15. The CDR sequences within the light chain of an antibody of the invention may be identified at: amino acids 24 to 34, 50 to 56 and 89 to 97 of SEQ ID NO: 7; amino acids 24 to 33, 49 to 55 and 88 to 96 of SEQ ID NO: 11; amino acids 24 to 38, 54 to 60 and 93 to 101 of SEQ ID NOs: 15. The CDR sequences within the heavy chain of an antibody of the invention may be identified at: amino acids 31 to 35, 50 to 66 and 99-
106 of SEQ ID NO: 9; amino acids 31 to 35, 50 to 66 and 99-106 of SEQ ID NO: 9; at amino acids 31 to 35, 50 to 66 and 99-111 of SEQ ID NO: 13.

An antibody of the invention may comprise any one or more of these CDR sequences. An antibody of the invention may comprise the CDR3 heavy chain sequence of one of the antibodies described herein, e.g. amino acids 99 to 107 of SEQ ID NO: 5, 99 to 106 of SEQ ID NO: 9 or 99 to 111 of SEQ ID NO: 13. An antibody of the invention may comprise all six CDRs from one of the specific antibodies described herein such as the CDR amino acids indicated above from SEQ ID NO: 5 and SEQ ID NO: 7, the CDR amino acids indicated above from SEQ ID NO: 9 and SEQ ID NO: 11 or the CDR amino acids indicated above from SEQ ID NO: 13 and SEQ ID NO: 15.

The term "epitope", as used herein, is defined in the context of a molecular interaction between an "antigen binding polypeptide" (Ab) and its corresponding "antigen" (Ag). The term antigen (Ag) refers to the molecular entity used for immunization 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 specifically recognized by the Ab, thus including fragments or mimics of the molecule used in the immunization process for raising the Ab. Thus, for Abs that bind to the C-terminal of TFPI, both full-length TFPI, truncated TFPI and other variants of TFPI that comprise the C-terminal portion of TFPI are referred to as an Ag.

Generally, the term "epitope" refers to the area or region on an Ag to which an Ab specifically binds, i.e. the area or region in physical contact with the Ab. A protein epitope may comprise amino acid residues in the Ag that are directly involved in binding to a Ab (also called the immunodominant component of the epitope) and other amino acid residues, which are not directly involved in the binding, such as amino acid residues of the Ag which are effectively blocked by the Ab (in other words, the amino acid residue is within the "solvent-excluded surface" and/or the "footprint" of the Ab). The term epitope herein includes both types of binding sites in any particular region of the K3 domain or the C-terminal domain of TFPI that specifically binds to an anti-TFPI antibody, or another "C-terminal"-specific agent according to the invention, unless otherwise stated (e.g., in some contexts the invention relates to antibiotics that bind directly to particular amino acid residues). The "C-terminal" may comprise a number of different epitopes, which may include, without limitation, (1) linear peptide antigenic determinants, (2) conformational antigenic determinants which consist of one or more non-contiguous amino acids located near each other in the mature C-terminal conformation; and (3) post-translational antigenic determinants which consist, either in whole or part, of molecular structures covalently attached to the "C-terminal", such as carbohydrate groups.

The epitope for a given antibody (Ab)/antigen (Ag) pair can be defined 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, Hydrogde deuterium exchange Mass Spectrometry (HX-MS) and various competition binding methods. 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, the epitope for a given Ab/Ag pair will be defined differently depending on the epitope mapping method.
employed.

At its most detailed level, the epitope for the interaction between the Ag and the Ab can be defined by the spatial coordinates defining the atomic contacts present in the Ag-Ab interaction, as well as information about their relative contributions to the binding thermodynamics. At a less detailed level the epitope can be characterized by the spatial coordinates defining the atomic contacts between the Ag and Ab. At a further less detailed level the epitope can be characterized by the amino acid residues that it comprises as defined by a specific criterion, e.g. distance between atoms in the Ab and the Ag. At a further, less detailed, level the epitope can be characterized through function, e.g. by competition binding with other Abs. The epitope can also be defined more generically as comprising amino acid residues for which substitution by another amino acid will alter the characteristics of the interaction between the Ab and Ag.

In the context of an X-ray derived crystal structure defined by spatial coordinates of a complex between an Ab, e.g. a Fab fragment, and its Ag, the term epitope is herein, unless otherwise specified or contradicted by context, specifically defined as K3 or C-terminal residues characterized by having a heavy atom (i.e. a non-hydrogen atom) within a distance of 2-6 Å, such as 3 Å, such as 4 Å, such as 5 Å from a heavy atom in the Ab.

From the fact that descriptions and definitions of epitopes, dependent on the epitope mapping method used, are obtained at different levels of detail, it follows that comparison of epitopes for different Abs on the same Ag can similarly be conducted at different levels of detail.

Epitopes described at the amino acid residue level, e.g. determined from an X-ray structure, are said to be identical if they contain the same set of amino acid residues. Epitopes are said to overlap if at least one amino acid residue is shared by the epitopes. Epitopes are said to be separate (unique) if no amino acid residue are shared by the epitopes.

Epitopes characterized by competition binding are said to be overlapping if the binding of corresponding Ab’s are mutually exclusive, i.e. if the binding of one Ab excludes simultaneous binding of the other Ab. The epitopes are said to be separate (unique) if the Ag is able to accommodate binding of both corresponding Ab’s simultaneously.

The definition of the term “paratope” is derived from the above definition of “epitope” by reversing the perspective. Thus, the term “paratope” refers to the area or region on the Ab to which an Ag specifically binds, i.e. to which it makes physical contact to the Ag.

In the context of an X-ray derived crystal structure defined by spatial coordinates of a complex between an Ab, e.g. a Fab fragment, and its Ag, the term paratope is herein, unless otherwise specified or contradicted by context, specifically defined as Ag residues characterized by having a heavy atom (i.e. a non-hydrogen atom) within a distance of 2-6 Å, such as 3 Å, such as 4 Å, such as 5 Å from a heavy atom in the C-terminal domain.

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 variant TFPI polypeptides. The specific amino acids within TFPI that make contact with an antibody (epitope) and the specific amino acids in an antibody that make contact with TFPI (paratope) may also be determined using routine methods, such as those described in the examples. For example, the antibody and target molecule
may be combined and the Ab/Ag complex may be crystallised. The crystal structure of the complex may be determined and used to identify specific sites of interaction between the antibody and its target.

An antibody according to the current invention may bind to the same epitope, domain or portion of TFPI as the antibodies of the invention that are specifically disclosed herein. For example, other yet unidentified antibodies of the invention may be identified by comparing their binding to TFPI with that of the monoclonal antibodies, MuTFPI4F10, MuTFPI22F66 and MuTFPI22F71; or by comparing the function of yet unidentified antibodies with that of MuTFPI4F10, MuTFPI22F66 and MuTFPI22F71. Analyses and assays that may be used for the purpose of such identification include TFPI neutralizing assays such as: a FXa inhibition assay; an ELISA and binding interaction analyses, such as those described in the examples.

An antibody of the invention may bind an epitope comprising one or more amino acid residues, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46 or 47 amino acid residues, such as 6-10 amino acid residues or 16-21 amino acid residues within the C terminal of full length TFPI, wherein said one or more amino acids have a relative accessibility of more than 40% when measured as described in the Examples. Thus, an antibody of the invention may bind an epitope comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46 or 47 amino acid residues, such as 6-10 amino acid residues or 16-21 amino acid residues selected from the group consisting of amino acid residues 186-187, 190, 192-208, 213, 215-220, 225-228, 230-234, 236-237 and 240-276 of SEQ ID NO: 1.

An antibody of the invention may bind to an epitope that comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46 or 47 amino acid residues, such as 6-10 amino acid residues or 16-21 amino acid residues, selected from the group consisting of P186, S187, L190, P192, A193, D194, R195, G196, L197, C198, R199, A200, N201, E202, N203, R204, F205, Y206, Y207, N208, K213, R215, P216, F217, K218, Y219, S220, N225, E226, N227, N228, T230, S231, K232, Q233, E234, L236, R237, K240, K241, G242, F243, 1244, Q245, R246, 1247, S248, K249, G250, G251, L252, 1253, K254, T255, K256,
An antibody of the invention may have the ability to compete with another antibody of the invention for binding to TFPI or another appropriate target as described herein. For example, an antibody of the invention may cross-compete with the antibodies identified as MuTFPI4F110, MuTFPI22F66 and MuTFPI22F71, described herein, for binding to TFPI, or to a suitable fragment or variant of TFPI that is bound by MuTFPI4F110, MuTFPI22F66 and MuTFPI22F71 antibodies. Such cross-competing antibodies can be identified based on their ability to cross-compete with a known antibody of the invention in standard binding assays. For example, SPR e.g. by using a Biacore™ system, ELISA assays or flow cytometry may be used to demonstrate cross-competition. Such cross-competition may suggest that the two antibodies bind to identical, overlapping or similar epitopes.

"Epitope binning" refers to the use of competitive binding assays to identify pairs of antibodies that are, or are not, capable of binding an antigen, such as TFPI, simultaneously, thereby identifying antibodies that bind to the same, or overlapping epitopes of TFPI. Families of antibodies (or bins) that have the same, or overlapping, binding specificity can then be used to help define specific epitopes on TFPI. Epitope binning experiments provide evidence that antigenically distinct epitopes are present. However, by themselves, they do not identify, or "map" the epitope to a specific amino acid sequence or location on TFPI. Competition for binding can be evaluated for any pair of antibodies or fragments. Favourable properties of a family (or bin) of antibodies can be correlated with binding to a specific epitope defined in terms of the antibody bin.

As explained above, TFPI downregulates blood coagulation. It does this by inhibiting the activity of FXa and by inhibiting the TF-FVIIa complex in the presence of FXa. The activity of TFPI that is inhibited by an antibody of the invention may be any of these activities or any downstream effect thereof. For example, an antibody of the invention may lead to an increase in blood coagulation, an increase in the presence or levels of FXa or an increased activity of TF-FVIIa. Preferably, an antibody of the invention reduces clotting time when contacted with (a) human FVIII deficient plasma or (b) human whole blood.

The measurement of TFPI activity may comprise assessing the activity of free TFPI in inhibiting coagulation or reducing clotting time in a blood sample. For example, such a method may comprise contacting TFPI with a sample of blood, or a blood product such as plasma or serum that comprises blood coagulation factors, under conditions in which coagulation should occur, and determining whether coagulation of the blood is inhibited or clotting time is reduced by the presence of the TFPI. The level of blood coagulation or clotting time in such a sample may then be compared to that in an equivalent sample in which a test antibody is also present. If the level of coagulation is increased or clotting time is reduced in the antibody sample, this suggests that the antibody is inhibiting the activity of TFPI in the sample.

Blood coagulation may be detected by looking for coagulation of the blood itself, of plasma, or for one or more characteristics of the coagulation cascade that lie downstream to the
point of action of TFPI. For example, the method may assess levels of FXa or activation of TF-FVIIa in the sample.

Various other methods for assessing blood coagulation and clotting time are well known in the art. For example, any effect of an antibody on blood clotting time may be assessed using a dilute prothrombin time analysis (dPT analysis) as described in the examples. Briefly, human plasma is contacted with human thromboplastin. The time taken for the plasma to clot is measured in the presence and absence of the test antibody. A positive control may be used in such an analysis, such as addition of FVIIa (NovoSeven®), which would be expected to reduce clotting time. An antibody of the invention should be capable of reducing clotting time in such a method.

Preferably, an antibody of the invention should be capable of reducing clotting time in a dose-dependent manner.

Thromboelastography (TEG) may be used to assess the kinetics of clot formation and fibrinolysis in samples of whole blood, such as in FVIII-deficient whole blood. The ability of an antibody to reduce clotting time or to stimulate blood coagulation may thus be similarly assessed in a whole blood sample by comparing the time taken for clot formation in the presence and absence of the antibody.

Methods to assess the functional effects of an antibody of the invention may thus be carried out in vitro. Such methods are preferably carried out on samples of human blood or plasma. Such samples may be normal human blood or plasma or may be deficient in, or supplemented with, one or more factors involved in blood coagulation. For example, these methods may be carried out using normal human whole blood, normal human plasma or FVIII-deficient plasma or whole blood. FVIII-deficient blood or plasma may be generated by contacting a suitable blood or plasma sample with neutralising anti-FVIII antibody. Such in vitro methods may be binding interaction analyses or TFPI neutralisation analyses, such as those described in the examples.

Once a suitable antibody has been identified and selected, the amino acid sequence of the antibody may be identified by methods known in the art. The genes encoding the antibody can be cloned using specific and/or degenerate primers. The antibody may be recombinantly produced by routine methods.

The invention also relates to polynucleotides that encode antibodies of the invention. Thus, a polynucleotide of the invention may encode any antibody as described herein. The terms "nucleic acid molecule" and "polynucleotide" are used interchangeably herein and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Non-limiting examples of polynucleotides include a gene, a gene fragment, messenger RNA (mRNA), cDNA, recombinant polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide of the invention may be provided in isolated or purified form.

A nucleic acid sequence which "encodes" a selected polypeptide is a nucleic acid molecule which is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the
coding sequence are determined by a start codon at the 5’ (amino) terminus and a translation stop
codon at the 3’ (carboxy) terminus. For the purposes of the invention, such nucleic acid sequences
can include, but are not limited to, cDNA from viral, prokaryotic or eukaryotic mRNA, genomic
sequences from viral or prokaryotic DNA or RNA, and even synthetic DNA sequences. A
transcription termination sequence may be located 3’ to the coding sequence.

A polynucleotide of the invention may comprise a sequence which encodes a VH or VL
amino acid sequence as described above. For example, a polynucleotide of the invention may
code a polypeptide comprising any one or more of the sequences selected from the group
consisting of: SEQ ID NOs: 5, 7, 9, 11, 13 and 15; or variants or fragments thereof.

Polynucleotides of the invention may be synthesised according to methods well known in
the art, as described by way of example in Sambrook et al (1989, Molecular Cloning - a laboratory
manual; Cold Spring Harbor Press).

The nucleic acid molecules of the present invention may be provided in the form of an
expression cassette which includes control sequences, signal peptide sequences operably linked to
the inserted sequence, thus allowing for expression of the antibody of the invention in vivo. These
expression cassettes, in turn, are typically provided within vectors (e.g., plasmids or recombinant
viral vectors). Such an expression cassette may be administered directly to a host subject.
Alternatively, a vector comprising a polynucleotide of the invention may be administered to a host
subject. Preferably the polynucleotide is prepared and/or administered using a genetic vector. A
suitable vector may be any vector which is capable of carrying a sufficient amount of genetic
information, and allowing expression of a polypeptide of the invention.

The present invention thus includes expression vectors that comprise such polynucleotide
sequences. Such expression vectors are routinely constructed in the art of molecular biology and
may for example involve the use of plasmid DNA and appropriate initiators, promoters, enhancers,
signal peptide sequences and other elements, such as for example polyadenylation signals which
may be necessary, and which are positioned in the correct orientation, in order to allow for
expression of a peptide of the invention. Other suitable vectors would be apparent to persons
skilled in the art. By way of further example in this regard we refer to Sambrook et al.

The invention also includes cells that have been modified to express an antibody of the
invention. Such cells include transient, or preferably stable higher eukaryotic cell lines, such as
mammalian cells or insect cells, lower eukaryotic cells, such as yeast or prokaryotic cells such as
bacterial cells. Particular examples of cells which may be modified by insertion of vectors or
expression cassettes encoding for an antibody of the invention include mammalian HEK293, CHO,
BHK, NSO and human retina cells. Preferably the cell line selected will be one which is not only
stable, but also allows for mature glycosylation and cell surface expression of a polypeptide.

In another aspect, the present invention provides compositions and formulations
comprising molecules of the invention, such as the antibodies, polynucleotides, vectors and cells
described herein. For example, the invention provides a pharmaceutical composition that
comprises one or more antibodies of the invention, formulated together with a pharmaceutically
acceptable carrier.
Accordingly, one object of the invention is to provide a pharmaceutical formulation comprising such an antibody which is present in a concentration from 1 mg/ml to 200 mg/ml, and wherein said formulation has a pH from 2.0 to 10.0. The formulation may further comprise a buffer system, preservative(s), tonicity agent(s), chelating agent(s), stabilizers and surfactants. The use of preservatives, isotonic agents, chelating agents, stabilizers and surfactants in 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. The terms "aqueous formulation" is defined as a 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 the physician or the patient adds solvents and/or diluents 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 of 1-200 mg/ml, and wherein said formulation has a pH from about 2.0 to about 10.0.

An antibody or a pharmaceutical formulation of the invention may be used to treat a subject with a coagulopathy.

As used herein, the term "subject" includes any human patient, or non-human vertebrate, with a coagulopathy.

The term "treatment", as used herein, refers to the medical therapy of any human or other vertebrate subject in need thereof. Said subject is expected to have undergone physical examination by a medical practitioner or a veterinary medical practitioner, who has given a tentative or definitive diagnosis which would indicate that the use of said specific treatment is beneficial to the health of said human or other vertebrate. The timing and purpose of said treatment may vary from one individual to another, according to the status quo of the subject's health. Thus, said treatment may be prophylactic, palliative, symptomatic and/or curative. In terms of the present invention, prophylactic, palliative, symptomatic and/or curative treatments may represent separate aspects of the invention.

The term "coagulopathy", as used herein, refers to an increased haemorrhagic tendency which may be caused by any qualitative or quantitative deficiency of any pro-coagulative component of the normal coagulation cascade, or any upregulation of fibrinolysis. Such coagulopathies may be congenital and/or acquired and/or iatrogenic and are identified by a person skilled in the art.

Non-limiting examples of congenital hypocoagulopathies are haemophilia A, haemophilia B, Factor VII deficiency, Factor XI deficiency, von Willebrand's disease and thrombocytopenias such as Glanzmann's thrombasthenia and Bernard-Soulier syndrome. Haemophilia A with "inhibitors" (that is, allo-antibodies against factor VIII) and haemophilia B with "inhibitors" (that is, allo-
antibodies against factor IX) are non-limiting examples of coagulopathies that are partly congenital and partly acquired.

A non-limiting example of an acquired coagulopathy is serine protease deficiency caused by vitamin K deficiency; such vitamin K-deficiency may be caused by administration of a vitamin K antagonist, such as warfarin. Acquired coagulopathy may also occur following extensive trauma. In this case otherwise known as the "bloody vicious cycle", it is characterised by haemodilution (dilutional thrombocytopenia and dilution of clotting factors), hypothermia, consumption of clotting factors and metabolic derangements (acidosis). Fluid therapy and increased fibrinolysis may exacerbate this situation. Said haemorrhage may be from any part of the body.

A non-limiting example of an iatrogenic coagulopathy is an overdosage of anticoagulant medication - such as heparin, aspirin, warfarin and other platelet aggregation inhibitors - that may be prescribed to treat thromboembolic disease. A second, non-limiting example of iatrogenic coagulopathy is that which is induced by excessive and/or inappropriate fluid therapy, such as that which may be induced by a blood transfusion.

In one embodiment of the current invention, haemorrhage is associated with haemophilia A or B. In another embodiment, haemorrhage is associated with haemophilia A or B with acquired inhibitors. In another embodiment, haemorrhage is associated with thrombocytopenia. In another embodiment, haemorrhage is associated with von Willebrand's disease. In another embodiment, haemorrhage is associated with severe tissue damage. In another embodiment, haemorrhage is associated with severe trauma. In another embodiment, haemorrhage is associated with surgery. In another embodiment, haemorrhage is associated with haemorrhagic gastritis and/or enteritis. In another embodiment, the haemorrhage is profuse uterine bleeding, such as in placental abruption. In another embodiment, haemorrhage occurs in organs with a limited possibility for mechanical haemostasis, such as intracranially, intraaurally or intraocularly. In another embodiment, haemorrhage is associated with anticoagulant therapy.

The use of an antibody or formulation of the invention may significantly reduce blood loss in subjects in need thereof. The use of said antibody or formulation may significantly reduce bleeding time. Thus, the invention is also the use of an antibody that is capable of binding the C-terminal of TFPI, for the treatment of a subject with a coagulopathy. Furthermore, the invention is a method of treating a subject in need thereof with a monoclonal antibody that is capable of binding to the C-terminal of TFPI. Use of said monoclonal antibody of the invention will, preferably, reduce in vivo clotting time without causing transient thrombocytopenia.

An antibody of the invention may be administered parenterally, such as intravenously, such as intramuscularly, such as subcutaneously. Alternatively, an antibody of the invention may be administered via a non-parenteral route, such as perorally or topically. An antibody of the invention may be administered prophylactically. An antibody of the invention may be administered therapeutically (on demand).

A suitable dosage of an antibody of the invention may be determined by a skilled medical or veterinary medical practitioner. A suitable dose of an antibody of the invention may be in the range of from about 0.1 Mg/kg to about 100mg/kg body weight of the patient to be treated.
Furthermore, antibodies of the invention may be co-administered with one or more other therapeutic agents or formulations. The other agent may be an agent that enhances haemostasis, such as a Factor VIII polypeptide, a Factor VIII polypeptide or a Factor IX polypeptide. The other agent may be intended to treat other symptoms or conditions of the patient. For example, the other agent may be an analgesic, an immunosuppressant or an anti-inflammatory agent. The other agent may be a monoclonal antibody, such as one of those disclosed in international patent application WO2010072691.

Co-administration of an antibody of the invention and said one or more other agents may be achieved in a number of different ways. In one embodiment, an antibody of the invention and the other agent may be administered together in a single composition. In another embodiment, an antibody of the invention and the other agent may be administered separately but as part of a combined therapy. For example, an antibody of the invention may be administered before, after, or concurrently with the other agent. In its broadest sense, co-administration according to the current invention refers to an antibody to the invention and the other agent being present in human blood at the same time, irrespective of the time when the two or more agents were administered. Thus, an antibody of the invention may be present in the blood at the same time as an exogenous FVIIa polypeptide, FVIII polypeptide or FIX polypeptide.

The term "Factor VII(a)" herein encompasses the uncleaved zymogen, Factor VII (FVII), as well as the cloven and thus activated protease, Factor Vila (FVIIa). "Factor VII(a)" includes natural allelic variants of FVII(a) that may exist and occur from one individual to another. A wild type human Factor Vila sequence is provided in SEQ ID NO: 19, as well as in Proc Natl Acad Sci USA 1986;83:2412-2416.

**Wild type human coagulation Factor VII(a) (SEQ ID NO: 19):**

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ANAFLYYLPRGSLRYCKKKYQCSFYARYIKFDAYRTKLFISYSGDGDCASSPCQNGGSCKDQLOSYICF
CLPAFEGRNCETHKKDDLICVNENGGGEQYCSHDHTGKRSCRCEGYSLLADGVSCTPTVEYPCGK1
PILEKRNASKPQGRIVGKVPKGECWPQVLLVNGAQLCGGTLLINTIVVSAACDFIKKINWRNL1
AVLGEHDLSEHDGEQSSRRVAQVIPSTYVPPTNH DIALLRHQPVVLTDHVPLCPERTFSERTLA
FVRFSLYSVGWQLLDRGATAELMVNVPRLMTQDCLQSRKVGDSPNITEYM FCAGYSDGSKDSC
30 KGDSGGPPHATHYRGTYOLDLTVGIVSWGQGCAVGHGFVYTRVSQYIELQKLMRSEPRPGVLLRAPFP
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Wild type FVII consists of 406 amino acid residues and is composed of four domains as defined by homology. There is an N-terminal Gla domain followed by two epidermal growth factor (EGF)-like domains and a C-terminal serine protease domain. FVII circulates in plasma as a single-chain molecule. Upon activation to activated FVII (FVIIa), the molecule is cleaved between residues Arg I52 and IleI53, resulting in a two-chain protein held together by a disulphide bond. The light chain contains the Gla and EGF-like domains, whereas the heavy chain is the protease domain. FVIIa requires binding to its cell-surface co-factor tissue factor (TF) to become biologically active.

Factor VII(a) may be plasma-derived or recombinantly produced, using well known methods of production and purification. The degree and location of glycosylation, gamma-carboxylation
and other post-translational modifications may vary depending on the chosen host cell and its growth conditions. In SEQ ID NO. 19, "y" (gamma) represents gamma-carboxylated Glu (E') remains. The term "Factor VII(a) polypeptide" herein refers to wild type Factor Vila molecules as well as FVII(a) variants, FVII(a) derivatives and FVII(a) conjugates. Such variants, derivatives and conjugates may exhibit substantially the same, or improved, biological activity relative to wild-type human Factor Vila.

The term "FVII(a) variant", as used herein, is intended to designate Factor FVII having the sequence of SEQ ID NO: 19, wherein one or more amino acids of the parent protein have been substituted by another amino acid and/or wherein one or more amino acids of the parent protein have been deleted and/or wherein one or more amino acids have been inserted in protein and/or wherein one or more amino acids have been added to the parent protein. Such addition can take place either at the N-terminal end or at the C-terminal end of the parent protein or both. The "analogue" or "analogues" within this definition still have FVII activity in its activated form. In one embodiment a variant is at least 90 % identical with the sequence of SEQ ID NO: 19. In another embodiment a variant is at least 95 % identical with the sequence of SEQ ID NO: 19. As used herein, any reference to a specific position refers to the corresponding position in SEQ ID NO: 19.

Non-limiting examples of FVII(a) variants that have substantially the same or increased proteolytic activity compared to recombinant wild type human Factor VII(a) include those disclosed in WO 01/83725, WO 02/22776, WO 02/077218, WO 03/027147, WO 03/037932, WO 04/029090, WO 05/024006, and EP 05108713.8, US 7173000 B2; and JP4451514 B2.

The term "Factor VII(a) derivative" as used herein, is intended to designate a FVII polypeptide that exhibits substantially the same or improved biological activity relative to wild-type Factor Vila, in which one or more of the amino acids of the parent peptide have been genetically and/or chemically and/or enzymatically modified, such as by alkylation, glycosylation, PEGylation, acylation, ester formation, disulfide bond formation, or amide formation.

The term "PEGylated human Factor VII(a)" refers to a human Factor VII(a) polypeptide, to which a PEG molecule has been conjugated. Such a PEG molecule may be attached to any part of the Factor Vila polypeptide, including any amino acid residue or carbohydrate moiety of the Factor Vila polypeptide. This includes but is not limited to PEGylated human Factor Vila, cysteine-PEGylated human Factor Vila and variants thereof. Non-limiting examples of Factor VII derivatives includes glycoPEGylated FVII(a) derivatives as disclosed in WO 03/03 1464 and WO 04/09923 1 and WO 02/077218.

The term "cysteine-PEGylated human Factor VII(a)" refers to a Factor VII(a) polypeptide in which a PEG molecule is conjugated to a sulfhydryl group of a cysteine that has been introduced into said human Factor Vila.

The term "improved biological activity" refers to FVII(a) polypeptides that exhibit i) substantially the same or increased proteolytic activity compared to recombinant wild type human Factor Vila in the presence and/or absence of tissue factor or ii) to FVII(a) polypeptides with substantially the same or increased TF affinity compared to recombinant wild type human Factor Vila or iii) to FVII(a) polypeptides with substantially the same or increased half life in plasma compared to
recombinant wild type human Factor Vila, or iv) to FVII(a) polypeptides with substantially the same or increased affinity for the activated platelet. The activity of FVIIa polypeptides may be tested using, for example, the *in vitro* hydrolysis assay or the *in vitro* proteolysis assay, as described in the examples.

"Factor VIII" or "FVIII" herein refers to a human plasma glycoprotein that is a member of the intrinsic coagulation pathway and is essential to blood coagulation. "Native FVIII" is the human FVIII molecule derived from the full length sequence as shown in SEQ ID NO: 20 (amino acid 1-2332). The terms "Factor VIII(a)" and "FVIII(a)" herein include both FVIII and FVIIa. "FVIII(a)" includes natural allelic variants of FVIII(a) that may exist and occur from one individual to another. FVIII(a) may be plasma-derived or recombinantly produced, using well known methods of production and purification. The degree and location of glycosylation, tyrosine sulfation and other post-translation modifications may vary, depending on the chosen host cell and its growth conditions.

Factor VIII (FVIII) is a large, complex glycoprotein that is primarily produced by hepatocytes. FVIII consists of 2351 amino acids, including a signal peptide, and contains several distinct domains as defined by homology. There are three A-domains, a unique B-domain, and two C-domains. The domain order can be listed as NH2-A1-A2-B-A3-C1-C2-COOH. FVIII circulates in plasma as two chains, separated at the B-A3 border. The chains are connected by bivalent metal ion-bindings. The A1-A2-B chain is termed the heavy chain (HC) while the A3-C1-C2 is termed the light chain (LC). Small acidic regions C-terminal of the A1 (the ai region) and A2 (the a2 region) and N-terminal of the A3 domain (the a3 region) play important roles in its interaction with other coagulation proteins, including thrombin and von Willebrand factor (vWF or VWF), the carrier protein for FVIII.

Endogenous FVIII molecules circulate *in vivo* as a pool of molecules with B domains of various sizes, the shortest having C-terminal at position 740, i.e. at the C-terminal of A2-a2. These FVIII molecules with B-domains of different length all have full procoagulant activity. Upon activation with thrombin, FVIII is cleaved C-terminal of Al-ai at position 372, C-terminal of A2-a2 at position 740, and between a3 and A3 at position 1689, the latter cleavage releasing the a3 region with concomitant loss of affinity for VWF. The activated FVIII molecule is termed FVIIIa. The activation allows interaction of FVIIIa with phospholipid surfaces like activated platelets and activated factor IX (FIXa), i.e. the tenase complex is formed, allowing efficient activation of factor X (FX).

FVIII molecules/variants may be B domain-truncated FVIII molecules wherein the remaining domains correspond closely to the sequences as set forth in amino acid numbers 1-740 and 1649-2332 of SEQ ID NO: 20. In such variants, as well as in FVIII derived from the full-length sequence, mutations may be introduced in order to, for example, reduce vWF binding capacity.

Amino acid modifications, such as substitutions and deletions, may be introduced into the molecule in order to modify the binding capacity of FVIII with various other components such as LRP, various receptors, other coagulation factors, cell surfaces, introduction and/or abolishment of glycosylation sites, etc. Other mutations that do not abolish FVIII activity may also be accommodated in a FVIII molecule/variant according to the present invention.
FVIII molecules that are administered according to the present invention are capable of functioning in the coagulation cascade in a manner that is functionally similar, or equivalent, to FVIII, inducing the formation of FXa via interaction with FIXa on an activated platelet and supporting the formation of a blood clot. FVIII activity can be assessed in vitro using techniques well known in the art. Clot analyses, FX activation assays (often termed chromogenic assays), thrombin generation assays and whole blood thromboelastography are examples of such in vitro techniques. FVIII molecules according to the present invention have FVIII activity that is at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, 100% or even more than 100% of that of native human FVIII.

The B domain in FVIII spans amino acids 741-1648 of SEQ ID NO: 20. The B domain is cleaved at several different sites, generating large heterogeneity in circulating plasma FVIII molecules. The exact function of the heavily glycosylated B domain is unknown. What is known is that the B domain is dispensable for FVIII activity in the coagulation cascade. Recombinant FVIII is thus frequently produced in the form of B domain-deleted/truncated variants.

Endogenous full length FVIII is synthesized as a single-chain precursor molecule. Prior to secretion, the precursor is cleaved into the heavy chain and the light chain. Recombinant B domain-deleted FVIII can be produced by means of two different strategies. Either the heavy chain without the B-domain and the light chain are synthesized individually as two different polypeptide chains (two-chain strategy) or the B domain-deleted FVIII is synthesized as a single precursor polypeptide chain (single-chain strategy) that is cleaved into the heavy and light chains in the same way as the full-length FVIII precursor.

In a B domain-deleted FVIII precursor polypeptide, produced by the single-chain strategy, the heavy and light chain moieties are often separated by a linker. To minimize the risk of introducing immunogenic epitopes in the B domain-deleted FVIII, the sequence of the linker is preferably derived from the FVIII B-domain. As a minimum, the linker must comprise a recognition site for the protease that cleaves the B-domain-deleted FVIII precursor polypeptide into the heavy and light chain. In the B domain of full length FVIII, amino acid 1644-1648 constitutes this recognition site. The thrombin cleavage site leading to removal of the linker on activation of B domain-deleted FVIII is located in the heavy chain. Thus, the size and amino acid sequence of the linker is unlikely to influence its removal from the remaining FVIII molecule by thrombin activation.

Deletion/truncation of the B domain is an advantage for production of FVIII. Nevertheless, parts of the B domain can be included in the linker without reducing the productivity. The negative effect of the B domain on productivity has not been attributed to any specific size or sequence of the B domain.

Factor IXa (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 factor Xa required to support proper thrombin formation during coagulation (reviewed in (Hoffman and Monroe, III 2001)).

Factor IX (FIX) is a vitamin K-dependent coagulation factor with structural similarities to factor VII, prothrombin, factor X, and protein C. The circulating zymogen form consists of 415 amino acids 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. Activation of FIX occurs by limited proteolysis at Arg\textsuperscript{145}-Ala\textsuperscript{146} and Arg\textsuperscript{180}-Val\textsuperscript{181} releasing a 35-aa fragment, the so-called activation peptide (Schmidt and Bajaj 2003). The activation peptide is heavily glycosylated, containing two N-linked and up to four O-linked glycans.

"Factor IX" or "FIX", as used herein, refers to a human plasma Factor IX glycoprotein that is a member of the intrinsic coagulation pathway and is essential to blood coagulation. "Factor IX(a)" includes natural allelic variants of FIX(a) that may exist and occur from one individual to another. Factor IX(a) may be plasma-derived or recombinantly produced using well-known methods of production and purification. The degree and location of glycosylation, gamma-carboxylation and other post-translation modifications may vary depending on the chosen host cell and its growth conditions. Unless otherwise specified or indicated, Factor IX means any functional human Factor IX protein molecule in its normal role in coagulation, including any fragment, analogue and derivative thereof.

One example of a "wild type FIX" is the full length human FIX molecule, as shown in SEQ ID NO: 21.

**Wild type human coagulation Factor IX (SEQ ID NO: 21):**

YNSGKLYYFQGNYRMYKCSFYYAYRFYNYRTTRYFWKQYVGDQCESNPCDNGGSCKDDINSYE CWCPFGFEKGNCLEDVTCNINKGRCEQFOCNASSDNKVCTEYRGLANQKSCPAPVFPYGRVSV SQTSDKLRAVEFVPDYYVVSTEATEILDNITQTGSTQSFNDFTRVGGEDAKPGQFQWQVVLNGKVDW FCGGSIVNEKWIVTAAHCETGKVITVAGHEHNEETEHTQKRNVRIFPHNNAYNAINKYNDIALL ELDEPLVNSYVTPIADKEYTNIFLFKFGSGYGSVGRVFTKGRSALVQLYLVRPVLDVRATCLRSTKF TYYNNM FCAGFHEGGGRDSCQGDSGPHVTVEGTSLFTGIIIWGECECM KGKYGIYTKVSYVNWKEKTKLTL

In SEQ ID NO: 21, "γ" represents gamma-carboxylated Glu (Glu). In fully gamma-carboxylated FIX, the first 12 Glu residues are gamma-carboxylated, but there are variants, especially in the case of recombinant FIX, in which less gamma-carboxylation takes place. Note, also, that a dimorphism occurs in FIX at position 148, which can be either Ala or Thr (see McGraw et al. (1985) PNAS, 82:2847). Both are "wild type" FIX.

The terms "FIX analogue", as used herein, is intended to designate Factor FIX having the sequence of SEQ ID NO: 21, wherein one or more amino acids of the parent protein have been substituted by another amino acid and/or wherein one or more amino acids of the parent protein have been deleted and/or wherein one or more amino acids have been inserted in protein and/or wherein one or more amino acids have been added to the parent protein. Such addition can take place either at the N-terminal end or at the C-terminal end of the parent protein or both. The "analogue" or "analougues" within this definition still have FIX activity in its activated form. In one embodiment a variant is at least 90% identical with the sequence of of SEQ ID NO: 21. In a further embodiment a variant is at least 95% identical with the sequence of of SEQ ID NO: 21. As used herein any reference to a specific positions refers to the corresponding position in SEQ ID NO: 21.
Unless otherwise specified, factor IX domains include the following amino acid residues: Gla domain being the region from residue Tyr1 to residue Lys43; EGF1 being the region from residue Gln44 to residue Leu84; EGF2 being the region from residue Asp85 to residue Arg145; the Activation Peptide being the region from residue Ala146 to residue Arg180; and the Protease Domain being the region from residue Val181 to Thr414. The light chain refers to the region encompassing the Gla domain, EGF1 and EGF2, while the heavy chain refers to the Protease Domain.

The clotting activity of procoagulant agents such as FVIIa polypeptide, a FVIII polypeptide or a Factor IX polypeptide may be determined using clotting assays that are known to the person skilled in the art, such as those described in the Examples.

The time at which antibodies of the invention are to be co-administered with a second agent, such as a Factor VIIa polypeptide, a Factor VIII polypeptide or a Factor IX polypeptide, may be determined by the skilled medical or veterinary medical practitioner.

Following is a non-limiting list of embodiments of the present invention:

Embodiment 1: An antibody that is capable of specifically binding the C-terminal of full length TFPI.

Embodiment 1a: The antibody according to embodiment 1, wherein said C-terminal is amino acids 186-276 of human TFPI (SEQ ID NO: 1).

Embodiment 1b: The antibody according to any one of embodiments 1 or 1a, which is a monoclonal antibody.


Embodiment 3: The antibody according to any one of embodiments 1-1b, wherein the epitope of said antibody comprises one or more amino acid residues selected from the group consisting of P186, S187, L190, P192, A193, D194, R195, G196, L197, C198, R199, A200, N201, E202, N203, R204, F205, Y206, Y207, N208, K213, R215, P216, F217, K218, Y219, S220, N225, E226, N227, N228, T230, S231, K232, Q233, E234, L236 and R237 of SEQ ID NO: 1.
Embodiment 4: The antibody according to any one of embodiments 1-1b, wherein the epitope of said antibody comprises one or more amino acid residues selected from the group consisting of K240, K241, G242, F243, 1244, Q245, R246, 1247, S248, K249, G250, G251, L252, 1253, K254, T255, K256, R257, K258, R259, K260, K261, Q262, 263, V264, K265, 1266, A267, Y268, E269, E270, 1271, F272, V273, 274, N275 and M276 of SEQ ID NO: 1.

Embodiment 5: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises a CDR1 sequence of amino acids 31 to 35 (SYMYM) of SEQ ID NO: 5, wherein one of these amino acids may be substituted by a different amino acid.

Embodiment 6: The antibody according to any one of embodiments 1-5, wherein the heavy chain of said antibody comprises a CDR2 sequence of amino acids 50-66 (EINPSNGDTNLNFKKS) of SEQ ID NO: 5, wherein one, two or three of these amino acids may be substituted by a different amino acid.

Embodiment 7: The antibody according to any one of embodiments 1-6, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-107 (WDRFDGFVY) of SEQ ID NO: 5, wherein one or two of these amino acids may be substituted by a different amino acid.

Embodiment 8: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises a CDR1 sequence of amino acids 31-35 (GYPMN) of SEQ ID NO: 9, wherein one of these amino acids may be substituted by a different amino acid.

Embodiment 9: The antibody according to any one of embodiments 1-4 and 8, wherein the heavy chain of said antibody comprises a CDR2 sequence of amino acids 50-66 (LINPYNGDTTFNQKFG) of SEQ ID NO: 9, wherein one, two or three of these amino acids may be substituted by a different amino acid.

Embodiment 10: The antibody according to any one of embodiments 1-4 and 8-9, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-106 (GTYEYVDY) of SEQ ID NO: 9, wherein one or two of these amino acids may be substituted by a different amino acid.

Embodiment 11: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises a CDR1 sequence of amino acids 31-35 (TYWIH) of SEQ ID NO: 13, wherein one of these amino acids may be substituted by a different amino acid.

Embodiment 12: The antibody according to any one of embodiments 1-4 and 11, wherein the heavy chain of said antibody comprises a CDR2 sequence of amino acids 50-66 (AIDPGNSDATYSQKF) of SEQ ID NO: 13, wherein one, two or three of these amino acids may be substituted by a different amino acid.

Embodiment 13: The antibody according to any one of embodiments 1-4 and 11-12, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-111 (EVYYGIGDYFDY) of SEQ ID NO: 13, wherein one, two or three of these amino acids may be substituted by a different amino acid.

Embodiment 14: The antibody according to any one of embodiments 1-7, wherein the light chain of said antibody comprises a CDR1 sequence of amino acids 24-34 (ILLSTNNDDDDIN) of
SEQ ID NO: 7, wherein one, two or three of these amino acids may be substituted with a different amino acid.

Embodiment 15: The antibody according to any one of embodiments 1-7 and 14, wherein the light chain of said antibody comprises a CDR2 sequence of amino acids 50-56 (EGNLTRP) of SEQ ID NO: 7, wherein one of these amino acids may be substituted with a different amino acid.

Embodiment 16: The antibody according to any one of embodiments 1-7 and 14-15, wherein the light chain of said antibody comprises a CDR3 sequence of amino acids 89-97 (LQSDDLPYT) of SEQ ID NO: 7, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 17: The antibody according to any one of embodiments 1-4 and 8-10, wherein the light chain of said antibody comprises a CDR1 sequence of amino acids 24-33 (SASSSVFYMH) of SEQ ID NO: 11, wherein one, two or three of these amino acids may be substituted with a different amino acid.

Embodiment 18: The antibody according to any one of embodiments 1-4, 8-10 and 17, wherein the light chain of said antibody comprises a CDR2 sequence of amino acids 49-55 (DTSILSS) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 19: The antibody according to any one of embodiments 1-4, 8-10 and 17-18, wherein the light chain of said antibody comprises a CDR3 sequence of amino acids 88-96 (QQWSSYPYLT) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 20: The antibody according to any one of embodiments 1-4 and 11-13, wherein the light chain of said antibody comprises a CDR1 sequence of amino acids 24-38 (RASESVSVHGTHLMH) of SEQ ID NO: 15, wherein one, two or three of these amino acids may be substituted with a different amino acid.

Embodiment 21: The antibody according to any one of embodiments 1-4, 11-13 and 20, wherein the light chain of said antibody comprises a CDR2 sequence of amino acids 54-60 (AASKLES) of SEQ ID NO: 15, wherein one of these amino acids may be substituted with a different amino acid.

Embodiment 22: The antibody according to any one of embodiments 1-4, 11-13 and 20-21, wherein the light chain of said antibody comprises a CDR3 sequence of amino acids 93-101 (QOSIGDPWT) of SEQ ID NO: 15, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 23: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

- a CDR1 sequence of amino acids 31 to 35 (SYMY) of SEQ ID NO: 5, wherein one of these amino acids may be substituted by a different amino acid; and/or
- a CDR2 sequence of amino acids 50-66 (EINPSNGDNLNEKFKS) of SEQ ID NO: 5, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or
• a CDR3 sequence of amino acids 99-107 (WDRFDGFVY) of SEQ ID NO: 5, wherein one or two of these amino acids may be substituted by a different amino acid.

Embodiment 24: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

5 • a CDR1 sequence of amino acids 31-35 (GYPMN) of SEQ ID NO: 9, wherein one of these amino acids may be substituted by a different amino acid; and/or

• a CDR2 sequence of amino acids 50-66 (LINPYNQDTTFNQKFG) of SEQ ID NO: 9, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or

• a CDR3 sequence of amino acids 99-106 (GTYEYVDY) of SEQ ID NO: 9, wherein one or two of these amino acids may be substituted by a different amino acid.

Embodiment 25: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

• a CDR1 sequence of amino acids 31-35 (TYWIH) of SEQ ID NO: 13, wherein one of these amino acids may be substituted by a different amino acid; and/or

• a CDR2 sequence of amino acids 50-66 (AIDPGNSATYSQKFD) of SEQ ID NO: 13, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or

• a CDR3 sequence of amino acids 99-111 (EYVYGDPYDY) of SEQ ID NO: 13, wherein one or two of these amino acids may be substituted by a different amino acid.

Embodiment 26: The antibody according to any one of embodiments 1-4, wherein the light chain of said antibody comprises:

• a CDR1 sequence of amino acids 24-34 (IISTNIDDIN) of SEQ ID NO: 7, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or

• a CDR2 sequence of amino acids 50-56 (EGNTLRP) of SEQ ID NO: 7, wherein one or two of these amino acids may be substituted with a different amino acid; and/or

• a CDR3 sequence of amino acids 89-97 (LQSDLPYT) of SEQ ID NO: 7, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 27: The antibody according to any one of embodiments 1-4, wherein the light chain of said antibody comprises:

• a CDR1 sequence of amino acids 24-33 (SASSSVFYM) of SEQ ID NO: 11, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or

• a CDR2 sequence of amino acids 49-55 (DTSILSS) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid; and/or

• a CDR3 sequence of amino acids 88-96 (QQWSSYPLT) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 28: The antibody according to any one of embodiments 1-4, wherein the light chain of said antibody comprises:

• a CDR1 sequence of amino acids 24-38 (RASESVSVHGTHLM) of SEQ ID NO: 15, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or

• a CDR2 sequence of amino acids 54-60 (AASKLES) of SEQ ID NO: 15, wherein one or two of these amino acids may be substituted with a different amino acid; and/or
• a CDR3 sequence of amino acids 93-101 (QQSIGDPWT) of SEQ ID NO: 15, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 29: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

   5  • a CDR1 sequence of amino acids 31 to 35 (SYMYM) of SEQ ID NO: 5, wherein one of these amino acids may be substituted by a different amino acid; and/or
   • a CDR2 sequence of amino acids 50-66 (EIPNSGDTNLNEKFKS) of SEQ ID NO: 5, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or
   • a CDR3 sequence of amino acids 99-107 (WDRFDGFVY) of SEQ ID NO: 5, wherein one or two of these amino acids may be substituted by a different amino acid.

   and wherein the light chain of said antibody comprises:

   • a CDR1 sequence of amino acids 24-34 (IISTNIDDDIN) of SEQ ID NO: 7, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or
   • a CDR2 sequence of amino acids 50-56 (EGNTRLR) of SEQ ID NO: 7, wherein one or two of these amino acids may be substituted with a different amino acid; and/or
   • a CDR3 sequence of amino acids 89-97 (LQSDDLPYT) of SEQ ID NO: 7, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 30: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

   • a CDR1 sequence of amino acids 31-35 (GYPMN) of SEQ ID NO: 9, wherein one of these amino acids may be substituted by a different amino acid; and/or
   • a CDR2 sequence of amino acids 50-66 (LNPYNGDFTFNQKFKG) of SEQ ID NO: 9, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or
   • a CDR3 sequence of amino acids 99-106 (GTYEYVDD) of SEQ ID NO: 9, wherein one or two of these amino acids may be substituted by a different amino acid.

   and wherein the light chain of said antibody comprises:

   • a CDR1 sequence of amino acids 24-33 (SASSSVFYMYH) of SEQ ID NO: 11, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or
   • a CDR2 sequence of amino acids 49-55 (DTSILSS) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid; and/or
   • a CDR3 sequence of amino acids 88-96 (QQWSSYPLT) of SEQ ID NO: 11, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodiment 31: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises:

   • a CDR1 sequence of amino acids 31-35 (TYWIH) of SEQ ID NO: 13, wherein one of these amino acids may be substituted by a different amino acid; and/or
   • a CDR2 sequence of amino acids 50-66 (AIDPGNSDATYSQKFKD) of SEQ ID NO: 13, wherein one, two or three of these amino acids may be substituted by a different amino acid; and/or
   • a CDR3 sequence of amino acids 99-111 (EYYYGIDGDYFDY) of SEQ ID NO: 13, wherein one or two of these amino acids may be substituted by a different amino acid.
and wherein the light chain of said antibody comprises:

- a CDR1 sequence of amino acids 24-38 (RASESVSHGTHLMH) of SEQ ID NO: 15, wherein one, two or three of these amino acids may be substituted with a different amino acid; and/or
- a CDR2 sequence of amino acids 54-60 (AASKLES) of SEQ ID NO: 15, wherein one or two of these amino acids may be substituted with a different amino acid; and/or
- a CDR3 sequence of amino acids 93-101 (QQSIGDPWT) of SEQ ID NO: 15, wherein one or two of these amino acids may be substituted with a different amino acid.

Embodyment 32: The antibody according to any one of embodiments 5-31, wherein said amino acid substitution is a conservative substitution.

Embodyment 33: The antibody according to any one of embodiments 1-4, wherein the heavy chain comprises:

- a CDR1 sequence of amino acids 31 to 35 (SYMY) of SEQ ID NO: 5 and/or
  - a CDR2 sequence of amino acids 50-66 (EINSNGDXTNLNEFKS) of SEQ ID NO: 5 and/or
  - a CDR3 sequence of amino acids 99-107 (WDRFDGFLVY) of SEQ ID NO: 5;

and wherein the light chain of said antibody comprises:

- a CDR1 sequence of amino acids 24-34 (IISNIDDDIN) of SEQ ID NO: 7 and/or
- a CDR2 sequence of amino acids 50-56 (EGNTRLP) of SEQ ID NO: 7 and/or
- a CDR3 sequence of amino acids 89-97 (LQSSDLPYT) of SEQ ID NO: 7.

Embodyment 34: The antibody according to any one of embodiments 1-4, wherein the heavy chain comprises:

- a CDR1 sequence of amino acids 31-35 (GYPMN) of SEQ ID NO: 9,
  - a CDR2 sequence of amino acids 50-66 (LINPYNGDXTFNQKFS) of SEQ ID NO: 9 and
  - a CDR3 sequence of amino acids 99-106 (GTGEYDYDY) of SEQ ID NO: 9;

and wherein the light chain comprises:

- a CDR1 sequence of amino acids 24-33 (SASSSVFYMH) of SEQ ID NO: 11,
- a CDR2 sequence of amino acids 49-55 (DTSILSS) of SEQ ID NO: 11 and
- a CDR3 sequence of amino acids 88-96 (QQWSSYPLT) of SEQ ID NO: 11.

Embodyment 35: The antibody according to any one of embodiments 1-4, wherein the heavy chain comprises:

- a CDR1 sequence of amino acids 31-35 (TYWH) of SEQ ID NO: 13,
  - a CDR2 sequence of amino acids 50-66 (AIDPGNSDATYSQKFKD) of SEQ ID NO: 13 and
  - a CDR3 sequence of amino acids 99-111 (EYVYGYGDYFDY) of SEQ ID NO: 13;

and wherein the light chain comprises:

- a CDR1 sequence of amino acids 24-38 (RASESVSHGTHLMH) of SEQ ID NO: 15,
- a CDR2 sequence of amino acids 54-60 (AASKLES) of SEQ ID NO: 15 and
- a CDR3 sequence of amino acids 93-101 (QQSIGDPWT) of SEQ ID NO: 15.

Embodyment 36: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises SEQ ID NO: 5.

Embodyment 37: The antibody according to any one of embodiments 1-4 and 36, wherein the light chain of said antibody comprises SEQ ID NO: 7.
Embodiment 38: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises SEQ ID NO: 9.

Embodiment 39: The antibody according to any one of embodiments 1-4 and 38, wherein the light chain of said antibody comprises SEQ ID NO: 11.

Embodiment 40: The antibody according to any one of embodiments 1-4, wherein the heavy chain of said antibody comprises SEQ ID NO: 13.

Embodiment 41: The antibody according to any one of embodiments 1-4 and 40, wherein the light chain of said antibody comprises SEQ ID NO: 15.

Embodiment 42: The antibody according to any one of embodiments 1-4, wherein said antibody comprises SEQ ID NO: 5 and SEQ ID NO: 7.

Embodiment 43: The antibody according to any one of embodiments 1-4, wherein said antibody comprises SEQ ID NO: 9 and SEQ ID NO: 11.

Embodiment 44: The antibody according to any one of embodiments 1-4, wherein said antibody comprises SEQ ID NO: 13 and SEQ ID NO: 15.

Embodiment 45: The antibody according to any one of the embodiments 1-44, which is a humanized antibody.

Embodiment 46: The antibody according to any one of the embodiments 1-45, wherein the isotype of said antibody is IgG.

Embodiment 47: The antibody according to embodiment 46, wherein said isotype is IgG1, IgG2 or IgG4.

Embodiment 48: The antibody according to embodiment 47, wherein the isotype of said antibody is IgG4.

Embodiment 49: The antibody, according to any one of embodiments 1-48, wherein the $K_d$ of said antibody is less than 4.0 nM, such as less than 3.0 nM, such as less than 2.0 nM, such as less than 1.0 nM, such as less than 0.8 nM, such as less than 0.7 nM, such as less than 0.6 nM, such as less than 0.5 nM, such as less than 0.4 nM, such as less than 0.3 nM, such as less than 0.2 nM, such as less than 0.1 nM, such as less than 0.05 nM, such as less than 0.02 nM, such as less than 0.01 nM.

Embodiment 50: The antibody according to any one of embodiments 1-49, which is not capable of binding truncated TFPI (1-185).

Embodiment 51: The antibody according to any one of embodiments 1-49, which is not capable of binding truncated TFPI (1-239).

Embodiment 52: The antibody according to any one of embodiments 1-51, which is not capable of binding the KI or the K2 domain of TFPI.

Embodiment 53: The antibody according to any one of embodiments 1-52, which is not capable of binding GPI-anchored TFPI and/or lipoprotein bound TFPI.

Embodiment 54: The antibody according to any one of embodiments 1-53, which is capable of neutralizing TFPI inhibition of TF/FVIIa/FXa in the presence of phospholipid.

Embodiment 55: The antibody according to any one of embodiments 1-54, which is capable of binding the C-terminal of TFPI such that the percentage of free TFPI in a subject is...
reduced to less than 50%, such as less than 40%, such as less than 30%, such as less than 20%, such as less than 10%.

Embodiment 55a: The antibody according to any one of embodiments 1-55, which is capable of competing with MuTFPI4F1 10 for binding to TFPI.

Embodiment 55b: The antibody according to any one of embodiments 1-55, which is not capable of competing with MuTFPI4F1 10 for binding to TFPI.

Embodiment 56: The antibody according to any one of embodiments 1-55a, which reduces in vivo clotting time without significantly reducing the platelet count.

Embodiment 57: The antibody, according to embodiment 56, wherein said platelet count is not reduced to approximately 80%, such as approximately 75%, such as approximately 70%, such as approximately 65%, such as approximately 60%, such as approximately 55%, such as approximately 50%, such as approximately 45%, such as approximately 40%, such as approximately 35%, such as approximately 30%, such as approximately 25% of the original platelet count.

Embodiment 58: The antibody according to any one of embodiments 1-57, which reduces in vivo clotting time without causing transient thrombocytopenia.

Embodiment 59: A pharmaceutical formulation comprising the antibody according to any one of embodiments 1-58.

Embodiment 59a: A pharmaceutical formulation comprising the antibody according to any one of embodiments 1-58 and a Factor Vila, Factor VIII or Factor IX polypeptide.

Embodiment 60: The pharmaceutical formulation according to embodiment 59, which is suitable for parenteral use.

Embodiment 61: The pharmaceutical formulation according to embodiment 60, which is suitable for intravenous use.

Embodiment 62: The pharmaceutical formulation according to embodiment 60, which is suitable for subcutaneous use.

Embodiment 63: The antibody according to any one of embodiments 1-58, or the pharmaceutical formulation according to any one of embodiments 58-62, for the treatment of a subject with a coagulopathy.

Embodiment 64: The antibody according to any one of embodiments 1-58, or the pharmaceutical formulation according to any one of embodiments 58-62, for the treatment of any congenital, acquired and/or iatrogenic coagulopathy, such as may be selected from the group consisting of haemophilia A, with or without inhibitors, and haemophilia B, with or without inhibitors.

Embodiment 64a: The antibody according to any one of claims 1-9 and second coagulation agent, selected from the list consisting of a FVIIa polypeptide, a FVIII polypeptide or a FIX polypeptide, for the treatment of a subject with a coagulopathy.

Embodiment 64b: The antibody according to any one of embodiments 1-58 and a FVIII polypeptide for the treatment of haemophilia A.

Embodiment 64c: The antibody according to any one of embodiments 1-58 and a FIX polypeptide for the treatment of haemophilia B.
Embodiment 64d: The antibody according to any one of embodiments 1-58 and a FVIIa polypeptide for the treatment of haemophilia A or B with inhibitors.

Embodiment 65: A method of treating a subject with a coagulopathy, comprising administering to said subject the antibody according to any one of embodiments 1-58.

Embodiment 65a: A method of treating a subject with haemophilia A comprising administering to said subject the antibody according to any one of embodiments 1-58 and a FVIII polypeptide.

Embodiment 65b: A method of treating a subject with haemophilia B comprising administering to said subject the antibody according to any one of embodiments 1-58 and a FIX polypeptide.

Embodiment 65c: A method of treating a subject with FVII deficiency comprising administering to said subject the antibody according to any one of embodiments 1-58 and a FVII polypeptide.

Embodiment 65d: A method of treating a subject with haemophilia A with inhibitors, comprising administering to said subject the antibody according to any one of embodiments 1-58 and a FVII polypeptide.

Embodiment 65e: A method of treating a subject with haemophilia B with inhibitors, comprising administering to said subject the antibody according to any one of embodiments 1-58 and a FVII polypeptide.

Embodiment 66: The method according to embodiment 61, wherein said coagulopathy is any congenital, acquired and/or iatrogenic coagulopathy, such as may be selected from the group consisting of haemophilia A, with or without inhibitors, and haemophilia B, with or without inhibitors.

Embodiment 67: A polynucleotide that encodes the antibody according to any one of embodiments 1-58.

Embodiment 68: A polynucleotide according to embodiment 67, which comprises at least one sequence selected from the group consisting of SEQ ID NOs: 4, 6, 8, 10, 12 and 14.

Embodiment 69: A eukaryotic cell which comprises the polynucleotide according to any one of embodiments 67-69.

Embodiment 70: A eukaryotic cell which expresses the antibody, or fragment thereof, according to any one of embodiments 1-58.

Embodiment 71: The eukaryotic cell according to embodiment 70, which is a mammalian cell.

Embodiment 72: The mammalian cell according to embodiment 71, which is selected from the group consisting of HEK293, CHO, BHK, NSO and human retina cells.

The present invention is further illustrated by the following examples which should not be construed as further limiting. The contents of all figures and all references, patents and published patent applications cited throughout this application are expressly incorporated herein by reference.
EXAM PLES

Example 1: Immunisation and fusion

Mice were immunized with full length TFPI (SEQ ID NO: 1).

RBF mice were used for immunizations and production of mouse monoclonal antibodies.

Injections were made subcutaneously in the back of the mice. 20μg TFPI was mixed with complete Freund’s adjuvant for the first injection. In the subsequent immunizations, incomplete Freund’s adjuvant was used with same concentration of the antigen. Ten days after the last immunization, eye-blood from mice was screened, using ELISA, for TFPI specific antibodies. Mice with positive serum titres were boosted with 10 μg of TFPI by intravenous injection, and sacrificed after three days. The spleens were removed aseptically and dispersed to a single cell suspension. Fusion of spleen cells and myeloma cells was done by the PEG-method or by electrofusion.

Screening procedure

- Screening for binding to full length TFPI and no binding to TFPI(1-161)
- Cellular assays with endothelial cell lines or TF & TFPI transfected cells
- TFPI neutralizing activity in plasma (dilute prothrombin time)
- Clot dynamics measured in human plasma (Endogenous thrombin potential; ETP) and in human whole blood (thrombelastography; TEG)
- Identification of the specific inhibitory epitopes on full length soluble TFPI involved in binding of the monoclonal antibodies with the above characteristics

Purification of mAbs

Monoclonal antibodies were purified by means of protein A affinity chromatography.

Example 2: Cloning and sequencing of mouse anti-TFPI K3/C-terminal specific mAbs

This example describes cloning and sequencing of the murine heavy chain and light chain sequences of anti-TFPI antibodies MuTFPI4F1 10, MuTFPI22F66 and MuTFPI22F71.

Total RNA was extracted from hybridoma cells using the RNeasy-Mini Kit from Qiagen and used as template for cDNA synthesis. cDNA was synthesized in a 5’-RACE reaction using the SMART™ RACE cDNA amplification kit from Clontech. Subsequent target amplification of HC and LC sequences was performed by PCR using Phusion Hot Start polymerase (Finnzymes) and the universal primer mix (UPM) included in the SMART™ RACE kit as forward primer. The sequence of the reverse primer used for HC (VH domain) amplification is given in SEQ ID NO: 16. The sequence of the reverse primer used for MuTFPI22F66 and MuTFPI22F71 LC (VL domain) amplification is given in SEQ ID NO: 17. The sequence of the reverse primer used for MuTFPI4F1 10 LC amplification is given in SEQ ID NO: 18.

PCR products were separated by gel electrophoresis, extracted using the GFX PCR DNA & Gel Band Purification Kit from GE Healthcare Bio-Sciences and cloned for sequencing using a Zero Blunt TOPO PCR Cloning Kit and chemically competent TOP10 E.coli (Invitrogen). Colony PCR was performed on selected colonies using an AmpliTaq Gold Master Mix from Applied Biosystems and
M13uni/M 13rev primers. Colony PCR clean-up was performed using the ExoSAP-IT enzyme mix (USB). Sequencing was performed at MWG Biotech, Martinsried Germany using M13uni(-21)/M 13rev(-29) sequencing primers. Sequences were analyzed and annotated using the VectorNTI program. All kits and reagents were used according to the manufacturer’s instructions.

A single unique murine kappa type LC and a single unique murine HC, subclass IgGl was identified for each of the hybridomas: MuTFPI4F110, MuTFPI22F66 and MuTFPI22F71. Nucleic acid and amino acid sequences are as shown in the sequence listing; leader peptide sequences are not included.

**Example 3: Dilute prothrombin time (dPT)**

A dilute prothrombin (PT) analysis with human plasma in combination with diluted human thromboplastin. Clot time in the plasma was measured upon addition of increasing protein A purified TFPI monoclonal antibody concentrations to look for dose dependent reduction of clotting time with the mAbs of interest.

120 µl citrate-stabilized FVIII-depleted plasma (Helena) was mixed with 5 µl MuTFPI4F110 at various final concentrations (0.0-1.0 nM) and incubated for 15 min at room temperature. Clotting was measured by ACL300 analysis at 37°C. Coagulation was initiated by mixing 75 µl plasma with 75 µl reagent containing 0.02 M CaCl2 and 1:3,750; 1:7,500; or 1:15,000 dilution of lipidated tissue factor (TF) (Innovin®) in 20 mM Heps, 150 mM NaCl, pH 7.4. As shown in figure 1, MuTFPI4F110 shortened the clotting time in a concentration dependent manner at all three TF concentrations.

Only a fraction of TFPI present in plasma contains an intact C-terminal. This data suggests that binding of an antibody to this full length TFPI fraction efficiently promotes TF-induced clotting in FVIII-depleted plasma.

**Example 4: Endogenous thrombin formation**

Thrombin activity was assessed continuously following the conversion of the fluorogenic substrate Z-Gly-Gly-Arg-AMC. HCl (1-1140), from Bachendorf, Switzerland. Fluorescence was measured in a microtiterplate Fluorskan Ascent fluorometer (Thermo Labsystems, Helsinki, Finland) with excitation and emission wavelengths set at 368 and 460 nm, respectively. A calibrator was used to allow calculation of the amount of thrombin formed and correction of the obtained relative fluorescence units for inner-filter effects and fluorogenic substrate consumption. In addition, the contribution to substrate conversion by thrombin-a2-macroglobulin complexes was subtracted (9). These corrections were performed automatically by means of the calibrated automated thrombogram (CAT) computer software provided by Synapse BV (Maastricht, the Netherlands). Finally, the first derivative of the data was taken that yielded the thrombin generation curve, allowing calculation of the total area under the curve, the endogenous thrombin potential (ETP).

The effect of MuTFPI4F110 on thrombin generation in FVIII-depleted plasma supplemented with 10 µM PS/PC is studied in figure 2. Triggering of coagulation by re-calcification
and addition of Innovin® to a final dilution of 1/50,000 did not induce a measurable thrombin generation in the absence of anti-TFPI. In contrast, thrombin generation occurred in the presence of 10 nM MuTFPI4F1 10. After an initial increase the thrombin concentration reached a steady-state level of about 2 nM.

MuTFPI4F1 10 was studied in the presence of sub-normal levels of FVIII, typical for severe and moderate hemophilia A, to see if it is capable of improving or normalising the thrombin generation. The results in figure 3 show the effect on TF-induced thrombin generation of replenishing FVIII-depleted plasma with 0-2 IU/ml rFVIII (REFacto®) in absence and presence of 10 nM MuTFPI4F1 10. Thrombin generation was below the detection level in the absence of added rFVIII and was measurable only when rFVIII was added to a level higher than ~ 0.3 IU/ml rFVIII. Supplementation with higher levels of rFVIII resulted in a dose-dependent increase in the thrombin activity peak and shortened the lag time to thrombin generation. Thrombin generation experiments in the presence of 10 nM MuTFPI4F1 10 showed that neutralization of TFPI in FVIII-depleted plasma resulted in enhancement of thrombin generation, as illustrated in Fig. 2, at a higher resolution.

After a lag time of about 13 min the thrombin concentration increased and reached a steady-state level of about 2 nM. Addition of rFVIII to levels higher than about 0.05 IU/ml changed this pattern and induced an additional transient thrombin peak on top of the basal steady-state level induced by MuTFPI4F1 10 alone. The results showed that MuTFPI4F1 10 directed towards the C-terminal of TFPI alone promotes initiation of coagulation, and, in combination with sub-optimal levels of FVIII, it also enhances the generation of a thrombin burst.

**Example 5: Thrombelastography (TEG) measurements**

Citrate-stabilized FVIII-depleted plasma (Helena) was supplemented with (final concentrations): 0.12 pM TF (Innovin®, 1:50,000), 150,000 washed platelets/μl and various concentrations (0.0; 0.005; 0.05; 0.1 and 1.0 U/ml) of recombinant FVIII (ReFacto®). Clotting in the absence or presence of 10 nM MuTFPI4F1 10 was initiated when 320 μl of this premix was transferred to a thrombelastograph cup containing 20 μl 0.2 M CaCl₂. The TEG trace was followed continuously for up to 120 min (5000 series TEG analyzer, Haemoscope Corporation, Niles, IL, USA). The following TEG variables were recorded: R time (clotting time i.e. the time from initiation of coagulation until an amplitude of 2 mm was obtained), α-angle (clot development measured as the angle between the R value and the inflection point of the TEG trace), K (speed of clot kinetics to reach a certain level of clot strength, amplitude = 20 mm), and MA (maximal amplitude of the TEG trace reflecting the maximal mechanical strength of the clot).

The results showed that MuTFPI4F1 10 enhanced the TF-induced clot formation i.e. shortened the clotting time (R value) and enhanced the rate of clot development (angle value) both in the absence of rFVIII and at low concentrations of rFVIII, corresponding to severe and moderate hemophilia.

**Example 6: FACS analysis**
The TFPI-positive human endothelial-like immortalised cell line EAHy926WT (derived from umbilical vein endothelial cells) were used as a positive control for binding of membrane bound TFPI. The aerolysin-resistant EAHy926AR cells do not express TFPI on their surface and were used as a negative control.

Staining with anti TFPI antibodies and the corresponding isotype control antibody hzATNP were done as follows: Washed cell-line preparations (50000 cells pr well) were added to 96 well plates (Greiner, cat no. 65021) together with 50 µl of diluted TFPI antibody or isotype control in titration giving final concentrations 5 µg/ml. Cell preparations were then incubated at 4 degrees Celsius for 1 hour. After incubation and wash (PBS buffer with 5 % Fetal calf serum, centrifuge for 5 minutes at 200g) the secondary RPE-labelled anti-human antibody (diluted in PBS buffer 1:200) was added and incubated for another 1 hour at 4 degrees of Celsius. Finally, cells were washed and fixed by paraformaldehyde (1 % weight in volume (w/v) paraformaldehyde) and analysed in the flow cytometer within 36 hours.

In figure 5, the binding of C-terminal specific anti TFPI antibodies (4F100 and 4F110) and the isotype control antibody hzATNP (0.5 µg/ml) to EAHy926WT and EAHy926AR is shown.

It is here clear that anti-TFPI antibodies directed against the C-terminal of TFPI do not bind TFPI anchored via GPI expressed by endothelial cell line EAHy926WT, whereas antibodies to Kunitz 2 bind selectively to the EAHy926WT and not to the aerolysin resistant TFPI negative cell line EAHy926AR.

**Example 7: ELISA**

The effect of truncating the C-terminal tail of TFPI on TFPI's binding affinity to MuTFPI22F66, MuTFPI22F71, MuTFPI22F74, MuTFPI22F79 and MuTFPI22F132 was analyzed by means of ELISA, or real-time binding analysis, using the ForteBio platform. The TFPI variants, which were either wild type (wt) TFPI (SEQ ID NO: 1) or truncated TFPI mutants encompassing amino acids 1-239 (SEQ ID NO: 2), 1-240 (SEQ ID NO: 22), 1-241 (SEQ ID NO: 23), 1-242 (SEQ ID NO: 24), 1-243 (SEQ ID NO: 25), 1-244 (SEQ ID NO: 26) or 1-245 (SEQ ID NO: 3), were expressed in HEK293-F cells. The ELISAs, or the real-time binding analyses, were carried out using the conditioned medium from the cell cultures.

The concentrations of wt TFPI and truncated TFPI mutants in the conditioned medium were estimated by means of an ELISA that binds TFPI K1-K2 (Goat anti-TFPI, in-house) and K2 (MAB4F36, in-house). The binding to these antibodies is not affected by the truncations. Alternatively, biotin-labelled MAB4F36 was captured on streptavidin coated BioSensor tips (ForteBio) and used for concentration estimations.

In the ELISA setting, the effect of the mutations on TFPI's ability to bind to MuTFPI22F66, MuTFPI22F71, MuTFPI22F74, MuTFPI22F79 or MuTFPI22F132 was analyzed using each of the listed MAbs as capturing antibody and using MAB4F36 for detection. Direct binding of TFPI variants to biotin-labelled MuTFPI22F66, MuTFPI22F71, MuTFPI22F74, MuTFPI22F79, and MuTFPI22F132, captured on streptavidin coated BioSensor tips (ForteBio), was measured using the ForteBio platform.
Figure 7 reflects the effect of the truncations calculated, relative to the expression level and relative to wt. It was demonstrated that mAb 4F110 binding to the three truncated forms 1-243, 1-244 and 1-245 was not affected, compared to their binding to full length TFPI, whereas binding of mAb 22F74 to all of the truncated TFPI forms was strongly reduced. The rest of the tested antibodies lay within this range.

Example 8: Neutralizing TFPI inhibition of FVIIa/TF/FXa activity in the presence of PS/PC vesicles

Materials used were BSA buffer (50 mM HEPES; 0.1 M NaCl, 5 mM CaCl₂, 0.1 mg/ml BSA, pH 7.4) EDTA: 50 mM and the reagents listed in the tables below.

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<td>6 TFPI-4F110</td>
<td>OP001</td>
<td>3.5</td>
<td>23333</td>
<td>400</td>
<td>58.3</td>
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<tr>
<th>Reagent</th>
<th>Batch - lot no.</th>
<th>Cone</th>
<th>Final cone in well</th>
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<tbody>
<tr>
<td>EDTA</td>
<td>MERCK 8418</td>
<td>0.5 M</td>
<td></td>
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<tr>
<td>mAb</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>50 nM 12.5 3.13 0.78 0.2 0.05 0.01 0</td>
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<tr>
<td>FVIIa</td>
<td>LASa 13200-008</td>
<td>27 µM</td>
<td>10 pM</td>
</tr>
<tr>
<td></td>
<td>frozen in aliquots storage -80°C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>vesicles</td>
<td>HTI Phospholipids vesicles cat#PCPS-02 #W1115-75% PC - 25% PS (0.02% azid added)</td>
<td>2.0 mM</td>
<td>12.5 µM</td>
</tr>
<tr>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>S-2765</td>
<td>Chromogenix 82 1413 39 lot# N0574120 2010-50</td>
<td>35 mM</td>
<td>0.5 mM</td>
</tr>
<tr>
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</tr>
<tr>
<td>FX</td>
<td>Enzyme Research HXF 3064 A2L dissolved in 50 % Glycerol 08-dec-2009 frozen in aliquots storage -80°C</td>
<td>34 µM</td>
<td>160 nM</td>
</tr>
<tr>
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<tr>
<td>TFPI Fl.</td>
<td>0172-0000-0001-6A</td>
<td>21.9 µM</td>
<td>1 nM</td>
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All of the components, in final concentrations as indicated in the table above, were added together. 25 \( \mu \)M FX and 25 \( \mu \)M TFPI mAb were added in varying concentrations to 25 \( \mu \)M human TFPI, 25 \( \mu \)M FVIIa-TF (Innovin) and PS/PC vesicles in microtiter wells. Mixtures were incubated for 15 min at room temperature. 50 \( \mu \)M EDTA was added, followed by 50 \( \mu \)M S-2765. Plates were mixed and read for 15 min at 405 nm in Spectramax. 100% activity was the activity of FVIIa/TF/FX obtained with no TFPI present.

The six C-terminal TFPI mAbs listed in the table above were capable of neutralising TFPI inhibition of the complex FVIIa/TF/FX in the presence of PS/PC vesicles. The antibodies also neutralised TFPI in the absence of PS/PC.

**Example 9: Binding interaction analysis**

Binding interaction analysis was obtained by Surface Plasmon Resonance in a Biacore 3000. Capture of the relevant monoclonal antibody at a fixed concentration was obtained with immobilised mouse anti-IgG. Different concentrations of TFPI were tested. Determination of binding constants \( (k_{on}, k_{off}, K_d) \) was obtained assuming a 1:1 interaction of TFPI and the antibody of interest.

<table>
<thead>
<tr>
<th>mAb ID</th>
<th>TFPI binding constant nM</th>
<th>Human TFPI</th>
<th>Human TFPI161</th>
<th>Rabbit TFPI</th>
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<td>MuTFPI22F66</td>
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<td>3.76</td>
<td>-</td>
<td>-</td>
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<td>MuTFPI22F71</td>
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<td>-</td>
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<td>-</td>
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<tr>
<td>MuTFPI22F74</td>
<td>nd</td>
<td>-</td>
<td>2.73</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>MuTFPI22F132</td>
<td>nd</td>
<td>-</td>
<td>0.1</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>MuTFPI4F110</td>
<td>0.002</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
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Competition of the different mAbs for binding to TFPI when bound to mAb 4F110 was obtained by immobilisation of mAb 4F110 at a CM5 chip followed by binding of 50 nM TFPI followed by varying concentrations the mAbs (22F66, 22F71, 22F74, 22F79, 22F132, 22F158, 22F174, 4F110) to be tested for competition. Results are shown in the table below. Regeneration of the chip was obtained by 10 mM Glycine, pH 1.7.

**mAb ID**

**Competition with mAb 4F110 for binding to TFPI**

TFPI-22F66  YES
TFPI-22F71 YES
TFPI-22F74 NO
TFPI-22F79 NO
TFPI-22F132 NO
TFPI-22F158 YES
TFPI-22F174 YES
TFPI-4F1 10 YES

The C-terminal mAbs fall into two groups with respect to competition with mAb 4F1 10. Antibodies in both groups display TFPI neutralizing activity.

Example 10: Epitope determination by means of comparative modelling

Epitope models were generated by means of the commercially available computer program, Modeller [N. Eswar, M. A. Marti-Renom, B. Webb, M. S. Madhusudhan, D. Eramian, M. Shen, U. Pieper, A. Sali. Comparative Protein Structure Modeling With MODELLER. Current Protocols in Bioinformatics, John Wiley & Sons, Inc., Supplement 15, 5.6.1-5.6.30, 2006] based on published x-ray crystallographic structures of TFPI-1-2. For the TFPI-1-3, residues with a relative accessibility larger than 40% were found to be: 186-187, 190, 192-208, 213, 215-220, 225-228, 230-234 and 236-237. For the C-terminal, residues 240-276 had a relative accessibility that was larger than 40%.

Example 11: Factor Vila Variant Activity Assay (In Vitro Hydrolysis Assay)

Native (wild-type) Factor Vila and Factor Vila variant (both hereafter referred to as "Factor Vila") are assayed in parallel to directly compare their specific activities. The assay is carried out in a microtiter plate (MaxiSorp, Nunc, Denmark). The chromogenic substrate D-Ile-Pro-Arg-p-nitroanilide (S-2288, Chromogenix, Sweden), final concentration 1 mM, is added to Factor Vila (final concentration 100 nM) in 50 mM Hapes, pH 7.4, containing 0.1 M NaCl, 5 mM CaCl₂ and 1 mg/ml bovine serum albumin. The absorbance at 405 nm is measured continuously in a Spectra-Max™ 340 plate reader (Molecular Devices, USA). The absorbance developed during a 20-minute incubation, after subtraction of the absorbance in a blank well containing no enzyme, is used to calculate the ratio between the activities of variant and wild-type Factor Vila:

\[
\text{Ratio} = \frac{(A_{405 \text{nm}} \text{ Factor Vila variant})}{(A_{405 \text{nm}} \text{ Factor Vila wild-type})}
\]

Example 12: Factor Vila Variant Activity Assay (In Vitro Proteolysis Assay)

Native (wild-type) Factor Vila and Factor Vila variant (both hereafter referred to as "Factor Vila") are assayed in parallel to directly compare their specific activities. The assay is carried out in a microtiter plate (MaxiSorp, Nunc, Denmark). Factor Vila (10 nM) and Factor X (0.8 mM) in 100 microL 50 mM Hapes, pH 7.4, containing 0.1 M NaCl, 5 mM CaCl₂ and 1 mg/ml bovine serum albumin, are incubated for 15 min. Factor X cleavage is then stopped by the addition of 50
microL 50 mM Hepes, pH 7.4, containing 0.1 M NaCl, 20 mM EDTA and 1 mg/ml bovine serum albumin. The amount of Factor Xa generated is measured by addition of the chromogenic substrate Z-D-Arg-Gly-Arg-p-nitroanilide (S-2765, Chromogenix, Sweden), final concentration 0.5 mM. The absorbance at 405 nm is measured continuously in a SpectraMax™ 340 plate reader (Molecular Devices, USA). The absorbance developed during 10 minutes, after subtraction of the absorbance in a blank well containing no FVIIa, is used to calculate the ratio between the proteolytic activities of variant and wild-type Factor Vila:

\[
\text{Ratio} = \frac{A_{405 \text{ nm Factor Vila variant}}}{A_{405 \text{ nm Factor Vila wild-type}}}.
\]

**Example 13: Factor VIII Activity Assay (Chromogenic Assay)**

The FVIII activity (FVIII :C) of the rFVIII compound is evaluated in a chromogenic FVIII assay using Coatest SP reagents (Chromogenix) as follows: rFVIII samples and a FVIII standard (e.g. purified wild-type rFVIII calibrated against the 7th international FVIII standard from NIBSC) are diluted in Coatest assay buffer (50 mM Tris, 150 mM NaCl, 1 % BSA, pH 7.3, with preservative). Fifty \( \mu \)l of samples, standards, and buffer negative control are added to 96-well microtiter plates (Nunc) in duplicates. The factor IXa/factor X reagent, the phospholipid reagent and CaCl\(_2\) from the Coatest SP kit are mixed 5:1:3 (vol:vol:vol) and 75 \( \mu \)l of this added to the wells. After 15 min incubation at room temperature, 50 \( \mu \)l of the factor Xa substrate S-2765/thrombin inhibitor 1-2581 mix is added and the reagents incubated for 10 minutes at room temperature before 25 \( \mu \)l 1 M citric acid, pH 3, is added. The absorbance at 415 nm is measured on a Spectramax microtiter plate reader (Molecular Devices) with absorbance at 620 nm used as reference wavelength. The value for the negative control is subtracted from all samples and a calibration curve prepared by linear regression of the absorbance values plotted vs. FVIII concentration. Specific activity is calculated by dividing the activity of the samples with the protein concentration determined by HPLC. The concentration of the sample is determined by integrating the area under the peak in the chromatogram corresponding to the light chain and compare with the area of the same peak in a parallel analysis of a wild-type unmodified rFVIII, where the concentration is determined by amino acid analyses.

**Example 14: Factor VIII Activity Assay (One-Stage Clot Assay)**

FVIII activity (FVIII :C) of the rFVIII compounds is further evaluated in a one-stage FVIII clot assay as follows: rFVIII samples and a FVIII standard (e.g. purified wild-type rFVIII calibrated against the 7th international FVIII standard from NIBSC) are diluted in HBS/BSA buffer (20 mM hepes, 150 mM NaCl, pH 7.4 with 1 % BSA) to approximately 10 U/ml, followed by 10-fold dilution in FVIII-deficient plasma containing VWF (Dade Behring). Samples are subsequently diluted in HBS/BSA buffer. The APTT clot time is measured using an ACL300R or an ACL5000 instrument (Instrumentation Laboratory) using the single factor program. FVIII-deficient plasma with VWF (Dade Behring) is used as assay plasma and SynthASil, (HemosIL™, Instrumentation Laboratory) as aPTT reagent. In the clot instrument, the diluted sample or standard is mixed with FVIII-deficient plasma.
and aPTT reagents at 37°C. Calcium chloride is added and time until clot formation is determined by measuring turbidity. The FVIII:C in the sample is calculated based on a standard curve of the clot formation times of the dilutions of the FVIII standard.

All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference in their entirety and to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein (to the maximum extent permitted by law).

All headings and sub-headings are used herein for convenience only and should not be construed as limiting the invention in any way.

The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

The citation and incorporation of patent documents herein is done for convenience only and does not reflect any view of the validity, patentability, and/or enforceability of such patent documents.

This invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law.
1. An antibody that is capable of specifically binding the C-terminal of full length TFPI.

2. The antibody according to claim 1, wherein said C-terminal corresponds to amino acids 186-276 of TFPI (SEQ ID NO: 1).

3. The antibody according to any one of claims 1-2, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-107 (WDRFDFVY) of SEQ ID NO: 5, wherein one or two of these amino acids may be substituted by a different amino acid.

4. The antibody according to any one of claims 1-2, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-106 (GTYEYVDY) of SEQ ID NO: 9, wherein one or two of these amino acids may be substituted by a different amino acid.

5. The antibody according to any one of claims 1-2, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-111 (EVYYGYGDDYFDY) of SEQ ID NO: 13, wherein one, two or three of these amino acids may be substituted by a different amino acid.

6. The antibody according to any one of claims 1-4, wherein the heavy chain comprises:
   • a CDR1 sequence of amino acids 31 to 35 (SYMYM) of SEQ ID NO: 5 and/or
     a CDR2 sequence of amino acids 50-66 (EINPSNGDNLNEKFS) of SEQ ID NO: 5 and/or
     a CDR3 sequence of amino acids 99-107 (WDRFDFVY) of SEQ ID NO: 5, and the light chain comprises:
     • a CDR1 sequence of amino acids 24-34 (IISTNDDIDIN) of SEQ ID NO: 7 and/or
     • a CDR2 sequence of amino acids 50-56 (EGNTLRP) of SEQ ID NO: 7 and/or
     • a CDR3 sequence of amino acids 89-97 (LQSDDLPYT) of SEQ ID NO: 7;
   or wherein the heavy chain comprises
     • a CDR1 sequence of amino acids 31-35 (GYPMN) of SEQ ID NO: 9, and/or
     • a CDR2 sequence of amino acids 50-66 (LINPYNGDHTFNQKFG) of SEQ ID NO: 9 and/or
     • a CDR3 sequence of amino acids 99-106 (GTYEYVDY) of SEQ ID NO: 9, and the light chain comprises:
     • a CDR1 sequence of amino acids 24-33 (SASSSVFYMH) of SEQ ID NO: 11, and/or
     • a CDR2 sequence of amino acids 49-55 (DTSILSS) of SEQ ID NO: 11 and/or
     • a CDR3 sequence of amino acids 88-96 (QQWSSYPLT) of SEQ ID NO: 11;
   or wherein the heavy chain comprises
     • a CDR1 sequence of amino acids 31-35 (TYWIH) of SEQ ID NO: 13, and/or
     • a CDR2 sequence of amino acids 50-66 (AIDPGNSDATYSQKFD) of SEQ ID NO: 13 and/or
     • a CDR3 sequence of amino acids 99-111 (EVYYGYGDDYFDY) of SEQ ID NO: 13; and the light chain comprises:
     • a CDR1 sequence of amino acids 24-38 (RASESVSVDHGLM) of SEQ ID NO: 15, and/or
• a CDR2 sequence of amino acids 54-60 (AASKLES) of SEQ ID NO.: 15 and/or
• a CDR3 sequence of amino acids 93-101 (QQSIGDPWT) of SEQ ID NO.: 15.

7. The antibody according to any one of claims 1-4, wherein said antibody comprises SEQ ID NOs: 5 and 7; or SEQ ID NOs: 9 and 11; or SEQ ID NOs: 13 and 15.

8. The antibody according to any one of claims 1-9, which is not capable of specifically binding truncated TFPI selected from the group consisting of TFPI (1-161), truncated TFPI (1-185), truncated TFPI (1-239) or truncated TFPI (1-245).

9. The antibody according to any one of claims 1-8, which is capable of neutralizing TFPI inhibition of TF/FVIIa/FXa in the presence of phospholipid.

10. A pharmaceutical formulation comprising the monoclonal antibody according to any one of claims 1-9.

11. The antibody according to any one of claims 1-9, or the pharmaceutical formulation according to claim 10, for the treatment of a subject with a coagulopathy.

12. The antibody according to any one of claims 1-9 and another agent that enhances haemostasis, selected from the list consisting of a Factor Vila polypeptide, a Factor VIII polypeptide or a Factor IX polypeptide, for the treatment of a subject with a coagulopathy.

13. The antibody according to any one of claims 1-9 and a Factor VIII polypeptide for the treatment of haemophilia A.

14. The antibody according to any one of claims 1-9 and a Factor IX polypeptide for the treatment of haemophilia B.

15. The antibody according to any one of claims 1-9 and a Factor Vila polypeptide for the treatment of haemophilia A or B with inhibitors.
Fig. 1

- TF 1:7,500
- TF 1:15,000
- TF 1:30,000

![Graph showing dPT (Sec) vs. [4F110] (nM)]
Fig. 2

![Graph showing Thrombin (nM) over time (min) with Control and 4F110 traces.](image-url)
Fig. 3
Fig. 4

![Graph showing R (Clot time) min vs. ReFacto (IU/ml) with bars for buffer and F110 at different concentrations.](image-url)
Fig. 4 cont.
Fig. 5

- **K2-binding Antibody**
- **K2-binding Antibody**
- **4F100-C terminal**
- **4F110 C-terminal**

(Conc. 5μg/ml)

- **MFI (FACSCARRAY)**

Values:
- K2-binding Antibody: 34,400
- K2-binding Antibody: 29,500
- 4F100-C terminal: 24,600
- 4F110 C-terminal: 19,700
Fig. 6

Reactivity to MAb (relative to expression level and WT)

WT, 1-239, 1-246

TFPI truncations

- 4F110
- 22F66
- 22F71
- 22F74
- 22F79
- 22F132
Fig. 7

Binding of TFPI variants to αTFPI MAbs relative to TFPI WT

- 4F110
- 22F71
- 22F66
- 22F132
- 22F79
- 22F74

Key:
- WT
- 1-239
- 1-240
- 1-241
- 1-242
- 1-243
- 1-244
- 1-245
Fig. 8

![Graph showing FXa generation (arb. u.) vs. Concentration (nM).]
Fig. 9

TFPI w. 3 Kunitz domains

Endothelial cells

TFPI in platelets
free TFPI
Lipoprotein-bound TFPI
GPI-anchored TFPI
HSPG-associated TFPI
Heparin releasable TFPI
**INTERNATIONAL SEARCH REPORT**

**International application No**

PCT/EP2011/06980

**A. CLASSIFICATION OF SUBJECT MATTER**

INV. C07K16/38 A61K39/395 A61P7/Q4

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 A61K A61P

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 practical, search terms used)

EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

<table>
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<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
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<td>X</td>
<td>EP 0 539 975 AI (TEIJIN LTD [JP]) 5 May 1993 (1993-05-05) the whole document in particular abstract page 2, line 38 - page 3, line 41 page 5, line 40 - page 7, line 8 claims 1-18; figures 1-4; examples 1-12 ------ /--</td>
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* Further documents are listed in the continuation of Box C. See patent family annex.

X

* 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 document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "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**

3 August 2011

**Date of mailing of the international search report**

16/08/2011

**Name and mailing address of the ISA/Authorized officer**

European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk

Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016

Ferreira, Roger
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<td>X</td>
<td>ABUMIYA T ET AL: &quot;An anti-tissue factor pathway inhibitor (TFPI) monoclonal antibody recognizes the Kunitz domain (K3) of free-form TFPI but not the protease associated forms in plasma&quot;, JOURNAL OF BIOCHEMISTRY, JAPANESE BIOCHEMICAL SOCIETY / OUP, TOKYO; JP, vol. 118, no. 1, 1 July 1995 (1995-07-01), pages 178-182, XP001207171, ISSN: 0021-924X</td>
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<td>TANG HAIWANG ET AL: &quot;Septic induced coagulation in the baboon lung is associated with decreased tissue factor pathway inhibitor&quot;, AMERICAN JOURNAL OF PATHOLOGY, AMERICAN SOCIETY FOR INVESTIGATIVE PATHOLOGY, US, vol. 171, no. 3, 1 September 2007 (2007-09-01), pages 1066-1077, XP002574356, ISSN: 0002-9440</td>
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<td>KOKAWA T ET AL: &quot;Measurement of the free form of TFPI anti-gen in hyperplastic tissue&quot;, ARTERIOSCLEROSIS, THROMBOSIS, AND VASCULAR BIOLOGY, vol. 16, no. 6, June 1996 (1996-06), pages 802-808, XP009140258, ISSN: 1079-5642</td>
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<td>OHKURA N ET AL: &quot;Monoclonal anti-body specific for tissue factor pathway inhibitor Xa complex&quot;, BLOOD COAGULATION &amp; FIBRINOLYSIS: AN INTERNATIONAL JOURNAL, vol. 10, no. 6, September 1999 (1999-09), pages 309-319, XP009140267, ISSN: 0957-5235</td>
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<td>CARTER P J: &quot;POTENT ANTIBODY THERAPEUTICS BY DESIGN&quot;, NATURE REVIEWS IMUNOLOGY, NATURE PUBLISHING GROUP, GB, vol. 6, 7 April 2006 (2006-04-07), pages 343-357, XP007901440, ISSN: 1474-1733, DOI: DOI: 10.1038/NR1837</td>
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<td>WO 2008/136848 A2 (GENENTECH INC [US]; LI KANG [US]; FUNG SEK CHUNG [US]; YAO ZHENG [U]) 13 November 2008 (2008-11-13) claims 4, 10; figure 2A; sequences 2, 10</td>
<td>5, 6</td>
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<td>A</td>
<td>US 6 171 587 BI (WUN TZE CHEIN [US] ET AL) 9 January 2001 (2001-01-09), the whole document</td>
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<td>WO 2010/072691 (NOVO NORDISK AS [DK]; HILDEN IDA [DK]; KROGH BERIT 0LSEN [DK]; CLAUSEN) 1 July 2010 (2010-07-01) cited in the application</td>
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<td>WO 2010/072687 (NOVO NORDISK AS [DK]; HILDEN IDA [DK]; CLAUSEN JES THORN [DK]) 1 July 2010 (2010-07-01)</td>
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<tr>
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<td></td>
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<td>a.</td>
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<td>subsequently to this Authority for the purpose of search</td>
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<td>2.</td>
<td>In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.</td>
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<td>3.</td>
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**INTERNATIONAL SEARCH REPORT**

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<td>This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:</td>
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<td>1. ☐ Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:</td>
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<td>2. ☐ Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:</td>
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<td>3. ☐ Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).</td>
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<td>This International Searching Authority found multiple inventions in this international application, as follows:</td>
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|               | As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. |
|               | ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees. |
|               | ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: |
|               | ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: |

**Remark on Protest**

- ☐ The additional search fees were accompanied by the applicant’s protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant’s protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.
# INTERNATIONAL SEARCH REPORT

Information on patent family members

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<td>AT 273322 T 15-08-2004</td>
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This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1, 2, 8-15 (fully)

   Subject-matter of claims 1, 2 and 8-15 insofar as it relates to a monoclonal antibody that is capable of specifically binding the C-terminal TFPI (tissue factor pathway inhibitor), wherein said C-terminal is amino acids 186-276 of TFPI (SEQ ID No. 1).

2. claims: 3 (completely); 1, 2, 6-15 (partially)

   Subject-matter of claims 1-3 and 6-15, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-107 (WDRFDGFVY) of SEQ ID No. 5, wherein one or two of these amino acids may be substituted by a different amino acid.

3. claims: 4 (completely); 1, 2, 6-15 (partially)

   Subject-matter of claims 1, 2, 4 and 6-15, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-106 (GTYEYVDY) of SEQ ID No. 9, wherein one or two of these amino acids may be substituted by a different amino acid.

4. claims: 5 (completely); 1, 2, 6-15 (partially)

   Subject-matter of claims 1, 2 and 5-15, wherein the heavy chain of said antibody comprises a CDR3 sequence of amino acids 99-111 (EVVYGYGFDY) of SEQ ID No. 13, wherein one or two of these amino acids may be substituted by a different amino acid.