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(54) **TISSUE FACTOR COMPOSITIONS AND METHODS**

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(57) **ABSTRACT**

Tissue Factor (natural or recombinant truncated) can be incorporated into stable, soluble nanoscale particles so that activity is maintained. These particles can be used as a reagent in prothrombin clotting time assays or they can be used in therapeutic compositions for use in humans or animals. Therapeutic settings can include supplementation in the case of a genetic deficiency, uncontrolled bleeding, surgical incisions or seepage, thrombocytopenia, soft tissue trauma or other trauma, to effect tumor regression or to inhibit tumor growth.

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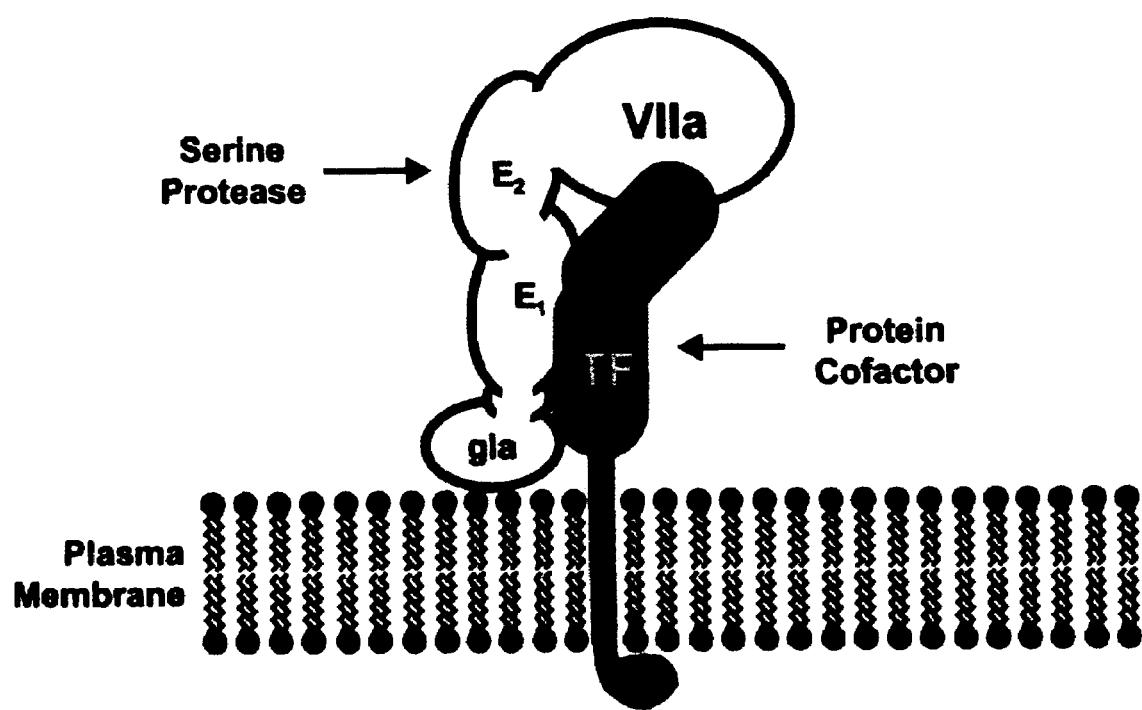
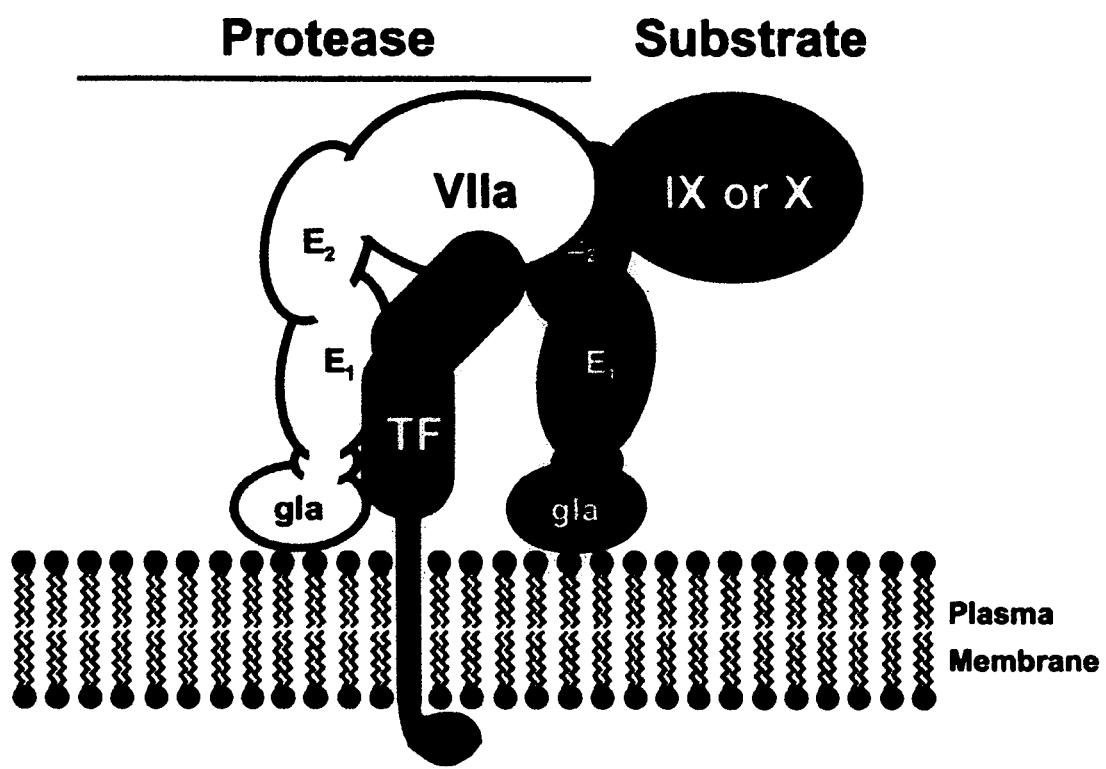
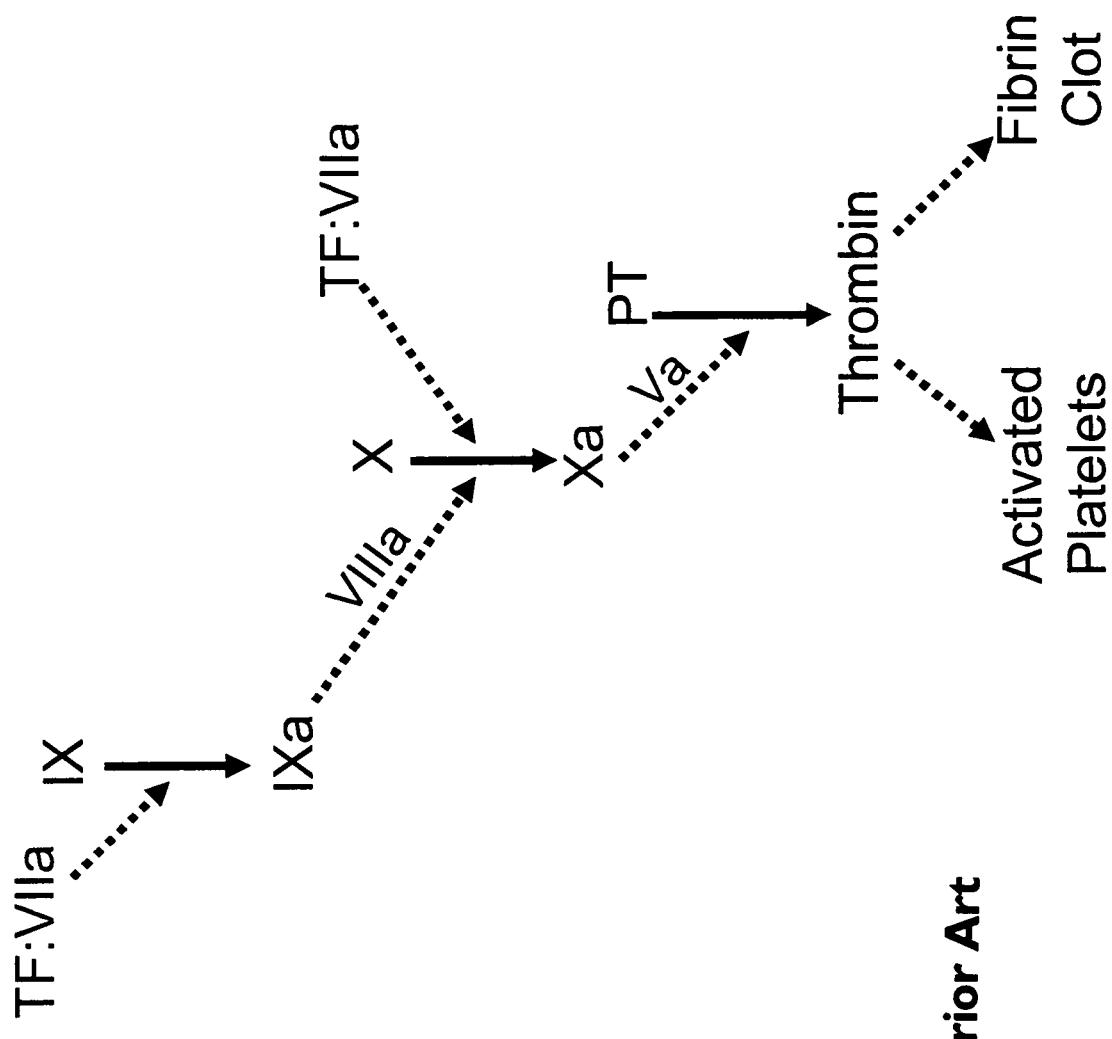


FIGURE 1A - PRIOR ART



**FIGURE 1B - PRIOR ART**



**FIG. 2 Prior Art**

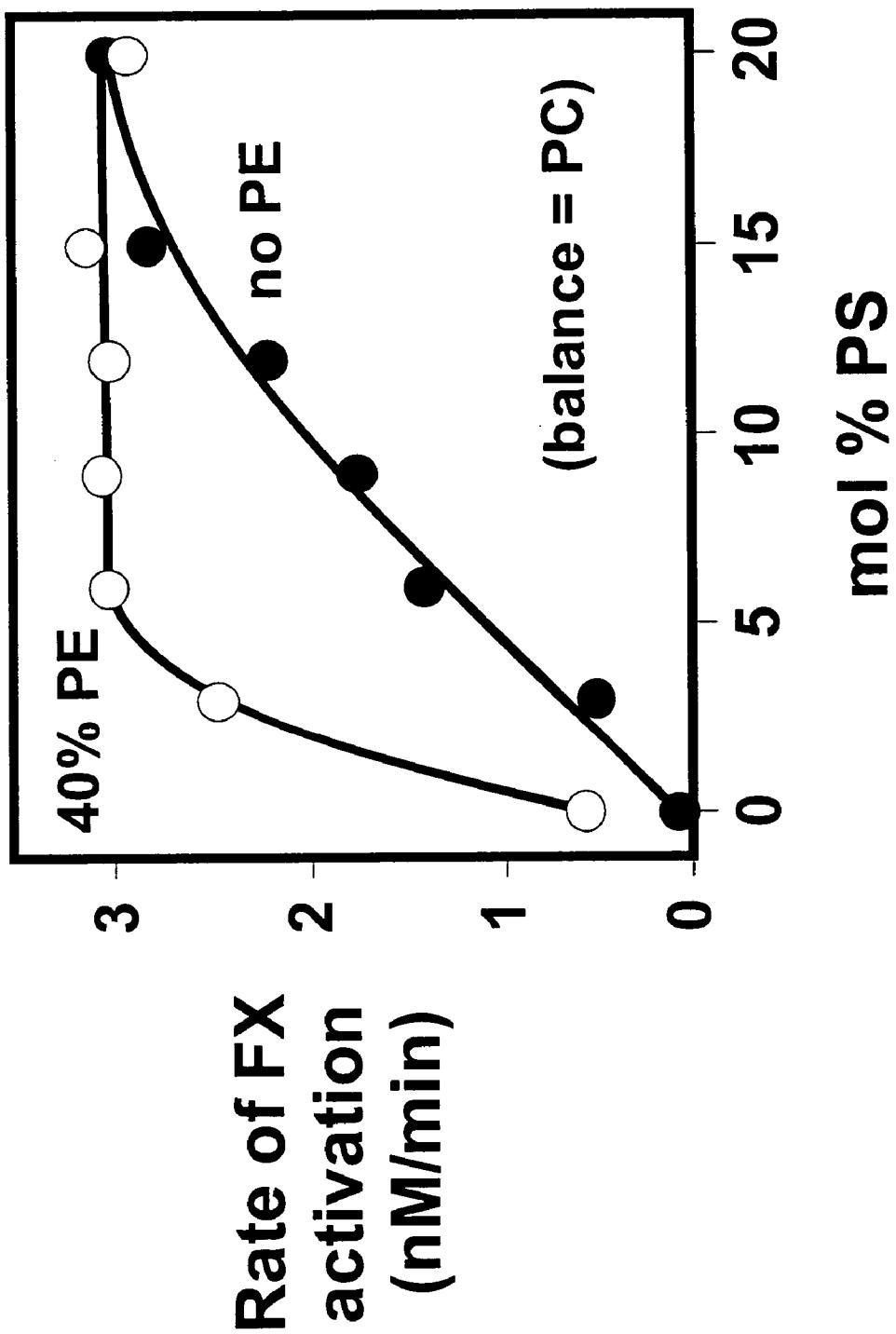
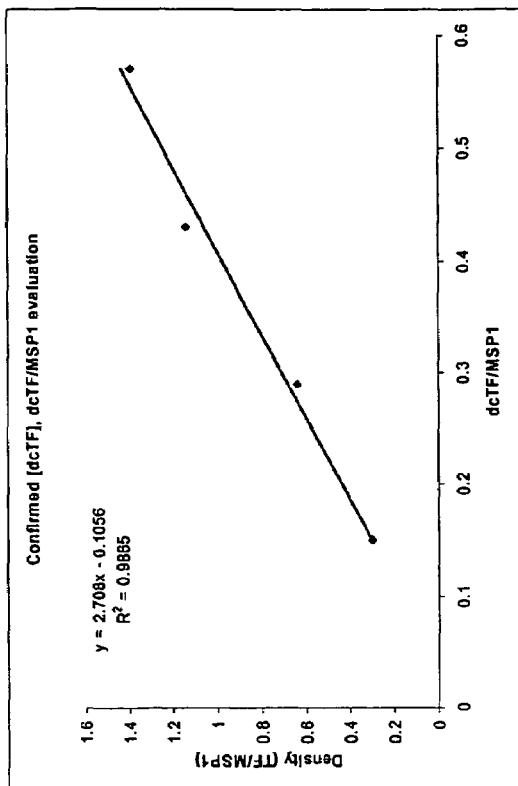
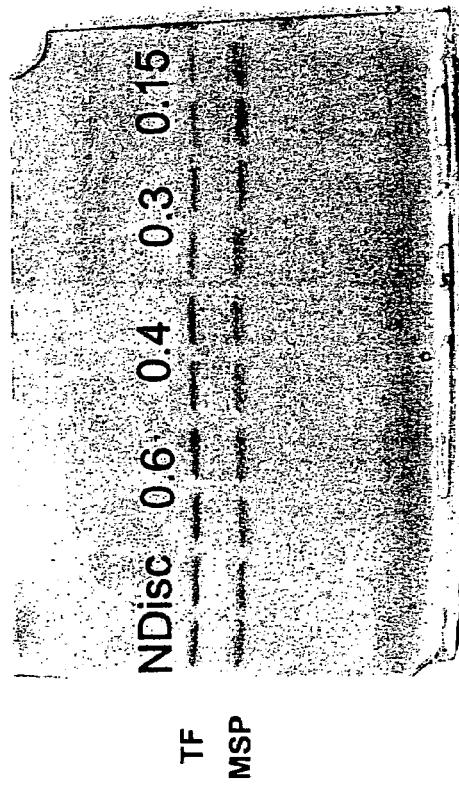
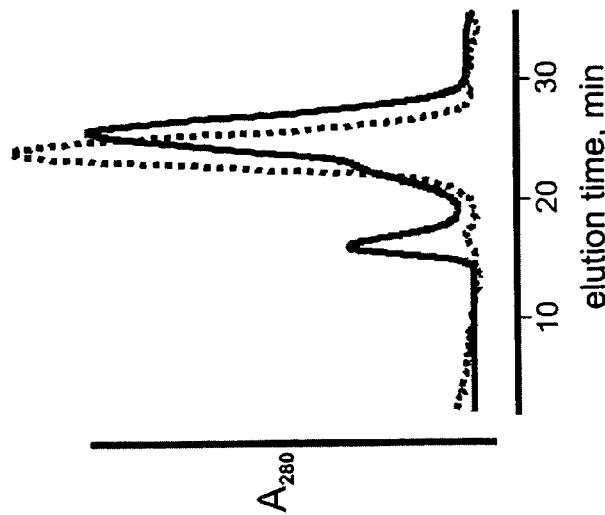
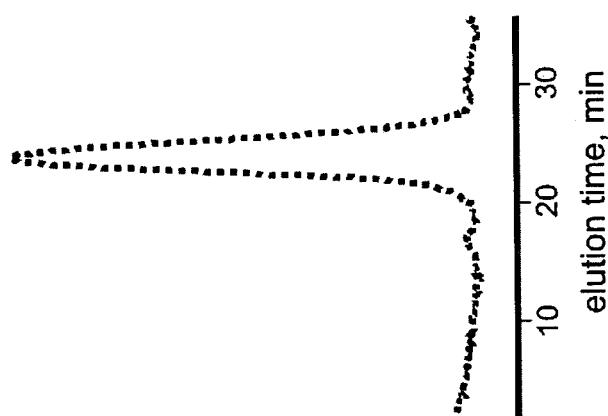
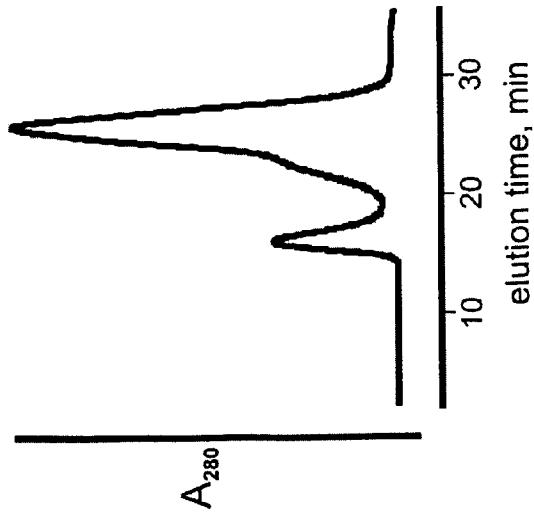


FIG. 3 Prior Art

**FIG. 4B**

Numbers indicate TF/MSP

**FIG. 4A**

**FIG. 5C****FIG. 5B****FIG. 5A**

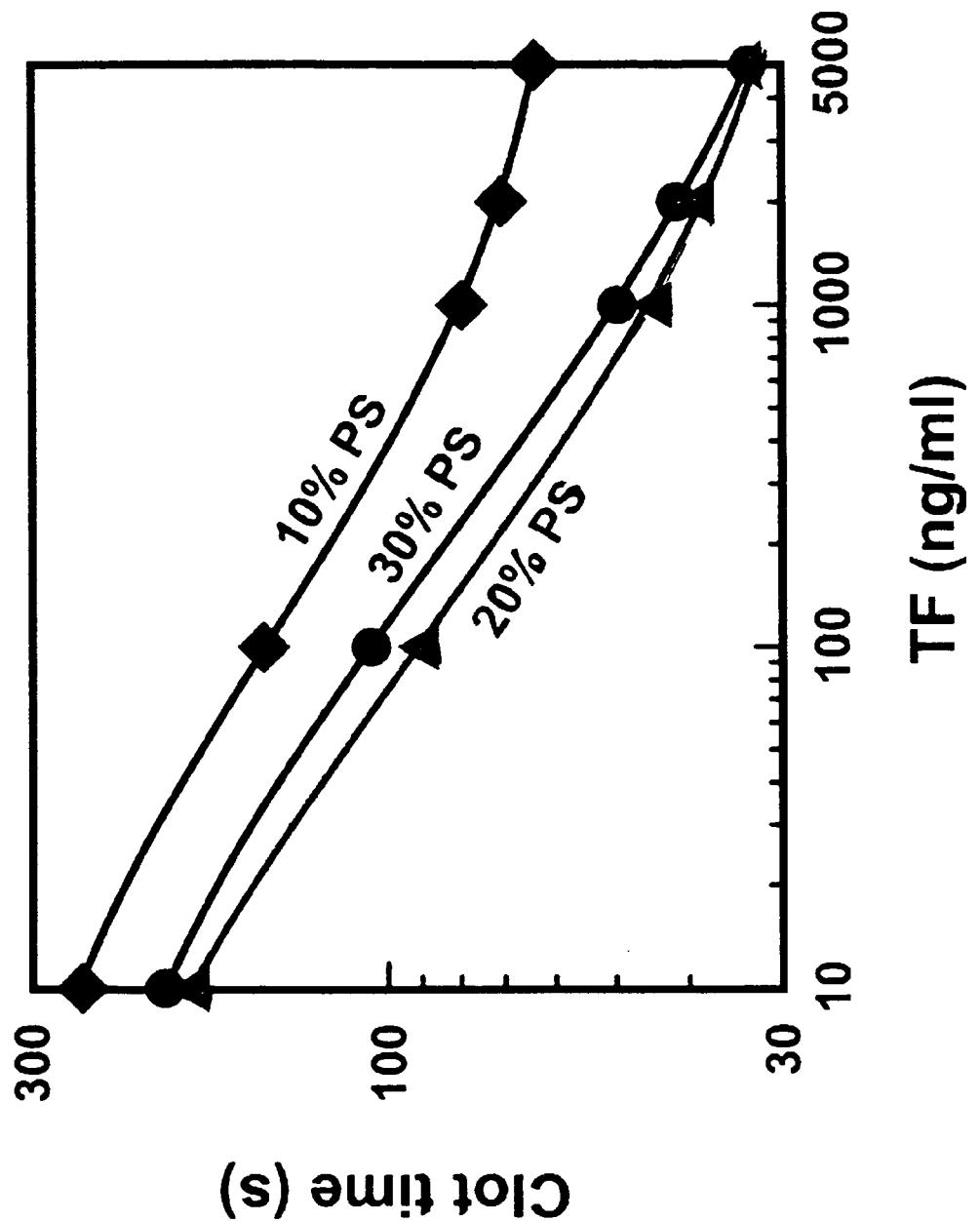


FIG. 6

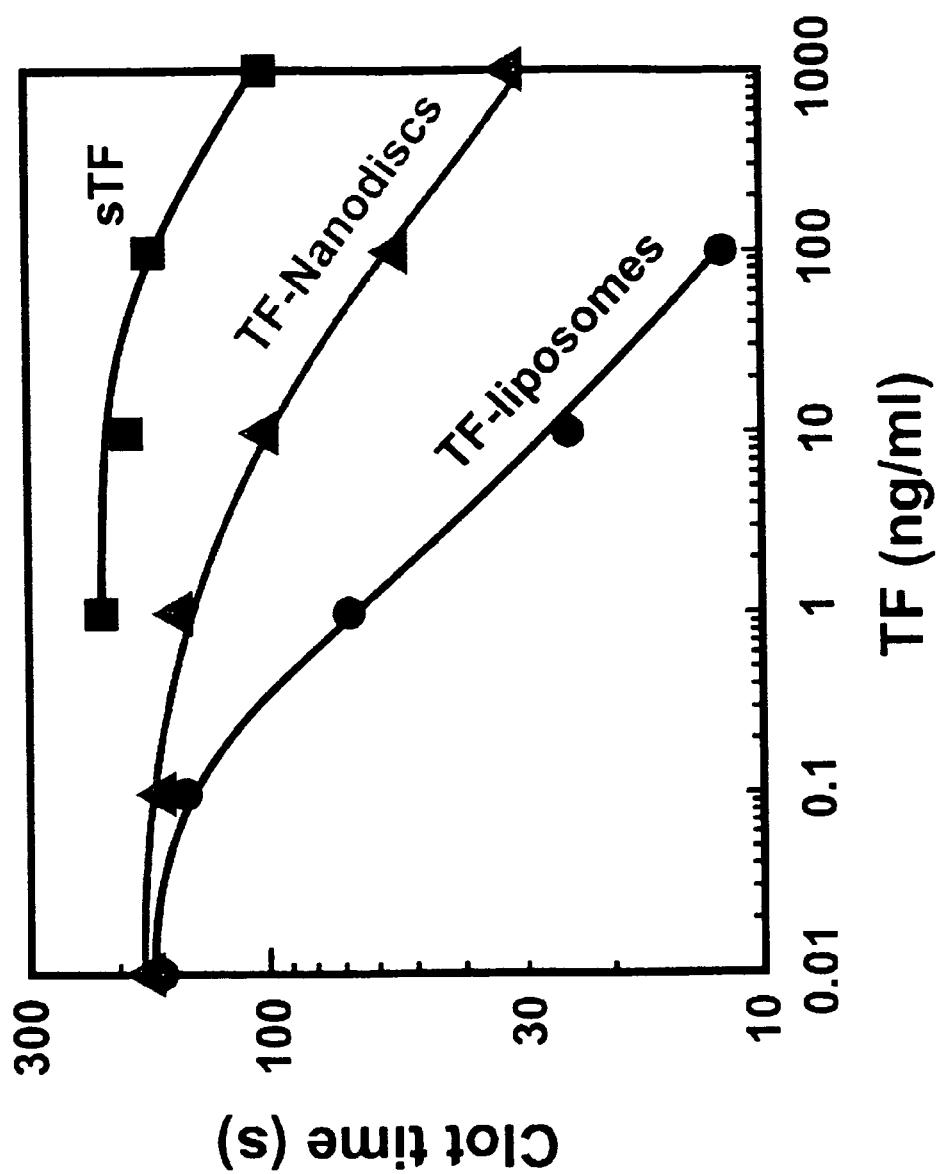


FIG. 7

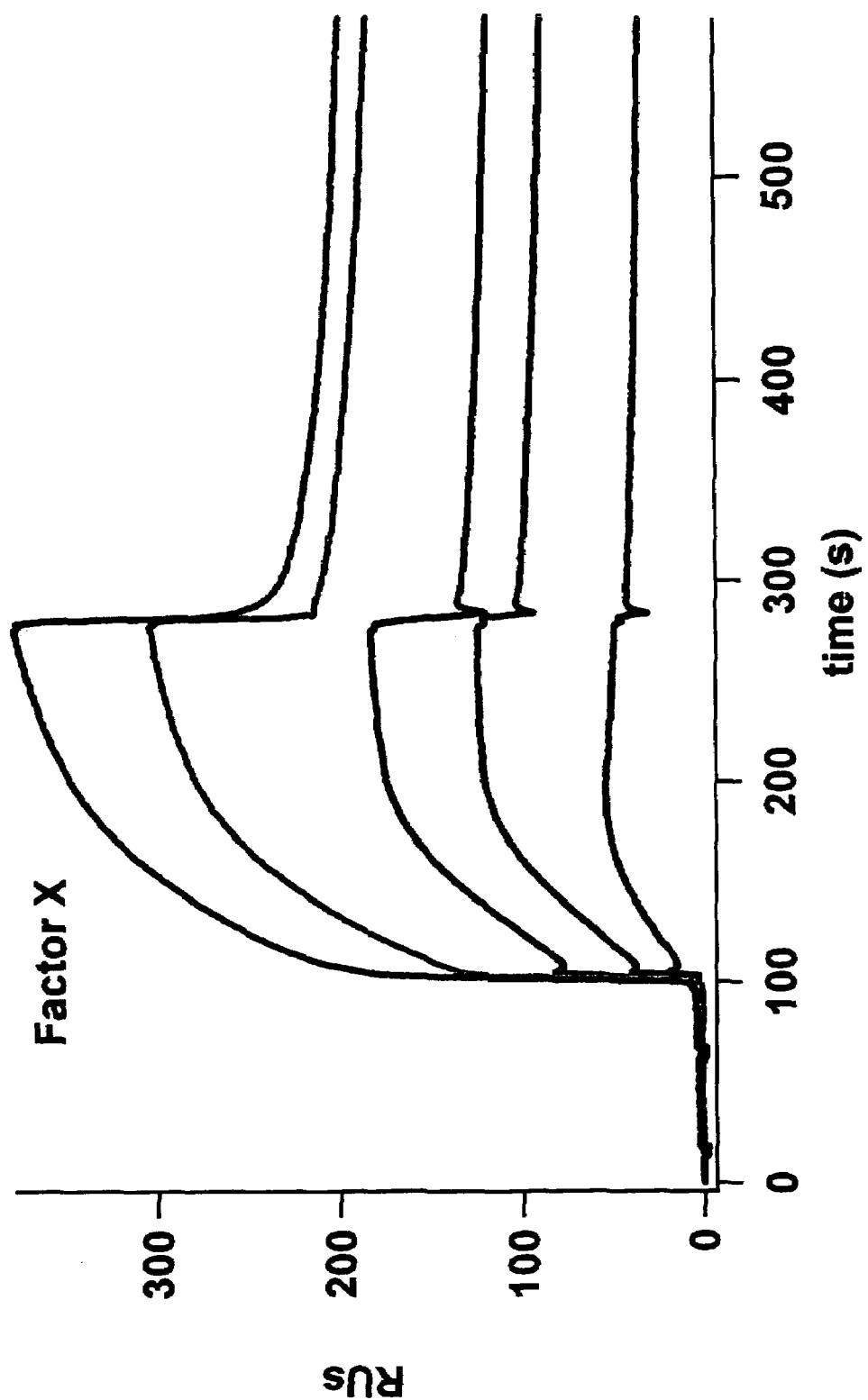


FIG. 8

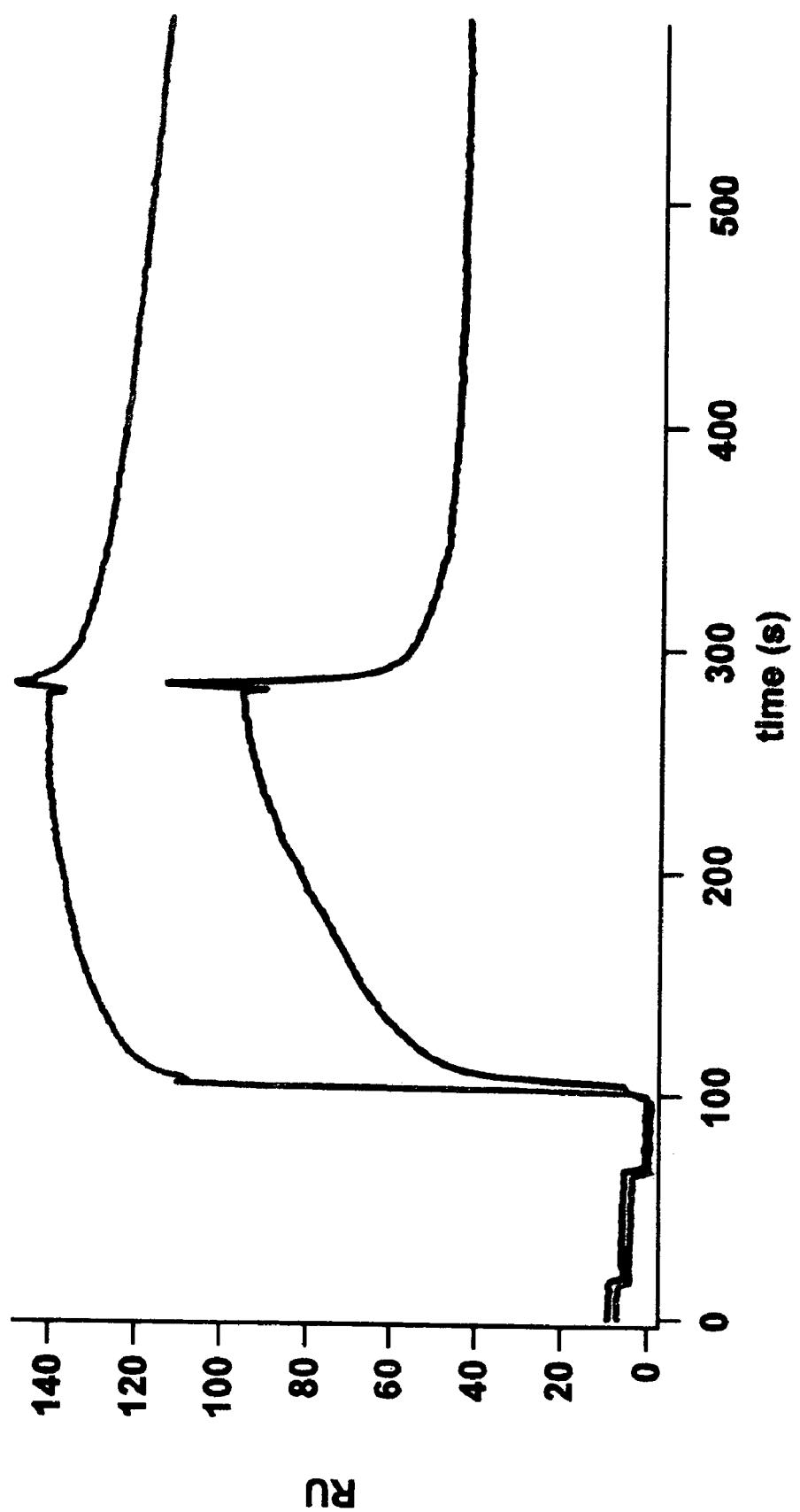


FIGURE 9

## TISSUE FACTOR COMPOSITIONS AND METHODS

## CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims benefit of U.S. Provisional Application No. 60/622,737, filed Oct. 27, 2004, and is a Continuation-in-Part of U.S. patent application Ser. No. 11/033,489, filed Jan. 11, 2005, which claims benefit of U.S. Provisional Application 60/536,281, filed Jan. 13, 2004 and is a Continuation-in-Part of U.S. patent application Ser. No. 10/465,789, filed Jun. 18, 2003, which is a Continuation-in-Part of U.S. patent application Ser. No. 09/990,087, filed Nov. 20, 2001, which claims benefit of U.S. Provisional Application No. 60/252,233, filed Nov. 20, 2000. All prior applications are incorporated by reference in their entirities to the extent there is no inconsistency with the present disclosure.

## STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under Grant Nos. GM33775 and R01 HL 47014 awarded by the National Institutes of Health. The government has certain rights in the invention.

## BACKGROUND OF THE INVENTION

The field of this invention is the area of therapeutic nanoscale particulate compositions, in particular to formulations of improved solubility and stability for the delivery of tissue factor. These formulations can be used to kill tumors, to stop bleeding, as topical hemostatic agents and as reagents in prothrombin time assays.

Tissue factor (TF) is the integral membrane protein that triggers blood coagulation. TF is composed of two fibronectin type 3 domains, a single membrane-spanning domain, and a short cytoplasmic domain (FIG. 1A). TF is typically expressed on the cell surface. A type I integral membrane protein, TF has its N-terminus located outside the cell and its C-terminus is in the cytoplasm.

TF is abundant in adventitial cells, found exterior to the smooth muscle of blood vessels. This layer can be considered a hemostatic envelope (Drake et al. 1989. Amer. J. Pathol. 134:1087-1097). Where there is damage to a blood vessel, TF participates in the clotting cascade to form a "patch" to stop further blood loss from the vasculature. Where blood vessels contain plaque and there is a rupture of the plaque, TF participates in the formation of a hemostatic "patch" at the point of rupture. This serves as a focus for clotting, leading to further occlusion of the blood vessel at that location.

TF functions to initiate blood clotting by selectively binding one of the soluble plasma proteins (factor VII or the activated form, factor VIIa) with high affinity. This results in the formation of TF:VIIa complexes on the cell surface. Factor VIIa, the first enzyme in the blood clotting cascade, is a serine protease that circulates as a soluble protein in the plasma. Factor VIIa is an extremely weak enzyme (low activity) unless it is bound to its protein cofactor (TF). Factor VIIa is allosterically activated when it binds TF, creating an extremely potent, two subunit enzyme (TF:VIIa). The TF:VIIa complex then triggers blood clotting by proteolytically activating two plasma serine protease zymogens (factors IX and X), which then go on to propagate the clotting cascade. The ultimate result is the formation of blood clots composed of polymerized fibrin and activated platelets. TF is

thought to be involved in thrombotic diseases in addition to its beneficial role in preventing blood loss from the vasculature.

Structurally, TF is a type I integral membrane protein composed of an extracellular domain, a single membrane-spanning domain and a short cytoplasmic tail. TF must be incorporated into suitable phospholipid membranes in order to exhibit maximal activity. Soluble TF is thousands of times less active than TF embedded in a suitable membrane, underscoring the essential role of membrane anchoring for TF function. In order for TF to exhibit strong procoagulant activity, the membrane or disc in which it is embedded must contain negatively charged phospholipids, desirably phosphatidylserine. There are several methods available for incorporating purified TF into phospholipid vesicles and nanoscale disc-like structures of varying composition.

Nanoscale disc-like particles comprising a membrane scaffold protein (MSP, naturally occurring or engineered) and phospholipid have been successfully used to provide stable, soluble and biologically active hydrophobic proteins. See, for example, WO 02/40501 and US Published Applications 2004/0053384 and 2005/0182243 for a thorough discussion of these particles, the structural proteins in them and their formation. These particles contain the phospholipid in the form of a disc which is surrounded by a "belt" formed of the amphiphilic membrane scaffold protein (MSP). Where there is a hydrophobic protein incorporated, it is bound in, within or to the phospholipid portion and may or may not have peripheral association with the encircling MSP. These particles are typically from about 5 to about 50 nm, usually about 5 to about 20 nm, in diameter, depending on the specific composition.

## SUMMARY OF THE INVENTION

It is an object of the present invention to provide improved compositions comprising tissue factor, including but not limited to human tissue factor, which compositions are improved in stability, solubility and handling characteristics. As specifically exemplified herein, tissue factor is incorporated into nanoscale particles comprising at least one membrane scaffold protein and phospholipid, desirably but not necessarily including at least one net negatively charged phospholipid. Desirably, the phospholipid is phosphatidylserine (PS) and phosphatidylcholine (PC) at a molar ratio of 1:99 to 50:50, or from 5:95, 10:40 or 20:80. If phosphatidylethanolamine (PE) is present instead of PC, then the proportion of PS or other net negatively charged phospholipid can be lower. Where a net negatively charged phospholipid is incorporated, it can make up from 1 to 50% (molar basis) of the total phospholipid. The membrane scaffold protein can be a naturally occurring protein such as apolipoprotein A1, apolipoprotein C or E, or other predominantly amphipathic helical protein, or it can be any of a number of engineered (designed and produced by the hand of man) membrane scaffold proteins, for example as described in United States Patent Publications 2005/0182243 and 2004/0053384, both of which are incorporated by reference to the extent there is no inconsistency with the present disclosure. For coding and amino acid sequences of MSPs useful in the practice of the present invention, see Tables 4-56 herein below. Specifically exemplified MSPs include, but are not limited to, SEQ ID NO:2, SEQ ID NO: 4, SEQ ID NO:6, SEQ ID NO:8, amino acids 13-414 of SEQ ID NO:8, SEQ ID NO:10, amino acids 13-422 of SEQ ID NO:10, SEQ ID NO:12, amino acids 13-168 of SEQ ID NO:12, SEQ ID NO:14, amino acids 13-168 of SEQ ID NO:14, SEQ ID NO:16, amino acids 13-201 of SEQ ID NO:16, SEQ ID NO:17, amino acids 13-201 of SEQ ID NO:17, SEQ ID

NO:18, amino acids 13-392 of SEQ ID NO:18, SEQ ID NO:50, amino acids 13-234 of SEQ ID NO:50, SEQ ID NO:51, amino acids 13-256 of SEQ ID NO:51, SEQ ID NO:52, amino acids 13-278 of SEQ ID NO:52, SEQ ID NO:53, amino acids 24-223 of SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, amino acids 24-212 of SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, amino acids 24-201 of SEQ ID NO:57, SEQ ID NO:58, amino acids 13-190 of SEQ ID NO:58, SEQ ID NO:59, amino acids 13-201 of SEQ ID NO:59, SEQ ID NO:60, amino acids 13-190 of SEQ ID NO:60, SEQ ID NO:61, amino acids 24-201 of SEQ ID NO:61, SEQ ID NO:62, amino acids 24-190 of SEQ ID NO:62, SEQ ID NO:63, amino acids 24-179 of SEQ ID NO:63, SEQ ID NO:64, amino acids 24-289 of SEQ ID NO:64, SEQ ID NO:65, amino acids 24-289 of SEQ ID NO:64, SEQ ID NO:65, amino acids 24-278 of SEQ ID NO:65, SEQ ID NO:66, amino acids 24-423 of SEQ ID NO:66, SEQ ID NO:67, amino acids 24-199 of SEQ ID NO:67, SEQ ID NO:68, amino acids 24-401 of SEQ ID NO:68, SEQ ID NO:69, amino acids 24-392 of SEQ ID NO:69, SEQ ID NO:81, amino acids 24-397 of SEQ ID NO:81, SEQ ID NO:83, amino acids 24-383 of SEQ ID NO:83, SEQ ID NO:85, amino acids 24-379 of SEQ ID NO:85, SEQ ID NO:87, amino acids 24-381 of SEQ ID NO:87, SEQ ID NO:89, amino acids 25-212 of SEQ ID NO:89, SEQ ID NO:91, amino acids 25-212 of SEQ ID NO:91, SEQ ID NO:93 and amino acids 13-212 of SEQ ID 93.

The molar ratio of phospholipid to membrane scaffold protein to tissue factor or truncated recombinant tissue factor in the mixture from which the nanoscale particles are prepared can be from about 45:1:0.1 to about 80:1:0.1, desirably about 50:1:0.1 to 70:1:0.1, or 65:1:0.1, where the membrane scaffold protein in MSP1, rTF and a 20:80 molar ratio of PS:PC. Other phospholipid mixtures can comprise net-negative charged phospholipids (including but not limited to PS) present from 1 to 50, from 3 to 50, from 10 to 40 or 20, on a mol % basis, with the balance being net-neutral phospholipids such as phosphatidylcholine (PC) or phosphatidylethanolamine (PE). In the specifically exemplified case where an MSP is larger than MSP1, for example MSP1E3D1, then a higher molar ratio of lipid to MSP is used (from 70:1 to 140:1, from 90:1 to 125:1, or from 115:1). It is understood that if more than one TF (or rTF) molecule per nanoscale particle is acceptable the ratio of that TF or rTF in the preparation mixture can be higher than those specified above.

It is a further object of the present invention to provide tissue factor-containing compositions useful as topical hemostatic agents. These compositions comprise tissue factor incorporated into nanoscale particles as described above. The topical hemostatic agent can be applied to a site of trauma in a human or animal patient, or it can be applied to a surgical incision, a site of post-surgical bleeding, soft tissue trauma or to patient afflicted with hemophilia or thrombocytopenia, in an amount sufficient to control bleeding in the patient. The nanoparticles containing the tissue factor can be attached to or adsorbed onto a solid support such as to a collagen sponge or netting, or microcrystalline collagen powder, which is convenient for use at a surgical or trauma locus. Alternatively, such nanoparticles can be attached to a solid support such as beads or coated onto biologically inert particles or to materials such as ground chitin, chitosan or chitosan derivatives, which can then be applied at a trauma site in a patient or introduced into a solid tumor. In some embodiments, tissue factor is attached to solid supports so that it will not be allowed to migrate freely into and/or throughout the bloodstream, and so that it will not be washed out of a wound by

hemorrhaging blood. Alternatively, the TF-containing particles can be embedded in a slow release composition.

The present invention provides a useful therapeutic composition to supplement a deficiency in the clotting system in a human or animal patient, for example, as a result of a genetic or acquired deficiency, due to chemotherapy, or as a result of inhibitory antibodies. Desirably, the tissue factor and the membrane scaffold protein in the nanoparticles are from the same species as the patient to which the composition is administered.

It is another object of the invention to provide a method for stopping bleeding in a human or animal patient, said method comprising the step of administering a therapeutic composition comprising tissue factor-containing nanoscale particles as described above to the patient in need of said treatment, in an amount sufficient to control or stop bleeding in said patient. Advantageously, the TF-containing particles are immobilized on a solid support so that migration into the bloodstream or loss of the particles from the wound site is limited.

It is further object of the invention to provide a method for killing or inhibiting growth of a tumor in a human or animal patient, said method comprising the step of administering a therapeutic composition comprising tissue factor-containing nanoscale particles as described above to the patient in need of said treatment. The tumor can be a neoplastic growth in the patient. Especially in this method, the particles further comprise a targeting agent which specifically binds to the tumor cells and tissue, including but not limited to a lectin an antibody, single chain body, or an antigen-binding antibody fragment.

It is yet another object of the invention to provide a reagent for use in prothrombin time assays, specifically nanoscale particles comprising tissue factor, as described above.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A (prior art) diagrammatically illustrates the catalytically active, membrane-bound complex of TF and factor VIIa. FIG. 1B diagrammatically illustrates the TF:VIIa complex bound to factor IX or X, which is activated by the proteolytic action of the TF:VIIa complex bound to the membrane.

FIG. 1B (prior art) shows the complex of Factor VIIa, TF and Factor IX or X with the relative position of the membrane.

FIG. 2 (prior art) is a simplified schematic of the clotting cascades, with the two action points of the TF:VIIa complex shown.

FIG. 3 (prior art, Neuenschwander and Morrissey. 1993. Biochemistry 34:13988-13993) shows the response of TF:VIIa to the phospholipid content.

FIG. 4A shows the results of sodium dodecyl sulfate polyacrylamide gel electrophoresis of solubilized TF-containing, MSP1-supported nanoscale disc-like particles purified by HPLC, where those particles were prepared under different conditions. FIG. 4B shows that the ratio of TF:MSP1 is 0.51 in the nanoscale particle preparation.

FIG. 5A shows the results of gel filtration (on a Superdex 200 sizing column) of a crude preparation of nanoscale disc-like particles containing rTF that were prepared using the detergent, deoxycholate. The x-axis is retention time on the column and the y-axis is A280. The nanoscale disc-like particles eluted from the column between 20 and 30 min. FIG. 5B shows the results of gel filtration (on a Superdex 200 sizing column) of the same preparation of nanoscale disc-like particles containing rTF shown in FIG. 5A, after they were enriched for TF-containing nanodiscs by immunoaffinity

chromatography using immobilized HPC4 antibody. Note that the elution profile is more symmetrical and therefore the preparation appears to be more homogeneous than the crude nanoscale particle preparation exhibited in FIG. 5A. FIG. 5C shows the superimposition of the chromatograms from FIG. 5A and FIG. 5B.

FIG. 6 shows the clotting activity of TF-Nanodiscs containing varying proportions of PS (remainder of phospholipid is PC). Clotting time is measured as a function time.

FIG. 7 provides a comparison of the clotting activities of TF-liposomes, TF-Nanodiscs and a mixture of sTF and PCPS vesicles.

FIG. 8 shows the results of SPR (Biacore 3000) analysis of factor X binding to Nanodiscs of varying phospholipid content. Nanodiscs (no TF) were prepared using mixtures of the indicated percent POPS, with the balance being POPC. The Nanodiscs were then immobilized on NTA chips via the oligohistidine tag present as part of MSP1. Factor X was flowed over the immobilized discs starting at 100 seconds (association phase) followed by buffer only at 280 seconds (dissociation phase). Nanodiscs containing 100% POPC employed as a control showed no evidence of factor X binding; they only exhibited the RU shift due to the refractive index of the factor X solution (not shown). Sensorgrams for POPC Nanodiscs run in parallel were therefore subtracted from the sensorgrams presented herein. Traces from top to bottom are 25%, 20%, 15%, 10% and 5% POPS.

FIG. 9 demonstrates that factor VIIa binding to TF-Nanodiscs is faster than to Nanodiscs containing only MSP and phospholipids, as measured by SPR. The upper trace is that of the TF-Nanodiscs and the lower is that for containing only MSP and phospholipids.

#### DETAILED DESCRIPTION OF THE INVENTION

Abbreviations used herein include DOPC, 1,2-dioleoyl-sn-glycero-3-phosphocholine; DOPS, 1,2-dioleoyl-sn-glycero-3-phosphoserine; DPPC, 1,2-dipalmitoyl-sn-glycero-phosphocholine; Gla,  $\gamma$ -carboxyglutamate; Gla-domain, Gla-rich domain; PC, phosphatidylcholine; PCPS, vesicles composed of mixtures of PC and PS, typically 80% PC, 20% PS; PE, phosphatidylethanolamine; PS, phosphatidylserine; SPR, surface plasmon resonance; sTF, soluble TF (extracellular domain of TF); TF:VIIa, the 1:1 complex of TF and factor VIIa; rTF, recombinant truncated TF; PL, phospholipid; POPC, palmitoyl-oleoyl-sn-glycero-3-phosphatidylcholine; POPS, palmitoyl-oleoyl-sn-glycero-3-phosphatidylserine.

Tissue factor (TF) is the integral membrane protein that triggers blood coagulation (Morrissey, J.H. Tissue Factor and Factor VII Initiation of Coagulation. In: Hemostasis and Thrombosis: Basic Principles and Clinical Practice (Fourth Edition), R W Colman, J Hirsh, V J Marder, A W Clowes, and J N George, eds. (Lippincott Williams & Wilkins, Philadelphia), pp 89-101, 2001). TF is composed of two fibronectin type 3 domains, a single membrane-spanning domain, and a short cytoplasmic domain (FIG. 1A). TF is typically expressed on the cell surface. A type I integral membrane protein, TF has its N-terminus located outside the cell and its C-terminus is in the cytoplasm.

Membrane (or Matrix) Scaffold Proteins (MSPs) as used herein may be naturally occurring, recombinant or artificial (do not occur in nature) amphiphilic proteins which self-assemble phospholipids and phospholipid mixtures into nanometer size membrane bilayers. A subset of these nanometer size assemblies are discoidal in shape, and are referred to as nanoscale discs or nanoscale disc-like particles. Typical nanoscale disc-like particles are from about 9 to about 13 nm

in diameter. Such particles comprise about 65 to about 120 phospholipid molecules per side, ringed by one or more amphipathic membrane scaffold proteins, also call matrix scaffold protein. Desirably the MSPs comprise several helical domains, wherein successive helical domains are separated by a punctuation region, made up of one to five amino acids which do not favor helix formation or which tend to stop helix formation of adjacent amino acids. These assembled structures of MSP and phospholipid preserve the overall bilayer structure of normal membranes but provide a system which is both soluble in solution and can be assembled or affixed to a variety of surfaces.

An example of a naturally occurring MSP is apolipoprotein A1. In addition, MSPs can be designed using helical segments of proteins other than human apolipoprotein A-1, for example, apo A-1 of other species, or apo C, apo E, myoglobin or hemoglobin proteins of various species. Helical segments from more than one protein can be combined, with the appropriate punctuation sequences (where the punctuation sequence confers flexibility it can also be called a hinge region or hinge sequence) to form an MSP having the useful properties described herein. See Tables 4-56 below for specifically exemplified MSPs and their coding sequences. Additionally, functional MSPs can be generated by de novo protein design wherein the desired traits of amphiphilic helical protein structures are produced. It is also understood that conservative amino acid substitutions can be made in the sequences specifically exemplified, with the proviso that the self-association function is maintained. Such substitution variants can be termed homologs of the specifically exemplified sequences. Various helix-forming, amphiphilic proteins of interest are described in Bolanos-Garcia et al. (2003) *Progress in Biophys. Molec. Biol.* 83:47-68.

It is also readily within the grasp of the skilled artisan to design other MSPs for packaging tissue factor (natural or truncated) proteins or complexes where the MSP assumes an amphiphilic conformation based on beta sheets, where the amino acid sequence of the protein is punctuated so that there are regions of beta sheet forming portions separated by a flexible region of amino acids. The region of beta sheet-forming sequence is desirably from about 10 to about 30 amino acids, and the punctuation region can include from 3 to 10 amino acids, where there are antiparallel beta sheets in the MSP or from about 10 to about 30 amino acids where the beta sheets are parallel.

Functional MSPs may or may not have punctuation regions between domains of secondary structure within the protein. The punctuation region disrupts regions of secondary structure within a protein. Proline and/or glycine residues are preferred punctuation regions in a protein having helical domains. Besides disrupting a domain with a particular characteristic secondary structure, the punctuation regions can provide flexibility to the structure of a protein, especially in the case of two to three amino acids, desirably including glycine and alanine residues. A punctuation region (or sequence) can include from 5 to 30 amino acids, especially 1 or 2 when the secondary structure elements or domains are alpha helices and 3 to 10, where there are antiparallel beta sheets in the MSP.

Sequences of several apolipoproteins, hemoglobins and myoglobins are available on the internet at the site of The National Center for Biotechnology Information (NCIB), National Institutes of Health. The coding sequences can be found on the internet and used in the construction of artificial MSP coding sequences or the sequences can be tailored to optimize expression in the recombinant host cell of choice. There is a large body of information about codon choice and

nontranslated sequences in the art. Apolipoprotein C sequences include, without limitation, bovine, XP 77416; mouse, AAH 28816; human NP 000032; and monkey, Q28995. Myoglobin sequences include, for example, those of mouse, NP 038621; bovine, NP 776306; rat, NP 067599; and human, NP 005359. Hemoglobin alpha chain sequences include human, AAH 32122 or NP 000549; beta chain sequences include human, NP 000509 or PO20203; rat, NP 150237; mouse NP032246; bovine, NP 776342. Others may be found at the NCBI website and in the scientific literature.

As used herein, amphiphilic and amphipathic are used synonymously in reference to membrane scaffold proteins. An amphiphilic protein or an amphiphilic helical region of a protein is one which has both hydrophobic and hydrophilic regions.

The MSPs used in preparing the nanoscale disc-like particles of the present invention must be amphipathic, with one part of its structure more or less hydrophilic and facing the aqueous solvent and another part more or less hydrophobic and facing the center of the hydrophobic bilayer that is to be stabilized. The elements of secondary structure of the protein generate the hydrophilic and hydrophobic regions in three dimensional space. Examination of the basic biochemical literature reveals two candidate protein structures that can have this required amphipathic character: the helix and the pleated sheet. The MSPs useful in packaging TF into soluble and stable nanoscale discs have a helix as the fundamental amphipathic building block. Each MSP has an amino acid sequence which forms amphipathic helices with more hydrophobic residues (such as A, C, F, I, L, M, V, W or Y, using one letter abbreviations for amino acids as well known to the art) predominantly on one face of the helix and more polar or charged residues (such as D, E, N, Q, S, T, H, K or R and sometimes C) on the other face of the helix. In addition, each helical building block can be punctuated (but punctuation is not necessary) with residues such as proline (P) or glycine (G) periodically, which can introduce flexibility into the overall structure by interrupting the general topology of the helix. In one embodiment, these punctuations occur about every 20-25 amino acids to form "kinks" or to initiate turns to facilitate the "wrapping" of the MSP around the edge of a discoidal phospholipid bilayer. The punctuation region (or sequence) can include from one to 10 amino acids, especially 3 to 10 where there are antiparallel beta sheets in the MSP.

In order to generate smaller belts around the bilayer structure, the overall length of the helical building blocks can be reduced, and the punctuations may be introduced more frequently. The exact amino acid sequence can vary in the positioning and number of the hydrophobic amino acids within the designed linear sequence. Simple models in which either the helical axis is parallel or perpendicular to the normal of the nanoscale disc bilayer can be generated. To generate a disc with a diameter of roughly 10 nm, an MSP comprises about 12 to about 20 or more repeating units having this generalized amphipathic sequence. Preferably, this protein would be composed of amphipathic alpha helices each with a length of between 14 and 25 amino acids, punctuated in the linear sequence by a residue unfavorable for helix formation, such as proline or glycine or a sequence from about 1 to 5 amino acids which does not favor helix formation, which form small helical building blocks that stabilize the hydrophobic core of the phospholipid bilayer. A helix of about 20-25 amino acids (a small helical building block) has a length comparable to the thickness of a membrane bilayer. These small helical segments are linked together (punctuated) with from 0 to about 5, optimally 1 or 2, amino acid residues, especially G or P. To cover the edge of a 10 nm discoidal particle in either of the

"belt" models presented, one would need between 10-20 such helices, with 16 being a useful number. Desirably, the helix contains from about 3 to about 18 amino acids per turn, and the type of helix can be an alpha, pi or 3,10 helix, among others. Helices with three to sixteen, three to eight, desirably three to four, amino acids per turn of the helix are useful in the present invention. An MSP of the present invention can comprise from 50 to 400 turns.

Secondary structure predictions can be determined using 10 programs readily accessible to the art; see, for example, on the internet at the ExPASy proteomics server of the Swiss Institute of Bioinformatics. Guidance in predicting secondary structure is also given in publications such as Chou et al. (1974) *Biochemistry* 13:211, 222; Chou et al. (1978) *Ann. Rev. Biochem.* 47:251-278; Fasman (1987) *Biopolymers* 26(suppl.):S59-S79. Where there is a dimer or higher oligomer of a protein such as a 7-TM membrane protein or where more than one protein is to be incorporated within a single nanoscale disc, for example a reductase and a cytochrome, the 15 MSP used is ideally capable of forming a nanoscale disc-like particle with a diameter greater than 9-10 nm. Many of the examples described herein utilize MSP1, but MSP1T2 and others can be used as well. See, e.g., U.S. Patent Publication 2004/0053384 or U.S. 2005/0182243 and herein below. The 20 MSP used is ideally capable of forming a nanoscale disc-like particle with a diameter greater than 9-10 nm. Many of the examples described herein utilize MSP1, but MSP1T2 and others can be used as well. See, e.g., U.S. Patent Publication 2004/0053384 or U.S. 2005/0182243 and herein below. The 25 increasingly larger nanoscale discs are prepared using increasingly longer MSP sequences, such as MSP1E1, MSP1E2 or MSP1E3, with or without polyhistidine tags (see U.S. 2004/0053384 and U.S. 2005/0182243). MSP1 yields a particle 8.5 nm in diameter. MSP1E1 9.7 nm, MSP1E2, 10.9 nm and MspE3 12.1 nm, when assembled only with phospholipids. Concomitantly, the average number of DPPC (fully saturated phospholipid) molecules assembled in these particles increases from 164±2 for MSP1 particles to 334±12 for MSP1E3 particles. With the unsaturated phospholipids, 30 e.g., POPC (1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine) the numbers of phospholipid molecules for MSP1 particles was 122±10 and for MSP1E3 particles there were 248±24 molecules per disc. Without wishing to be bound by theory, it is believed that using a larger rather than a smaller 35 MSP results in TF-containing nanoscale with improved clotting, antitumor or hemostatic activity.

In an alternative embodiment, the engineered amphiphilic MSP contains regions of secondary structure in three dimensional space, such as parallel or antiparallel beta sheets, with 40 spacer regions of appropriate length to allow association of hydrophobic regions with a target hydrophobic molecule which is protected from the aqueous milieu, and thus stabilized and solubilized.

As specifically exemplified herein, the compositions and 45 methods of the present invention utilize recombinant human tissue factor (rTF) that has been expressed in, and purified from, *Escherichia coli*, although other forms of native tissue factor and recombinant tissue factor can be used. The human rTF used in the experiments described herein differs from 50 wild-type human TF in several ways. First, a small peptide epitope (HPC4 epitope) has been added to the N-terminus of rTF for ease of purification (Rezaie et al. 1992. *Protein Express. Purif.* 3: 453-460). The presence of this epitope on the N-terminus of TF does not affect its function in blood 55 clotting. Second, all but two of the amino acids in the cytoplasmic domain of TF have been deleted (this is also termed des-cyto-TF, dcTF or rTF). The reason for removing most of the cytoplasmic domain is that it causes problems in expression and purification of rTF. The cytoplasmic domain of TF is 60 dispensable for TF clotting functions, so there is no harm in removing this portion of TF. (See FIGS. 1A-1B). Third, rTF expressed in bacteria lacks the N-linked carbohydrate chains 65

normally found on human TF, but the carbohydrate chains are not required for TF procoagulant activity (Paborsky et al. 1989. *Biochemistry* 28:8072-8077).

In order for TF to have optimal activity, it must be embedded into a phospholipid (PL) membrane which contains net-negatively charged phospholipids (Neuenschwander et al. 1995. *Biochemistry* 34, 13988-13993). The most active negatively charged phospholipid is phosphatidylserine (PS), although other phospholipids with a net negative charge, e.g., phosphatidic acid, phosphatidylglycerol or phosphatidylinositol, can be used. However, it is not possible to prepare phospholipid bilayers composed of just PS or other net negatively charged phospholipid. Therefore, PS is mixed with a net-neutral phospholipid, usually phosphatidylcholine (PC). Typically, PS is used in these phospholipid mixtures at levels ranging from 3 to 50 mol %. Most commonly, the phospholipid preparations used in the present invention contain 20 mol % PS and 80 mol % PC. This mixture is referred to herein as PCPS. Other neutral phospholipids, such as phosphatidylethanolamine (PE), can be incorporated into the mixture in place of some of the PC. An example of such a mixture is 10 mol % PS, 40 mol % PE and 50 mol % PC. Phospholipids, purchased from Avanti Polar Lipids, Inc., Alabaster, Ala., are derived from natural sources, although synthetic phospholipids can also be used.

TF functions as the cell-surface binding protein (and essential protein cofactor) for coagulation factor VIIa (FVIIa). FVIIa is a trypsin-like plasma serine protease (see FIG. 2 for clotting cascade). TF binds to FVIIa with high affinity ( $K_d < 50$  pM) and with 1:1 stoichiometry. The TF:VIIa complex is the first enzyme in the extrinsic pathway of the blood clotting cascade, in which TF can be considered the regulatory subunit, and FVIIa the catalytic subunit. TF:VIIa activates the clotting cascade by converting two serine protease zymogens (factors IX and X) into active enzymes (factors IXa and Xa) via limited proteolysis.

The isolated extracellular domain of TF has been expressed and purified using recombinant means. This truncated protein is water-soluble, so it is often referred to as soluble tissue factor (sTF). sTF has drastically reduced procoagulant activity relative to membrane-anchored TF (Neuenschwander and Morrissey. 1992. *J. Biol. Chem.* 267: 14477-14482; Fiore, M. M et al. 1994. *J. Biol. Chem.* 269: 143-149; Paborsky et al. 1991. *J. Biol. Chem.* 266:21911-21916) This underscores the importance of the membrane surface in supporting the enzymatic activity of the TF:VIIa complex.

rTF can be incorporated into supported phospholipid bilayers (nanoscale disc-like particles) in such a way as to retain procoagulant activity. To do this, it was necessary to identify conditions under which TF could be reliably inserted into the nanoscale disc bilayer. In addition, it was necessary to incorporate a mixture of negatively charged phospholipids (in this case, a mixture of PC and PS) into the supported phospholipid bilayer to insure optimal activity, although activity can be modulated (i.e., damped) by increasing the proportion of neutral phospholipids in the core of the particle.

Initial studies were carried out to optimize PCPS nanoscale disc assembly without rTF. Our first optimization studies were aimed at determining which molar ratios of phospholipids (PL) to scaffold protein (MSP1) yielded the most homogeneous preparations of nanoscale discs when using PCPS as phospholipid. A molar ratio of 65:1 (PL:MSP) gave satisfactory result, with quite homogeneous preparations of nanoscale discs, as judged by size-exclusion chromatography.

When preparing TF-Nanodiscs, we typically use molar ratios of phospholipid:MSP1:membTF of 140:2:0.2. Using a

tenfold molar excess of MSP over TF means that, on average, one TF molecule is incorporated for every five Nanodiscs. This ensures that, statistically, the majority of TF-Nanodiscs contain only one TF molecule, but only about 20% of the Nanodiscs contain TF. Pure populations of TF-Nanodiscs are isolated from the Nanodisc mixture as follows. First, the products of the Nanodisc self-assembly reactions are chromatographed by size-exclusion chromatography. A small peak consisting of aggregated material elutes first and is discarded, while Nanodiscs elute between 20 and 27 min on this column and are collected. The Nanodisc fraction, which contains a mixture of Nanodiscs with and without membTF, is then subjected to immunoaffinity chromatography using immobilized HPC4 monoclonal antibody. A small epitope tag incorporated at the N-terminus of membTF facilitates purification from the *E. coli* expression system (Rezaie et al. 1992. *Prot. Expr. Purif.* 3:453-460). The HPC4 antibody binds to this peptide epitope with very high affinity in a  $\text{Ca}^{2+}$ -dependent manner, which allows for gentle elution of the tagged protein using EDTA. The presence of this epitope tag on the N-terminus of TF has no effect on its activity. The HPC4 epitope tag enables isolation of a pure population of TF-Nanodiscs. When re-chromatographed on size-exclusion chromatography, TF-Nanodiscs elute in a much more symmetrical peak whose Stokes diameter is slightly larger than that of Nanodiscs not containing TF (FIG. 5B).

The TF and MSP content of the purified TF-Nanodisc preparation was analyzed by SDS-PAGE followed by Coomassie staining. Densitometry scanning of the lane (calibrated against known quantities of TF and MSP loaded on the same gel) revealed a 0.51 molar ratio of TF:MSP protein. Since each Nanodisc contains two MSP molecules, this equates to 1.02 TF molecules per Nanodisc. We have also quantified the TF content of Nanodisc preparations using a TF ELISA (after detergent solubilization), and by titrating a fixed concentration of factor VIIa with increasing TF-Nanodisc concentrations, using the increase in factor VIIa amidolytic activity as the readout. These approaches all confirm an average of one TF molecule per Nanodisc.

It was demonstrated that we could make Nanodiscs with a phospholipid composition that was known, at least in liposomes, to optimally support blood clotting reactions and that we could incorporate a single molecule of TF per Nanodisc. TF-Nanodiscs function was evaluated in plasma clotting assays using three different preparations of TF-Nanodiscs in which the PS content was varied from 10 to 30 mol % (FIG. 6). The ability of TF-Nanodiscs to shorten the clotting time of plasma in a standard Prothrombin Time (PT) clotting test was tested as a function of TF concentration. This result demonstrated that TF-Nanodiscs do indeed possess procoagulant activity, and furthermore, that 20% PS was optimal. This finding parallels the known PS-dependence of TF procoagulant activity in liposomes (Neuenschwander et al. 1995. *Biochemistry* 34:13988-13993). We next compared the procoagulant activity of TF-Nanodiscs (containing 20% PS) to that of TF-liposomes (also containing 20% PS), and to a mixture of sTF and phospholipid vesicles containing 20% PS (FIG. 7). These results showed that TF-Nanodiscs exhibit appreciable procoagulant activity, although their specific activity is somewhat lower than that of TF-liposomes. Interestingly, the procoagulant activity of TF-Nanodiscs was at least 100-fold higher than that of sTF. Clotting of plasma in PT assays is dependent upon the sequential functioning of two membrane-bound protease-cofactor complexes: The first is the TF:VIIa complex, and the second is the prothrombinase complex (factor Va:factor Xa complex). The procoagulant activity of TF-

Nanodiscs indicates that at least the first reaction (TF:VIIa activation of factor X) can occur on the Nanodisc surface.

A comparison of sodium cholate-solubilized phospholipids vs. sodium deoxycholate-solubilized phospholipids in discs was carried out. The detergent, sodium cholate, has typically been used previously in the preparation of nanoscale disc-like particles. However, recent studies have shown that sodium cholate is a relatively poor detergent for incorporating TF into phospholipid vesicles (Smith and Morrissey. 2004. *J. Thromb. Haemost.* 2: 1155-1162). Sodium deoxycholate, on the other hand, works very well for reconstituting TF into PCPS vesicles. We reasoned that sodium deoxycholate may also be preferable to cholate for incorporating rTF into PCPS-containing nanoscale discs. Our studies confirmed that more homogeneous preparations of PCPS-nanoscale discs were obtained using sodium deoxycholate than sodium cholate, as determined by size-exclusion chromatography. TF, MSP, deoxycholate and phospholipids (especially 80% PC, 20% PS) are incubated together at room temperature. Detergent is removed, for example using Biobeads, and the nanoscale disc-like particles self-assemble so that the TF is biologically active and associated with the particles. Size exclusion chromatography separates unincorporated molecules and aggregates from the nanoscale-disc-like particles. Those disc-like particles containing TF which has been engineered to contain an HPC4 epitope tag can be purified by chromatography over an immunoaffinity column to which HPC4-specific antibody is bound.

While sodium deoxycholate has been used successfully in the preparation of the tissue factor-containing nanoscale particles, other detergents can be used as well. In addition to cholate and deoxycholate, other detergents can be used to assist in the incorporation of tissue factor into phospholipid bilayers, including t-octylphenoxypolyethoxyethanol (Triton X-100, Union Carbide Chemicals and Plastics Co., Inc.), n-octyl-beta-D-glucopyranoside (octylglucoside), octaethylene glycol monododecyl ether ( $C_{12}E_8$ ), and nonaethylene glycol monododecyl ether ( $C_{12}E_9$ ).

Once we had determined the optimal PL:MSP ratio for preparing PCPS-nanoscale discs and had found that sodium deoxycholate was preferable to sodium cholate, we incorporated rTF into PCPS-nanoscale discs. In this experiment, a molar ratio of 65:1:0.1 was used (PL:MSP:rTF) in the preparation mixture. This resulted in apparently homogeneous rTF-PCPS-nanoscale disc assemblies (as judged by size-exclusion chromatography). Further experiments identified an advantageous molar ratio of phospholipid:MSP:TF of 70:1:0.1. Useful range includes from 50:1:0.1 to 80:1:0.1. The proportion of rTF in the mixture from which the nanoscale particles is greater where more rTF molecules on average per particle is acceptable.

Tissue factor activity of rTF containing nanoscale disc-like particles, prepared as described herein, was then studied. The nanoscale discoid particles were fractionated using size-exclusion chromatography, and the various fractions were tested for TF procoagulant activity (the ability to shorten the clotting time of pooled normal human plasma). The shortest clotting times (highest TF activity) corresponded to the major absorption peak on the chromatogram. This indicates that active rTF was successfully incorporated into the nanoscale discs. By contrast, rTF that is not incorporated into a suitable phospholipid surface has negligible activity in this clotting test.

Because the starting ratio of MSP:rTF was 1:0.1 (i.e., a tenfold excess of MSP over rTF), and because there are two MSP molecules per nanoscale disc, it is estimated that even if one obtained 100% incorporation of rTF into discs, only

about 20% of the discs would have rTF in them under these conditions. If the rate of rTF incorporation were less, then even fewer than 20% of the nanoscale discs would contain rTF. Therefore it is desirable to enrich for those nanoscale discs containing rTF. To do so, we took advantage of the HPC4 epitope tag on the N-terminus of rTF to purify the discs that contained rTF. The nanoscale disc preparation was made 5 mM in  $CaCl_2$ , and then the preparation was pumped over an HPC4 column, which column consists of the monoclonal antibody HPC4 attached covalently to AffiGel beads. HPC4 binds tightly, in a calcium-dependent manner, to the HPC4 epitope. HPC4 beads can be readily used to purify recombinant proteins containing this tag (Rezaie et al. 1992. *vide infra*). Purified HPC4 IgG is attached to a N-hydroxysuccinimide ester chromatography matrix (AffiGel, Bio-Rad Laboratories, Hercules, Calif.). HPC4 IgG and HPC4 attached to beads can also be purchased from Roche Applied Science. The nanoscale discs containing rTF bind to the HPC4 column, while "empty" nanoscale discs do not bind. After washing the column to remove any unbound particles, the rTF-containing particles were eluted with buffer containing 10 mM EDTA. Some material eluted from the HPC4 column in this initial experiment; it appeared to be severely aggregated material, as determined by size-exclusion chromatography. The published procedure for purifying rTF and sTF on HPC4 columns includes a step in which the column is washed in a "high-salt" (contains 1 M NaCl) buffer just prior to elution. Without wishing to be bound by theory, it is believed that the 1 M NaCl disrupted the nanoscale discs and promoted aggregation. The HPC4 purification procedure was repeated using a fresh preparation of nanoscale discs, and the HPC4 column was washed with a buffer containing 0.1 M NaCl instead of 1 M NaCl. This was successful and yielded a homogeneous preparation of nanoscale discs that eluted at the correct position when analyzed by size-exclusion chromatography (FIG. 5B).

An experiment was carried out to examine the optimum ratio of MSP:rTF when making rTF-PCPS-nanoscale disc-like particles. As the rTF content was increased, an increasingly large shoulder on the nanoparticle peak was observed when the preparations were subjected to size-exclusion chromatography. The shoulder region elutes before the main nanoscale disc peak, and is therefore apparently larger than nanoscale discs which did not contain TF. TF procoagulant activity eluted approximately with the main disc peak. Without wishing to be bound by any particular theory, it is believed that the shoulder includes aggregated material. A ratio of 1:0.1 MSP:rTF is used routinely, but higher proportions of rTF result in greater average incorporation of rTF per particle.

Some clotting tests were carried out with unoptimized nanoscale disc preparations. The experiments showed that even the unoptimized particles had readily measurable TF procoagulant activity.

More extensive studies with optimized rTF-PCPS-nanoscale disc-like particles were conducted, including measuring the  $K_d$  for binding of factor VIIa to rTF within nanoscale discs. Factor VIIa binds to rTF in PCPS vesicles with a  $K_d < 50$  pM. On the other hand, it binds to sTF, or to rTF in pure PC vesicles, with a  $K_d$  of about 2 to 5 nM. The explanation for the difference in binding affinity between rTF and sTF is that the protein-protein interactions between factor VIIa and TF are sufficient to provide a  $K_d$  of 2 to 5 nM. When factor VIIa binds to rTF in PCPS vesicles, however, there are both protein-protein interactions (between factor VIIa and TF) and protein-phospholipid interactions (between the Gla domain of factor VIIa and negatively-charged phospholipids). The protein-phospholipid interactions are thought to provide additional

binding energy, giving rise to the tighter  $K_d$ . We have observed that factor VIIa binds to rTF-PCPS-nanoscale discs with a  $K_d$  that is also in the pM range, and is only slightly higher than that observed for binding of factor VIIa to rTF in PCPS vesicles. This indicates that rTF-PCPS-nanoscale discs provide an environment for binding factor VIIa that is very similar to rTF incorporated into phospholipid vesicles.

The purpose of this study was to compare the binding and enzyme kinetic properties of recombinant human tissue factor (rTF) incorporated into PCPS-nanoscale discs to rTF incorporated into PCPS vesicles. The rTF used in these studies is recombinant human tissue factor produced in bacteria. rTF was incorporated into PCPS-nanoscale discs as described, and then further purified on an HPC4 column to isolate nanoscale disc-like particles that contain rTF. For comparison purposes, rTF was also incorporated into PCPS vesicles using a Bio-Bead method (Smith and Morrissey. 2004. *supra*). The compositions of the two preparations are given as follows:

- rTF-PCPS-nanoscale discs:
  - 20 mol % phosphatidylserine (PS)
  - 80 mol % phosphatidylcholine (PC)
  - molar ratio of PL:MSP was 65:1
- rTF in PCPS vesicles:
  - 20 mol % PS
  - 80 mol % PC
  - molar ratio of PL:rTF was 8700:1

We determined the apparent  $K_d$  for binding of factor VIIa to rTF in both settings using the TF-dependent enhancement of factor VIIa enzymatic activity as the readout for complex formation. We also determined apparent  $K_m$  and  $k_{cat}$  values for factor X activation by the rTF:VIIa complex using either 500 pM factor VIIa and 5 pM rTF. Factor X concentrations varied from 0 to 800 nM. Table 2 lists the  $K_d$ ,  $K_m$ , and  $k_{cat}$  values obtained.

TABLE 1

Kinetic parameters for Factor X Activation			
	$K_d$ , app (pM)	$K_m$ , app (nM)	$k_{cat}^{-1}$ (s)
rTF in PCPS vesicles	26.4 $\pm$ 2.8	20.2 $\pm$ 1.0	2.4 $\pm$ 0.4
rTF-PCPS-nanoscale discs	65.1 $\pm$ 3.7	68.6 $\pm$ 4.3	1.5 $\pm$ 0.3

As can be seen from this data, factor VIIa bound to rTF very tightly when rTF was incorporated into either nanoscale discs or phospholipid vesicles. Both  $K_d$  values were in the low pM range, in agreement with literature values (Neuenschwander and Morrissey. 1994. *J. Biol. Chem.* 269: 8007-8013). The binding of factor VIIa to rTF was slightly stronger when rTF was in phospholipid vesicles compared to nanoscale discs, but in both cases the binding was sufficiently tight to ensure complete binding of factor VII to rTF at plasma concentrations of factor VII, which is approximately 10 nM (Fair. 1983. *Blood* 62: 784-791).

We have also measured  $k_{cat}$  and  $K_m$  values for the activation of factor X by factor VIIa bound to rTF-PCPS-nanoscale discs; kinetic constants for this reaction are very similar to those of factor VIIa bound to rTF in PCPS vesicles. This is another important test of the ability of factor VIIa bound to rTF within nanoscale discs to function as the activating enzyme of the blood clotting system. A priori, it was unclear whether or not rTF-PCPS-nanoscale discs would be comparable to rTF in PCPS vesicles in supporting factor VIIa proteolytic activity. The lipid bilayer encompassed by the nanoscale discs is relatively small, with only approximately 65

phospholipid molecules per side. This relatively tiny lipid bilayer has to bind both the enzyme (factor VIIa) and the substrate (factor X) onto the same side of the nanoscale disc-like particle in order for catalysis to occur efficiently.

- 5 The  $K_m$  and  $k_{cat}$  values obtained for factor VIIa bound to rTF in PCPS vesicles (given in the table above) are comparable to literature values (Fiore et al. 1994. *supra*). Note that the  $K_m$  values for factor X activation by rTF:VIIa are given as apparent  $K_m$  values because this number depends strongly on 10 the phospholipid concentration used in the assay. The  $K_m$  and  $k_{cat}$  values obtained for the two forms of rTF:VIIa complexes were similar. Both forms of the enzyme exhibited  $K_m$  values that are below the factor X concentration in plasma, indicating that they are both efficient in recognizing factor X as a 15 substrate in plasma. The  $k_{cat}$  value obtained with factor VIIa bound to rTF-PCPS-nanoscale disc-like particles was approximately 1.6-fold lower than the value obtained for factor VIIa bound to PCPS vesicles. This indicates that the rTF:VIIa complex on nanoscale discs is only slightly less 20 active than rTF:VIIa complexes in phospholipid vesicles in converting factor X to Xa. This may be a consequence of the much smaller membrane surface available for binding factor X or Xa in a nanoscale disc of about 10 nm to about 14 nm in diameter, compared to a phospholipid vesicle of some 300 nm 25 diameter.

We have shown TF can be incorporated into Nanodiscs with high yield, and that TF-Nanodiscs can be purified from mixtures containing Nanodiscs lacking TF using immunoaffinity chromatography, providing a highly homogeneous 30 population, containing on average one TF molecule per disc. We also showed that TF-Nanodiscs exhibit significant procoagulant activity, orders of magnitude more active in clotting assays than is the combination of sTF and PCPS vesicles. TF incorporated into Nanodiscs containing PS is highly functional, and the TF-Nanodisc system is capable of supporting 35 membrane-dependent blood clotting reactions.

A priori, it had been uncertain whether or not TF could efficiently initiate clotting when embedded in such small membrane bilayers (approximately 65 phospholipid molecules per side) because TF, as an integral membrane protein, occupies some of the membrane surface, and factor VIIa occupies a bit more, owing to interactions between its Gla domain and phospholipids. We previously quantified the ability of interactions between the factor VIIa Gla domain and PS 40 to stabilize the TF:VIIa complex (Neuenschwander and Morrissey 1994. *J. Biol. Chem.* 269:8007-8013). TF incorporated into pure PC vesicles binds factor VIIa with a  $K_d$  in the nM range, while TF-liposomes containing 20% PS bind factor VIIa with a  $K_d$  in the low pM range. Therefore, we expect that 45 some of the PS molecules in TF-Nanodiscs are bound to factor VIIa's Gla domain when the TF:VIIa complex forms on these discs.

In order for TF:VIIa complexes on TF-Nanodiscs to exhibit 50 significant procoagulant activity, the remaining phospholipid surface must have sufficient room, and sufficient free PS, to reversibly bind protein substrates, which in the case of the clotting assay is factor X. Like factor VIIa, factor X also 55 interacts with negatively charged phospholipids including PS via its Gla domain, and these interactions are important for efficient recognition as a substrate by TF:VIIa. With conventional TF-liposomes, the apparent  $K_m$  for factor X activation by the TF:VIIa complex is in the pM range in the absence of PS, but this falls to the nM range (generally, 20 to 100 nM 60 depending upon the experimental conditions) in the presence of PS. Binding of factor X's Gla domain to PS molecules in the immediate vicinity of TF:VIIa therefore contributes to 65 stabilizing the enzyme-substrate complex, lowering the

apparent  $K_m$ . The TF-Nanodisc system provides a system for analyzing highly localized protein-phospholipid interactions within the immediate vicinity of the membrane-bound enzyme and the binding characteristics of the enzyme, factor VIIa, to TF-Nanodiscs, and also the binding of substrates (factors IX and X) to both Nanodiscs and TF-Nanodiscs.

Two methods are used for quantifying the binding affinity of factor VIIa to TF-Nanodiscs. In the first method, we use the large increase in factor VIIa enzymatic activity as the readout for complex formation (see Neuenschwander and Morrissey. 1994. *supra*). In the second method, surface plasmon resonance (SPR) in a Biacore 3000 instrument is used to quantify association of factor VIIa with TF-Nanodiscs. We have used the first method (change in enzyme activity) to quantify binding of factor VIIa to TF-Nanodiscs in which the supported phospholipid bilayer contained 10, 20 or 30% PS (with the balance being PC). This was compared to binding of factor VIIa to TF in liposomes containing 20% PS using the same method. Table 2 shows that factor VIIa bound to TF-liposomes with a 26.4 pM  $K_d$ , which is in agreement with published values (Neuenschwander and Morrissey. 1994. *supra*). Factor VIIa bound to TF in Nanodiscs with similarly tight  $K_d$  values (in the low pM range) when the TF-Nanodiscs contained 10, 20 or 30% PS. TF in Nanodiscs containing mixtures of PS and PC binds factor VIIa with similarly high affinity with which TF in conventional liposomes binds factor VIIa.

TABLE 2

Binding constants for TF:VIIa complexes		
	Phospholipid	Factor VIIa binding $K_d$ (pM)
TF-liposomes	20% PS, 80% PC	26.4 $\pm$ 2.8
TF- Nanodiscs	10% PS, 90% PC	83.7 $\pm$ 6.0
	20% PS, 80% PC	65.1 $\pm$ 3.7
	30% PS, 70% PC	57.4 $\pm$ 1.3
sTF		about 3000

The TF-dependent enhancement of factor VIIa enzymatic activity is used to quantify the binding affinity of factor VIIa to TF on Nanodiscs of variable phospholipid composition and variable Nanodisc size.

SPR (Biacore) approaches are used to quantify the equilibrium binding affinities as well as association and dissociation rate constants for the binding of clotting factors to Nanodiscs of varying size and composition. Nanodiscs of a desired composition are bound to a sensorchip and then the protein of interest is allowed to flow over the Nanodisc-chip to quantify binding. While other types of immobilized phospholipid membrane surfaces can be prepared on sensorchips, immobilizing Nanodiscs has the advantage that the binding rates of various membrane-binding proteins are measured as they associate with the identical membrane surface that are used in functional studies, in solution, of the catalytic activities of membrane-bound protease complexes.

Nanodiscs can be attached to the sensorchip surface using a variety of approaches, owing to the adaptability built into the recombinant MSPs that encircle them. One approach used successfully is to simply flow Nanodiscs over an NTA chip. The MSP encircling the Nanodiscs have an oligohistidine tag engineered therein for ease of purification, and this same oligohistidine tag can be exploited to immobilize the Nanodiscs onto a Nickel-Nitrilotriacetic acid (NTA) chip. Nickel chelated by nitrilotriacetic acid (NTA) is pre-immobilized on a carboxymethylated dextran matrix of the sensor chip. The

sensor chip can be regenerated with the use of the metal chelating compound (ethylenedinitrilo)tetraacetic acid (EDTA).

To form a more specific linkage to sensor chips, as well as one that could be used in the presence of other divalent cations, such as calcium, which can disrupt the histidine tag binding to nickel, a second method was developed. This attachment involves covalently labeling the MSP with a single-stranded DNA; a biotinylated complementary strand of DNA is bound to a sensor chip with pre-immobilized streptavidin and used to capture the DNA-tagged Nanodiscs. The heterobifunctional linker sulfosuccinimidyl 4-N-maleimidomethyl cyclohexane-1-carboxylate (Sulfo-SMCC) has been used to bind amine-labeled DNA to the thiol group of a cysteine mutant engineered into MSPs. The same DNA has also been attached to carboxyl groups present on MSPs using (1-Ethyl-3-[3-dimethylaminopropyl]carbodiimide hydrochloride) (EDC). Both methods of DNA attachment show specific binding to the complementary strand immobilized on Biacore chips, and the chips are regenerated using a high salt solution containing sodium hydroxide which separates the strands of DNA. The use of these DNA-tagged Nanodiscs has been extended to patterning the discs on DNA chips where highly-fluorescent Nanodiscs have been arrayed and imaged upon binding to microarrayed spots of complementary DNA. When Nanodiscs with oligonucleotide-tagged MSPs are flowed over the sensorchip containing the immobilized complementary oligonucleotide, the discs become immobilized via hybridization between the complementary oligonucleotide sequences. Both approaches work well, and each approach has its own advantages.

An example of immobilizing Nanodiscs on an NTA sensorchip surface is given in FIG. 8. Nanodiscs lacking TF but containing 5 to 25% POPS (with the balance being POPC) were immobilized on NTA Biacore chips and analyzed using a Biacore 3000 instrument. Nanodiscs were loaded onto the chips at a concentration of 50 nM MSP using a flow rate of 5  $\mu$ L/min. Nanodisc loading was monitored by the Biacore sensogram and was stopped when 500 RU of discs were loaded for each sample. We chose to examine factor X binding to these immobilized Nanodiscs. Factor X was injected at a concentration of 1  $\mu$ M using a flow rate of 10  $\mu$ L/min. All portions of the experiment were performed using a buffer solution containing 10 mM HEPES pH 7.4, 150 mM NaCl, 2.5 mM CaCl<sub>2</sub>. Immobilized Nanodiscs containing only POPC were run simultaneously as a control and were subtracted from each sample yielding the binding curves shown in FIG. 8.

FIG. 8 demonstrates that we can successfully use Biacore analysis to study binding of vitamin K-dependent clotting factor (factor X) to immobilized Nanodiscs. As can be seen from the experiment in FIG. 8, factor X binding to the immobilized Nanodiscs depended strongly on the PS content of the supported bilayers, with both the rate and extent of binding being highest at the highest PS contents. Furthermore, dissociation rates were slowest in Nanodiscs containing the highest % PS. This system can be used to quantify the binding of factors VIIa, IX and X to immobilized Nanodiscs containing varying phospholipid compositions. Data obtained from such studies are used to characterize the Nanodisc system and to provide a baseline from which to calculate affinities of both enzyme and substrate to the same membrane microenvironment enclosed within Nanodiscs, with care taken to ensure that apparent binding and dissociation rate constants are not complicated by artifacts arising from mass transport limitations and rebinding effects, for example, by limiting the quantity of Nanodiscs attached to the membrane surface and

examining the effects of altering the flow rate and concentration of the ligand that is being flowed over the sensorchip. It is understood that other strategies can be employed to immobilize the nanoscale particles comprising TF, for example by anchoring via the cytoplasmic tail or truncated cytoplasmic tail of the TF, or via at least one phospholipid molecule.

We have shown that TF-Nanodiscs have substantial procoagulant activity, although their specific activities in clotting assays were somewhat lower than TF-liposomes when compared at the same TF concentrations (FIG. 7). The lower specific activity in clotting assays could be due to lower catalytic efficiency of TF:VIIa complexes on Nanodiscs compared to TF-liposomes, or it could be due to lower ability to support the prothrombinase complex, since both reactions are required in a typical PT clotting assay. We therefore examined, in preliminary experiments, how well the TF:VIIa complex activated factor X on Nanodiscs compared to TF-liposomes with the same phospholipid composition. We already showed that TF-Nanodiscs bound factor VIIa with affinities that were comparable to TF-liposomes (Table 3), so we know that assembly of the TF:VIIa complex is not impaired on Nanodiscs. We therefore addressed the catalytic competence of the TF:VIIa complex toward activation of factor X. Initial rates of factor X activation were quantified using TF:VIIa complexes assembled on liposomes and Nanodiscs as a function of increasing factor X concentration. Initial estimates of the rate constants for factor X activation are given in Table 3.

TABLE 3

Kinetic constants for TF:VIIa complexes			
	Factor X activation		
	Phospholipid	Km (nM)	kcat (s <sup>-1</sup> )
TF-liposomes	20% PS, 80% PC	20.2 ± 1	2.4 ± 0.24
TF-Nanodiscs	10% PS, 90% PC	131.8 ± 12.1	1.4 ± 0.2
	20% PS, 80% PC	68.6 ± 4.3	1.5 ± 0.3
	30% PS, 70% PC	45.2 ± 2.4	1.4 ± 0.3

Remarkably, TF:VIIa complexes assembled on Nanodiscs exhibited kcat values that differed from by less than a factor of two from those of TF:VIIa complexes assembled on liposomes of the same phospholipid composition. TF:VIIa complexes assembled on liposomes exhibited lower apparent Km values than did TF:VIIa complexes assembled on Nanodiscs. There was a trend toward lower Km values as the PS content of the Nanodiscs increased. The higher apparent Km values of TF-Nanodiscs compared with TF-liposomes may explain, at least in part, the somewhat lower specific procoagulant activity of TF-Nanodiscs compared with TF-liposomes in PT clotting assays. In a typical PT assay, the plasma is diluted three-fold in the final clotting reaction. The plasma concentration of factor X is approximately 170 nM, so diluting the plasma in the PT clotting assay reduces its concentration to about 57 nM. This tends to exaggerate the difference in apparent specific activity between TF-liposomes and TF-Nanodiscs; therefore these clotting assays are desirably supplemented with sufficient factor X to keep its final concentration at 170 nM, as a more direct estimation of specific activities that these various TF complexes exhibit in undiluted plasma.

In summary, rTF in nanoscale discs exhibits properties that are surprisingly similar to rTF in large unilamellar vesicles. Factor VIIa bound very tightly to rTF in nanoscale discs, and the rTF:VIIa complex on these discs exhibited enzyme kinetic properties that are surprisingly similar to rTF:VIIa complexes on the surface of phospholipid vesicles. These

studies demonstrate the feasibility of using rTF-PCPS-nanoscale discs as nanoreactors for the activation of plasma factor X to factor Xa, thereby triggering the blood coagulation cascade.

TF (especially as rTF) formulated within nanoscale disc-like particles as described herein can be administered for killing tumors. Previous studies by others have shown that truncated recombinant TF (sTF) can be attached to a bispecific targeting antibody for delivery of sTF to the vascular bed of tumors in experimental animals, resulting in killing of the tumor (Huang et al. 1997. *Science* 275: 547-550). This general targeting strategy appears to work by concentrating sTF at the surface of the tumor vasculature, whereupon sTF triggers the blood clotting cascade locally, forming a thrombus that infarcts the tumor vascular bed and kills the tumor. Delivery of sTF to tumor vascular beds as a means of tumor killing has been successfully employed in a number of other model studies, which have used different targeting molecules for addressing the sTF payload to the tumor vasculature. This includes coupling sTF to antibodies to vascular cell adhesion molecule-1 (VCAM-1) (Ran et al. 1998. *Cancer Res.* 58: 4646-4653); coupling sTF to antibodies to the receptor for vascular endothelial growth factor (VEGFR1) (Brekken and Thorpe 2001. *Anticancer Res.* 21: 4221-4229); coupling sTF to single-chain antibody fragments to fibroblast activation protein (FAP) (Rippmann et al. 2000. *Biochem. J.* 349: 805-812); creating a fusion protein between sTF and portions of fibronectin (Nilsson et al. 2001. *Cancer Res.* 61: 711-716; Liu et al. 2004. *Mol. Cancer Ther.*); and coupling sTF to a catalytic site inhibitor of prostate-specific antigen (PSMA) (Liu et al. 2002. *Cancer Res.* 62: 5470-5475).

TF formulated within nanoscale disc-like particles can be targeted to the tumor vasculature using the same targeting strategies and targeting molecules as have been used to target sTF. This can be accomplished by linking the targeting antibody (or other suitable targeting molecule) directly to rTF within the nanoscale disc-like particles, or it can be accomplished by linking the targeting antibody (or other suitable targeting molecule) directly to the matrix scaffold protein within the nanoscale disc-like particles. Alternatively, targeting can be accomplished by linking the targeting antibody (or other suitable targeting molecule) to the supported phospholipid bilayers within the nanoscale disc-like particles. TF formulated within nanoscale disc-like particles has much higher procoagulant activities than sTF and therefore has superior efficacy in triggering the blood clotting cascade locally once targeted. In addition to the targeting strategies discussed above for targeting sTF to vascular beds, other targeting strategies, both general and specific, have been discussed in the scientific literature which can be utilized for targeting rTF within nanoscale disc-like particles to tumor vasculature, including bispecific antibodies, conjugates with monoclonal antibodies, recombinant single-chain antibodies, and other targeting molecules (Cao and Lam 2003. *Adv. Drug Del. Rev.* 55: 171-197; Trail et al. 2003. *Cancer Immunol. Immunother.* 52: 328-337; Carter 2001. *Nat. Rev. Cancer* 1: 118-129; Gottstein et al. 2001. *Biotechniques* 30: 190-194; Ruoslahti 2002 *Drug Discov. Today* 7: 1138-1143; and Konig et al. 2002. *Endothelium* 9:161-171; Ran et al. 1998. *Cancer Res.* 58:4646-4653).

The TF-containing particles can be administered locally to the tumor, for example, incorporated within slowly dissolved materials, or they can be administered intravenously and targeted to the tumor by incorporating targeting molecules, such as antibodies, single chain tumor-binding antibodies or tumor-binding fragments of antibodies, within the nanoscale particles so that the tumor-binding portion is external to the

disc and free to bind to the target tissue. Desirably, the dose of TF administered should be about 0.5 mg TF incorporated in particles per kg body weight to about 5 mg TF incorporated in particles per kg body weight. It is preferred that a targeting molecule be included within the particle either within the MSP or TF derivative so that clotting activity is not systemic or excessive so as to cause harm to the patient to whom the particles have been administered.

Clinical situations in which excessive bleeding is encountered include surgery or trauma in patients with hereditary or acquired deficiencies in the blood clotting system. Patients with such deficiencies include patients with thrombocytopenia and hemophilia (patients lacking factor VIII or IX), especially patients who have developed inhibitory antibodies against therapeutically administered factor VII or IX. Current therapies for such refractory patients include injection of coagulation factor concentrates or recombinant factor VIIa, which are generally very expensive (Carr and Martin, 2004. Expert Rev. Cardiovasc. Ther. 2: 661-674). Additionally, bleeding (especially surgical bleeding) is sometimes treated using topical hemostatic agents such as collagen sponges, oxidized cellulose, chitosan derivatives, and "fibrin glue" (which contains a mixture of thrombin, fibrinogen and factor XIII). Topical agents containing materials like collagen, cellulose or chitosan are designed to activate blood platelets and stimulate vasoconstriction, both of which can facilitate hemostasis. Additionally, these agents may be used in conjunction with thrombin or "fibrin glue" to stimulate the formation of cross-linked fibrin in order to enhance the formation of hemostatic plugs, thereby helping to control bleeding (Pusateri et al. 2003. J. Trauma 55: 518-526; Soffer et al. 2003. Oral Surg. Oral Med. Oral Pathol. Oral Radiol. Endod. 95: 521-528). TF in a suitable phospholipid membrane is the most potent known initiator of blood clotting and, because of its extremely potent procoagulant activity, would be advantageous to incorporate into topical hemostatic agents in place of thrombin. However, phospholipid vesicles containing TF are relatively unstable and are difficult to immobilize onto solid surfaces. Nanoscale, disc-like particles comprising a membrane scaffold protein, on the other hand, are known to be stable after lyophilization and they can be attached to solid supports via crosslinking between the membrane scaffold protein and sites on the solid support matrices. It would therefore be highly desirable to immobilize nanoscale particles comprising TF in or on topical hemostatic agents in order to stop bleeding.

The present invention provides nanoscale particles comprising TF, which can be applied topically, either alone or administered bound to a solid support, desirably a macroscopic support material, such as a collagen sponge, microcrystalline collagen, chitosan derivatives, cellulose or latex beads, in applications of nanoscale disc-like particles containing TF (or rTF) as described herein for controlling bleeding. An example of a cellulosic material useful in the present context is a gauze used in bandages or wound dressings. An example of topical application of nanoscale particles comprising TF alone is a mouthwash containing a suspension of such particles, which can be used to control bleeding in the oral cavity following dental surgery. In other examples, nanoscale particles comprising TF in which the nanoscale particles are bound to solid support matrices can be applied to surgical sites and sites of trauma in order to activate the blood clotting cascade locally. In these settings, immobilization of nanoscale particles comprising TF has the additional advantage that the TF particle is not washed out of the wound site by hemorrhaging blood, and furthermore, that the TF particle is not readily released back into the circulation of the patient. Similarly, such bound TF can be advantageously adminis-

tered to a patient who does not suffer from a hemophilia but who is experiencing bleeding due to trauma or surgery or any other reason. The target incorporated into the nanoscale disc-like particles can be attached to the surface of a solid support, including collagen sponges or other macroscopic pieces, microcrystalline collagen, or latex beads, in a variety of ways. The first is the easiest and nonspecific way, which is to rely on physisorption to the surface of the material using either hydrophobic or electrostatic forces. More stable incorporation or attachment can be via covalent bonding. This can be accomplished through chemical cross-linking between the scaffold protein and the solid support. There are a number of chemical cross-linking reagents that can be used to form covalent crosslinks between the scaffold protein and the support matrix, including homobifunctional amine reagents such as glutaraldehyde, bis(imido esters), and bis(succinimidyl esters), and heterobifunctional reagents such as 1-ethyl-3-[3-dimethylaminopropyl]carbodiimide hydrochloride. The nanoscale disc-like particles can also be immobilized through incorporation of derivatized phospholipids or fatty acyl chains, or including biotinylated phospholipids, which can then be attached to the support matrix via interaction with immobilized avidin or streptavidin. The TF is bound to a collagen sponge or similar solid support at a density of from about 1 ng to about 100 µg rTF (incorporated in nanoscale particles) per gram (dry weight) of solid support matrix. The use of a cysteine-containing MSP allows the use of a heterofunctional cross linker where one reactive group reacts with a free sulfhydryl to effect bonding the TF particle to the solid material (such as a collagen sponge). Descriptions of immobilization reactions using bifunctional cross linking molecules are given herein.

Alternatively, the particles containing the TF can be injected intravenously and targeted to adhesion molecules that are exposed on activated platelets or to other molecules such as collagen or tissue adhesive proteins that are not normally exposed to blood in intact blood vessels but are exposed to blood at sites of wounds. This can be achieved by binding or crosslinking a targeting antibody or other targeting agent to the MSP with nanoscale particles containing TF, although care must be taken to avoid excessive or uncontrolled clotting factor activation in circulation.

In addition to hemophiliac patients, other patients subject to excessive bleeding can also benefit from the administration, especially local administration, of nanoscale particles containing TF. Victims of accidents or other traumatic injuries or surgical patients, including but not limited to liver surgery patients, can be treated with the particles of the present invention. Other types of patients who can be treated by administration of nanoscale particles containing TF to control bleeding include patients with acquired or congenital coagulopathies including patients with thrombocytopenia, sepsis, liver failure, disseminated intravascular coagulation, and other coagulopathies.

The target incorporated into nanoscale disc-like particles can be attached to a surface, either a sponge or latex bead, in one of three ways. The first, easiest but also non-specific, is to rely on physisorption to the material using either hydrophobic or electrostatic forces. More stable incorporation is via covalent linkages. This can be accomplished through crosslinking with the scaffold protein or through incorporation of labeled phospholipids or fatty acyl chains.

An additional application of the TF-containing nanoscale disc-like particles of the present invention is as a reagent in Prothrombin Time (PT) assays which are employed to screen for defects in the blood clotting system and to monitor patients who are being treated with anticoagulants. This assay

uses a source of TF activity (a thromboplastin reagent) to trigger clotting of blood or plasma in vitro, and the time interval between adding the TF reagent and the formation of the blood or plasma clot is the PT value. Previously, the thromboplastin reagent was simply an extract of homogenized tissue, most commonly animal or human brain or human placenta. More recently recombinant thromboplastins have been developed based on purified recombinant human or rabbit TF that has been reconstituted into suitable phospholipid vesicles. TF-containing nanoscale discs-like particles can be used as the thromboplastin reagent in PT assays. They have the advantages of stability to aggregation in aqueous environments as well as excellent stability of the procoagulant activity of TF in these particles.

TF can be embedded into the phospholipid portion of membrane scaffold protein-supported nanoscale disc-like particles by virtue of the interaction of the membrane-spanning domain of TF with the phospholipid of the particles. The nanoscale particles provide the necessary phospholipid surface to support the TF:VIIa enzymatic activity. Clearly, TF in the nanoscale discs can bind and allosterically activate factor VIIa, because the resultant discs exhibit strong procoagulant activity. It is also clear from the clotting studies that the TF:VIIa complex in the nanoscale particles can proteolytically activate its natural substrate, factor X. The TF in the nanoscale particles provides a unique way to deliver and control TF activity. The procoagulant activity of TF can, for example, be controlled by modulating the content of negatively charged phospholipids in the nanoscale disc-like particles.

To study the half-life in circulation, fluorescein-labeled nanoscale discs, which served as a model for rTF-containing discs, were prepared using MSP1 and phospholipid (PSPC 80:1) and injected intravenously into a rat. Based on measurement of the absorbance at 280 nm, 20.6  $\mu$ M particles (about 255  $\mu$ g particles) were injected in a 0.5 ml bolus. The estimate based on absorbance at 497 nm was 16.7  $\mu$ M particles, with an assumption of 2 molecules fluorescein conjugated per particle. The rats used were about 200 g, with an estimated blood volume of about 13 ml. 0.2 ml aliquots of blood were taken at time intervals after injection. The blood was collected into dry heparin, with a final concentration of heparin of 333 U/ml. The heparinized blood was centrifuged to remove cells, and the emission of fluorescein was measured at 520 nm. The estimated half-life of the particles in circulation was about 5.5 hours. The equation describing the persistence in circulation is  $y = -0.055x + 1.64$ ;  $R^2 = 0.9663$ .

Recombinant tissue factor consists of an extracellular domain, a transmembrane anchor and a truncated cytosolic domain. The truncation increases the homogeneity of the protein by removing the C-terminal portions of the protein which are subject to proteolysis by bacterial enzymes, but this modification does not affect TF activity. Additional modifications to the protein include an N-terminal trafficking peptide and an HPC4 epitope tag. The trafficking peptide directs the expressed protein to the intermembrane space of the recombinant *E. coli* host cell, in which space the peptide sequence is cleaved. The HPC4 epitope allows for affinity purification with  $\text{Ca}^{2+}$  dependent antibody (Rezaie et al., 1992) and does not affect TF activity.

rTF-containing nanoscale disc-like particles can be prepared using cholate and dialysis as follows. A 25 mM lipid mixture containing 80% phosphatidylcholine and 20% phosphatidylserine was solubilized with 50 mM sodium cholate in 10 mM Tris Cl, 150 mM NaCl at pH 8.0. TF, MSP1 and phospholipid (in a ratio of 1:10:1000) were combined and incubated overnight at 37°C. The sample was then dialyzed at

37°C. (10,000 dalton molecular weight cutoff membrane) against buffer containing 10 mM Tris Cl, 150 mM NaCl at pH 8.0 (lacking sodium cholate) for 2 hours. Dialysis was then continued at 400 for an additional 6 hours with buffer changes every 2 hours. The approximately 1 ml sample was then concentrated to <250  $\mu$ l using a YM-10 centrifuge concentrator and injected into a Pharmacia 10/30 Superdex 200 HR gel filtration column. Samples were eluted with buffer identical to that described above (no sodium cholate) at 0.5 ml per minute. Fractions from chromatography were run on an 8-25% gradient SDS polyacrylamide gel to determine apparent size and then checked for coagulation activity.

The activity of TF in several disc fractions was determined by coagulation assays with human plasma. Activity was monitored in fractions 25-28 as the inverse of coagulation time. Activity was highest in fraction 25 at 40 and decreased through fraction 28 at 30 hr<sup>-1</sup>. This is expected from the size chromatogram in that the leading edge of the nanoscale disc peak has a larger effective mass due to the incorporation of TF in the MSP-supported bilayer. This assay thus demonstrates that TF is incorporated into nanoscale discs in an active conformation and that the membrane environment of the nanoscale disc closely mimics that of the native membrane system.

Alternatively, rTF-containing nanoscale disc-like particles can be prepared using deoxycholate and Bio-Beads as follows. Purified phospholipids for these studies were obtained from Avanti Polar Lipids (Alabaster, Ala.) and consisted of egg yolk L- $\alpha$ -phosphatidylcholine (PC) and porcine brain L- $\alpha$ -phosphatidylserine (PS), both of which were provided as solutions in chloroform. Before use, aliquots of the phospholipid solutions were dispensed into a glass test tube and the chloroform was evaporated under a stream of nitrogen. To ensure the removal of any traces of remaining chloroform, the dried-down lipids were placed under high vacuum overnight. The next day, the dried phospholipids were dissolved in a solution of 10.4 mM sodium deoxycholate in TBS buffer (50 mM Tris Cl, 100 mM NaCl, 0.1% sodium azide at pH 7.5) to yield a final concentration of 5.2 mM total phospholipid, with sonication being used to facilitate the complete solubilization of the phospholipids. Typically, the phospholipids were mixed to give 80% PC and 20% PS (abbreviated PCPS). Recombinant human TF (rTF) was combined with the solubilized lipid mixture and incubated for 1 hour at room temperature, after which MSP1 was added and incubated at room temperature for an additional 4 hours. The final reaction mixture contained 8  $\mu$ M rTF and 80  $\mu$ M MSP1, with a molar ratio of rTF to MSP1 to total phospholipid of 1:10:650. The deoxycholate detergent was then selectively removed from the sample by adsorption to Bio-Beads SM2 (Bio-Rad Laboratories, Hercules, Calif.). This was achieved by adding 0.5 mg washed Bio-Beads per ml of sample and incubating for an additional hour at room temperature with gentle agitation on a rocking platform. The Bio-Beads were then removed by filtration through a 0.22  $\mu$ M sterilizing filter, yielding a crude preparation of rTF in nanoscale disc-like particles. The sample was then injected into a gel filtration column (10/30 Superdex 200 HR, Pharmacia, Piscataway, N.J.). Samples were eluted with TBS buffer at 0.5 ml per minute and the elution profile monitored by  $A_{280}$ . Fractions from chromatography were analyzed using an 8-25% gradient SDS polyacrylamide gel to determine apparent size and protein content, and then checked for procoagulant activity. The chromatogram showing elution of rTF incorporated into an excess population of MSP1 nanoscale discs is shown in FIG. 5A.

When desired, the rTF-containing nanoscale discs were further purified by immunoaffinity chromatography using the calcium-dependent antibody, HPC4, essentially as described

(Rezaie, A. R. et al. 1992. *Protein Expr. Purif.* 3:453-460), except that the wash step with 1 M NaCl was not performed because this appeared to disrupt the integrity of the nanodiscs. This purification method takes advantage of the fact that the peptide epitope for the HPC4 antibody was engineered into the N-terminus of recombinant TF. It resulted in an essentially pure population of nanodiscs into which rTF was embedded. When a sample of this highly purified material was rechromatographed on a 10/30 Superdex 200 HR gel filtration column, it eluted as a single, highly homogeneous peak.

The procoagulant activity of TF in disc fractions was determined by clotting assays with pooled human plasma essentially as described (Smith, S. A. and Morrissey, J. H. 2004. *J. Thromb. Haemost.* 2:1155-1162).

Derivatives of MSP that have a single cysteine residue engineered into the "belt" surrounding Nanodiscs have been designed and prepared. These single cysteine residues have successfully been used to attach compounds that react with sulphydryls, allowing the incorporation of desired chemical functionalities onto Nanodiscs at defined spatial locations. A heterobifunctional crosslinker can be attached to these SH groups. An example of such a crosslinker is APDP (N-[4-(p-Azidosalicylamido) butyl]-3'-(2'-pyridylidithio)propionamide), available from Pierce Biotechnology, Inc., Rockford, Ill. TF-Nanodiscs are prepared using these cysteine-containing versions of MSP by the same methodology as for preparing TF-Nanodiscs using conventional MSP. After TF-Nanodiscs are prepared, they are reacted with APDP as follows (with all of the following steps carried out in the dark): First, 3 mg APDP is dissolved in 50  $\mu$ l of dimethylsulfoxide (DMSO). Then, 1 microliter of the APDP/DMSO solution is added to 199  $\mu$ l of phosphate-buffered saline (PBS: 20 mM sodium phosphate, 150 mM NaCl, pH 7.2). The crosslinking reaction is commenced by mixing 0.1 ml of the APDP/PBS solution to 0.3 ml of a preparation of TF-Nanodiscs that had previously been dialyzed into 0.1 M sodium borate buffer, pH 8.4, and allowing the reaction mixture to incubate for 30 minutes at room temperature in the dark. (The TF-Nanodisc preparation in borate buffer can contain up to 2 mg/ml MSP, in order to maintain an excess of APDP over MSP to ensure complete labeling.) Excess unreacted APDP is then separated from labeled TF-Nanodiscs by applying the mixture to a desalting column, such as a D-Salt Execellulose Desalting Column (Pierce Biotechnology, Inc.), that has previously been equilibrated with PBS. TF-Nanodiscs elute in the void volume of such desalting columns, yielding TF-Nanodiscs that are specifically derivatized with APDP on the cysteine residues in the MSP protein.

The APDP-labeled TF-Nanodiscs can be immobilized onto solid supports by photoactivatable crosslinking as follows: The APDP-labeled TF-Nanodiscs are mixed in the dark with the substance to which they are to be crosslinked (for example, collagen sponges). The mixture is then irradiated with an ultraviolet light (302 nm) for 5 minutes at a distance of 3.5 cm at room temperature. Ultraviolet light activates the hydroxyphenyl azide functional group of APDP, allowing it to react covalently and non-selectively with proteins or other organic compounds. Any TF-Nanodiscs that fail to react with the collagen sponge are removed by gentle washing of the sponges with PBS. Once the APD-labeled TF-Nanodiscs have been crosslinked to a solid support, they can be handled in the light.

Examples of publications using APDP to react with free cysteine residues of target proteins, and then crosslinking the derivatized protein to other molecules include, without limi-

tation, Yasui N, and Koide T. *J. Am. Chem. Soc.* 125:15728-15729, 2003 and van Voorst et al. *FEBS Lett.* 486:57-62, 2000.

As an alternative to using MSPs with engineered cysteine residues, conventional TF-Nanodiscs (that is, using conventional MSP that do not contain cysteines) can also be immobilized onto solid supports using amine-reactive crosslinking agents such as Sulfo-SASD (Sulfosuccinimidyl-2-[p-azidosalicylamido]ethyl-1,3'-dithiopropionate), also available from Pierce. Sulfo-SASD is reacted with TF-Nanodiscs in the dark according to the manufacturer's directions, which allows the crosslinker to react with primary amines present on the TF-Nanodiscs. The derivatized TF-Nanodiscs are then reacted with solid supports such as collagen sponges using ultraviolet light as above. The final result is immobilized TF-Nanodiscs. This method is slightly less preferable since the site of attachment of the crosslinker to the TF-Nanodiscs cannot be as precisely controlled as with the combination of MSP containing cysteine residues and a sulphydryl-specific crosslinker such as APDP.

For targeting TF-Nanodiscs to specific anatomic sites in vivo, it is desirable to attach targeting sequences to the TF-Nanodiscs. Targeted TF-Nanodiscs can be used to confer hemostasis or to induce the formation of an occlusive thrombus in the vasculature of a tumor, killing it by infarction. This depends on the in vivo location to which the TF-Nanodiscs are targeted.

Targeting of TF-Nanodiscs to specific in vivo locations can be accomplished in several ways. Monoclonal antibodies specific for desired in vivo targets can be chemically cross-linked to the TF-Nanodiscs using the Sulfo-SASD or APDP crosslinkers as described above. In this case, the crosslinker is first attached to the TF-Nanodiscs using the same methodology described above for immobilizing TF-Nanodiscs on solid supports. Once the crosslinker is attached to TF-Nanodiscs, the purified targeting antibody IgG is added and crosslinking between the TF-Nanodiscs and IgG molecules is initiated by exposing the reaction mixture to ultraviolet light as described above and according to the manufacturer's instructions. Alternatively, fusion proteins between a targeting molecule (such as the antibody combining regions of monoclonal antibodies) and either TF or MSP can be created in order to target TF-Nanodiscs to desired in vivo locations. This can be accomplished as has been described previously by others for making fusion proteins between targeting antibodies and a truncated form of TF (soluble tissue factor, or sTF). In the present invention, however, the membrane-anchored form of TF is used for preparing the fusion proteins. The targeting molecule can be fused either to the N- or C-terminus of membrane TF. As an alternative, the targeting molecule can be fused to either the N- or C-terminus of MSP. The advantages to using fusion proteins with MSP instead of TF is that there is less likelihood of steric hindrance between the TF fusion protein and its ligands (factors VIIa, IX and X) when the targeting molecule is attached to MSP. Alternatively, attaching the targeting molecule to the C-terminus of TF (which is uniquely accessible to the solution in TF-Nanodiscs but not in TF-liposomes) is expected also to avoid problems with steric hindrance, since the targeting molecule is on the other side of the membrane bilayer relative to the ligand binding surface of TF.

Published examples describing how to prepare such targeting molecules using fusion proteins with sTF include Hu et al. 2003. *Cancer Res.* 63:5046-5053; Nilsson et al. 2001. *Cancer Res.* 61:711-6; Rippmann et al. 2000. *Biochem J.* 349 Pt 3:805-812. Examples of specific targeting molecules that can be used to target TF-Nanodiscs include antibody sequences

chTNT-3 and chTV-1 (Hu et al. 2003); antibody sequence scFV(L19) (Nilsson et al. 2001) and antibody sequence scSV OS4 (Rippmann et al. 2000); RGD peptide sequence (for example, the amino acid sequence CDCRGDCFC, using the single amino acid abbreviations) (Hu et al. 2003). Any of these targeting molecules could be fused to the N- or C-terminus of either membrane TF or MSP. An important advantage of targeting TF-Nanodiscs instead of sTF using such fusion proteins or cross-linked proteins is the much greater procoagulant activity of TF-Nanodiscs compared with sTF.

The following provides numerous sequences of specifically exemplified MSPs (including the precursor of the naturally occurring apolipoprotein A1) and their coding sequences which could be employed in preparing the TF-nanoscale disc-like particles of the present invention.

TABLE 4

ProApo A-I coding sequence (SEQ ID NO:1)  
Restriction sites used in cloning are underlined,  
and the translation start and stop signals are  
shown in bold.

CCATGGCCCATTTCTGGCAGCAAGATGAACCCCCCCCAGAGGCCCTGGATC  
GAGTGAAGGACCTGGCCACTGTGTCAGTGGATGTGCTAAAGACAGCGCA  
GAGACTATGTGTCCTTGGAGCTGCCCTTGGGAAACAGCTAAACC  
TAAGAGCTCTTGTGACATGGGAGCAGCTGACATCCCTTGAGCAAGCTG  
GCGAACAGCTCGGCTGTGACCAGGAGTTCTGGGATACTGGAAAAGG  
AGACAGAGGCCCTGAGGCAAGAGATGAGCAAGGATCTGGAGGAGGTGAAGG  
CCAAGGTCAGGCCCTACCTGGAGCACTTCTCAGAAAGAATGGCAGGAGGA  
TGGAGCTCTACCGCCAGAAAGTGGAGCCCTGCGCCAGCTTCAAGAGG  
GGCGGCCGCAAGAGCTGACAGCTCAGAAGAGTGGCCACTTGGGGC  
AGGAGAGTGGCGACCGGGCGCCATGTGAGCGCTGGCACCCATC  
TGGCCCCCTACAGCAGACAGCTGCGCCAGCGCTTGGCGCGCCCTTGGG  
CTCTCAAGGAGAACGGCGCGCCAGACTGGCCGAGTACCAACCCCAAGGC  
CACCGAGCATCTGAGCACGCTCAGCGAGAAGGCCAGCCGCTGAGGACC  
TCCGGCAAGGGCTGCTGCCCTGCTGGAGGACTTCAAGGTGAGCTTCTGA  
GGCCTCTGAGGAGTACACTAAGAAGCTAACACCCAGTAATAAGCTT

TABLE 5

ProApo A-I amino acid sequence (SEQ ID NO:2)

MAHFWQQDDEPPQSPWDRVKLDLATYVVDVLKDSGRDYVSQFEGSALGKQLN  
LKLNDNWDSVTFSKLRERQGLGPVTFQEWFVNLDKETEGLRQEMSKDLEEV  
KAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQLHEQKLSP  
LGEEMRDRARAHDLRALTHAPYSDELRQLRAARLEALKENGARLAEYH  
AKATEHLSLSEKAKPALEDLRQGLLPVLESFKVFSLSALEEYTTKLNTO

TABLE 6

Histidine-tagged MSPII coding sequence  
(SEQ ID NO:3). Restriction sites used in cloning  
are underlined, and the translation start and stop  
signals are shown in bold.

TATACCATGGGCCATCATCATCATCATCATATAGAAGGAAGACTAAAGCT  
CCTTGACAACTGGGACAGCTGAGCTCCACCTTCAGCAAGCTGCGCAAC  
AGCTCGGCCCTGTGACCCAGGAGTCTGGGATAACCTGGAAAAGGAGAC  
GAGGGCTGAGGAGGAGATGAGAAGGATTGGAGGGGGTGAAGGCCAA  
GGTGCAGCCCTACCTGGACGACTTCAGAGAAGTGGCAGGAGGAGATGG  
AGCTCTACGCCAGAAGGTGGAGCGCTGCGCAGAGCTCCAAGGGC  
GCCGCCAGAAGTCGACAGCTCAAGAAGGAGTGGAGCCACTGGGCA  
GGAGATGCGCAGCCGCGCCGCGCCATGGACGCGCTGCGCAGCATC  
TGCCCCCTACAGCGACGAGCTGGCCAGGCTTGCCGCGCCATTGAG  
GCTCTCAAGGAGAACGGCGGCCAGACTGGCGAGTACACGCCAAGGC  
CACCGAGCATCTGAGCACCTCAGCGAGAAGGCCAACCCCGCTCGAGG  
ACCTCCGCCAAGGCCCTGCTGCCCGTCTGGAGAGCTTCAGGTCAGCTC  
CTGAGCGCTCTCAGGAGTACACTAAGAAGCTCAACCCAGTAATAATA  
AGCTTGC

TABLE 7

Histidine-tagged MSP1 amino acid sequence  
(SEQ ID NO:4)

MGGHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDNLEKETEG  
LQEEMSKDLEEVAKAVQPYLDFQKKWQEEMELYRKVEPLRRAELQEGAR  
QKLHLQEKLSPGLEEMRDRARAHVDALRTHLAPSYDELQRQLAARLEAL  
KEENGARRAELYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVUSFLS  
AEEYTKKLNTQ

TABLE 8

Non-Histidine-tagged MSP1 DNA sequence (SEQ ID NO:5).  
Restriction sites used in cloning are underlined,  
and the translation start and stop signals are  
shown in bold.

20 TACCATGGCAAAGCTCTTGACAAGCTGGGACAGCGTGAACCTCCACCTTCA  
GCAAGCTGCGGAACAGCTCGCCCTGTGACCCAGGAGTTCTGGGATAAC  
20 CTGAAAGGAGACAGAGGCTGGAGCAGGAGATGAGCAAGGTCTGGA  
GGAGGTTGAAGGGCAAGGTGCAAGGCCCTACCTGGACGACTTCAGAAGAGT  
GGCAGGAGGAGATGGAGCTTACCGCCAGAAGGTGGAGCCCTGCGGCCA  
GAGCTCAAGAGGGCGCGCAGAAGCTGCACTGCAAGAGAAGTT  
GAGCCCACTGGCGAGGAGATGGCGACCGCCGCGCCCATGGACG  
CGCTGCGCACGATCTGGCCCCCTACAGCGAGACTGCGCAGCGCTTGG  
25 GCGCCGCGCTTGAGCTCTCAAGGAGAACGGCGGGCCAGACTGGCGA  
GTACACGCCAAGGCCACCGAGCATCTGAGCACGCTCAGCGAGAACGCCA  
AACCCCGCTCGAGGAGCTCCGCCAAGGCCCTGCTGCCGTGCTGGAGAGC  
TTCAAGGTCAGCTTCTGAGCGCTCTCGAGGAGTACACTAAGAACGCTCAA  
CACCCAGATAAGCTTGC

TABLE 9

Non-Histidine-tagged MSP1 amino acid sequence  
(SEQ ID NO:6).

35 MAKLLDNWDTSVTSFSLRQELGPVTQEWFWDNLKEKETEGLRQEMSKDLEE  
VKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQLKLHELQEKLS  
PLGEEMRDRARAHVDALRTHLAPYSDELRQLRAARLEALKENGARLAEY  
HAKATEHLSLTSEKAPALEDLRQGLLPVLESFKVSPLSALEEYTTKLLNT  
Q

TABLE 10

45 MSP2 (with histidine tag, without long linker) DNA sequence (SEQ ID NO:7). The translation start and stop codons are in bold type, and the restriction endonuclease recognition sites used in cloning are underlined.

50 TATAACCATGGGCCATCATCATCATCATCATATAGAAGGAAGACTAAAGCT  
CCTTGACAACAGGGACAGCGTGACCTCACCTTCAGCAAGCTGCGCGAAC  
AGCTCGCCCTGTGACCGAGGATCTGGATTAACCTGGAAAAGGAGACAGAGGGCCTGAGGGCAGGAGATGAGCAAGGATCTGGAGGAGGTGAAGGCAAAGGTGAGGCTTACCTGGACGACTTCAGAAAGATGGCAGGAGGAGATGGAGCTCTACCCGAGAGGTGGAGGCCGTGCGCAGAGCTCAAGAGGGCAGCGCAGAAGCTGACGAGCTGCAAGAGAAGCTGAGCCCAGTGGCGA

55 TGGCCCCCTACAGCGACGAGCTGCGCAGCGCTTGCGCGCGCCTTGAG  
GCTCTCAAGGAGACGGCGGCCAGACTGGCGGAGTACCCAGGCAAGGC  
CACCAGGACATCTGAGCACGCTCAGCGAGAAGGCCAGCCGCGCTCGAGG  
ACCTCGCCAAGGGCTGCTGCCGCTGGAGAGCTTCAGGTCAGGTTCTC  
CTGAGGCGCTCGAGGAGTACACTAAGAAGCTAACACCCAGGGTACCCCT  
AAAGCTCTTGCACATCTGGGACAGCTGACCTCCACCTTCAGCAAGCTGC  
60 GCGAACAGCTGGGCCCTGTGGGACCCAGGAGTCTGGGAACTACCTGGAAAG  
GAGACAGGGCCCTGAGGGCAGGAGATGAGCAAGGATCTGGAGGGGGTGA  
GGCCAAGGTGCAAGCCCTACCTGGACGACTTCCAGAAGAAGTGGCAGGGAG  
AGATGGAGCTTACCCAGGAGTGGAGGCGCTGGCCGAGCTCCAA  
GAGGGCGCCGCGCAGAAGCTGCAAGCGCTGCAAGAGAAGCTGACCCACT  
GGGGCAGGGAGATGGCGGACCCGGCGGCCATGTGGACGGCTGGCA  
65 CGCATCTGGCCCCCTACAGCGACGAGCTGCGCAGCGCTTGCGCGCC  
CTTGGAGGCTCTCAAGGAGAACGGCGGCCAGACTGGCCGAGTACACCGC  
CAAGGCCACCGAGGACTCTGAGCACGCTCAGCGAGAAGGCCAGCCGCGC

TABLE 10-continued

MSP2 (with histidine tag, without long linker) DNA sequence (SEQ ID NO:7). The translation start and stop codons are in bold type, and the restriction endonuclease recognition sites used in cloning are underlined.

TCGAGGACCTCCGCCAAGGCTGCTGCCGTGGAGAGCTTCAGGTC  
AGCTTCTGAGGCTCTCGAGGAGTACACTAAGAAGCTAACACCCAGTA  
**ATAAGCTTGC**

TABLE 11

MSP2 (with histidine tag, without long linker) amino acid sequence (SEQ ID NO:8)

MGHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGAR  
QLKHELQEKLSPGLEEMRDRARAHVDALRTHLAPYSDELRQLRAARLEAL  
KENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLS  
AEEYTKKLNTQGTLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKET  
EGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEG  
ARQKLHELQEKLSPGLEEMRDRARAHVDALRTHLAPYSDELRQLRAARLE  
ALKENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFL  
LSALEEYTKKLNTQ

TABLE 12

MSP2L (with histidine tag, with long linker) DNA sequence (SEQ ID NO:9). Translation start and stop codons are in bold type; restriction endonuclease sites used in cloning are underlined.

TACCATGGGCCATCATCATCATCATCATATAGAAGGAAGACTAAAGCTCC  
TTGACAACCTGGACACGGTGACCTCACCCTCAGAAGCTCGCGAACAG  
CTCGGCCCTGTGACCCGGAGTCTGGGATAACCTGGAAAAGGAGACAGA  
GGCCTGAGGAGATGAGCAAGGCTGGAGGAGGTGAAGGGCAAGG  
TGCAGCCCCATACCTGGGACACTGGCAGACTTCAAGAGAAGTGGCAGGAGGAGATGGAG  
CTCTACGGCCAGAGGGTGGAGCCGCGCAGACTGGCGCAGACTCCAAAGGGCGC  
GCGCCAGAGCTGCACGAGCTGCAAGAGAAGCTGAGCCCACTGGCGAGG  
AGATGGCGCGACGGCGCGCGCCATGTGGACCGCTGCGCACGCATCTG  
GCCCCCTACAGCGACGACTGGCGCGCGCCATGGCGCGCGCTTGAGGC  
TCTCAAGGAGAACGGCGGCCAGACTGGCGAGTACCCAGCCAAGGCCA  
CCGAGCATCTGAGCACGCTCAGCGAGAAGGCCAACGCCGCGCTCGAGGAC  
CTCCGCCAAAGGCTGCTGCCGTGCTGGAGAGCTCAAGGTAGCTTCC  
GAGCGCTCTGGAGGAGTACAAAGAGCTAACACCCAGGTACCGGTG  
GAGGTTAGTGGAGGTGGTACCTTAAAGCTCTTGACAACTGGGACAGCTG  
ACCTTACACCTTCAGCAAGCTCGCGAACAGCTGGCCCTGTGACCCAGGA  
GTTCTGGGATAACCTGGAAAAGGAGACAGAGGCCCTGAGGCAGGAGATGA  
GCAAGGATCTGGAGGAGGTAGGGCTAACAGGTGAGCCCTAACGGACGAC  
TTCCAGAAGAAGTGGAGGAGATGAGCTTACCGCCAGAAGGTGAC  
GCCCGCTGCCAGACTTCAAGAGGGCGCCGCCAGAAGCTGCACGAGC  
TGCAAGAGAAGCTGAGCCACTGGCGAGGAGATGCGCGACCGCGCGC  
GCCCCATGGAGCGCTGCGCACGCTTGGCCCTTACAGCGACAGCTG  
GCCCCAGCTGGCCCTGGCCGCCGCCAGCTGAGCTCTCAAGGAGAACGCCG  
CCAGACTGGCCAGTACCCAGCAAGGCCACCGAGCATCTGAGCACGCTC  
AGCGAGAAGGCCAACGCCGCGCTCGAGGACCTCCGCCAAGGCCCTGCTGCC  
CTGTGAGGAGCTCAAGGTCAAGGTCAAGGCTTCTGAGGCCTCTGAGGAGTACA  
CTAAAGAGCTCAACACCCAGTAATAAGCTTGC

TABLE 13

MSP2 (with histidine tag, with long linker, in bold type) amino acid sequence (SEQ ID NO:10).

MGHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGAR  
QLKHELQEKLSPGLEEMRDRARAHVDALRTHLAPYSDELRQLRAARLEAL  
KENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLS  
AEEYTKKLNTQGTGGGGGGTLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
WDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEP

TABLE 13-continued

5 MSP2 (with histidine tag, with long linker, in bold type) amino acid sequence (SEQ ID NO:10).

LRAELQEGARQKLHELQEKLSPGLEEMRDRARAHVDALRTHLAPYSDELR  
QRLAARLEALKENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPV  
10 LESFKVSFLSALEEYTKKLNTQ

TABLE 14

15 MSP1D5D6 DNA sequence (SEQ ID NO:11). Translations start and stop codons are in bold type; restriction endonuclease recognition sites are underlined.

20 TATACCATGGGCCATCATCATCATCATATAGAAGGAAGACTAAAGCT  
CCTTGACAACTGGACACGGCGTGACCTCCACCTTCAGAACGCTGCGCGAAC  
AGCTCGGCCCTGTGACCCAGGAGTCTGGGATAACCTGGAAAAGGAGACA  
GAGGGCCTGAGGAGATGAGCAAGGATCTGGAGGAGGTGAAGGCCAA  
GGTGCAGCCCTACCTGGACGACTTCCAGAAGAAGTGGCAGGAGGAGATGG  
AGCTctaccggcagaaggtggacCCTACAGCAGCAGCTGCGCCAGCG  
TTGGCCGGCGCTTGAGGCTCTCAAGGAGAACGGCGCCAGACTGGC  
CGAGTACACGCCAAGGCCACCGAGCATCTGAGCACGCTCAGCGAGAAGG  
CCAAAACCCGCGCTCGAGGACCTCCGCCAAGGCCCTGCTGCCGTGCTGGAG  
AGCTTCAGGTAGCTCTGAGCCTCGAGGAGTACACTAAGAAGCT  
30 CAACACCCAGTAATAAGCTTGC

TABLE 15

35 MSP1D5D6 amino acid sequence (SEQ ID NO:12).

MGHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQRLA  
ARLEALKENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPVLESF  
KVSFLSALEEYTKKLNTQ

TABLE 16

45 MSP1D6D7 DNA sequence (SEQ ID NO:13). Translation start and stop codons are shown in bold type, and restriction endonuclease recognition sites used in cloning are underlined.

50 TATACCATGGGCCATCATCATCATATAGAAGGAAGACTAAAGCT  
CCTTGACAACTGGACACGGCGTGACCTCCACCTTCAGAACGCTGCGCGAAC  
AGCTCGGCCCTGTGACCCAGGAGTCTGGGATAACCTGGAAAAGGAGACA  
GAGGGCCTGAGGAGATGAGCAAGGATCTGGAGGAGGTGAAGGCCAA  
GGTCGCCCTACCTGGAGCAGTCCAGAAGAAGTGGCAGGAGGAGATGG  
AGCTTACCGCCAGAACGGTGGAGCCGCTGCGCCAGAGCTCAAGAGGGC  
GCGCGCCAGAACGCTGCAAGAGCTGCAAGAGAAGTTGAGGCCAGGCTAGC  
CGAGTACACGCCAAGGCCACCGAGCATCTGAGCACGCTCAGCGAGAAGG  
CCAAAACCCGCGCTCGAGGACCTCCGCCAAGGCCCTGCTGCCGTGCTGGAG  
AGCTTCAGGTAGCTCTGAGCCTCGAGGAGTACACTAAGAAGCT  
55 CAACACCCAGTAATAAGCTTGC

TABLE 17

60 MSP1D6D7 amino acid sequence (SEQ ID NO:14).

MGHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGAR  
QLKHELQEKLSPGLEEMRDRARAHVDALRTHLAPYSDELRQLRAARLEAL  
KENGGARLAEHAKATEHLSTLSEKAKPALEDLRQGLLPVLESF  
KVSFLSALEEYTKKLNTQ

TABLE 18

Full synthetic gene sequence for MSP1 (SEQ ID NO:15). Restriction sites used in cloning are underlined, and the translation start and stop signals are shown in bold.

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ACCATGGTCATCATCATCATCACATTGAGGGACGTGAAAGCTGTT
GGACAATTGGACTCTGTTACGTCTACCTTCAGTAAACTTCGGAAACAC
TGGCCCGCTGACGCAGGAATTCTGGACAAACTCTGGAAAAGACCGAG
GAACTGGGTCAAGGAAATGTCAGGAGATTAGAAGAGGTGAAGGCCAAGGT
TCAGCCATATCTAGATGACTTCAGAAAAATGGCAGGAAGAGATGGAAT
TATATCGTCAAAGGTGGAACCTGGGTGCGGAACTCGCAAGAGGGGCA
CGCCAAAACTCATGAGCTCCAAAGAGCTCAGCCATTAGGCCAGAAGA
ATCGCGGATCGCCGGTGCACATTTGATGTCGACTCCGACTCATTTGG
CGCGTATTCGGATGAACTTCCGAGCTTGGCCGACGTCGAGGCG
CTGAAAGAAAAGGGGGTGGCCGCTTGAGGTACACGGAAAGCAGAC
AGAACACCTGAGCACCTTGAGCAGAAAAGCAGAAACGGCGTGGAGATC
TACGCCAGGGCTATTGCCCTGTCTTGAGACCTTAAAGTCAGTTCTG
TCAGCTCTGGAGAATATACTAAAAGCTGAATACCCAGTAAAGCTTG
G

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The following is the amino acid sequence of a MSP polypeptide in which half repeats are deleted:

TABLE 19

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MSP1D3 (SEQ ID NO:16).

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MGHHHHHHHIEGRKLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG
LRQEMSPLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLQEKLS
PLGEEMRDRARAHVDALRTHLAPYSDELRQLAARLEALKENGGARLAEY
HAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAEYTKKLNT
Q

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TABLE 20

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MSP1D9 (SEQ ID NO:17).

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MGHHHHHHHIEGRKLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG
LRQEMSKDLEEVVAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGAR
QKLHLQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQLAARLEALKENGGARLAEY
KENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAEYTKKLNT
Q

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TABLE 21

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MSP tandem repeat with first half-repeats deleted (MSP2delta1) (SEQ ID NO:18)

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MGHHHHHHHIEGRKLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEG
LRQEMSPLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLQEKLS
PLGEEMRDRARAHVDALRTHLAPYSDELRQLAARLEALKENGGARLAEY
HAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAEYTKKLNT
QGTKLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSPYL
DDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHLQEKLSPLGEEMRDR
ARAHDALRTHLAPYSDELRQLAARLEALKENGGARLAEYHAKATEHLS
TLSEKAKPALEDLRQGLLPVLESFKVSFLSAEYTKKLNTQ

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Plasmids for the expression of extended MSPs were constructed from plasmid for MSP1 described in Bayburt et al. (2002) *Nanoletters* 2:853-856 using a "Seamless" cloning kit (Stratagene) according to the manufacturer recommendations. An alternative N-terminus for MSP1TEV was added by PCR; the primers were designed to include Nco I and Hind III restriction sites. The PCR product was cloned into the pET28a plasmid (Novagen). Truncated mutants of MSP were produced with a Quick-change kit (Stratagene) using the MSP1TEV plasmid as a template. The presence of the desired insertions or deletions and absence of PCR-induced mutations were verified by DNA sequencing.

Expression and purification of the MSP proteins was performed as described herein. Protein purity was characterized by SDS-PAGE and Electrospray Mass Spectrometry; it was found to be greater than 95%. The TEV protease expression system was purchased (Science Reagents, Inc., Atlanta, Ga.) and used after some minor modifications. The sequences of new scaffold proteins were optimized with respect to salt link scores for the belt model of the antiparallel dimer as described in Segrest et al. (1999) *J. Biol. Chem.* 274:31755-31758. At 10 first, the amino acid sequences of the extended mutants were generated so that each of the central helices (from H3 to H7) was inserted sequentially at every position between other central helices, i.e. after H3, H4, H5, and H6, and the number of favorable salt links minus number of unfavorable contacts 15 of the same charges was calculated for all possible configurations of antiparallel dimers in the resulting scaffold protein (Segrest (1999) *supra*). As a result, the insertion mutants were selected as optimal for maximum salt link scores. These 20 extended scaffold proteins, as well as truncated scaffold proteins, also containing different tag sequences at the N. terminus, were engineered in *E. coli* and expressed with a high yield and purified by standard procedures.

With reference to the following protein and DNA sequences, the MSPs we have utilized can be summarized as 25 the following linked structures. Note H1, H2 refer to the sequences of Helix #1 etc. His is a (His)6 tag, TEV is the tobacco viral protease, X is the Factor X (ten) protease site.

TABLE 22

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Amino Acid Sequences of MSP Building Blocks

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30 GLOB	DEPPQSPWDRVKDLATVYDVLKDSGRDYVSQ FEGSALGKQLN (SEQ ID NO:21)
35 HisX	MGHHHHHHHIEGR (SEQ ID NO:20)
HisTEV	MGHHHHHHHDYDIP <b>TENLYFQG</b> (SEQ ID NO:21)
40 Helix 1 (H1) :	L <b>K</b> LLDNWDSVTSTFSKLREQLG (SEQ ID NO:22)
Helix 2 (H2) :	PVTQEFWDNLEKETEGLRQEMS (SEQ ID NO:23)
45 Helix 3 (H3) :	KD <b>L</b> EEV <b>V</b> AKV <b>Q</b> (SEQ ID NO:24)
Helix 4 (H4) :	PY <b>L</b> DDFQKKWQEEEMELYRQKVE (SEQ ID NO:25)
50 Helix 5 (H5) :	PLRAELQEGARQKL <b>HL</b> QEK <b>LS</b> (SEQ ID NO:26)
Helix 6 (H6) :	PLGEEMRDRARAHV <b>D</b> ALRTHLA (SEQ ID NO:27)
55 Helix 7 (H7) :	PYSDEL <b>R</b> QLAARLEALKENG <b>G</b> (SEQ ID NO:28)
Helix 8 (H8) :	ARLA <b>EY</b> HAKATEHL <b>ST</b> LS <b>E</b> KAK (SEQ ID NO:29)
60 Helix 9 (H9) :	PALED <b>L</b> RQGLL (SEQ ID NO:30)
Helix 10 (H10) :	PVLESFKV <b>S</b> FLSA <b>EY</b> TKKLNTQ (SEQ ID NO:31)
65 Helix 0.5 (H0.5) :	STFSKLREQLG (SEQ ID NO:32)

TABLE 22-continued

Amino Acid Sequences of MSP Building Blocks	
Helix 10.5 (H10.5) :	SALEEYTKKLNTQ (SEQ ID NO:33)
Helix 2S (H2) :	PVTQEFWDNLEKETEGLRQEMS (SEQ ID NO:34)

TABLE 23

Sequences encoding the MSP Building Blocks of Table 22.	
HisX	ATGGGTCATCATCATCATCATCACATTGAGGG ACGT (SEQ ID NO:35)
HisTEV	ATGGGTCATCATCATCATCATCACGATT TGATATTCTCTACTACTGAGAATTGTATTTC AGGGT (SEQ ID NO:36)
Helix 1 (H1) :	CTGAAGCTTGGACAATTGGGACTCTGTATC GTCTACCTTCAGTAACACTTCGCGAACACTGG GC (SEQ ID NO:37)
Helix 2 (H2) :	CCCGTGACGCAGGAATTCTGGGACAACCTGG AAAAGAAACCGAGGGACTCGCGTCAAGGAAATGT CC (SEQ ID NO:38)
Helix 3 (H3) :	AAAGATTTAGAAGAGGTGAAGGCCAAGGTTCA G (SEQ ID NO:39)
Helix 4 (H4) :	CCATATCTCGATGACTTCAGAAAAATGGCA GGAAGAGATGGAATATATCGTCAAAAGGTGG AA (SEQ ID NO:40)
Helix 5 (H5) :	CCGCTGCGTGGAACTGCAAGAGGGGACG CCAAAAACTCATGAGCTCAAGAGAACGCTCA GC (SEQ ID NO:41)
Helix 6 (H6) :	CCATTAGGCGAAGGAAATGCGCGATCGCGCCCG TGACATGTTGATCGCACTCCGGACTCATTTGG CG (SEQ ID NO:42)
Helix 7 (H7) :	CCGTATTGCGATGAACTTCGCCAGCGTTGGC CGCACGTCCTGAGGGCTGAAAGAAAACGGGG GT (SEQ ID NO:43)
Helix 8 (H8) :	GCCCCGTTGGCTGAGTACACCGCGAAAGCGAC AGAACACCTGAGCACCTTGAGCGAAAAAGCGA AA (SEQ ID NO:44)
Helix 9 (H9) :	CCGGCGCTGGAAGATCTACGCCAGGGCTTATT G (SEQ ID NO:45)
Helix 10 (H10) :	CCTGTTCTTGAGAGCTTTAAAGTCAGTTTCT GTCAGCTCTGGAAGAAATATACTAAAGCTGA ATACCCAG (SEQ ID NO:46)
Helix 0.5 (H0.5) :	TCTACCTTCAGTAAACTTCGCGAACACTGGG C (SEQ ID NO:47)
Helix 10.5 (H10.5) :	CAGTTTCTGTCAGCTCTGGAAAGAATATACTA AAAAGCTGAATACCCAG (SEQ ID NO:48)
Helix 2S (H2S) :	TCCGTGACGCAGGAATTCTGGGACAACCTGG AAAAGAAACCGAGGGACTCGCGTCAAGGAAATGT CC (SEQ ID NO:49)

Several particular MSP sequences useful in the present invention are the following combinations of the above sequences, as given in Table 24 and others.

TABLE 24

Engineered MSPs Useful in Nanodisc Preparation	
5	MSP1 HisX-H1-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:3)
10	MSP1E1 HisX-H1-H2-H3-H4-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:50)
15	MSP1E2 HisX-H1-H2-H3-H4-H5-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:51)
20	MSP1E3 HisX-H1-H2-H3-H4-H5-H6-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:52)
25	MSP1TEV HisTev-H1-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:53)
30	MSP1NH H1-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:54)
35	MSP1T2 HisTev-H0.5-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:55)
40	MSP1T2NH H0.5-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:56)
45	MSP1T3 HisTev-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:57)
50	MSP1D3 HisX-H1-H2-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:16)
55	MSP1D9 HisX-H1-H2-H3-H4-H5-H6-H7-H8-H10 (SEQ ID NO:17)
60	MSP1D5D6 HisX-H1-H2-H3-H4-H7-H8-H9-H10 (SEQ ID NO:12)
65	MSP1D6D7 HisX-H1-H2-H3-H4-H5-H8-H9-H10 (SEQ ID NO:14)
70	MSP1D3D9 HisX-H1-H2-H4-H5-H6-H7-H8-H10 (SEQ ID NO:58)
75	MSP1D10.5 HisX-H1-H2-H3-H4-H5-H6-H7-H8-H9-H10.5 (SEQ ID NO:59)
80	MSP1D3D10.5 HisX-H1-H2-H4-H5-H6-H7-H8-H9-H10.5 (SEQ ID NO:60)
85	MSP1T4 HisTEV-H25-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:61)
90	Apo A-I GLOB-H1-H2-H3-H4-H5-H6-H5-H6-H7-H8- H9-H10 (SEQ ID NO:2, exclusive of the signal peptide)
95	MSP1T5 HisTev-H2.5-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:62)
100	MSP1T6 HisTev-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:63)
105	MSP1E3TEV HisTev-H1-H2-H3-H4-H5-H6-H4-H5-H6-H7- H8-H9-H10 (SEQ ID NO:64)
110	MSP1E3D1 HisTev-H0.5-H2-H3-H4-H5-H6-H4-H5-H6- H7-H8-H9-H10 (SEQ ID NO:65)
115	MSP2TEV HisTev-H1-H2-H3-H4-H5-H6-H7-H8-H9-H10- GT-H1-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO:66)
120	MSP1N1 His-TEV-H2S-H3-H4-H4-H5-H6-H7-H8-H9 (SEQ ID NO:67)
125	MSP2N1 HisTev-H0.5-H2-H3-H4-H5-H6-H7-H8-H9- H10-GT-H0.5-H2-H3-H4-H5-H6-H7-H8-H9- H10 (SEQ ID NO:68)

TABLE 24-continued

Engineered MSPs Useful in Nanodisc Preparation
MSP2N2 : HisTev-H0-5-H2-H3-H4-H5-H6-H7-H8-H9-H10-GT-H2-H3-H4-H5-H6-H7-H8-H9-H10 (SEQ ID NO: 69)

In addition to these sequences, there are two fusion protein (tandem repeat MSP) constructs of reference. These are composed of two MSP1 constructs linked by a Gly-Thr linker:

MSP2 (MSP1-Gly-Thr-MSP1, SEQ ID NO: 8)  
and

MSP2D1D1  
(MSP1T3-Gly-Thr-H2-H3-H4-H5-H6-H7-H8-H9-H10,  
SEQ ID NO: 70).

Other constructs that can be readily produced include permutations of the above, i.e., MSP1 or a tandemly repeated MSP with either a short or long linker sequence with any combination of the following: hinge deletion, hinge replacement, half-repeat deletion, histidine tag, different linkers for MSP2 analogs.

The coding and amino acid sequences of MSP1T4 are given in Tables 25 and 26, respectively.

TABLE 25

DNA sequence encoding MSP1T4 (SEQ ID NO: 71)
atgggtcatcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatttcagggtaatcgtaatcgccggacaaatcgccgg aaaaaaacccggaggactcgctcggaaatgtccaaagatgttaga gtgaaggccaaatgttcagccatatctcgatgactttcagaaaaatggca ggaaagatggattatctgtccaaaggtggaaaccgctgcgtggaa tgcgaaggggccacggccaaactccatgcgtccaaagaaatcgcc ccattaggcgaaaatcgccgtccggccgtgcacatgttgcact ccggactcttggccgtattcgatqaaattccgcgcgttggcc cacgtctcgaggcgtaaagaaaaacgggggtccgcgttgcgt cacgcgaaacgcgaaacacttgcgcatttgcgcggaaaacgcgaaacc ggcgcgtccggaaatctgcgcggccgttattgcctgttgcgcgg aagtcaagttttgcgtccggaaatataactaaaaacgtgaatacc cag

TABLE 26

Amino acid sequence of MSP1T4 (SEQ ID NO: 61)
MGHHHHHHHHDYDIPPTENLYFQGSVTFQEFWDNLEKETEGLRQEMSKDLEE VKAKVQPYLDDFQKKWQEEEMLYRQKVEPLRAELQEGARQKLHELQEKLS PLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLA YHAKATEHLSTLS EKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLNT Q

In the schematic for MSP1T5, H2.5 indicates the second half of the H2 helical sequence, i.e. the last 33 nucleotides or 11 amino acids is not included in the MSP sequence. The coding and amino acid sequence for this protein is given in Tables 27 and 28, respectively.

TABLE 27

DNA sequence encoding MSP1T5 (SEQ ID NO: 72)
atgggtcatcatcatcatcagcattatgtatccctactactga gaatttgtatttcagggtaatcgtaatcgccggacaaatcgccgg aaaaaaacccggaggactcgctcggaaatgtccaaagatgttaga gtgaaggccaaatgttcagccatatctcgatgactttcagaaaaatggca ggaaagatggattatctgtccaaaggtggaaaccgctgcgtggaa tgcgtccggccgttattgcgttgcgcgg cacaatgttgcgtccggacttgcgtccggatccggatgcact ccgcgcgtccggccgttattgcgttgcgtccggatccggatgcact

TABLE 27-continued

DNA sequence encoding MSP1T5 (SEQ ID NO: 72)
5 tttcagaaaaatggcggaggatggattatatcgtaaaaagggtgg accgtcgctggaaatcgcaaggggggcagccaaaaactccatcgac tccaagaaagctcagggcattaggcgaaagaaatgcgcgatcgcc gcacatgttgcactccggactcattggccgttattcgatgact tcgcccggctttggccgcacgtctcgaggcgctgaaaagaaaacgggg cccgcttggctgactacccacgcggaaacacctgagcaccctg agcggaaaacgcgaaacccggcgctggaaatctacgcgcagg tggcttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc ctaaaaagctgaatacccg

TABLE 28

Amino acid sequence of MSP1T5 (SEQ ID NO: 62)
MGHHHHHHHHDYDIPPTENLYFQGSVTFQEFWDNLEKETEGLRQEMSKDLEE VKAKVQPYLDDFQKKWQEEEMLYRQKVEPLRAELQEGARQKLHELQEKLS PLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLA YHAKATEHLSTLS EKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLNT Q

TABLE 29

DNA sequence encoding MSP1T6 (SEQ ID NO: 73)
15 atgggtcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatttcagggtaatgttagaagggtgaaaggccagg agccatatctcgatgactttcagaaaaatggcggaggatgttaga tatcgtaaaaggtggaaaccgcgtgcgtgcggactcga aaggaggggggcactccggactcggccatattggcgaagaaa ccaaaaactccatgcgcgtccaaagagaactcgcggccatatt tgcgtccggatgcacttcgcgcgttgcgcgcgttgcgg ccgttattggatgcacttcgcgcgttgcgcgcgttgcgg gaaagaaaaacgggggtccgcgttgcgttgcgttgcgt aacacactgagcacttcgcgttgcgttgcgttgcgt ccgcgcggatccggatccggatccggatccggatccgg agctctggaaataactaaaaacgtgaatacccg

TABLE 30

Amino acid sequence of MSP1T6 (SEQ ID NO: 63)
MGHHHHHHHHDYDIPPTENLYFQGSVTFQEFWDNLEKETEGLRQEMSKDLEE VKAKVQPYLDDFQKKWQEEEMLYRQKVEPLRAELQEGARQKLHELQEKLS PLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGARLA YHAKATEHLSTLS EKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLNT Q

MSP1T5 and MSP1T6 discs preps are not homogeneous under all assembly conditions. The results are highly dependent on the particular assembly conditions.

50 In the following MSP construct (MSP1N1), H10 is not included, and two H4 motifs are inserted. The coding and amino acid sequences are given in Tables 31 and 32, respectively. This MSP is designed to increase the number of possible salt bridges on the interhelical interface.

TABLE 31

DNA sequence encoding MSP1N1 (SEQ ID NO: 74)
60 atgggtcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatttcagggtaatgttagaagggtgaaaggccagg aaaaaaacccggaggactcgctcggaaatgtccaaagatgttaga gtgaaggccaaatgttcgcgtccatatctcgatgactttc gaaagatggaaatataatcgtaaaagggtggaaaccatatctcg atctcgatgactttcgcgtccatatctcgatgactttc tgcgtccggccgttattgcgttgcgttgcgttgcgt ccgcgcggatccggatccggatccggatccggatccgg ccaaatgttgcgtccggacttgcgtccggatccggatccgg cacaatgttgcgtccggacttgcgtccggatccggatccgg ccgcgcggatccggatccggatccggatccggatccgg

TABLE 31-continued

DNA sequence encoding MSP1N1 (SEQ ID NO:74)  
ccgttggctgagtaccacgcgaaagcgacagaacacctggacccatgg  
gcggaaaaaggcgaaaccggcgctggaaagatctacggccagggttattg

TABLE 32

Amino acid sequence of MSPIN1 (SEQ ID NO:67)  
MGHHHHHHHHHDYDIPPTTENLYFQGSVTQEFWDNLEKETEGLRQEMSSKDLLEE  
VAKAVQPYLDDFQKKWQEEMELYRQKVEPYLDDFQKKWQEEMELYRQKVE  
PLRAELQGRGARQLKHLQEKLSPLGEEMDRARAHVDALRTHLAPYSDEL  
RQLAARLEALKENGGRALAEYHAKATEHLSTLSEKAKPALEDLRQGLL

The following “extended” MSPs incorporate a cleavable His-tag and use a TEV protease recognition site.

TABLE 33

TABLE 34

Amino acid sequence of MSP1E3TEV (SEQ ID NO:64)

MGHHHHHHHHHYDIDPTTENLYFQQLKLKLLDNWDSVTSTFSKLREQLGPVTQE  
FWDNLEKETEGLRQEMLSKEEVKAKVQPYLDDFQKKWQEEMELYRQKVE  
PLRAELQEGRQLKHLQEKLSPGEEMDRARAHVDALRTHLAPYLD  
QKKWQEEMELYRQKVEPLRAELQEGRQLKHLQEKLSPGEEMDRARAH  
HVDALRTHLAPYSDELRQKLAARLEALKENGARRLAEYHAKATEHLSTS  
EAKAPALEDLRLGGLPVLIESFKVSVFLSALLEYTKKLINTO

TABLE 35

DNA sequence encoding MSP1E3D1 (SEQ ID NO:76)  
(HisTev-H0.5-H2-H3-H4-H5-H6-H4-H5-H6-H7-H8-H9-H10)

---

```
atgggtcatcatcatcatcatcatcacgattatgatattctactactga
gaatttgtattttcagggttctaccctcgataaaactcgagaacaactgg
gccccgtacgcggcggaaattctggacaacctggaaaaaaaacccggaggaa
ctcgctcggaaaatgtccaaagatttagaaaggggtgaaggccaagggttca
ccatatctcgatgactttcagaaaaatggcggaggaaagagatggattat
atcgccaaaagggtggaaaggctgtcgctggaaactcgcaagggggccacgc
aaaaaactccatcgatgacttccaaagagaagctcgccatggcgaagaaaat
ggcgatcgccggccgtgcacatgttgcgtgcactccggactcattggcgc
catatctcgatgactttcagaaaaatggcggaggatggattatata
ctgtccaaaagggtggaaaggctgtcgctggaaactcgcaagggggccacgc
aaaaactccatcgatgacttccaaagagaagctcgccatggcgaagaaaatgc
qdcatcgccggccgtgcacatgttgcgtqactccggactcattggcgc
```

TABLE 35-continued

DNA sequence encoding MSP1E3D1 (SEQ\_ID\_NO: 76)  
(HisTev-H0-5-H2-H3-H4-H5-H6-H4-H5-H6-H7-H8-H9-H10)  
tatccggatgaacctccgcggcagcgttggccgcacgtctcgaggcgctgaa  
agaaaaacgggggtgtccggctgtggctgagatccacgcggaaacgcacagac  
acctgagccaccttggcggaaaaagcggaaacccggcgctggaaagatctacgc  
cagggtttatgcctgttcttggagcgtttaaaagtcaatttctgtcagc  
10 tctggaaagaataactaaaaagctgaatacccg

TABLE 36

15 Amino acid sequence of MSP1E3D1 (SEQ ID NO:65)  
MGHHHHHHHDYDIPPTENLYFQGSTFSKLRQELGPVTQEFWDNLEKETEG  
LRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMLYRQKVEPLRRAELQEGAR  
QKLHELQEKLSPLGLGEEMRDRARAHVDALRTHLAPYLDIFQKKWQEEEMLY  
RQKVEPLRRAELQEGARQKLHELQEKLSPLGLGEEMRDRARAHVDALRTHLAP  
20 YSDELRQLRQLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLR  
QGLLPVLESFKVFSFLSALEYTKKLNTQ

25 A protein corresponding to MSP2 with a N-terminal TEV cleavable His-tag has been designed. The coding and amino acid sequences are given in Tables 37 and 38, respectively.

TABLE 37

DNA sequence encoding MSP2TEV (HisTev-H1-H2-H3-H4-  
H5-H6-H7-H8-H9-H10-GT-H1-H2-H3-H4-H5-H6-H7-H8-H9-  
H10) (SEQ ID NO:77)

---

atgggtcatcatcatcatcatcatcatcagcattatgatattcctactactga  
gaatttgtatttcagggtctaaagctcttgacaactggacagcgtga  
cctccaccccttcaggcaactgctgcgcgaacagctcggccctgtgacccaggag  
35 ttctggggaaactctggaaaaaggagacaggggcttgaggcaggatgag  
caaggatctggaggaggatggaaaggccaaaggcttgaggcaggatgag  
tccagaagaagtggcaggaggatggatctaccggcagaaggctggag  
ccgctgcgcgcagagcttcaagaggggcgcgcgcagaaggctgcacgcagct  
gcaagagaaggctgaggccactttggcggaggatgcgcgcgcgcgc  
ccccatgtggacgcgcgcgcgcacatctggccccctacagcgcagcgc  
40 cggccaggcgttggccggcgccttgaggcttcagaaggaaaggccggc  
cagactggccgagtagaccacgcacccaggccaccgcacatctgagcgc  
gcgcgagaaggccaaaggccgcgcgcaggacccctggcccaaggctgc  
gtgtctggagaggatctcaaggctcaggtcttcgtgacccatctggaggat  
taagaactcaacaccaggatggatccctaaaggctcttgacaactgggaca  
45 gctgtgactccatggccatggccatggccatggccatggccatggcc  
caggatgtctgggataaccctggaaaaaggagacaggaggcttgaggcagg  
gatgacggaaaggatctggaggaggatggggccaaaggctgc  
acgactttcccaagaaggatgtggcaggaggatggagacttaccgcac  
gtggagccgtgcgcgcagagcttcaagaggggcgcgcgcagaaggctgc  
cgactgcacaaaggaaactgtggccactttggcggaggatgcgcgc  
cggccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc  
50 gagactgtggccatggccatggccatggccatggccatggccatggcc  
caggatgtctggccatggccatggccatggccatggccatggcc  
cgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc  
cgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc  
cgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc  
55 cggccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc  
cgctcaggcaaggccaaaggccgcgcgcgcgcgcgc  
ctggccctgtggaggatctcaaggctcaggtcttcgtgacccatctgg  
gtactactaaaggatctcaacaccagg  
60

TABLE 38

Amino acid sequence of HistEV-MSP2 (SEQ ID NO:66)

MGHHHHHHHDYDIPPTENLYFQGLKLLDNWDSVTSTFSKLRQLGPVTQE  
60 FWDNLEKETEGLRQEMSKDLEEVAKAKVQPYLDDPQKKWQEEMELYRQKVE  
PLRAELQEGARQKLHQLKQKLSPGLEEMRDRARAHVDALRTHLAPYSDEL  
RQLRAARLEALKENGARLAEYHAKATEHLSLSEKAPKALEDLRQGLLPP  
VLESFKVFSLFSALEYTTKLNQGTLKLLDNWDSVTSTFSKLRQLGPVTQE  
65 EFWDNLEKETEGLRQEMSKDLEEVAKAKVQPYLDDPQKKWQEEMELYRQKVE  
PLRAELQEGARQKLHQLKQKLSPGLEEMRDRARAHVDALRTHLAPYSDEL  
RQLRAARLEALKENGARLAEYHAKATEHLSLSEKAPKALEDLRQGLLPP  
VLESFKVFSLFSALEYTTKLNQ

New constructs have been designed to produce a “linear dimer” to generate Nanodisics with only a single polypeptide sequence. These are fusions that make use of our knowledge of the parts of the MSP1 sequences which are important and are thus are “MSP2 derivatives”. All have the TEV protease-cleavage His-tag.

TABLE 39

TABLE 40

Amino acid sequence of MSP2N1 (SEQ ID NO:68)

---

MGGHHHHHHHDYDIPPTENLYFQGSTFSKLRQQLGPVTQEFWDNLEKETEG  
LQEOMSKDLEEVKAQVQYLDDFQKKWQEEMELYRQKVEPLRAELQEGAR  
QKLHEQKLSPGLEEMRDRARAHDALRTHLAPYSDELRQRLAARLEA  
KENGQARLAELYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLS  
ALEEYTKLNTQGTFSKLRQQLGPVTQEFWDNLEKETEGLRQEEMSKDLEE  
VKAQVQYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHEQKL  
PLGEEMRDRARAHDALRTHLAPYSDELRQRLAARLEAALKENGQARLA  
YHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKLNT  
Q

TABLE 41

DNA sequence encoding MSP2N2 (SEQ ID NO:79)  
(HisTev-H0.5-H2-H3-H4-H5-H6-H7-H8-H9-H10-GT-H2-H3-  
H4-H5-H6-H7-H8-H9-H10)

---

atgggtcatcatcatcatcatcacgtatgtatccctactactgaa  
gaatttgcattttcagggttctacccatcgatccaaatccggaa  
ggccctgtacgcaggaaattctggacaaacctggaaaaaaaggaa  
ctgcgtcaggaaatgtccaaagatttagaagaggtgaaggccaagg  
tgcgcattatccatcgacttccatcgacggaaatggatattat  
atcgtaaaagggttgcacccgtcgccgtggaaactgcaggatgc  
aaaaactccatcgatgcctaaagagaaggtcgactccggactcat  
ggcgatcgcccccgtgcacatgttgcgcatttgcggacat  
cgatccatcgatgcacttgcgcaggcttgcgcgcacgttc  
aaaggaaacccgggggtgcggccgtgcgtgcacccgcggac  
acacccgtgcacccgtgcggaaaaaaaggcaacccggcgctgc  
gcggggcttattgcctgtcttgcggatccaaatgcgttgc  
gtctggaaataactaaaaaggctgaataccaggatccccgtgc  
gcaggaaatctggacaaacctggaaaaaaaggaaacccggggact  
atgtccaaagatgttagaagaggtgaaggccaaggatccat  
gtatccatcgatccatcgacggaaatggatattatcgtaaaa  
ggtggaaaccggctgcgtgcggaaactgcacggggacgc  
aaaaactccatcgatgcacttgcgcaggatccatcgatccat

TABLE 41-continued

TABLE 42

20 Amino acid sequence of MSP2N2 (SEQ\_ID NO:69)  
MGHHHHHHHDYDIPPTENLYFQGSTFSKLRQQLGPVTQEFDWDNLEKETEG  
LHQEMS KDLDEEVAKVAKVQPYDFFDQKKWQEEMLYRQKVEPLRAELQEARLE  
KQLHELQKLSPLGEEMDRDRARAHDALRTHLAPYSDELRQLRALELQ  
KENGGAARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSPFLS  
AEEYTKLNTQGTPVTQEFDWDNLEKETECLRQEMS KDLDEEVAKVAKVQPYL  
DDFQKKWQEEMLYRQKVEPLRAELQEGARQLKHLQKLSPLGEEMDRDR  
ARAHDALRTHLAPYSDELRQLRALELQENGGAARLAEYHAKATEHLS  
TLSEKAKPALEDLRQGLLPVLESFKVSPFLSALEYTKLNTQ

A further MSP2 derivative (MSP2N3) has been designed to include helices 2-10 following the linker part of the H1 helix sequence. The DNA coding and amino acid sequences are given in Tables 43 and 44, respectively.

TABLE 43

TABLE 44

65 Amino acid sequence of MSP2N3 (SEQ ID NO:81)  
MGHHHHHHHDYDIPPTENLYFQGSTFSKLRQELGPVTQEFDWDNLKEKETEG  
LQEEMS KDLLEEVKAKVQPYLDFFQKQWQEEMELYRQKVPLRAELQEGAR  
QKLHEQKLSPLSPLGEEMRDRARAHVDALRTHLAPYSDELDRQRLAARL  
KENGGARLAELYHAKATEHLSLSEKAKPAELEDQGLLPLVLESFKVSFLS  
ALEEYTKKLNTQGTREQLGPVTQEFDWDNLKEKETEGLRQEEMS KDLLEEVKAK

TABLE 44-continued

Amino acid sequence of MSP2N3 (SEQ ID NO:81)	
VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQLKHLQEKLSPLGE EMDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGARLAEYHAKA TEHLSTLSEKAKPALEDLRQGLLPVLESFKVFSFLSALEEYTKKLNTQ	

Unlike MSP2 and MSP2TEV these proteins self-assemble with lipids at 300:1 to 400:1 molar ratios with preferable formation of significantly bigger particles (Stokes diameter approximately 15.5 nm, corresponding to a calculated diameter assuming discoidal shape of about 17 nm).

Additional dimer sequences (i.e., tandem repeat MSP) have been designed with the fusion region to be composed of two different linkers which have high propensity to form beta-turns (Creighton, Proteins, p. 226). These scaffold proteins are specifically designed to promote the anti-parallel helix-turn-helix structure in Nanodiscs. The constituent scaffold proteins include MSP1T3, as well as the specially designed new scaffold proteins as described herein, MSP1N1 and the circularly permuted MSP2N5 which has a modified sequence of amphipathic helices to optimize the salt bridges formed between two scaffold proteins in the antiparallel helix-turn-helix structure.

The general scheme for a tandem repeat MSP is MSP-Linker-MSP, where linker may be either the Linker 1 or Linker 2 sequence defined below and MSP may be any of the monomeric membrane scaffold proteins previously defined. Linker 1 (Lb1) is composed of 4 amino acids, preferably the sequence Asn-Pro-Gly-Thr (SEQ ID NO:96). Linker 2 (Lb2) is composed of 6 amino acids with one additional residue on both ends to provide more flexibility, preferably the sequence Ser-Asn-Pro-Gly-Thr-Gln (SEQ ID NO:94).

TABLE 45

DNA sequence encoding MSP2N4 (His-TEV-H2S-H3-H4-H5-H6-H7-H8-H9-H10-NPGT-H2-H3-H4-H5-H6-H7-H8-H9-H10) (SEQ ID NO:82)	
atgggtcatcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatccagggttccgtgacgcaggaaattctggacaacctgg aaaaaaaacccaggactcgctcaggaaatgtccaaagattttagaagag gtgaaggccaagggttcagccatatctcgatgactttcagaaaaatggca ggaaagatgatggattatctcgcaaaagggtggaaacggctcgccggaaac tgcaagagggggcagccaaaactccatcgatgactccaaagagaactcagc ccataggcgaaatgcgcgatcgcccggtgcacatgttgcact ccggactcattggcccgatcgatgaaacttcgcgcagcggttggccg cactgtcgaggcgctgaaagaaaacgggggtgcggcgttgcgtgact cgcgcgaaagcagacaaacacctgagccatgttgcggatggatggatc ggcgtggaaatctcgccagggttattgcgttgcgttgcggatggatc aagtcatgttttgcgtcagcttgcggaaatatactaaaactgtaatacc cagaatccaggtaaaaaatcgatcgccaggaaatctggggacaacctggaaaa aaaaacccaggactcgctcaggaaatgtccaaagattttagaagaggta aggccaaagggttcaggccatatctcgatgactttcgcggatggatc gagatgaaattatatctcgcaaaagggtggaaaccgcgtcgccggaaactc agaggggggcagccaaaactccatcgatgactccaaagagaactcagcccat taggcgcgaaatgcgcgatcgcccggtgcacatgttgcact actcattttggcccgatcgatgaaatctccggcaggcttgcgttgcggccacg tctcgaggcgctgaaagaaaacgggggtgcggcgttgcgtgact cgaaaaggccaggaaacacctgagccatgttgcggatggatggatc tctggaaatctcgccagggttattgcgttgcgttgcggatggatc cgttttgcgtcagcttgcggaaatatactaaaactgtaatacc	

TABLE 46

Amino acid sequence of MSP2N4 (SEQ ID NO:83)	
MGHHHHHHHYDIPPTENLYFQGSVTQEFWDNLEKETEGLRQEMSKDLEE VKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQLKHLQEKLS	

TABLE 46-continued

Amino acid sequence of MSP2N4 (SEQ ID NO:83)	
PLGEEMDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGARLAEY HAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVFSFLSALEEYTKKLNT QNPGBTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEE EMELYRQKVEPLRAELQEGARQLKHLQEKLSPLGEEMDRARAHVDALR THLAPYSDELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPA LEDLRQGLLPVLESFKVFSFLSALEEYTKKLNTQ	

TABLE 47

DNA sequence encoding MSP2N5 (His-TEV-H2S-H3-H4-H4-H5-H6-H7-H8-H9-H2) (SEQ ID NO:84)	
atgggtcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatccagggttccgtgacgcaggaaattctggacaacctgg aaaaaaaacccaggactcgctcaggaaatgtccaaagattttagaagag gtgaaggccaagggttcagccatatctcgatgactttcagaaaaatggca ggaaagatgatggattatctcgcaaaagggtggaaacggctcgccggaaac tgcaagagggggcagccaaaactccatcgatgactccaaagagaactcagc ccataggcgaaatgcgcgatcgcccggtgcacatgttgcact ccggactcattggcccgatcgatgaaacttcgcgcagcggttggccg cactgtcgaggcgctgaaagaaaacgggggtgcggcgttgcgtgact cgcgtggaaatctcgccagggttattgcgttgcgttgcggatggatc ggcgtggaaatctcgccagggttattgcgttgcgttgcggatggatc gatctacgcaggcttgcgtcaggccatgttgcgttgcgttgcggatggatc aaaaaaaacccaggactcgctcaggaaatgtccaa	

TABLE 48

Amino acid sequence of MSP2N5 (SEQ ID NO:85)	
MGHHHHHHHYDIPPTENLYFQGSVTQEFWDNLEKETEGLRQEMSKDLEE VKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQLKHLQEKLS PLRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLN PGTKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLDDFQKKWQEE ELYRQKVEPLRAELQEGARQLKHLQEKLSPLGEEMDRARAHVDALRTH LAPYSDELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALE DLRQGLLPVTFQEFWDNLEKETEGLRQEMSKDLEE	

DNA sequence encoding MSP2N6 (His-TEV-H2S-H3-H4-H4-H5-H6-H7-H8-H9-H2) (SEQ ID NO:86)	
atgggtcatcatcatcatcatcagcattatgtatccctactactga gaatttgtatccagggttccgtgacgcaggaaattctggacaacctgg aaaaaaaacccaggactcgctcaggaaatgtccaaagattttagaagag gtgaaggccaagggttcagccatatctcgatgactttcagaaaaatggca ggaaagatgatggattatctcgcaaaagggtggaaacggctcgccggaaac tgcaagagggggcagccaaaactccatcgatgactccaaagagaactcagc ccataggcgaaatgcgcgatcgcccggtgcacatgttgcact actcattttggcccgatcgatgaaatctccggcaggcttgcgttgcggccacg tctcgaggcgctgaaagaaaacgggggtgcggcgttgcgtgact cgaaaaggccaggaaacacctgagccatgttgcggatggatggatc tctggaaatctcgccagggttattgcgttgcgttgcggatggatc cgttttgcgtcagcttgcggaaatatactaaaactgtaatacc	

TABLE 49-continued

DNA sequence encoding MSP2N6 (His-TEV-H2S-H3-H4-  
H4-H5-H6-H7-H8-H9-SNPGTQ-H3-H4-H4-H5-H6-H7-H8-  
H9-H2) (SEQ ID NO:86)

---

```
atatctcgatgactttcgaaaaaaatggcaggaagagatggattatatc  
gtcaaaagggtggaaacccatatctcgatgactttcgaaaaaaatggcagga  
gagatggaaatataatcgcaaaagggtggaaacccgtcgctggaaactgc  
agagggggcacgcacccaaactccatgagcttcagaaagactcagccat  
taggcgaaaatgcgcgatcgcccggtgcacatgttgatgcactccgg  
actcatttggcgcgtattcgatgaaacttcgcgcacgcgtttggccgcac  
tctcgaggcgctgaaaggaaacccgggggtgcgcgttgcgtgactaccacg  
cgaaaggcgacagaacacccgtgacccctgtggcgaaaaaggcgaaacccggc  
ctggaaagatctgcggccagggttattgcggctgtggcgaaatctggga  
caacctggaaaaaaaggaaacccggaggggactcgctcgaggaaatgtcc
```

TABLE 50

MSP derivatives have been prepared with the incorporation of cysteine residues into the scaffold proteins by point mutation. DNA coding and amino acid sequences are given in Tables 51 and 52, respectively. In MSP1RC12' a cysteine residue is incorporated at the last residue in the Factor X recognition site. This mutant is used to prepare fluorescently labeled discs and attach to surfaces or matrices, for example, using heterofunctional cross linker molecules. In MSP1K90C, Lysine90 is replaced by a cysteine. See Tables 53 and 54 for coding and amino acid sequences respectively. In MSP1K152C, Lysine 152 is replaced by cysteine; see Tables 55 and 56.

TABLE 51

TABLE 52

MSP1RC12' Protein Sequence (SEQ ID NO:89)  
MGHHHHHHIEGCLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLKEKETEG  
LRQEMSDLEEVAKQVYLLDFQKKWQEEMBLYRQKVEPLRAELQEGAR  
QKLHELQEKLSPLGEEMRDRARAHVDALRTHIAPYSDELRLQRLAARLEAL  
KENGGARLAEYAHAKATEHLSTLSEKAKPALEDLRQGLLPPVLESFKVSFLS  
AEEYTKKLNTQ

TABLE 53

TABLE 54

20 MSP1K90C Protein sequence (SEQ\_ID\_NO:91)  
MGHHHHHHIEGRLKLDDNWDTSVTSFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMKS DLEEVKAKVQPYLLDFQKKWQEEMELYRKVKEPLRAELQEGAR  
QCLHELQEQLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEL  
KENGGAARLAEHYAKATEHSTLSEKAKPALEDLRLQGLLPVLESFKVSPLS  
AEEYTKLNTQ

TABLE 55

TABLE 56

MSP1K152C Protein sequence (SEQ ID NO:93)  
45 MGHHHHHHHIEGRLKLLDNWDSVTSTFSKLREQLGPVTQEFDWNLEKETEG  
LRQEMS KDLLEEVKAKVQPYLLDFQKKWQEEAMELYRKVKEPLRAELQEGAR  
QLKHLHQLQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEAL  
KENGGAARLAHYAECATEHSLTSEKAKPALEDLRQGLLPVLESFKVSPLS  
AEEYFTKKLNTQ

50 The mutations in MSP1K90 C and in MSP1K152C are located on inter-helical interfaces. Discs were formed in the presence of DTT. The discs are more stable toward temperature-induced irreversible degradation. These are variants of the "Milano" mutations.

55 In addition to these sequences, there are two fusion protein constructs of reference. These are composed of two MSP1 constructs linked by a Gly-Ser linker: MSP2 (MSP1-Gly-Thr-MSP1, SEQ ID NO:8) and MSP2D1D1 (MSP1T3-Gly-Thr-H2-H3-H4-H5-H6-H7-H8-H9-H10, SEQ ID NO:70).

60 Other constructs that can be readily produced include permutations of the above, i.e. MSP1 or MSP2 or MSP2a with any combination of the following: hinge deletion, hinge replacement, half-repeat deletion, histidine tag, different linkers for MSP2 analogs.

65 To express MSP proteins, the nucleic acid constructs were inserted between the NcoI and HindIII sites in the pET28 expression vector and transformed into *E. coli* BL21(DE3).

Transformants were grown on LB plates using kanamycin for selection. Colonies were used to inoculate 5 ml starter cultures grown in LB broth containing 30 µg/ml kanamycin. For overexpression, cultures were inoculated by adding 1 volume overnight culture to 100 volumes LB broth containing 30 µg/ml kanamycin and grown in shaker flasks at 37°C. When the optical density at 600 nm reached 0.6-0.8, isopropyl-β-D-thiogalactopyranoside (IPTG) was added to a concentration of 1 mM to induce expression and cells were grown 3-4 hours longer before harvesting by centrifugation. Cell pellets were flash frozen and stored at -80°C.

Purification of histidine-tagged MSPs was carried out as follows. A frozen cell pellet from 1 liter of expression culture was resuspended in 25 milliliters of 20 mM Tris HCl pH 7.5 containing 1 mM phenylmethylsulfonyl fluoride. Triton X-100 (t-octylphenoxypolyethoxyethanol) was added from a 10% (w/v) stock in distilled H2O to a final concentration of 1%. The resuspended cells were sonicated on ice at 50% duty cycle at a power setting of 5 for four cycles of 1 minute on, 5 minutes off with a Branson probe sonifier. The resulting lysate was centrifuged for 30 minutes at 30,000 rpm in a Beckman Ti 45 rotor in an ultracentrifuge. The resulting supernatant was filtered through a 0.22 µm nylon syringe filter. The salt concentration was adjusted to 0.5 M from a 4 M NaCl stock in water and applied to a 5 ml Hi-Trap nickel loaded column (Pharmacia, Piscataway, N.J.).

For His-tagged-MSP1, the column is washed with 20 ml buffer (10 mM Tris pH 8, 0.5 M NaCl) containing 1% Triton X-100, followed by 20 ml buffer+50 mM sodium cholate, and then 20 ml buffer and 20 ml 100 mM imidazole in buffer. The His-tagged polypeptide is eluted with 15 ml 0.5 M imidazole in buffer.

For His-tagged-MSP2, the column is washed with 20 ml buffer (10 mM Tris pH 8, 0.5 M NaCl) containing 1% Triton X-100; 20 ml buffer+50 mM cholate; 20 ml buffer; 20 ml 35 mM imidazole in buffer. The His-tagged polypeptide is then eluted with 15 ml 0.5 M imidazole in buffer, and the purified protein is dialyzed against 10 mM Tris pH 8, 0.15 M NaCl using a 10,000 MW cutoff cellulose dialysis membrane.

The amino acid sequence of the recombinant TF is given in Table 57; see also SEQ ID NO:95. The mature rTF lacks the 22 N-terminal amino acids. The HPC4 epitope which allows immunoaffinity purification is at amino acids 23-35. The TF extracellular domain is amino acids 36-254; the transmembrane domain which inserts into the phospholipid bilayer of the disc-like nanoscale particles occurs at amino acids 255-277; and amino acids 278-279 are the remnants of the cytoplasmic domain (most of which has been deleted). Expression of this rTF is carried out as described in Rezaie et al. 1992. Protein Expr. Purif. 3:453-460, 1992 and Smith S A and Morrissey J. H. 2004. J. Thromb. Haemost. 2:1610-1616. In general, although TF may not be specified as rTF, TF incorporated into nanoscale disc-like particles is the truncated rTF.

All references cited herein are hereby incorporated by reference to the extent there is no inconsistency with the present disclosure; and the references cited herein reflect the level of skill in the relevant arts.

In general the terms and phrases used herein have their art-recognized meaning, which can be found by reference to standard texts, journal references and contexts known to those skilled in the art.

As used herein, "comprising" is synonymous with "including," "containing," or "characterized by," and is inclusive or open-ended and does not exclude additional, unrecited elements or method steps. As used herein, "consisting of" excludes any element, step, or ingredient not specified in the claim element. As used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim. Any recitation herein of the term "comprising", particularly in a description of components of a composition or in a description of elements of a device, is understood to encompass those compositions and methods consisting essentially of and consisting of the recited components or elements. The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations not specifically disclosed herein.

The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition (see e.g. Fingl et al., in *The Pharmacological Basis of Therapeutics*, 1975, Ch. 1 p. 1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions, or to other adverse effects. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the disorder of interest will vary with the severity of the condition to be treated and to the route of administration. The severity of the condition may, for example, be evaluated, in part, by standard prognostic evaluation methods. Further, the dose and dose frequency may also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above also may be used in veterinary medicine.

Depending on the specific conditions being treated and the targeting method selected, such agents may be formulated and administered systemically or locally. Techniques for formulation and administration may be found in Alfonso and Gennaro (1995). Suitable routes may include, for example, oral, rectal, transdermal, vaginal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, or intramedullary injections, as well as intrathecal, intravenous, or intraperitoneal injections.

TABLE 57

Amino Acid Sequence of rTF (see also SEQ ID NO:95)
1 MKYLLPTAAA GLLLAAQPA MAAEDQVDPK LIDGKSGTTN TVAAYNLWK STNFKTI
EW
61 EPKPVNQVYT VQ1STKSGDW KSKCFYTTDT ECDLTDEIVK DVKQTYLARV FSYPAGNVES
121 TGSAGEPLYE NSPEFTPYLE TNLGQPTIQS FEQVGTKVNV TVEDERTLVR RNNNTFLSLRD
181 VFGKDLIYTL YYWKSSSSKG KTAKTNTNEF LIDVDKGENY CFSVQAVIPS RTVNRKSTD
241 PVECMGQEKG EFREIFYIIG AVVFVVIILV IILAIISLHK

45

For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular those formulated as solutions, may be administered parenterally, such as by intravenous injection. Appropriate compounds can be formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated for oral administration may be in the form of tablets, dragees, capsules, or solutions, including those formulated for delayed release or only to be released when the pharmaceutical reaches the small or large intestine.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levitating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

46

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions to exclude any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by particular embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

Although the description herein contains certain specific examples and information, these should not be construed as limiting the scope of the invention but rather as merely providing illustrations of some of the presently preferred embodiments of the invention. For example, thus the scope of the invention should be determined by the appended claims and their equivalents, rather than by the examples given.

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SEQUENCE LISTING

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<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens

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ttgaaggctc cgccttggga aaacagctaa acctaaagct ccttgacaac tgggacagcg     180
tgacctccac cttcagcaag ctgcgcgaac agctcgccc tgtgaccag gagttctggg     240
ataacctgga aaaggagaca gagggcctga ggcaagagat gagcaaggat ctggaggagg     300
tgaaggccaa ggtcagccc tacctggacg acttccagaa gaagtggcag gaggagatgg     360
agctctaccg ccagaaggtg gagccgctgc gcgcagact ccaagaggc gcgcgcaga     420
agctgcacga gctgcaagag aagctgagcc cactggcga ggagatgcgc gaccgcgc     480
gcgcctatgt ggacgcgctg cgcacgcata tggcccccta cagcgcacgag ctgcgcacg     540
gcgtggccgc gcgcctttag gctctcaagg agaacggcgg cgccagactg gccgagtacc     600
acgccaaggc caccgagcat ctgagcacgc tcagcgagaa ggccaagccc gcgcctcgagg     660
acctccgcca aggctgctg cccgtgctgg agagcttcaa ggtcagctc ctgagcgctc     720
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&lt;211&gt; LENGTH: 250

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 2

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Met Ala His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp Asp
1           5           10          15

```

```

Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp Ser
20          25          30

```

```

Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln
35          40          45

```

```

Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe
50          55          60

```

```

Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp
65          70          75          80

```

```

Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp
85          90          95

```

```

Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln
100         105         110

```

```

Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro
115         120         125

```

```

Leu Arg Ala Glu Leu Gln Glu Ala Arg Gln Lys Leu His Glu Leu
130         135         140

```

```

Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg
145         150         155         160

```

```

Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu
165         170         175

```

```

Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly
180         185         190

```

```

Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser
195         200         205

```

```

Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly
210         215         220

```

```

Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu

```

-continued

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 225                    230                    235                    240

 Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 245                    250

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<400> SEQUENCE: 3

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tgggacacgc tgacctccac cttagcgaag ctgcgcgaac agctcgccccc tggaccagg    120
gagttctggg ataacctgga aaaggagaca gagggcctga ggcaggagat gagcaaggat    180
ctggaggagg tgaaggccaa ggtgcagccc tacctggacg acttccagaa gaagtggcag    240
gaggagatgg agctctaccg ccagaagggtg gagccgcgtgc ggcgcagact ccaagaggc    300
gcccgcgcaga agctgcacga gctgcaagag aagttgagcc cactggcgcg ggagatgcgc    360
gaccgcgcgc gcgcgcgcgc gacgcgcgtg cgcacgcac tggccccccta cagcgcacgag    420
ctgcgcgcgc gcttggccgc gcgccttgcg gctctcaagg agaacggccgg cgccagactg    480
gcccgcgcgc acgcgcaggc caccgagcat ctgagcgcgc tcagcgcagaa ggccaaaccc    540
gcccgcgcgc acctccgcgcaggc caccgagcat ctgagcgcgc tcagcgcagaa ggccaaaccc    600
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 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1

<400> SEQUENCE: 4

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1                    5                    10                    15
  
```

```

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
20                    25                    30
  
```

```

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
35                    40                    45
  
```

```

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
50                    55                    60
  
```

```

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
65                    70                    75                    80
  
```

```

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
85                    90                    95
  
```

```

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
100                    105                    110
  
```

```

Leu Gly Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
115                    120                    125
  
```

```

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
130                    135                    140
  
```

```

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
145                    150                    155                    160
  
```

```

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
165                    170                    175
  
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-continued

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu  
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Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys  
 195 200 205

Leu Asn Thr Gln  
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 cctgaggcgagatgagca agggatcttga ggaggtgaag gccaagggtgc agccctacct 180  
 ggacgacttc cagaagaagt ggcaggagga gatggagctc taccggcaga aggtggagcc 240  
 gctgcgcgca gagctccaag agggcgcgcg ccagaagctg caccgagctgc aagagaagtt 300  
 gagcccactg ggcgaggaga tgccgcgaccg cgccgcgcgc catgtggacg cgctgcgcac 360  
 gcatctggcc ccctacagcg acgagctcgcc ccagcgcttgc gccgcgcgc ttgaggctct 420  
 caaggagaac ggccgcgcga gactggccga gtaccacgccc aaggccaccc agcatctgag 480  
 cacgctcagc gagaaggcca aaccgcgcgt cgaggacctc cgccaaaggcc tgctgcccgt 540  
 gctggagagc ttcaagggtca gcttcctgag cgctctcgag gagtacacta agaagctcaa 600  
 cacccagtaa taagcttgc 619

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Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn  
 20 25 30

Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu  
 35 40 45

Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140

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Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160

Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 195 200

<210> SEQ ID NO 7

<211> LENGTH: 1260

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Nucleotide sequence encoding MSP2 with short linker

<400> SEQUENCE: 7

tataccatgg gccatcatca tcatacatcat atagaaggaa gactaaagct ccttgacaac 60

tgggacacgc tgacctccac cttagcaag ctgcgcgaac agctcgccc tggaccag 120

gagttctggg ataaccttggaa aaaggagaca gagggcctga ggcaggagat gagcaaggat 180

ctggaggagg tgaaggccaa ggtgcagccc tacctggacg acttccagaa gaatggcag 240

gaggagatgg agctctaccg ccagaagggtg gagccgctgc ggcagagct ccaagaggc 300

gwgccgcaga agctgcacga gctgcaagag aagctgacg cactggcga ggatgcgc 360

gaccggcgcc ggcgcgcgtg ggacgcgtc cgacgcattc tggcccccata cagcgcacg 420

ctgcgcgcgc gcttggccgc ggcgcgttag gctctcaagg agaacggcgg cggcagactg 480

gcccggatacc acgccaaggc caccgagcat ctgagcacgc tcagcgagaa ggccaaggccc 540

gwgctcgagg acctccgcgc aggcgtgtc cccgtgtgg agagcttcaa ggtcagcttc 600

ctgagcgctc tcgaggagta cactaagaag ctcaacaccc agggtaacct aaagctcctt 660

gacaactggg acagegtgac ctccaccc tc agcaagctgc gcaacagct cggccctgtg 720

acccaggagt tctggataa cctggaaaag gagacagagg gctgaggca ggagatgagc 780

aaggatctgg aggaggatgaa ggccaagggtg cagccctacc tggacgactt ccagaagaag 840

tggcaggagg agatggagct ctaccgcgc aaggtggacg cgctgacgc agagtc当地 900

gaggggcgcc gccagaagct gcacgcgtc caagagaagc tgagcccact gggcgaggag 960

atgcgcgcacc ggcgcgcgc ccatgtggac ggcgtgcgc cgcacgc cccctacacc 1020

gacgcgtgc gcaacgcgtt ggcgcgcgc cttgaggctc tcaaggagaa cggccgcgc 1080

agactggccg agtaccacgc caaggccacc gacatctga gacgcgtc cggagaaggcc 1140

aaggccgcgc tcgaggaccc cgcacacgc ctgctgcgc tgctggagag cttcaaggctc 1200

agcttctgtc ggcgtctgcg gaggatcacact aagaagctca acacccagta ataagctgc 1260

<210> SEQ ID NO 8

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: MSP2 with short linker

<400> SEQUENCE: 8

Met Gly His His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15

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Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
 65 70 75 80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln  
 85 90 95

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro  
 100 105 110

Leu Gly Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu  
 180 185 190

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys  
 195 200 205

Leu Asn Thr Gln Gly Thr Leu Lys Leu Leu Asp Asn Trp Asp Ser Val  
 210 215 220

Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln  
 225 230 235 240

Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu  
 245 250 255

Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu  
 260 265 270

Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln  
 275 280 285

Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys  
 290 295 300

Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg  
 305 310 315 320

Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro  
 325 330 335

Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu  
 340 345 350

Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr  
 355 360 365

Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp  
 370 375 380

Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe  
 385 390 395 400

Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 405 410

<210> SEQ ID NO 9  
 <211> LENGTH: 1282  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP2L (with long linker)

<400> SEQUENCE: 9

taccatgggc	catcatcatc	atcatcatat	agaaggaaga	ctaaagctcc	ttgacaactg	60
ggacagcgtg	acacctccac	ctcagcaagct	gcgcgaacag	ctcggeccctg	tgaccaggaa	120
gttctggat	aacctggaaa	aggagacaga	gggcctgagg	caggagatga	gcaaggatct	180
ggaggaggtg	aaggccaagg	tgcagcccta	cctggacgac	ttccagaaga	agtggcagga	240
ggagatggag	ctctaccg	agaaggtgga	gccgctgcgc	gcagagctcc	aagaggcgc	300
gcccagaag	ctgcacg	tgcaagagaa	gctgagccca	ctggcggagg	agatgcgcga	360
ccgcgcgcgc	gcccattgtgg	acgcgcgtcg	cacgcacatcg	gccccatata	gcgcacgact	420
gcgcgcgcgc	ttggccgcgc	gccttggaggc	tctcaaggag	aacggcggcg	ccagactggc	480
cgcgttacc	cccaaggcca	ccgagcatct	gaggcacgctc	agcgagaagg	ccaaggccgc	540
gcgcgcggac	ctccgc	caag	gcctgctgc	cgtgctggag	agcttcaagg	600
gagcgtctc	gaggagtaca	ctaagaagct	caacacccag	ggtaccgg	gaggtagtgg	660
aggttgttacc	ctaaagctcc	ttgacaactg	ggacagcgtg	acctccac	tcagcaagct	720
gcgcgcac	ctcgccctg	tgacccagga	gttctggat	aacctggaaa	aggagacaga	780
gggcctgagg	caggagat	gcaaggatct	ggaggaggtg	aaggccaagg	tgcagcccta	840
cctggacgac	ttccagaaga	agtggcagga	ggagatggag	ctctaccg	agaaggtgg	900
gcccgcgcgc	gcagagctcc	aagaggcgc	gcccagaag	ctgcacg	tgcaagagaa	960
gcgcgcgcgc	ctggcgcagg	agatgcgcga	ccgcgcgcgc	gcccattgtgg	acgcgcgtcg	1020
cacgcacatcg	gccccatata	gcgcacgact	gcgcacgcgc	ttggccgcgc	gccttggaggc	1080
tctcaaggag	aacggcggcg	ccagactggc	cgacttacc	gccaaggcca	ccgagcatct	1140
gagcgcgc	agcgcgcgc	ccaagcccgc	gcctcgagg	ctccgc	gcctgctgc	1200
cgtgctggag	agcttcaagg	tcagcttctc	gagcgtctc	gaggagtaca	ctaagaagct	1260
caacacccag	taataagctt	gc				1282

<210> SEQ ID NO 10  
 <211> LENGTH: 422  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP2L (with long linker)

<400> SEQUENCE: 10

Met	Gly	His	His	His	His	Ile	Glu	Gly	Arg	Leu	Lys	Leu	Leu
1						5		10		15			

Asp	Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln
						20		25		30					

Leu	Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr
						35		40		45					

Glu	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala
						50		55		60					

Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu
65						70		75		80					

Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln
						85		90		95					

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Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro  
 100 105 110

Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu  
 180 185 190

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys  
 195 200 205

Leu Asn Thr Gln Gly Thr Gly Gly Ser Gly Gly Gly Thr Leu Lys  
 210 215 220

Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg  
 225 230 235 240

Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys  
 245 250 255

Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val  
 260 265 270

Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln  
 275 280 285

Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu  
 290 295 300

Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu  
 305 310 315 320

Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp  
 325 330 335

Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg  
 340 345 350

Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu  
 355 360 365

Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu  
 370 375 380

Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val  
 385 390 395 400

Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr  
 405 410 415

Lys Lys Leu Asn Thr Gln  
 420

<210> SEQ ID NO 11  
 <211> LENGTH: 522  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1D5D6

<400> SEQUENCE: 11

tataccatgg gccatcatca tcatcatcat atagaaggaa gactaaagct ccttgacaac 60

tgggacacgctg tgacctccac cttagcgaag ctgcgcgaac agctcgcccc tggaccctgg 120

gagttctggg ataacctgga aaaggagaca gagggcctga ggcaggagat gagcaaggat 180

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ctggaggagg tgaaggccaa ggtgcagccc tacctggacg acttccagaa gaagtggcag	240
gaggagatgg agctctaccg ccagaaggtg gagccctaca gcgcacgagct gcgccagcgc	300
ttggccgcgc gccttggaggc tctcaaggag aacggcggcg ccagactggc cgagtaccac	360
gccaaggcca ccgagcatct gaggcacgctc agcgagaagg ccaaaccgc gctcgaggac	420
ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct gagcgctctc	480
gaggagtaca ctaagaagct caacacccag taataagctt gc	522

<210> SEQ ID NO 12  
<211> LENGTH: 168  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: MSP1D5D6

<400> SEQUENCE: 12

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu	
1 5 10 15	
Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln	
20 25 30	
Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr	
35 40 45	
Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala	
50 55 60	
Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu	
65 70 75 80	
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr Ser Asp Glu Leu Arg	
85 90 95	
Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala	
100 105 110	
Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu	
115 120 125	
Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu	
130 135 140	
Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu	
145 150 155 160	
Tyr Thr Lys Lys Leu Asn Thr Gln	
165	

<210> SEQ ID NO 13  
<211> LENGTH: 522  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP1D6D7

<400> SEQUENCE: 13

tataccatgg gccatcatca tcatcatcat atagaaggaa gactaaagct cttgacaac	60
tgggacacgc tgacccacat ctccatcaag ctgcgcgaac agctcgccc tgcgtacccag	120
gagttctggg ataacctgga aaaggagaca gagggcctga ggcaggagat gagcaaggat	180
ctggaggagg tgaaggccaa ggtgcagccc tacctggacg acttccagaa gaagtggcag	240
gaggagatgg agctctaccg ccagaagggtg gagccgtgc gcgcacgact ccaagaggc	300
gcgcgcaga agctgcacga gctcaagag aagttgagcc ccaaggatgc cgagtaccac	360
gccaaggcca ccgagcatct gaggcacgctc agcgagaagg ccaaaccgc gctcgaggac	420

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ctccggccaa ggcgtgtggcc cgtgtggag agcttcaagg tcagcttctc gagcgcttc 480  
gaggagtaca ctaagaagct caacaccagg taataaagctt qc 522

<210> SEQ ID NO 14  
<211> LENGTH: 168  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: MSP1D6D7

<400> SEQUENCE: 14

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
50 55 60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
65 70 75 80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln  
85 90 95

Glu Gly Ala Arg Gin Lys Leu His Glu Leu Gin Glu Lys Leu Ser Ala  
100 105 110

Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu  
115 120 125

Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gin Gly Leu Leu  
 130 135 140

145 150 155 160

165

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<210> SEQ ID NO: 15
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Fully synthetic sequence encoding MSP1
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<400> SEQUENCE: 15

accatgggtt atccatcatca tcacatcacatt gagggacgatc tggaaatgtt ggacaattgg	60
gactctgtt aatccatcatca tcacatcacatt gagggacgatc tggaaatgtt ggacaattgg	120
ttctgggaca acctggaaaa agaaaccgag ggactgcgtc aggaaatgtc caaagattta	180
gaagaggtga aggccaaggt tcagccatat ctagatgact ttcagaaaaa atggcaggaa	240
gagatggaat tatatacgatca aaaggtggaa ccgctgcgtg cgaaactgcgca agagggggca	300
cgccaaaaac tccatgagct ccaagagaag ctcagccat taggcaaga aatgcgcgat	360
cgcgccccgtg cacatgttga tgcaactccgg actcatttgg cgccgtattc ggatgaaactt	420
cgccagcggtt tggccgcacg tctcgaggcg ctgaaagaaa acgggggtgc ccgcttggct	480
gagttaccacg cgaaagcgac agaacacctg agcacccatc gcgaaaaagc gaaaccggcg	540
ctggaaagatc tacggccagggtt attttgcgtt gttttgaga gctttaaagt cagttttctgtt	600
tcaatgttgg aagaatatac taaaaagctg aataaccctgtt aataagcttg g	651

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<210> SEQ ID NO 16  
 <211> LENGTH: 201  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1D3

<400> SEQUENCE: 16

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Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu
1           5           10          15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
20          25          30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
35          40          45

Glu Gly Leu Arg Gln Glu Met Ser Pro Tyr Leu Asp Asp Phe Gln Lys
50          55          60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu
65          70          75          80

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln
85          90          95

Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala
100         105         110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly
130         135         140

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr
145         150         155         160

Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu
165         170         175

Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu
180         185         190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln
195         200
  
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<210> SEQ ID NO 17  
 <211> LENGTH: 201  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1D9

<400> SEQUENCE: 17

```

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu
1           5           10          15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
20          25          30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
35          40          45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
50          55          60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
65          70          75          80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
85          90          95

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
100         105         110
  
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Leu Gly Glu Glu Met Arg Asp Arg Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175

Lys Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 195 200

<210> SEQ ID NO 18

<211> LENGTH: 392

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: MSP2delta1

<400> SEQUENCE: 18

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160

Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln Gly Thr Leu Lys Leu Asp  
 195 200 205

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu  
 210 215 220

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu  
 225 230 235 240

Gly Leu Arg Gln Glu Met Ser Pro Tyr Leu Asp Asp Phe Gln Lys Lys  
 245 250 255

Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg  
 260 265 270

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Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu  
 275 280 285

Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His  
 290 295 300

Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg  
 305 310 315 320

Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala  
 325 330 335

Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu  
 340 345 350

Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu  
 355 360 365

Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu  
 370 375 380

Tyr Thr Lys Lys Leu Asn Thr Gln  
 385 390

<210> SEQ ID NO 19  
 <211> LENGTH: 43  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: globular domain of apolipoprotein A1

<400> SEQUENCE: 19

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr  
 1 5 10 15

Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln  
 20 25 30

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn  
 35 40

<210> SEQ ID NO 20  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His tag

<400> SEQUENCE: 20

Met Gly His His His His His Ile Glu Gly Arg  
 1 5 10

<210> SEQ ID NO 21  
 <211> LENGTH: 23  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: HisTEV sequence

<400> SEQUENCE: 21

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

Glu Asn Leu Tyr Phe Gln Gly  
 20

<210> SEQ ID NO 22  
 <211> LENGTH: 22  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Helix 1

&lt;400&gt; SEQUENCE: 22

Leu	Lys	Leu	Leu	Asp	Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys
1				5				10					15		

Leu	Arg	Glu	Gln	Leu	Gly
				20	

&lt;210&gt; SEQ ID NO 23

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Helix 2

&lt;400&gt; SEQUENCE: 23

Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu	Gly
1				5				10				15			

Leu	Arg	Gln	Glu	Met	Ser
				20	

&lt;210&gt; SEQ ID NO 24

&lt;211&gt; LENGTH: 11

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Helix 3

&lt;400&gt; SEQUENCE: 24

Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys	Val	Gln
1				5				10		

&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Helix 4

&lt;400&gt; SEQUENCE: 25

Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu
1				5				10				15			

Tyr	Arg	Gln	Lys	Val	Glu
				20	

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Helix 5

&lt;400&gt; SEQUENCE: 26

Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu
1				5				10				15			

Leu	Gln	Glu	Lys	Leu	Ser
				20	

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Helix 6

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<400> SEQUENCE: 27

Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala  
 1 5 10 15

Leu Arg Thr His Leu Ala  
 20

<210> SEQ ID NO 28

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Helix 7

<400> SEQUENCE: 28

Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala  
 1 5 10 15

Leu Lys Glu Asn Gly Gly  
 20

<210> SEQ ID NO 29

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Helix 8

<400> SEQUENCE: 29

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 1 5 10 15

Leu Ser Glu Lys Ala Lys  
 20

<210> SEQ ID NO 30

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Helix 9

<400> SEQUENCE: 30

Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu  
 1 5 10

<210> SEQ ID NO 31

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Helix 10

<400> SEQUENCE: 31

Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu  
 1 5 10 15

Tyr Thr Lys Lys Leu Asn Thr Gln  
 20

<210> SEQ ID NO 32

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Helix 0.5

<400> SEQUENCE: 32

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Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly  
 1 5 10

<210> SEQ ID NO 33  
 <211> LENGTH: 13  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Helix 10.5

<400> SEQUENCE: 33

Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 1 5 10

<210> SEQ ID NO 34  
 <211> LENGTH: 22  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Helix 2S

<400> SEQUENCE: 34

Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly  
 1 5 10 15

Leu Arg Gln Glu Met Ser  
 20

<210> SEQ ID NO 35  
 <211> LENGTH: 36  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding His tag

<400> SEQUENCE: 35

atgggtcatc atcatcatca tcacatttag ggacgt 36

<210> SEQ ID NO 36  
 <211> LENGTH: 69  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding HisTEV

<400> SEQUENCE: 36

atgggtcatc atcatcatca tcatcacgtat tatgatattt ctactactga gaatttgtat 60  
 tttcagggt 69

<210> SEQ ID NO 37  
 <211> LENGTH: 66  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 1

<400> SEQUENCE: 37

ctgaagctgt tggacaattt ggactctgtt acgtctacct tcagtaaact tcgcgaacaa 60  
 ctgggc 66

<210> SEQ ID NO 38  
 <211> LENGTH: 66  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 2

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<400> SEQUENCE: 38

```
cccggtacgc aggaattctg ggacaacctg gaaaaagaaa ccgagggact gcgtcaggaa      60
atgtcc                                         66
```

<210> SEQ ID NO 39
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding Helix 3

<400> SEQUENCE: 39

```
aaagatttag aagaggtgaa ggccaagggtt cag                                         33
```

<210> SEQ ID NO 40
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding Helix 4

<400> SEQUENCE: 40

```
ccatatctcg atgactttca gaaaaaatgg caggaagaga tggattata tcgtcaaaag      60
gtggaa                                         66
```

<210> SEQ ID NO 41
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding Helix 5

<400> SEQUENCE: 41

```
ccgctgcgtg cggaaactgca agagggggca cgccaaaaac tccatgagct ccaagagaag      60
ctcagc                                         66
```

<210> SEQ ID NO 42
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding Helix 6

<400> SEQUENCE: 42

```
ccattaggcg aagaaatgca cgatgcgcgc cgtcacatg ttgatgcact ccggactcat      60
ttggcg                                         66
```

<210> SEQ ID NO 43
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding Helix 7

<400> SEQUENCE: 43

```
ccgttattcg agaacttcg ccagcgtttgc cccgcacgtc tcgaggcgct gaaagaaaaac      60
gggggt                                         66
```

<210> SEQ ID NO 44
<211> LENGTH: 66
<212> TYPE: DNA

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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 8  
  
 <400> SEQUENCE: 44  
  
 gcccgcgttgg ctgagttacca cgcgaaagcg acagaacacc tgagcacctt gagcgaaaaa 60  
  
 gcgaaaa 66

<210> SEQ ID NO 45  
 <211> LENGTH: 33  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 9  
  
 <400> SEQUENCE: 45  
  
 cccggcgctgg aagatctacg ccagggctta ttg 33

<210> SEQ ID NO 46  
 <211> LENGTH: 72  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 10  
  
 <400> SEQUENCE: 46  
  
 cctgttcttg agagcttaa agtcagttt ctgtcagctc tggaagaata tactaaaaag 60  
  
 ctgaatacc 72

<210> SEQ ID NO 47  
 <211> LENGTH: 33  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 0.5  
  
 <400> SEQUENCE: 47  
  
 tctacacctca gttaaacttcg cgaacaactg ggc 33

<210> SEQ ID NO 48  
 <211> LENGTH: 49  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 10.5  
  
 <400> SEQUENCE: 48  
  
 cagtttctg tcaagctctgg aagaatatac taaaaagctg aatacccg 49

<210> SEQ ID NO 49  
 <211> LENGTH: 66  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding Helix 2S  
  
 <400> SEQUENCE: 49  
  
 tccgtgacgc aggaattctg ggacaacctg gaaaaagaaa ccgaggact gcgtcaggaa 60  
  
 atgtcc 66

<210> SEQ ID NO 50  
 <211> LENGTH: 234  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial

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&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1E1

&lt;400&gt; SEQUENCE: 50

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15  
 Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30  
 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45  
 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60  
 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Gln Glu  
 65 70 75 80  
 Met Glu Leu Tyr Arg Gln Cys Val Glu Pro Tyr Leu Asp Asp Phe Gln  
 85 90 95  
 Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro  
 100 105 110  
 Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu  
 115 120 125  
 Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg  
 130 135 140  
 Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu  
 145 150 155 160  
 Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly  
 165 170 175  
 Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser  
 180 185 190  
 Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly  
 195 200 205  
 Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu  
 210 215 220  
 Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 225 230

&lt;210&gt; SEQ ID NO 51

&lt;211&gt; LENGTH: 256

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1E2

&lt;400&gt; SEQUENCE: 51

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15  
 Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30  
 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45  
 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60  
 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
 65 70 75 80  
 Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr Leu Cys Cys Phe Gln  
 85 90 95  
 Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro

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100	105	110	
Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu			
115	120	125	
Gln Glu Lys Leu Ser Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg			
130	135	140	
Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu			
145	150	155	160
Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu			
165	170	175	
Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu			
180	185	190	
Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys			
195	200	205	
Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu			
210	215	220	
Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val			
225	230	235	240
Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln			
245	250	255	

&lt;210&gt; SEQ ID NO 52

&lt;211&gt; LENGTH: 278

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1E3

&lt;400&gt; SEQUENCE: 52

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu			
1	5	10	15
Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln			
20	25	30	
Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr			
35	40	45	
Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala			
50	55	60	
Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu			
65	70	75	80
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr Leu Asp Asp Phe Gln			
85	90	95	
Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro			
100	105	110	
Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu			
115	120	125	
Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg			
130	135	140	
Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Leu Arg Ala Glu			
145	150	155	160
Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu			
165	170	175	
Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp			
180	185	190	
Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg			
195	200	205	
Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu			

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210	215	220	
Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu			
225	230	235	240
Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val			
245	250	255	
Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Tyr Thr			
260	265	270	
Lys Lys Leu Asn Thr Gln			
275			

<210> SEQ ID NO 53  
 <211> LENGTH: 223  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1TEV

<400> SEQUENCE: 53

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr			
1	5	10	15
Glu Asn Leu Tyr Phe Gln Gly Leu Lys Leu Leu Asp Asn Trp Asp Ser			
20	25	30	
Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr			
35	40	45	
Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln			
50	55	60	
Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr			
65	70	75	80
Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg			
85	90	95	
Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln			
100	105	110	
Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met			
115	120	125	
Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala			
130	135	140	
Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala			
145	150	155	160
Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala			
165	170	175	
Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu			
180	185	190	
Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser			
195	200	205	
Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln			
210	215	220	

<210> SEQ ID NO 54  
 <211> LENGTH: 200  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1NH

<400> SEQUENCE: 54

Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys			
1	5	10	15

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Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu  
 20 25 30

Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu  
 35 40 45

Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys  
 50 55 60

Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg  
 65 70 75 80

Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu  
 85 90 95

Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala His  
 100 105 110

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

Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala  
 130 135 140

Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu  
 145 150 155 160

Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu  
 165 170 175

Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu  
 180 185 190

Tyr Thr Lys Lys Leu Ser Thr Gln  
 195 200

<210> SEQ ID NO 55  
 <211> LENGTH: 212  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1T2

<400> SEQUENCE: 55

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

Glu Asn Leu Tyr Phe Gln Gly Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
 65 70 75 80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln  
 85 90 95

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro  
 100 105 110

Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175

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Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu  
 180 185 190

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys  
 195 200 205

Leu Asn Thr Gln  
 210

<210> SEQ ID NO 56  
 <211> LENGTH: 189  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1T2NH

<400> SEQUENCE: 56

Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu  
 1 5 10 15

Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met  
 20 25 30

Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp  
 35 40 45

Asp Phe Gln Lys Lys Trp Gln Glu Met Glu Leu Tyr Arg Gln Lys  
 50 55 60

Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu  
 65 70 75 80

His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp  
 85 90 95

Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr  
 100 105 110

Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys  
 115 120 125

Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu  
 130 135 140

His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu  
 145 150 155 160

Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu  
 165 170 175

Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 180 185

<210> SEQ ID NO 57  
 <211> LENGTH: 201  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1T3

<400> SEQUENCE: 57

Met Gly His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

Glu Asn Leu Tyr Phe Gln Gly Pro Val Thr Gln Glu Phe Trp Asp Asn  
 20 25 30

Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu  
 35 40 45

Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

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Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Ser Gly Gly  
 130 135 140

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160

Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 195 200

<210> SEQ ID NO 58

<211> LENGTH: 190

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: MSP1D3D9

<400> SEQUENCE: 58

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160

Leu Ser Glu Lys Ala Lys Pro Val Leu Glu Ser Phe Lys Val Ser Phe  
 165 170 175

Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 180 185 190

<210> SEQ ID NO 59

<211> LENGTH: 201

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: MSP1D10.5

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&lt;400&gt; SEQUENCE: 59

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
 65 70 75 80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln  
 85 90 95

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro  
 100 105 110

Leu Gly Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Ser Ala Leu Glu  
 180 185 190

Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 195 200

&lt;210&gt; SEQ ID NO 60

&lt;211&gt; LENGTH: 190

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1D3D10.5

&lt;400&gt; SEQUENCE: 60

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr

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 145 150 155 160

 Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

 Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 180 185 190

&lt;210&gt; SEQ ID NO 61

&lt;211&gt; LENGTH: 201

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1T4

&lt;400&gt; SEQUENCE: 61

 Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

 Glu Asn Leu Tyr Phe Gln Gly Ser Val Thr Gln Glu Phe Trp Asp Asn  
 20 25 30

 Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu  
 35 40 45

 Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

 Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80

 Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95

 Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110

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

 Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140

 Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160

 Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

 Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190

 Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 195 200

&lt;210&gt; SEQ ID NO 62

&lt;211&gt; LENGTH: 190

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1T5

&lt;400&gt; SEQUENCE: 62

 Met Gly His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

 Glu Asn Leu Tyr Phe Gln Gly Lys Glu Thr Glu Gly Leu Arg Gln Glu  
 20 25 30

 Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu  
 35 40 45

 Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln  
 50 55 60

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Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys  
 65 70 75 80  
 Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg  
 85 90 95  
 Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro  
 100 105 110  
 Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu  
 115 120 125  
 Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr  
 130 135 140  
 Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp  
 145 150 155 160  
 Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe  
 165 170 175  
 Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 180 185 190

<210> SEQ ID NO 63  
 <211> LENGTH: 179  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1T6

<400> SEQUENCE: 63

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15  
 Glu Asn Leu Tyr Phe Gln Gly Lys Asp Leu Glu Glu Val Lys Ala Lys  
 20 25 30  
 Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met  
 35 40 45  
 Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu  
 50 55 60  
 Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu  
 65 70 75 80  
 Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg  
 85 90 95  
 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala  
 100 105 110  
 Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr  
 115 120 125  
 His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys  
 130 135 140  
 Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser  
 145 150 155 160  
 Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu  
 165 170 175

Asn Thr Gln

<210> SEQ ID NO 64  
 <211> LENGTH: 289  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1E3TEV

<400> SEQUENCE: 64

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Met Gly His His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15  
 Glu Asn Leu Tyr Phe Gln Gly Leu Lys Leu Leu Asp Asn Trp Asp Ser  
 20 25 30  
 Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr  
 35 40 45  
 Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln  
 50 55 60  
 Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr  
 65 70 75 80  
 Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg  
 85 90 95  
 Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln  
 100 105 110  
 Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met  
 115 120 125  
 Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala  
 130 135 140  
 Pro Tyr Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu  
 145 150 155 160  
 Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala  
 165 170 175  
 Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu  
 180 185 190  
 Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His  
 195 200 205  
 Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu  
 210 215 220  
 Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala  
 225 230 235 240  
 Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala  
 245 250 255  
 Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys  
 260 265 270  
 Val Ser Phe Leu Ser Ala Leu Glu Tyr Thr Lys Lys Leu Asn Thr  
 275 280 285  
 Gln

<210> SEQ ID NO 65  
 <211> LENGTH: 278  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP1E3D1  
 <400> SEQUENCE: 65

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15  
 Glu Asn Leu Tyr Phe Gln Gly Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30  
 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45  
 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60  
 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu

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65	70	75	80
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln			
85	90	95	
Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro			
100	105	110	
Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu			
115	120	125	
Arg Thr His Leu Ala Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln			
130	135	140	
Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu			
145	150	155	160
Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu			
165	170	175	
Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp			
180	185	190	
Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg			
195	200	205	
Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu			
210	215	220	
Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu			
225	230	235	240
Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val			
245	250	255	
Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Tyr Thr			
260	265	270	
Lys Lys Leu Asn Thr Gln			
275			

<210> SEQ ID NO 66  
 <211> LENGTH: 423  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP2TEV

<400> SEQUENCE: 66

Met Gly His His His His His Asp Tyr Asp Ile Pro Thr Thr			
1	5	10	15
Glu Asn Leu Tyr Phe Gln Gly Leu Lys Leu Asp Asn Trp Asp Ser			
20	25	30	
Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr			
35	40	45	
Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln			
50	55	60	
Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr			
65	70	75	80
Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg			
85	90	95	
Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln			
100	105	110	
Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Met			
115	120	125	
Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala			
130	135	140	
Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala			

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145	150	155	160												
Leu	Lys	Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala
				165				170				175			
Thr	Glu	His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala	Lys	Pro	Ala	Leu	Glu
			180			185			190						
Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu	Ser	Phe	Lys	Val	Ser
			195			200			205						
Phe	Leu	Ser	Ala	Leu	Glu	Tyr	Thr	Lys	Lys	Leu	Asn	Thr	Gln	Gly	Thr
			210			215			220						
Leu	Lys	Leu	Leu	Asp	Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys
	225			230			235			240					
Leu	Arg	Glu	Gln	Leu	Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu
			245			250			255						
Glu	Lys	Glu	Thr	Glu	Gly	Leu	Arg	Gln	Glu	Met	Lys	Asp	Leu	Glu	Glu
			260			265			270						
Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp
			275			280			285						
Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala
			290			295			300						
Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	Lys
	305			310			315			320					
Leu	Ser	Pro	Leu	Gly	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	
			325			330			335						
Asp	Ala	Leu	Arg	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	Gln
			340			345			350						
Arg	Leu	Ala	Ala	Arg	Leu	Ala	Lys	Glu	Asn	Gly	Gly	Ala	Arg		
			355			360			365						
Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	Ser
			370			375			380						
Glu	Lys	Ala	Lys	Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro
	385			390			395			400					
Val	Leu	Glu	Ser	Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu	Glu	Tyr
			405			410			415						
Thr	Lys	Lys	Leu	Asn	Thr	Gln									
			420												

<210> SEQ\_ID NO 67  
<211> LENGTH: 199  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: MSP1N1

<400> SEQUENCE: 67

Met	Gly	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr	Thr		
1		5		10		15									
Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ser	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn
		20		25		30									
Leu	Glu	Lys	Glu	Thr	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	
		35		40		45									
Glu	Glu	Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys
		50		55		60									
Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Tyr
	65			70		75			80						
Leu	Asp	Asp	Phe	Gln	Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	

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85	90	95	
Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln			
100	105	110	
Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met			
115	120	125	
Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala			
130	135	140	
Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala			
145	150	155	160
Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala			
165	170	175	
Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu			
180	185	190	
Asp Leu Arg Gln Gly Leu Leu			
195			

<210> SEQ ID NO 68  
 <211> LENGTH: 401  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP2N1

<400> SEQUENCE: 68

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr			
1	5	10	15
Glu Asn Leu Tyr Phe Gln Gly Ser Thr Phe Ser Lys Leu Arg Glu Gln			
20	25	30	
Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr			
35	40	45	
Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala			
50	55	60	
Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu			
65	70	75	80
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln			
85	90	95	
Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro			
100	105	110	
Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu			
115	120	125	
Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala			
130	135	140	
Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu			
145	150	155	160
Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala			
165	170	175	
Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu			
180	185	190	
Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys			
195	200	205	
Leu Asn Thr Gln Gly Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro			
210	215	220	
Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu			
225	230	235	240
Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln			

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245	250	255	
Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu			
260	265	270	
Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala			
275	280	285	
Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu			
290	295	300	
Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His			
305	310	315	320
Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu			
325	330	335	
Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala			
340	345	350	
Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala			
355	360	365	
Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys			
370	375	380	
Val Ser Phe Leu Ser Ala Leu Glu Tyr Thr Lys Lys Leu Asn Thr			
385	390	395	400
Gln			
<210> SEQ ID NO 69			
<211> LENGTH: 392			
<212> TYPE: PRT			
<213> ORGANISM: Artificial			
<220> FEATURE:			
<223> OTHER INFORMATION: MSP2N2			
<400> SEQUENCE: 69			
Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr			
1	5	10	15
Glu Asn Leu Tyr Phe Gln Gly Ser Thr Phe Ser Lys Leu Arg Glu Gln			
20	25	30	
Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr			
35	40	45	
Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala			
50	55	60	
Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu			
65	70	75	80
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln			
85	90	95	
Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro			
100	105	110	
Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu			
115	120	125	
Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala			
130	135	140	
Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu			
145	150	155	160
Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala			
165	170	175	
Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu			
180	185	190	
Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Tyr Thr Lys Lys			
195	200	205	

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Leu Asn Thr Gln Gly Thr Pro Val Thr Gln Glu Phe Trp Asp Asn Leu  
 210 215 220  
 Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu  
 225 230 235 240  
 Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys  
 245 250 255  
 Trp Gln Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg  
 260 265 270  
 Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu  
 275 280 285  
 Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His  
 290 295 300  
 Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg  
 305 310 315 320  
 Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala  
 325 330 335  
 Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu  
 340 345 350  
 Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu  
 355 360 365  
 Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu  
 370 375 380  
 Tyr Thr Lys Lys Leu Asn Thr Gln  
 385 390

<210> SEQ ID NO 70  
 <211> LENGTH: 381  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP2D1D1  
 <400> SEQUENCE: 70  
  
 Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15  
  
 Glu Asn Leu Tyr Phe Gln Gly Pro Val Thr Gln Glu Phe Trp Asp Asn  
 20 25 30  
  
 Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu  
 35 40 45  
  
 Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60  
  
 Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu  
 65 70 75 80  
  
 Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln  
 85 90 95  
  
 Glu Lys Leu Ser Pro Leu Gly Glu Met Arg Asp Arg Ala Arg Ala  
 100 105 110  
  
 His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu  
 115 120 125  
  
 Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly  
 130 135 140  
  
 Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr  
 145 150 155 160  
  
 Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu  
 165 170 175

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Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu  
 180 185 190  
 Glu Tyr Thr Lys Lys Leu Asn Thr Gln Gly Thr Pro Val Thr Gln Glu  
 195 200 205  
 Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met  
 210 215 220  
 Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp  
 225 230 235 240  
 Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys  
 245 250 255  
 Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu  
 260 265 270  
 His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp  
 275 280 285  
 Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr  
 290 295 300  
 Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys  
 305 310 315 320  
 Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu  
 325 330 335  
 His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu  
 340 345 350  
 Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu  
 355 360 365  
 Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 370 375 380

<210> SEQ ID NO 71  
 <211> LENGTH: 603  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1T4  
  
 <400> SEQUENCE: 71  
  
 atgggtcata atcatcatca tcatcacat tatgatattt ctactactga gaatttttat 60  
 tttcagggtt ccgtgacgca ggaattctgg gacaacctgg aaaaagaaac cgagggactg 120  
 cgtcaggaaa tgtccaaaga ttttagaagag gtgaaggcca aggttcagcc atatctcgat 180  
 gactttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaggt ggaaccgctg 240  
 cgtgcggAAC tgcaagaggg ggcacgccaa aaactccatg agctccaaga gaagtcagc 300  
 ccattaggcg aagaaatgca cgatcgccgc cgtgcacatg ttgatgcact ccggactcat 360  
 ttggcgcgtt attcggatga acttcgcccag cggttggccg cacgtctcgaa ggcgtgaaa 420  
 gaaaacgggg gtgcccgtt ggctgagttac cacgcgaaag cgacagaaca cctgagcacc 480  
 ttgagcgtttt aagtcaatttt tctgtcagttt ctggaaagaat atactaaaaa gctgaatacc 540  
 gagagcttta aagtcaatttt tctgtcagttt ctggaaagaat atactaaaaa gctgaatacc 600  
 cag 603

<210> SEQ ID NO 72  
 <211> LENGTH: 570  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1T5

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<400> SEQUENCE: 72

atgggtcatc atcatcatca tcatcacat	60
ttcagggta aagaaaaccga gggactg	120
aaggccaagg ttcagccata tctcgat	180
ttatatcgta aaaagggtga accgc	240
ctccatgagc tccaagagaa gctcagcc	300
gcacatgtt atgcactccg gactcattt	360
ttggccgcac gtctcgaggc gctgaaagaa	420
gaaaaagcga cagaacaccc gaggac	480
ctacgcagg gcttattgcc tggtttag	540
gaagaatata ctaaaaagct gaatacc	570

<210> SEQ ID NO 73  
 <211> LENGTH: 603  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1T6

<400> SEQUENCE: 73

atgggtcatc atcatcatca tcatcacat	60
ttcagggtt ccgtgacgca ggaattctgg	120
cgtcaggaaa tgtccaaaga tttagaagag	180
gactttcaga aaaaatggca ggaagagat	240
cgtgcggaaac tgcaagaggg ggcacgcca	300
ccattaggcg aagaatgcg cgatcgcc	360
ttggcgccgt attcgatga acttcgcag	420
aaaaacgggg gtgcccgtt ggctgag	480
ttgagcgaaa aagcgaaacc ggcgtggaa	540
gagagctta aagttagt tctgtcag	600
cag	603

<210> SEQ ID NO 74  
 <211> LENGTH: 597  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1N1

<400> SEQUENCE: 74

atgggtcatc atcatcatca tcatcacat	60
ttcagggtt ccgtgacgca ggaattctgg	120
cgtcaggaaa tgtccaaaga tttagaagag	180
gactttcaga aaaaatggca ggaagagat	240
ctcgatgact ttcagaaaaa atggcaggaa	300
ccgctgcgtg cggaaactgca aggggggc	360
ctcagccat taggcaaga aatgcgcgat	420

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actcatttgg cgccgttattc ggtatgaaactt cgccagcggt tggccgcacg tctcgaggcg	480
ctgaaaagaaa acgggggtgc ccgttggct gagtaccacg cgaaagcgac agaacacactg	540
agcaccttga gcgaaaaagc gaaaaccggcg ctggaagatc tacgccaggg cttattg	597

<210> SEQ ID NO 75  
<211> LENGTH: 867  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP1E3TEV

<400> SEQUENCE: 75

atgggtcatc atcatcatca tcatcacat tatgatattc ctactactga gaatttttat	60
tttcagggtc tgaagctgtt ggacaattgg gactctgtt cgtctacccctt cagtaaactt	120
cgcgaacaac tggggccctgt gacgcaggaa ttctggacca acctggaaaa agaaaccgag	180
ggactgcgtc aggaaatgtc caaagattta gaagagggtga aggccaaggt tcagccatat	240
ctcgatgact ttcagaaaaa atggcaggaa gagatggaaat tatatcgta aaaggtggaa	300
ccgctgcgtg cggaaactgca agagggggca cgccaaaaac tccatgagct ccaagagaag	360
ctcagcccat taggcaaga aatgcgcgtat cggccccgtg cacaatgttgc tgcaactccgg	420
actcatttgg cgccatatact cgtactttt cagaaaaat ggcaggaaaga gatggatta	480
tatcgtaaa aggtggaaacc gctgcgtgcg gaactgcaag agggggcacg cccaaaaactc	540
catgagctcc aagagaagct cagccattaa ggcaagaaaa tgcgcgatcg cgcccggtca	600
catgttgcgtg cactccggac tcatttggcg ccgtattcgg atgaacttcg ccagegtttg	660
ggcccacgtc tcgaggcgct gaaagaaaaac ggggggtgc gtttggctga gtaccacgcg	720
aaagcgacag aacacctgag cacatttgcg gaaaaagcga aaccggcgct ggaagatcta	780
cgccagggtc tattgcgtgt tcttgcgcg tttaaatgtca gttttctgtc agctctggaa	840
gaatataacta aaaagctgaa tacccag	867

<210> SEQ ID NO 76  
<211> LENGTH: 834  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP1E3D1

<400> SEQUENCE: 76

atgggtcatc atcatcatca tcatcacat tatgatattc ctactactga gaatttttat	60
tttcagggtt ctacattcgt taaacttcgc gaacaactgg gccccgtgac gcaggaaattc	120
tgggacaacc tggaaaaaaga aaccggggga ctgcgtcagg aaatgtccaa agattttagaa	180
gagggtgaagg ccaagggtca gccatatctc gatgactttc agaaaaatg gcaggaaagag	240
atggaaattat atcgtaaaa ggtggaaaccg ctgcgtgcgg aactgcaaga gggggcacgc	300
ccaaaaactcc atgagctcca agagaagctc agccattag gcaagaaat ggcgcgatcg	360
gccccgtgcac atgttgcgtc actccggact catttggcgcc catatctcgat tgactttcgt	420
aaaaaaatggc aggaagagat ggaatttatat cgtaaaaagg tggaaaccgct ggcgtgcggaa	480
ctgcaagagg gggcacgcca aaaactccat gagctccaag agaagctcag cccattaggc	540
gaagaaaatgc gcgatcgccg ccgtgcacat gttgtgcac tccggactca tttggcgccg	600
tattcggatg aacttcgcgc ggcgttggcc gcacgtctcg aggcgtgaa agaaaacggg	660
gggtccccgt tggctgagta ccacgcgaaa ggcacagaac acctgagcac cttgagcgaa	720

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aaagcgaaac	ccggcgctgga	agatctacgc	cagggcttat	tgccctgttct	tgagagcttt	780
aaagtcagtt	ttctgtcagc	tctgaaagaa	tatactaaaa	agctgaatac	ccag	834

<210> SEQ ID NO 77  
 <211> LENGTH: 1275  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP2TEV

<400> SEQUENCE: 77

atgggtcatc	atcatcatca	tcatcacat	tatgatattc	ctactactga	gaatttgtat	60
tttcagggtc	taaagctcct	tgacaactgg	gacagcgtga	cctccaccc	cagcaagctg	120
cgcgaacagc	tcggccctgt	gaccaggag	ttctgggata	acctggaaaa	ggagacagag	180
ggcctgaggc	aggagatgag	caaggatctg	gaggagggtga	aggccaaggt	gcagccctac	240
ctggacact	tccagaagaa	gtggcaggag	gagatggagc	tctaccgcca	gaagggtggag	300
cgcgtgcgc	cagagctcca	agagggcgcg	cgccagaagc	tgcacgagct	gcaagagaag	360
ctgagcccc	tggcggagga	gatgcgcgac	cgcgcgcg	ccatgtgga	cgcgctgcgc	420
acgcatactgg	ccccctacag	cgacgagctg	cgccagcgct	tggccgcgcg	ccttggggct	480
ctcaaggaga	acggcggcgc	cagactggcc	gagtaccacg	ccaaggccac	cgagcatctg	540
agcacgcgtca	gcgagaaggc	caagcccgcg	ctcgaggacc	tccgccaagg	cctgtgccc	600
gtgctggaga	gttcaaggt	cagttcctg	agcgctctcg	aggagtacac	taagaagctc	660
aacacccagg	gtaccctaaa	gctccttgac	aactggaca	gcgtgaccc	cacccatcg	720
aagctgcgcg	acacagctcg	ccctgtgacc	caggagtct	ggataaacct	ggaaaaggag	780
acagaggggc	tgaggcagga	gatgagcaag	gatctggagg	aggtgaaggc	caaggtgcag	840
ccctacctgg	acgacttcca	gaagaagtgg	caggaggaga	tggagctcta	ccgcccagaag	900
gtggagccgc	tgcgcgcaga	gctccaagag	ggcgccgcgc	agaagctgca	cgagctgcaa	960
gagaagctga	gccccactggg	cgaggagatg	cgcgaccgcg	cgcgcccca	tgtggacgcg	1020
ctgcgcacgc	atctggcccc	ctacagcgac	gagctgcgc	agcgcttggc	cgcgccctt	1080
gaggctctca	aggagaacgg	cgccgcaga	ctggccgagt	accacgcca	ggccaccggag	1140
catctgagca	cgctcagcga	gaaggccaag	cccgcgctcg	aggacctccg	ccaaggcctg	1200
ctgcccgtgc	tgagagcttt	caaggtcago	ttcctgagcg	ctctcgagga	gtacactaag	1260
aagctcaaca	cccaag					1275

<210> SEQ ID NO 78  
 <211> LENGTH: 1203  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP2N1

<400> SEQUENCE: 78

atgggtcatc	atcatcatca	tcatcacat	tatgatattc	ctactactga	gaatttgtat	60
tttcagggtt	ctacccatcg	taaacttcgc	gaacaactgg	gccccgtgac	gcaggaattc	120
tgggacaacc	tggaaaaaga	aaccgaggga	ctgcgtcagg	aatgtccaa	agatttagaa	180
gaggtgaagg	ccaagggttca	ccatatctc	gatgacttc	agaaaaaaatg	gcaggaagag	240
atggaattat	atcgtaaaa	ggtggaaaccg	ctgcgtgcgg	aactgcaaga	gggggcacgc	300

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caaaaactcc atgagctcca agagaagctc agcccattag gcgaagaat ggcgcatgc	360
gcccgtgcac atgttgcac actccggact catttggcgc cgtattcgaa tgaacttcgc	420
cagcgttgg ccgcacgtct cgaggcgctg aaagaaaacg ggggtgcccgg tttggctgag	480
taccacgcga aagcgacaga acacctgagc accttgcgac aaaaagcgaa accggcgctg	540
gaagatctac gccagggtt attgcctgtt cttgagagct taaaagtca gttttctgtca	600
gctctgaaag aataatactaa aaagctgaat acccagggtt ctttcgtt aaacttcgcgaa	660
caactggggcc ccgtgcacgc ggaattctgg gacaacctgg aaaaagaaaac cgaggggactg	720
cgtcaggaaa tgtccaaaga ttttagaagag gtgaaggccaa aggttcagcc atatctcgat	780
gactttcaga aaaaatggca ggaagagatg gaattatatac gtcaaaaggt ggaaccgctg	840
cgtgcggaaac tgcaagaggg ggcacgcacaa aaactccatg agctccaaga gaagctcgc	900
ccattaggcg aagaaatgcg cgatcgccgc cgtgcacatg ttgatgcact ccggactcat	960
ttggcgcgtt attcggatga acttcggccag cgtttggccg cacgtctcgaa ggcgcgtgaaa	1020
gaaaacgggg gtgcccgtt ggctgagttt caccgcgaaag cgacagaaca cctgagcacc	1080
ttgagcgaaa aagcgaaacc ggcgcgtggaa gatctacgcg agggttatt gcctgttctt	1140
gagagcttta aagtcaagttt tctgtca gttt ctggaaagaat atactaaaaa gctgaataacc	1200
cag	1203

<210> SEQ ID NO 79  
 <211> LENGTH: 1176  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP2N2

<400> SEQUENCE: 79

atgggtcatc atcatcatca tcatcacat tatgatattc ctactactga gaatttgcgtat	60
tttcagggtt ctacccatcg taaaacttcgc gaacaactgg gcccgtgcac gcaggaaattc	120
tgggacaacc tggaaaaga aaccggggca ctgcgtcagg aaatgtccaa agattttagaa	180
gaggtgaagg ccaagggttca gccatatctc gatgactttc agaaaaatgcgaggaaag	240
atgaaattat atcgtaaaaa ggtggaaaccg ctgcgtgcgg aactgcaga gggggcacgc	300
caaaaactcc atgagctcca agagaagctc agcccattag gcgaagaat ggcgcatgc	360
gcccgtgcac atgttgcac actccggact catttggcgc cgtattcgaa tgaacttcgc	420
cagcgttgg ccgcacgtct cgaggcgctg aaagaaaacg ggggtgcccgg tttggctgag	480
taccacgcga aagcgacaga acacctgagc accttgcgac aaaaagcgaa accggcgctg	540
gaagatctac gccagggtt attgcctgtt cttgagagct taaaagtca gttttctgtca	600
gctctgaaag aataatactaa aaagctgaat acccagggtt ccccggtgac gcaggaaattc	660
tgggacaacc tggaaaaga aaccggggca ctgcgtcagg aaatgtccaa agattttagaa	720
gaggtgaagg ccaagggttca gccatatctc gatgactttc agaaaaatgcgaggaaag	780
atgaaattat atcgtaaaaa ggtggaaaccg ctgcgtgcgg aactgcaga gggggcacgc	840
caaaaactcc atgagctcca agagaagctc agcccattag gcgaagaat ggcgcatgc	900
gcccgtgcac atgttgcac actccggact catttggcgc cgtattcgaa tgaacttcgc	960
cagcgttgg ccgcacgtct cgaggcgctg aaagaaaacg ggggtgcccgg tttggctgag	1020
taccacgcga aagcgacaga acacctgagc accttgcgac aaaaagcgaa accggcgctg	1080
gaagatctac gccagggtt attgcctgtt cttgagagct taaaagtca gttttctgtca	1140

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gctctggaag aataactaa aaagctgaat acccag 1176

<210> SEQ ID NO 80  
<211> LENGTH: 1198  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP2N3

<400> SEQUENCE: 80

atgggtcata	atcatcatca	tcatcacat	tatgatattc	ctactactga	gaatttgat	60
tttcagggtt	ctacccatcg	taaacttcgc	gaacaactgg	gccccgtgac	gcaggaattc	120
tgggacaacc	tggaaaaga	aaccgaggga	ctgcgtcagg	aatgtccaa	agatttagaa	180
gaggtgaagg	ccaagggtca	gccatatctc	gatgacttgc	agaaaaaatg	gcaggaagag	240
atgaaattat	atcgtaaaa	ggtggaaaccg	ctgcgtcgg	aactgcaaga	gggggcacgc	300
caaaaactcc	atgagctcca	agagaagctc	agccattag	gcgaagaat	gcgcgatcgc	360
gcccgtgcac	atgttgcac	actccggact	catttggcgc	cgatattcgg	tgaacttcgc	420
cagcgttgg	ccgcacgtct	cgagggcgtg	aaagaaaacg	gggggtgccc	cttggctgag	480
taccacgcga	aagcgcacaga	acacctgagc	accttggcgc	aaaaagcgaa	accggcgctg	540
gaagatctac	gccagggctt	attgcctgtt	cttgagagct	ttaaagtca	ttttctgtca	600
gctctggaag	aataactaa	aaagctgaat	accagggtt	cccgcgaaaca	actggggccc	660
gtgacgcagg	aattctggaa	caacctggaa	aaagaaacccg	agggactgcg	tcaggaaatg	720
tccaaagatt	tagaagaggt	gaaggccaag	gttcagccat	atctcgatga	ctttcagaaa	780
aaatggcagg	aagagatgga	attatatcg	caaagggtt	accgcgtgcg	tgcgaaactg	840
caagaggggg	cacgcacaaa	actccatgag	ctccaagaga	agctcagccc	attaggcgaa	900
gaaatgcgcg	atcgccccc	tgcacatgtt	gatgcactcc	ggactcattt	ggcgccgtat	960
tcggatgac	tccgcagcg	tttggccgc	cgtctcgagg	cgctgaaaga	aaacgggggt	1020
gcccgcgttgg	ctgagttacca	cgcgaaagcg	acagaacacc	tgagcacctt	gagcgaaaaa	1080
gcgaaacccg	cgctggaaga	tctacgccc	ggcttattgc	ctgttcttga	gagctttaaa	1140
gtcagtttc	tgtcagctct	ggaagaatat	actaaaaacg	tgaataccca	gtaaagctt	1198

<210> SEQ ID NO 81  
<211> LENGTH: 397  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: MSP2N3

<400> SEQUENCE: 81

Met	Gly	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr	Thr
1							5		10			15	

Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln
							20		25			30			

Leu	Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr
							35		40			45			

Glu	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala
						50		55			60				

Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu
						65		70			75			80	

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln

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85	90	95													
Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro
100								105							110
Leu	Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu
115								120							125
Arg	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	Gln	Arg	Leu	Ala
130								135							140
Ala	Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu
145						150			155						160
Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala
165						170			175						
Lys	Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu
180						185									190
Ser	Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu	Glu	Tyr	Thr	Lys	Lys
195						200						205			
Leu	Asn	Thr	Gln	Gly	Thr	Arg	Glu	Gln	Leu	Gly	Pro	Val	Thr	Gln	Glu
210						215						220			
Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu	Gly	Leu	Arg	Gln	Glu	Met
225						230			235						240
Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu	Asp
245						250			255						
Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	
260						265			270						
Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu
275						280						285			
His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu	Gly	Glu	Glu	Met	Arg	Asp
290						295			300						
Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	Arg	Thr	His	Leu	Ala	Pro	Tyr
305						310			315						320
Ser	Asp	Glu	Leu	Arg	Gln	Arg	Leu	Ala	Ala	Arg	Leu	Glu	Ala	Leu	Lys
325						330			335						
Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala	Thr	Glu
340						345			350						
His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala	Lys	Pro	Ala	Leu	Glu	Asp	Leu
355						360			365						
Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu	Ser	Phe	Lys	Val	Ser	Phe	Leu
370						375			380						
Ser	Ala	Leu	Glu	Glu	Tyr	Thr	Lys	Lys	Leu	Asn	Thr	Gln			
385						390			395						

<210> SEQ ID NO 82  
<211> LENGTH: 1149  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP2N4  
<400> SEQUENCE: 82

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atgggtcatc atcatcatca tcatcacat tatgatattc ctactactga gaatttgtat      60
tttcagggtt ccgtgacgca ggaattctgg gacaacctgg aaaaagaaac cgaggggactg      120
cgtcaggaaa tgtccaaaga ttttagaagag gtgaaggccca aggttcagcc atatctcgat      180
gactttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaaggt ggaaccgctg      240
cgtgcggAAC tgcaagaggg ggcacgccaa aaactccatg agctccaaga gaagctcagc      300
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ccattaggcg aagaaaatgct	cgatcgcgcc	cgtgcacatg	ttgatgcact	ccggactcat	360
ttggcgccgt	attcgatga	acttcgcccag	cgtttggccg	cacgtctcgaa	420
gaaaacgggg	gtgcccgtt	ggctgagttac	cacgcgaaag	cgacagaaca	480
ttgagcgaaa	aagcgaaacc	ggcgctggaa	gatctacgcc	agggcttatt	540
gagagcttta	aagtca	ttctgtcagct	ctggaagaat	atactaaaaa	600
cagaatccag	gtaccccg	gacgcaggaa	ttctggaca	acctggaaaa	660
ggactgcgtc	aggaaatgtc	caaagattt	gaagaggta	aggccaaggt	720
ctcgatgact	ttcagaaaaa	atggcaggaa	gagatggaa	tatatcgta	780
ccgctgcgtg	cggaactgca	agagggggca	cgcacaaaac	tccatgagct	840
ctcagccat	taggcaaga	aatgcgcgt	cgcgcgttgc	catgttgc	900
actcatttgg	cgcgttattc	ggatgaa	cgcgcgttgc	tggccgcacg	960
ctgaaagaaa	acgggggtgc	ccgcttgcgt	gagtaccacg	cgaaagcgac	1020
agcaccttga	gcgaaaaagc	gaaaccggcg	ctggaagatc	tacgcccagg	1080
gttcttggaa	gttttaagt	cagtttgcgt	tca	gatatac	1140
aatacccg					1149

&lt;210&gt; SEQ ID NO 83

&lt;211&gt; LENGTH: 383

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP2N4

&lt;400&gt; SEQUENCE: 83

Met	Gly	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr	Thr
1							5		10		15		

Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ser	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn
20							25		30						

Leu	Glu	Lys	Glu	Thr	Glu	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu
35							40		45						

Glu	Glu	Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys
50							55		60						

Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu
65							70		75		80				

Arg	Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln
85							90		95						

Glu	Lys	Leu	Ser	Pro	Leu	Gly	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	
100							105		110						

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

Arg	Gln	Arg	Leu	Ala	Ala	Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly
130							135		140						

Ala	Arg	Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr
145							150		155		160				

Leu	Ser	Glu	Lys	Ala	Lys	Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu
165							170		175						

Leu	Pro	Val	Leu	Glu	Ser	Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu
180							185		190						

Glu	Tyr	Thr	Lys	Lys	Leu	Asn	Thr	Gln	Asn	Pro	Gly	Thr	Pro	Val	Thr
195							200		205						

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Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln  
 210 215 220  
 Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr  
 225 230 235 240  
 Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg  
 245 250 255  
 Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln  
 260 265 270  
 Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met  
 275 280 285  
 Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala  
 290 295 300  
 Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala  
 305 310 315 320  
 Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala  
 325 330 335  
 Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu  
 340 345 350  
 Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser  
 355 360 365  
 Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 370 375 380

<210> SEQ ID NO 84  
 <211> LENGTH: 1137  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP2NS

<400> SEQUENCE: 84

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atgggtcata atcatcatca tcatacacat tatgatattc ctactactga gaatttttat 60
tttcagggtt ccgtgacgca ggaattctgg gacaacctgg aaaaagaaac cgagggactg 120
cgtcaggaaa tgtccaaaga ttttagaagag gtgaaggcca aggttcagcc atatctcgat 180
gactttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaggt ggaaccatat 240
ctcgatgact ttcagaaaaa atggcaggaa gagatggaa tatatcgtca aaaggtggaa 300
ccgctgcgtg cgaaactgca agagggggca cgccaaaaac tccatgagct ccaagagaag 360
ctcagcccat taggcaaga aatgcgcgtat cgcccccgtg cacaatgttgc tgcactccgg 420
actcatttgg cgccgtattc ggatgaaactt cgccagcgat tggccgcacg tctcgaggcg 480
ctgaaagaaa acgggggtgc ccgcctggct gatgtaccacg cgaaagcgcac agaacacctg 540
agcaccttga gcgaaaaagc gaaaccggcg ctggaagatc tacgccagg cttattgaat 600
ccaggttacca aagattttaga agaggtgaag gccaagggttc agccatatct cgatgacttt 660
cagaaaaaaat ggcaggaaga gatggaaatta tatcgtcaaa aggtggaaacc atatctcgat 720
gactttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaggt ggaaccgctg 780
cgtgcggAAC tgcaagaggg ggcacgcCAA aaactccatg agctccaaga gaagctcagc 840
ccatttagcg aagaaaatgcg cgatcgccgc cgtgcacatg ttgtatgcact ccggactcat 900
ttggcgcgtt attcggatga acttcgcccag cgttggccg cacgtctcga ggcgctgaaa 960
gaaaacgggg gtcggccgtt ggctgagttac cacgcgaaag cgacagaaca cctgagcacc 1020
ttgagcgaaa aagcgaaacc ggcgctggaa gatctacgccc agggcttatt gcccgtgacg 1080
  
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 caggaattct gggacaacct ggaaaaagaa accgagggac tgcgtcagga aatgtcc 1137
 

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<210> SEQ ID NO 85  
 <211> LENGTH: 379  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: MSP2N5

<400> SEQUENCE: 85

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr  
 1 5 10 15

Glu Asn Leu Tyr Phe Gln Gly Ser Val Thr Gln Glu Phe Trp Asp Asn  
 20 25 30

Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu  
 35 40 45

Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
 50 55 60

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr  
 65 70 75 80

Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg  
 85 90 95

Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln  
 100 105 110

Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met  
 115 120 125

Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala  
 130 135 140

Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala  
 145 150 155 160

Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala  
 165 170 175

Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu  
 180 185 190

Asp Leu Arg Gln Gly Leu Leu Asn Pro Gly Thr Lys Asp Leu Glu Glu  
 195 200 205

Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp  
 210 215 220

Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr Leu Asp  
 225 230 235 240

Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys  
 245 250 255

Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu  
 260 265 270

His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp  
 275 280 285

Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr  
 290 295 300

Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys  
 305 310 315 320

Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu  
 325 330 335

His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu  
 340 345 350

Arg Gln Gly Leu Leu Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu

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355	360	365
Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser		
370	375	
<210> SEQ ID NO 86		
<211> LENGTH: 1143		
<212> TYPE: DNA		
<213> ORGANISM: Artificial		
<220> FEATURE:		
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP2N6		
<400> SEQUENCE: 86		
atgggtcatc atcatcatca tcatacgtat tatgatattc ctactactga gaatttgtat		60
tttcagggtt ccgtgacgca ggaattctgg gacaacctgg aaaaagaaaa cgagggactg		120
cgtcaggaaa tgtccaaaga tttagaagag gtgaaggcca aggttcagcc atatctcgat		180
gacttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaggt ggaaccatat		240
ctcgatgact ttcagaaaaa atggcaggaa gagatggaat tataatcgta aaagggtggaa		300
ccgctgcgtg cggaaactgca agagggggca cgccaaaaac tccatgagct ccaagagaag		360
ctcagcccat taggcgaaga aatgcgcgat cgcgcgcgtg cacatgttga tgcactccgg		420
actcatttgg cgccgtattc ggtgaaactt cgccagcggt tggccgcacg tctcgaggcg		480
ctgaaaagaaa acgggggtgc ccgcattggct gagtaccacg cgaaagcgcac agaacacctg		540
agcaccttga gcgaaaaagc gaaaccggcg ctggaagatc tacgcccagg cttattgtcc		600
aatccaggtt cccaaaaaga tttagaagag gtgaaggcca aggttcagcc atatctcgat		660
gacttcaga aaaaatggca ggaagagatg gaattatatc gtcaaaaggt ggaaccatat		720
ctcgatgact ttcagaaaaa atggcaggaa gagatggaat tataatcgta aaagggtggaa		780
ccgctgcgtg cggaaactgca agagggggca cgccaaaaac tccatgagct ccaagagaag		840
ctcagcccat taggcgaaga aatgcgcgat cgcgcgcgtg cacatgttga tgcactccgg		900
actcatttgg cgccgtattc ggtgaaactt cgccagcggt tggccgcacg tctcgaggcg		960
ctgaaaagaaa acgggggtgc ccgcattggct gagtaccacg cgaaagcgcac agaacacctg		1020
agcaccttga gcgaaaaagc gaaaccggcg ctggaagatc tacgcccagg cttattgtcc		1080
gtgacgcagg aattctggaa caacctggaa aaagaaaccg agggactgcg tcaggaaatg		1140
tcc		1143
<210> SEQ ID NO 87		
<211> LENGTH: 381		
<212> TYPE: PRT		
<213> ORGANISM: Artificial		
<220> FEATURE:		
<223> OTHER INFORMATION: MSP2N6		
<400> SEQUENCE: 87		
Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr		
1	5	10
Glu Asn Leu Tyr Phe Gln Gly Ser Val Thr Gln Glu Phe Trp Asp Asn		
20	25	30
Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu		
35	40	45
Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys		
50	55	60
Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr		
65	70	75
80		

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Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg  
                   85                  90                  95  
 Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln  
                   100              105              110  
 Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met  
                   115              120              125  
 Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala  
                   130              135              140  
 Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala  
                   145              150              155              160  
 Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala  
                   165              170              175  
 Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu  
                   180              185              190  
 Asp Leu Arg Gln Gly Leu Leu Ser Asn Pro Gly Thr Gln Lys Asp Leu  
                   195              200              205  
 Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys  
                   210              215              220  
 Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Tyr  
                   225              230              235              240  
 Leu Asp Asp Phe Gln Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg  
                   245              250              255  
 Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln  
                   260              265              270  
 Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met  
                   275              280              285  
 Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala  
                   290              295              300  
 Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala  
                   305              310              315              320  
 Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala  
                   325              330              335  
 Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu  
                   340              345              350  
 Asp Leu Arg Gln Gly Leu Leu Pro Val Thr Gln Glu Phe Trp Asp Asn  
                   355              360              365  
 Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser  
                   370              375              380

<210> SEQ ID NO 88  
 <211> LENGTH: 636  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Nucleotide sequence encoding MSP1RC12'

<400> SEQUENCE: 88

atgggtcata atcatcatca tcacatttag ggatgtctga agctgttggaa caattggac 60  
 tctgttacgt ctacattcag taaaacttcgc gaacaactgg gccccgtgac gcaggaattc 120  
 tgggacaacc tggaaaaaga aaccgaggga ctgcgtcagg aaatgtccaa agatttagaa 180  
 gaggtgaagg ccaaggttca gccatatctc gatgactttc agaaaaaatg gcaggaagag 240  
 atggaattat atcgtaaaa ggtggAACCG ctgcgtgcgg aactgcaaga gggggcacgc 300  
 caaaaaactcc atgagctcca agagaagctc agcccattag gcgaagaaat gcgcgatcgc 360

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gcccgtgcac atgttcatgc actccggact catttggcgc cgtattcgga tgaacttcgc 420
cagcgttgg ccgcacgtct cgaggcgctg aaagaaaacg ggggtgcccgg cttggctgag 480
taccacgcga aagcgacaga acacctgagc accttgagcg aaaaagcgaa accggcgctg 540
gaagatctac gccaggggctt attgcctgtt cttgagagct tttaaagtca gtttctgtca 600
gctctggaa aataatactaa aaagctgaat acccag 636

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<210> SEQ ID NO 89
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: MSP1RC12'

<400> SEQUENCE: 89

```

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Met Gly His His His His His Ile Glu Gly Cys Leu Lys Leu Leu
1 5 10 15

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
20 25 30

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
35 40 45

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
50 55 60

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
65 70 75 80

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
85 90 95

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
100 105 110

Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
115 120 125

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
130 135 140

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
145 150 155 160

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
165 170 175

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu
180 185 190

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys
195 200 205

Leu Asn Thr Gln
210

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```

<210> SEQ ID NO 90
<211> LENGTH: 636
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding MSP1K90C

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<400> SEQUENCE: 90
atgggtcatc atcatcatca tcacatttag ggacgtctga agctgttggca aattgggac 60
tctgttacgt ctaccttcag taaacttcgc gaacaactgg gccccgtgac gcaggaaattc 120
tgggacaacc tggaaaaaga aaccgaggga ctgcgtcagg aatgtccaa agattttagaa 180

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gagggtgaagg ccaagggttca	gccatatctc	gatgactttc	agaaaaaaatg	gcagggaaagag	240
atcgtcaaaa	gggtggaaaccg	ctgcgtgcgg	aactgcaaga	gggggcacgc	300
caatgtctcc	atgagctcca	agagaagctc	agcccattag	gcgaagaaat	360
gcccgtgcac	atgttgatgc	actccggact	catttggcgc	cgtattcgga	420
cagcgtttgg	ccgcacgtct	cgaggcgctg	aaagaaaacg	gggggtgcccgg	480
taccacgcga	aagcgacaga	acacctgagc	accttggagc	aaaaagcgaa	540
gaagatctac	gccagggtt	attgcctgtt	cttgagagct	ttaaagtca	600
gctcttggaa	aataatactaa	aaagctgaat	acccag		636

&lt;210&gt; SEQ ID NO 91

&lt;211&gt; LENGTH: 212

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1K90C

&lt;400&gt; SEQUENCE: 91

Met	Gly	His	His	His	His	His	Ile	Glu	Gly	Arg	Leu	Lys	Leu	Leu	
1							5	10			15				
Asp	Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln
		20				25					30				
Leu	Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr
		35			40						45				
Glu	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala
		50			55					60					
Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Trp	Gln	Glu	Glu	
		65			70				75			80			
Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln
		85			90					95					
Glu	Gly	Ala	Arg	Gln	Cys	Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro
		100			105					110					
Leu	Gly	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	
		115			120					125					
Arg	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	Gln	Arg	Leu	Ala
		130			135					140					
Ala	Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu
		145			150				155			160			
Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala
		165			170				175						
Lys	Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu
		180			185					190					
Ser	Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu	Glu	Tyr	Thr	Lys	Lys
		195			200					205					
Leu	Asn	Thr	Gln												
		210													

&lt;210&gt; SEQ ID NO 92

&lt;211&gt; LENGTH: 636

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Nucleotide sequence encoding MSP1K152C

&lt;400&gt; SEQUENCE: 92

atgggtcata tcatcatca tcacatttggag ggacgtctga agctgttggaa caattggac 60

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tctgttacgt ctaccttcag taaaacttcgc gaacaactgg gccccgtgac gcaggaattc 120  
 tgggacaacc tggaaaaaga aacccgaggga ctgcgtcagg aaatgtccaa agatttagaa 180  
 gaggtgtaaagg ccaaggttca gccatatctc gatgacttcc agaaaaaaatg gcaggaagag 240  
 atggaaattat atcgtcaaaa ggtggaaaccg ctgcgtgcgg aactgcaaga gggggcacgc 300  
 caaaaaactcc atgagctcca agagaagctc agcccatctt ggcgaaat ggcgcgtcgc 360  
 gccccgtgcac atgttgatgc actccggact catttggcgc cgtattcggta gacttcgc 420  
 cagcgttgg ccgcacgtct cgaggcgctg aaagaaaaacg ggggtgcctt cttggctgag 480  
 taccacgcat ggcgcacaga acacctgagc accttgagcg aaaaagcgaa accggcgctg 540  
 gaagatctac gccagggtt attgcctt cttgagagct tttaaagtca gtttctgtca 600  
 gctcttggaaag aataactaa aaagctgaat acccag 636

&lt;210&gt; SEQ ID NO 93

&lt;211&gt; LENGTH: 212

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MSP1K152C

&lt;400&gt; SEQUENCE: 93

Met Gly His His His His His Ile Glu Gly Arg Leu Lys Leu Leu  
 1 5 10 15  
 Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln  
 20 25 30  
 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr  
 35 40 45  
 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala  
 50 55 60  
 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu  
 65 70 75 80  
 Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln  
 85 90 95  
 Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro  
 100 105 110  
 Leu Gly Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu  
 115 120 125  
 Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala  
 130 135 140  
 Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu  
 145 150 155 160  
 Tyr His Ala Cys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala  
 165 170 175  
 Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu  
 180 185 190  
 Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys  
 195 200 205  
 Leu Asn Thr Gln  
 210

&lt;210&gt; SEQ ID NO 94

&lt;211&gt; LENGTH: 6

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

-continued

&lt;223&gt; OTHER INFORMATION: peptide segment

&lt;400&gt; SEQUENCE: 94

Ser Asn Pro Gly Thr Gln  
1 5<210> SEQ ID NO 95  
<211> LENGTH: 279  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Recombinant Tissue Factor with truncated  
cytoplasmic domain

&lt;400&gt; SEQUENCE: 95

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
1 5 10 15Ala Gln Pro Ala Met Ala Ala Glu Asp Gln Val Asp Pro Arg Leu Ile  
20 25 30Asp Gly Lys Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr  
35 40 45Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro  
50 55 60Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp  
65 70 75 80Lys Ser Lys Cys Phe Tyr Thr Asp Thr Glu Cys Asp Leu Thr Asp  
85 90 95Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser  
100 105 110Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu  
115 120 125Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly  
130 135 140Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val  
145 150 155 160Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu  
165 170 175Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr  
180 185 190Trp Lys Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn  
195 200 205Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val  
210 215 220Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser  
225 230 235 240Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe  
245 250 255Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile  
260 265 270Leu Ala Ile Ser Leu His Lys  
275

&lt;210&gt; SEQ ID NO 96

&lt;211&gt; LENGTH: 4

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: linker peptide segment

-continued

&lt;400&gt; SEQUENCE: 96

Asn Pro Gly Thr  
1

What is claimed is:

1. A method for controlling bleeding in a human or animal patient, said method comprising the step of administering, in an amount effective to control bleeding in said patient a composition comprising nanoscale particles comprising tissue factor or recombinant tissue factor, a membrane scaffold protein and phospholipid, wherein the phospholipid comprises a net-negatively charged phospholipid, and wherein said nanoscale particles are attached to a solid support, whereby bleeding in said patient is controlled.
2. The method of claim 1, wherein the phospholipid comprises from 1 to 50% on a molar basis of net-negative charged phospholipid and from 50 to 99% net-neutral phospholipid.
3. The method of claim 1, wherein the phospholipid consists essentially of phosphatidylserine and phosphatidylcholine or phosphatidylserine and phosphatidylethanolamine in a molar ratio of 20:80 or consists essentially of phosphatidylserine, phosphatidylcholine and phosphatidylethanolamine in a molar ratio of 20:40:40.
4. The method of claim 1, wherein the human or animal patient has hemophilia, a thrombocytopenia or other bleeding diathesis.
5. The method of claim 1, wherein the patient has a surgical, wound or soft tissue trauma resulting in bleeding.
6. The method of claim 1, wherein the solid support is a collagen containing material.
7. The method of claim 1, wherein the membrane scaffold protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO: 4, SEQ ID NO:6, SEQ ID NO:8, amino acids 13-414 of SEQ ID NO:8, SEQ ID NO:10, amino acids 13-422 of SEQ ID NO:10, SEQ ID NO:12, amino acids 13-168 of SEQ ID NO:12, SEQ ID NO:14, amino acids 13-168 of SEQ ID NO:14, SEQ ID NO:16, amino acids 13-201 of SEQ ID NO:16, SEQ ID
- 10 NO:17, amino acids 13-201 of SEQ ID NO:17, SEQ ID NO:18, amino acids 13-392 of SEQ ID NO:18, SEQ ID NO:50, amino acids 13-234 of SEQ ID NO:50, SEQ ID NO:51, amino acids 13-256 of SEQ ID NO:51, SEQ ID NO:52, amino acids 13-278 of SEQ ID NO:52, SEQ ID NO:53, amino acids 24-223 of SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, amino acids 24-212 of SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, amino acids 24-201 of SEQ ID NO:57, SEQ ID NO:58, amino acids 13-190 of SEQ ID NO:58, SEQ ID NO:59, amino acids 13-201 of SEQ ID NO:59, SEQ ID NO:60, amino acids 13-190 of SEQ ID NO:60, SEQ ID NO:61, amino acids 24-201 of SEQ ID NO:61, SEQ ID NO:62, amino acids 24-190 of SEQ ID NO:62, SEQ ID NO:63, amino acids 24-179 of SEQ ID NO:63, SEQ ID NO:64, amino acids 24-289 of SEQ ID NO:64, SEQ ID NO:65, amino acids 24-289 of SEQ ID NO:64, SEQ ID NO:65, amino acids 24-278 of SEQ ID NO:65, SEQ ID NO:66, amino acids 24-423 of SEQ ID NO:66, SEQ ID NO:67, amino acids 24-199 of SEQ ID NO:67, SEQ ID NO:68, amino acids 24-401 of SEQ ID NO:68, SEQ ID NO:69, amino acids 24-392 of SEQ ID NO:69, SEQ ID NO:81, amino acids 24-397 of SEQ ID NO:81, SEQ ID NO:83, amino acids 24-383 of SEQ ID NO:83, SEQ ID NO:85, amino acids 24-379 of SEQ ID NO:85, SEQ ID NO:87, amino acids 24-381 of SEQ ID NO:87, SEQ ID NO:89, amino acids 25-212 of SEQ ID NO:89, SEQ ID NO:91, amino acids 25-212 of SEQ ID NO:91, SEQ ID NO:93 and amino acids 13-212 of SEQ ID NO:93.
8. The method of claim 1, wherein the tissue factor is a recombinant tissue factor consisting of amino acids 23 to 277 of SEQ ID NO:95.

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