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(54) **Title**: METHODS FOR MAINTAINING PEGYLATION OF POLYPEPTIDES

(57) **Abstract**: Described herein are methods for maintaining PEGylation and inhibiting dePEGylation of polypeptides, such as fibronectin-based scaffold proteins, during storage.

METHODS FOR MAINTAINING PEGYLATION OF POLYPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional application No. 61/487,027 filed on May 17, 2011, the contents of which are specifically incorporated by reference herein.

BACKGROUND

[0002] PEGylation is a process by which polyethylene glycol (PEG) polymer chains are covalently conjugated to other molecules such as drugs or proteins. This chemical modification confers on the conjugate molecules many of the properties of PEG polymers, including hydrophilicity, structural flexibility, high mobility in solution, and low toxicity. With these new properties, PEGylated therapeutic agents show improved efficacy as compared to their unconjugated counterparts, due to increased serum half life, water solubility, protection from proteolytic degradation, low immunogenicity, and/or stability of the PEGylated molecules.

[0003] It is generally desirable to maintain therapeutic agents in a PEGylated state, particularly when drugs are manufactured and stored for a period of time before use. However, PEGylation is a reversible reaction and dePEGylation has been observed during formulation development, stability monitoring, and storage of some therapeutic proteins. This creates a heterogeneous mixture of PEGylated and dePEGylated molecules, which may lose efficacy, safety, and other benefits of PEGylation. Accordingly, there remains a need for maintaining PEGylation of therapeutic molecules during storage of these molecules.

SUMMARY

[0004] The present invention relates to methods for maintaining the PEGylation state of PEGylated polypeptides during periods of storage. Disclosed herein are compositions comprising a polypeptide conjugated to a PEG moiety through a maleimide linker, wherein the composition has a pH between pH 2.0 and pH 6.0. The composition may have a pH between pH 3.0 and pH 5.0. The composition may have a pH between pH 3.5 and pH 4.5. In certain embodiments, less than 5% of the maleimide linkers are cleaved

over a 4, 8, 12 or more week storage period. The polypeptide may comprise a domain or region that binds specifically to a target protein, such as a tenth fibronectin type III (^{10}Fn3) domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM. The ^{10}Fn3 domain may comprise at least one loop region that differs from a naturally occurring loop region and at least one beta strand that differs from the naturally occurring beta strand. In certain embodiments, the ^{10}Fn3 domain does not contain a DK sequence in the C-terminal tail region. The C-terminal tail of the ^{10}Fn3 domain may comprise a cysteine residue, to which the PEG moiety is linked. In certain embodiments, less than 1% of the maleimide linkers are cleaved over a four week storage period. The polypeptide may further comprise a second ^{10}Fn3 domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM. The first and second ^{10}Fn3 domains may bind to different targets. The first and second ^{10}Fn3 domains may be connected by a polypeptide linker comprising from 1-30 amino acids. The polypeptide linker may be selected from the group consisting of: a glycine-serine linker, a glycine-proline linker, a proline-alanine linker and an Fn linker. The maleimide linker may form a thioether bond with a sulfhydryl group on the polypeptide. The ^{10}Fn3 domain may comprise at least two loop regions that differ from the corresponding naturally occurring loop regions. An exemplary composition comprises a polypeptide conjugated to a PEG moiety through a maleimide linker, wherein the composition has a pH between pH 3.0 and pH 5.0 and wherein (i) the polypeptide comprises a ^{10}Fn3 domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM; (ii) the ^{10}Fn3 domain comprises at least one loop region that differs from the naturally occurring corresponding loop region and at least one beta strand that differs from the naturally occurring corresponding beta strand; (iii) the ^{10}Fn3 domain does not contain a DK sequence in the C-terminal tail region; and the ^{10}Fn3 domain comprises a cysteine residue, to which the PEG moiety is linked. In certain embodiments, less than 5% of the maleimide linkers are cleaved over a four week storage period.

[0005] Further disclosed herein are methods for maintaining PEGylation of polypeptides during storage by storing the polypeptides in a solution buffered to a pH between 2.0-6.0, 2.0-5.0, 2.0-4.0, 2.0-3.0, 3.0-6.0, 3.0-5.0, 3.0-4.0, 3.5-4.5, 4.0-5.0, 4.5-

5.5, or 5.0-6.0. The polypeptides are conjugated to a polyethylene glycol (PEG) moiety through a maleimide linker. The maleimide linker may connect the PEG moiety to the polypeptide via a thioether bond with a sulfhydryl group on the polypeptide. In exemplary embodiments, less than 25%, 20%, 15%, 10%, 5%, 2%, 1%, 0.5%, 0.2% or 0.1% of the maleimide linkers are cleaved over a storage period of at least four weeks, eight weeks, six months, or one year.

[0006] In certain embodiments, the PEGylated polypeptides comprise a tenth fibronectin type III (^{10}Fn3) domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM. The ^{10}Fn3 domain may have a C-terminal tail that does not contain a DK sequence, which has been found to be susceptible to cleavage in certain instances at pHs below 6.0. The ^{10}Fn3 domain may contain a cysteine residue that serves as the site for attachment of the PEG moiety, preferably in the C-terminal tail region.

[0007] In certain embodiments, the PEGylated polypeptides are a multivalent polypeptide comprising two or more ^{10}Fn3 domains. Each ^{10}Fn3 domain may comprise an altered amino acid sequence relative to the wild-type sequence such that it binds to a target molecule with a K_D of less than 500 nM. The first and second ^{10}Fn3 domains bind to the same or different targets. The first and second ^{10}Fn3 domains may be connected by a polypeptide linker comprising from 1-30 amino acids. Exemplary polypeptide linkers include, for example, a glycine-serine linker, a glycine-proline linker, a proline-alanine linker or an Fn linker.

[0008] In exemplary embodiments, the PEGylated polypeptides are stored in a formulation comprising (a) 25 mM succinate, 5% sorbitol; (b) 10 mM sodium acetate, 5% mannitol; or (c) 10 mM sodium acetate/2% mannitol, 100 mM sodium chloride.

[0009] In certain embodiments, the concentration of PEGylated polypeptides in the storage solution is from 1-10 mg/mL, 1-5 mg/mL, 0.5-2 mg/mL, or 4-6 mg/mL, or is about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 mg/mL.

[0010] In certain embodiments, the methods involve storing the PEGylated polypeptides at a temperature from 4-30 °C, 4-25 °C, 4-15 °C, 4-10 °C, 10-30 °C, or 10-25 °C, or at 4, 10, 15, 20, 25 or 30 °C.

[0011] In another aspect, the application provides a method for improving the stability of PEGylated polypeptides in a solution, wherein the polypeptides are conjugated

to a polyethylene glycol (PEG) moiety through a maleimide linker, comprising the steps of: (a) determining the amount of PEG cleaved from the polypeptides over a fixed storage period in the solution; and (b) if PEG is cleaved from more than 5% of the polypeptides over the storage period, reformulating the PEGylated polypeptides in a storage solution buffered to a pH of between 2.0-6.0.

BRIEF DESCRIPTION OF DRAWINGS

[0012] Figure 1 illustrates the mechanism of Michael Addition, showing the ligation between a protein (R′) via its sulfhydryl group and the PEG molecule (R).

[0013] Figure 2A-B shows the RP-HPLC profile of a FBSP-P stability sample (10 mg/mL, formulated in 10 mM succinate, 5% (w/v) sorbitol, 1.2% (w/v) alanine, pH 6.0; incubated at 25 °C for four weeks). A: UV trace at 280 nm depicting the detection of free (unPEGylated) FBSP-P ADNECTIN™. B: ELSD trace showing the detection of free intact PEG.

[0014] Figure 3 shows UV (280 nm) profile of a FBSP-P stability sample (1 mg/mL, formulated in 25 mM succinate, 1% glycine, pH 7.5; incubated at 25 °C for two weeks) from an LC-MS analysis.

[0015] Figure 4 presents a graph showing an increase in mole % of free PEG in FBSP-P samples formulated at different pH, during 25 °C stability testing for two weeks. Protein was formulated at 1 mg/mL in 25 mM succinate, 5% (w/v) sorbitol, at the pH indicated.

[0016] Figure 5 is a graph showing an increase in mole % of free PEG in FBSP-P samples formulated at different pH, during 37 °C stability testing for two weeks. Protein was formulated at 1 mg/mL in 25 mM succinate, 5% (w/v) sorbitol, at the pH indicated.

[0017] Figure 6A-B shows the increase in % free (unPEGylated) ADNECTIN™ in FBSP-P samples formulated at different pH, during 25 °C stability testing for two weeks. Free ADNECTIN™ refers to the sum of both the monomeric and dimeric form of the unPEGylated protein. Protein was formulated at 1 mg/mL in 25 mM succinate, 5% (w/v) sorbitol, at the pH indicated.

[0018] Figure 7 shows the increase in % free (unPEGylated) ADNECTIN™ in FBSP-P samples formulated at different pH, during 37 °C stability testing for two weeks. Free ADNECTIN™ refers to the sum of both the monomeric and dimeric form of the

unPEGylated protein. Protein was formulated at 1 mg/mL in 25 mM succinate, 5% (w/v) sorbitol, at the pH indicated.

[0019] Figure 8A-D is a series of UV profiles (at 280 nm) of FBSP-V stressed samples at different pH values, obtained from LC-MS analysis. FBSP-V_{free} refers to the free (unPEGylated) ADNECTIN™ of FBSP-V. Only the pre-peak region of the UV profile is shown. All samples (10 mM sodium acetate, 5% mannitol) were stressed at 25 °C for a period of 6 months. Figure 8A shows the UV profile of a sample at 5 mg/mL protein concentration, pH 4.5. Figure 8B shows the UV profile of a sample at 5 mg/mL, pH 5.5. Figure 8C shows the UV profile of a sample at 5 mg/mL, pH 6.5. Figure 8D shows the UV profile a sample at 10 mg/mL, 10 mM NaOAc, 5% mannitol, pH 6.5.

[0020] Figure 9 illustrates the results of non-reduced SDS-PAGE analysis of FBSP-V stability samples at T=0 and T=6 months at 25 °C. Lanes 1 and 5 are FBSP-V formulated in 10 mM sodium acetate, 2% mannitol, 100 mM sodium chloride, pH 4.5 at 5 mg/mL. Lanes 2 and 6 are each FBSP-V formulated in 10 mM sodium acetate, 5% mannitol, pH 4.5, at 5 mg/mL protein concentration. Lanes 3 and 7 are FBSP-V formulated in 10 mM sodium acetate, 5% mannitol, pH 5.5, at 5 mg/mL protein concentration. Lanes 4 and 8 are FBSP-V formulated in 10 mM sodium acetate, 5% mannitol, pH 6.5, at 5 mg/mL protein concentration. All FBSP-V lanes were loaded equally at 10 µg each. The arrow indicates the presence of a band corresponding to the free FBSP-V_{free} ADNECTIN™.

[0021] Figure 10 is the UV profile (280 nm) of a stressed FBSP-V/I sample (10 mM acetate, 150 mM sodium chloride, pH 5.5, 5 mg/mL; 25C for 4 weeks). Peak assignments shown were based on LC-MS analysis.

[0022] Figure 11 shows a comparison of dePEGylation in several ADNECTINS™, as a measure of free PEG over the course of 1-4 weeks. The exemplary ADNECTINS™ are FBSP-P (samples F1, F2, and F3) stored at pH6.0; FBSP-V/I stored at pH 5.5 (VI); FBSP-V stored at pH 5.0 (V); and FBSP-E/I stored at pH 4.0 (EI).

[0023] Figure 12 shows the structure of a 2-branched PEG-MAL with a C2 alkyl linker, conjugated to a protein through cysteine residue.

[0024] Figure 13 shows HPLC profiles of a synthetic peptide conjugated to three different 40kD PEG-MALs in a composition at pH 8.3 and at T=0. The profiles from top to bottom are those of: (1) free peptide; (2) peptide conjugated to ME-400MA (C2 linker)

linear PEG; (3) peptide conjugated to GLE-400MA3 (C5 linker) 2-branched PEG; and peptide conjugated to GLE-400MA (C2 linker) 2-branched PEG.

[0025] Figure 14 shows HPLC profiles of a synthetic peptide conjugated to three different 40kD PEG-MALs in a composition at pH 8.3 (same as in Figure 13), after one week at 37 °C. The profiles from top to bottom are those of: (1) free peptide; (2) peptide conjugated to ME-400MA (C2 linker) linear PEG; (3) peptide conjugated to GLE-400MA3 (C5 linker) 2-branched PEG; and peptide conjugated to GLE-400MA (C2 linker) 2-branched PEG.

[0026] Figure 15 shows the percentage of free peptide observed in samples of a peptide conjugated to three different 40kD PEG-MALs in compositions at pH 8.3, at T0 and T=1 week after heat stress at 37 °C (histogram based on results shown in Figures 13 and 14).

[0027] Figure 16 shows HPLC profiles of samples of PEGylated peptides at pH 5.5 or pH 8.0 at T=0 or after 1 week at 37 °C.

[0028] Figure 17 is a histogram showing the increased percentage of free C7 protein derived from PEGylated C7 proteins after one week of heat stress of the PEGylated C7 proteins at 37 °C relative to T0, comparing samples formulated in pH 4.5 sodium acetate and pH 8.0 Tris.

DETAILED DESCRIPTION

Overview

[0029] The methods of the present application may be used to maintain a polyethylene glycol (PEG) moiety on PEGylated conjugates, particularly protein or peptide therapeutics, during manufacture and/or storage of the PEGylated conjugates. These methods have broad applicability to proteins and peptides that have been PEGylated to overcome issues with stability, degradation, clearance, and tolerance in subjects. The process of PEGylation links polyethylene glycol chains to candidate therapeutics to produce larger conjugates that show improved efficacy as compared to their unconjugated counterparts, due to increased serum half life, increased solubility, increased protection from proteolytic degradation, reduced immunogenicity, and/or increased stability of the PEGylated molecules.

[0030] The present application describes methods to preserve PEGylation and all of its associated benefits and methods to inhibit dePEGylation of PEGylated conjugates. Specifically, the application provides methods to inhibit cleavage of PEG moieties conjugated to polypeptides through a maleimide linker by formulating and storing the PEGylated polypeptides in a solution buffered to a pH value between pH 2.0 and pH 6.0. The methods described herein are based on the observation that certain PEGylated conjugates are subject to significant cleavage of the PEG moiety from the polypeptide resulting in regeneration of the free (unPEGylated) polypeptide and formation of protein aggregates and/or disulfide-linked polypeptide dimers. It was observed that the amount of dePEGylation depended on the pH of the formulation, and that formulations with higher pHs led to higher levels of dePEGylation. As dePEGylation has been found to be most prominent at higher pH (≥6), the present methods inhibit dePEGylation by maintaining PEGylated polypeptide conjugates at a pH below 6.0. Notably, the methods may apply to PEGylated polypeptides that are conjugated to PEG through a maleimide moiety.

Definitions

[0031] By a "polypeptide" is meant any sequence of two or more amino acids, regardless of length, post-translation modification, or function. "Polypeptide", "peptide", and "protein" are used interchangeably herein. Polypeptides can include natural amino acids and non-natural amino acids such as those described in U.S. Patent No. 6,559,126, incorporated herein by reference. Polypeptides can also be modified in any of a variety of standard chemical ways (*e.g.*, an amino acid can be modified with a protecting group; the carboxy-terminal amino acid can be made into a terminal amide group; the amino-terminal residue can be modified with groups to, *e.g.*, enhance lipophilicity; or the polypeptide can be chemically glycosylated or otherwise modified to increase stability or *in vivo* half-life). Polypeptide modifications can include the attachment of another structure such as a cyclic compound or other molecule to the polypeptide and can also include polypeptides that contain one or more amino acids in an altered configuration (*i.e.*, R or S; or, L or D).

[0032] "Percent (%) amino acid sequence identity" herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid

residues in a selected sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR®) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are obtained as described below by using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087, and is publicly available through Genentech, Inc., South San Francisco, Calif. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0033] For purposes herein, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0034] The "half-life" of a polypeptide is the time taken for the concentration of the polypeptide to fall to half its original value. The "serum half-life" of a polypeptide can generally be defined as the time taken for the serum concentration of the polypeptide to be reduced by 50%, *in vivo*, for example due to degradation of the polypeptide and/or clearance or sequestration of the polypeptide by natural mechanisms. The half-life can be

determined in any manner known per se, such as by pharmacokinetic analysis. Suitable techniques for determining half-life, *e.g.*, serum half-life, will be clear to the person skilled in the art, and may, for example, generally involve the steps of administering a suitable dose of a polypeptide to a primate; collecting blood samples or other samples from said primate at regular intervals; determining the level or concentration of the polypeptide in said blood sample; and calculating, from (a plot of) the data thus obtained, the time until the level or concentration of the polypeptide has been reduced by 50% compared to the initial level upon dosing. Methods for determining half-life may be found, for example, in Kenneth et al., *Chemical Stability of Pharmaceuticals: A Handbook for Pharmacists* (1986); Peters et al., *Pharmacokinetic Analysis: A Practical Approach* (1996); and Gibaldi, M. et al., *Pharmacokinetics*, 2nd Rev. Edition, Marcel Dekker (1982).

[0035] Half-life can be expressed using parameters such as the t1/2-alpha, t1/2-beta and the area under the curve (AUC). In the present specification, an "increase in half-life" refers to an increase in any one of these parameters, any two of these parameters, or in all three these parameters. In certain embodiments, an increase in half-life refers to an increase in the t1/2-beta, either with or without an increase in the t1/2-alpha and/or the AUC or both.

[0036] "Shelf-life" of a pharmaceutical product *e.g.*, a PEGylated polypeptide, is the length of time the product is stored before decomposition occurs. For example, shelf-life may be defined as the time for decomposition of 0.1%, 0.5%, 1%, 5%, or 10% of the product.

[0037] A "purified" polypeptide or PEGylated polypeptide is preferably at least 85% pure, more preferably at least 95% pure, and most preferably at least 98% or 99% pure. Regardless of the exact numerical value of the purity, the polypeptide or PEGylated polypeptide is sufficiently pure for use as a pharmaceutical product.

Methods for Inhibiting DePEGylation

[0038] Given the benefits of PEGylation, it is clear that dePEGylation of PEG-protein conjugates is undesirable in many situations. DePEGylation is defined as the loss of at least one PEG moiety from a PEGylated conjugate molecule, resulting in the regeneration of the intact free polypeptide and the intact free PEG moiety. This reaction may result in

decreased bioavailability, decreased blood circulation, increased immunogenicity, and decreased efficacy of a therapeutic agent, as compared to its PEGylated form. Following dePEGylation, the free polypeptides may undesirably form dimers or aggregates. For example, when the PEG molecules are attached to cysteine residues on protein molecules, dePEGylation exposes free cysteine residues that could interact with one another through intermolecular disulfide linkages to form protein dimers. Alternatively, dePEGylation may result in exposure of hydrophobic surfaces that could lead to protein aggregation.

[0039] DePEGylation may be measured using methods known in the art, such as reverse phase high performance liquid chromatography (RP-HPLC). Dual absorbance detectors may be used, for example, UV absorbance may be used for the detection of polypeptide species, while an evaporative light scattering detector (ELSD) may be used to detect the PEG moieties. In addition, liquid chromatograph-mass spectrometry (LC-MS) may be used to determine the amount of free protein molecules as well as characterize the form of the free protein as monomers, dimers, or aggregates. RP-HPLC may be used to characterize the integrity of the free PEG released from the conjugate using retention time of the released PEG as compared to the retention time for a PEG standard. For those PEGylated conjugates that were generated by maleimide chemistry, the free PEG produced by dePEGylation of the conjugate may contain the maleimide functional group.

[0040] Factors which affect PEGylation include, but are not limited to, conditions of the original PEGylation reaction, length of storage of the PEGylated molecules, storage temperature, composition of the buffers and/or solutions in which the molecules are made and/or stored, pH of the storage buffers and/or solutions, and identity of the proteins that have been conjugated to PEG.

[0041] In some embodiments of the present application, PEGylation is maintained by storing the PEGylated polypeptides in a solution buffered to a pH value between pH 2.0 and pH 6.0. In some embodiments, the PEGylated polypeptides are stored in a solution buffered to a pH value between pH 2.0-6.0, 2.0-5.0, 2.0-4.0, 2.0-3.0, 2.0-2.5, 3.0-6.0, 3.0-5.0, 3.0-4.0, 3.0-3.5, 4.0-6.0, 4.0-5.0, 4.0-4.5, 2.5-3.5, or 2.5-3.5. In some embodiments, the PEGylated polypeptides are stored in a solution buffered to a pH of 4.0, 4.5, 5.0, 5.5, or 6.0.

[0042] Suitable formulations for storing PEGylated polypeptides in accordance with the methods described herein are pharmaceutically acceptable compositions comprising a

PEGylated polypeptide as described herein, wherein the composition is essentially endotoxin or pyrogen free. Formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0043] Therapeutic formulations comprising PEGylated polypeptides are prepared for storage by mixing the PEGylated polypeptides having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Osol, A., ed., *Remington's Pharmaceutical Sciences*, 16th Edition (1980)), in the form of aqueous solutions, lyophilized or other dried formulations. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, sodium acetate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyidimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as alanine, glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars or sugar alcohols such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as Tween, PLURONIC® or polyethylene glycol (PEG).

[0044] Suitable solutions for storing the PEGylated polypeptides generally contain from 1-100 mM, 10-100 mM, 25-100 mM, 50-100 mM, 1-50 mM, 1-25 mM, 1-10 mM, 10-50 mM 10-25 mM, 10-20 mM, 10-15 mM of a buffering agent. In certain embodiments, the solutions for storing the PEGylated polypeptides contain 10 mM buffer or 25 mM of a buffering agent. Exemplary buffering agents include, for example, citrate, histidine, succinate or sodium acetate.

[0045] Exemplary formulations for storing PEGylated polypeptides may be selected from (a) 25mM succinate, 5% sorbitol; (b) 10mM sodium acetate, 5% mannitol; and (c) 10 mM sodium acetate/2% mannitol, 100 mM sodium chloride.

[0046] In certain embodiments, the concentration of PEGylated polypeptide in a formulation for storage ranges from 0.5-15 mg/mL, 0.5-5 mg/mL, 0.5-2 mg/mL, 1-10 mg/mL, 1-5 mg/mL, 1-2 mg/Ml, 3-10 mg/mL, 3-8 mg/mL, 3-6 mg/mL, 3-5 mg/mL, 4-10 mg/mL, 4-8 mg/mL, 4-6 mg/mL, 5-10 mg/mL, 5-8 mg/mL, or 5-6 mg/mL. In other embodiments, the concentration of PEGylated polypeptide in a formulation for storage may be about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 mg/mL.

[0047] In certain embodiments, the methods described herein may be used to maintain PEGylation and/or inhibit dePEGylation of polypeptides having one, two, three, four or more PEG moieties per polypeptide molecule. In exemplary embodiments, the methods described herein are used in connection with PEGylated polypeptides having only a single PEG per polypeptide.

[0048] Formulations of PEGylated polypeptides may be suitable for administration via any desirable route. For example, the formulations may be suitable for administration intravenously as a bolus or by continuous infusion over a period of time, by intramuscular, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes.

[0049] In certain embodiments, at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% of PEGylation is maintained for at least 2 weeks, 4 weeks, 3 months, 6 months, 1 year or more. PEGylation may also be maintained for over 1 year, or for as long as the activity of the PEGylated conjugate remains at therapeutically effective levels. There percentage of PEGylation maintained is determined relative to the initial level of PEGylation of the PEGylated polypeptide. For example, at least 98% of PEGylation is maintained for a two week period if less than 2% of the polypeptides have lost a PEG moiety after storage for two weeks as compared to the level of PEGylation at time zero.

[0050] The methods described herein may involve maintaining PEGylation during storage of a PEGylated polypeptide at a fixed temperature over time or during storage at variable temperatures. For example, PEGylation may be maintained during storage at 4 ºC, 15 ºC, 20 ºC, 25 ºC, 30 ºC, or 37 ºC. Alternatively, PEGylation may be maintained, for example, during storage at 4 ºC for 2 weeks followed by storage at 25 ºC for 1 week. In any case, the level of dePEGylation should be determined relative the initial level of PEGylation of the polypeptide.

[0051] In certain embodiments, the methods described herein may involve first determining whether a PEGylated polypeptide is subject to dePEGylation at an undesirable level when stored at pH ≥ 6.0. For example, the methods may comprise determining the level of dePEGylation of a PEGylated polypeptide during storage at pH ≥ 6.0. If the level of dePEGylation is greater than 1%, 2%, 5%, 10% or 15%, the PEGylated polypeptide is reformulated in a solution having a pH ≤ 6.0. Similarly, the methods may involve monitoring the PEGylation level of a PEGylated polypeptide formulated in a solution having a pH ≥ 6.0 for a period of time. If more than 1%, 2%, 5%, 10% or 15% of the polypeptide is dePEGylated over a period of 2 weeks, 4 weeks, 3 months or 6 months, then the polypeptide may be reformulated in a solution having a pH ≤ 6.0.

[0052] In one embodiment, dePEGylation may be inhibited by a method comprising the steps of: (a) measuring PEGylation of the PEGylated polypeptides at an initial reference time point; (b) comparing PEGylation of the PEGylated polypeptides after an interval; (c) reducing pH of the solution to a value between pH 2.0 and pH 6.0; and (d) comparing PEGylation of the PEGylated polypeptides after an interval, wherein a decrease in dePEGylation of the PEGylated polypeptides after step (c) indicates inhibition of dePEGylation. In another embodiment, a method for inhibiting dePEGylation when storing PEGylated polypeptides may comprise: (a) storing the PEGylated polypeptides in a solution; (b) monitoring the PEGylation of the PEGylated polypeptides; and (c) lowering the pH of the solution to a value in between pH 2.0 and pH 6.0, wherein the pH is a value sufficient to inhibit dePEGylation.

PEGylated Polypeptides

[0053] The methods and formulations described herein may be applied to any PEGylated polypeptide. The methods described herein are particularly suited to maintaining PEGylation of polypeptides that are susceptible to dePEGylation when stored in solutions having a pH ≥ 6.0. In exemplary embodiments, the PEGylated polypeptides are therapeutic proteins, such as, for example, interferon alpha, adenosine deaminase, L-asparaginase, granulocyte colony-stimulating factor and antibodies, such as, for example, anti-tumor necrosis factor alpha antibodies. A PEGylated protein may be a protein binding specifically to a target, such as an antibody or an antigen binding fragment

thereof and may be any of the following: a Fab, a F(ab')2, an Fv, a single chain Fv fragment, a single domain antibody or a variant thereof (*e.g.*, a heavy or light chain variable domain monomer or dimer, *e.g.*, V_H, V_{HH}); a single chain Fc fragment, a diabody (dAb), a camelid antibody; one, two, or all three complementarity determining regions (CDRs) grafted onto a repertoire of VH or VL domains, or other scaffolds, an Affibody molecule (*e.g.*, an Affibody protein Z scaffold or other molecules as described, *e.g.*, in Lee et al., *Clin. Cancer Res.*, 14(12):3840-3849 (2008); Ahlgren et al., *Nucl. Med.*, 50:781-789 (2009)), lipocalin, ankyrin repeats, LDL receptor domain, RNA aptamer, PDZ domain, a multispecific (*e.g.*, bivalent or bispecific) antibody or fragment thereof, a human antibody or antigen binding fragment thereof, a humanized antibody or antigen binding fragment thereof, a chimeric antibody or antigen binding fragment thereof, a camelid antibody or antigen binding fragment thereof, a shark antibody or antigen binding fragment thereof, or an *in vitro* generated antibody or antigen binding fragment thereof.

[0054] In an exemplary embodiment, the PEGylated polypeptide is a fibronectin based scaffold protein (FBSP) as described further below. Exemplary FBSP include, for example, monovalent FBSP that bind to, for example, PCSK9 (FBSP-P) or VEGFR2 (FBSP-V), or multivalent FBSP, including, for example, bivalent FBSP that bind to VEGFR2 and IGF-1R (FBSP-VI).

Fibronectin-Based Scaffold Proteins (FBSP)

[0055] In some embodiments, the methods disclosed herein may be used to maintain PEGylation of fibronectin based scaffold proteins. This family of proteins is capable of evolving to bind any compound of interest. These proteins generally make use of a scaffold derived from a fibronectin type III (Fn3) or Fn3-like domain and function in a manner characteristic of natural or engineered antibodies (that is, polyclonal, monoclonal, or single-chain antibodies) and, in addition, possess structural advantages. Specifically, the structure of these antibody mimics has been designed for optimal folding, stability, and solubility, even under conditions that normally lead to the loss of structure and function in antibodies. An example of fibronectin-based scaffold proteins are ADNECTINS™ (Adnexus, a wholly owned subsidiary of Bristol-Myers Squibb).

Fibronectin-based scaffold proteins and ADNECTINS™ may be monovalent or multivalent.

[0056] An Fn3 domain is small, monomeric, soluble, and stable. It lacks disulfide bonds and, therefore, is stable under reducing conditions. The overall structure of Fn3 resembles the immunoglobulin fold. Fn3 domains comprise, in order from N-terminus to C-terminus, a beta or beta-like strand, A; a loop, AB; a beta or beta-like strand, B; a loop, BC; a beta or beta-like strand, C; a loop, CD; a beta or beta-like strand, D; a loop, DE; a beta or beta-like strand, E; a loop, EF; a beta or beta-like strand, F; a loop, FG; and a beta or beta-like strand, G. The seven antiparallel β-strands are arranged as two beta sheets that form a stable core, while creating two "faces" composed of the loops that connect the beta or beta-like strands. Loops AB, CD, and EF are located at one face and loops BC, DE, and FG are located on the opposing face. Any or all of loops AB, BC, CD, DE, EF and FG may participate in ligand binding. There are at least 15 different modules of Fn3, and while the sequence homology between the modules is low, they all share a high similarity in tertiary structure.

[0057] The amino acid sequence of the naturally occurring human tenth fibronectin type III domain, *i.e.*, the tenth module of human Fn3 (^{10}Fn3), is set forth in SEQ ID NO: 1:

*VSDVPRDL*EVVAATPTSLLI**SWDAPAVTVR**YYRITYGETGGNSPVQEFTV**PGSKS T** ATISGLKPGVDYTITVYAV**TGRGDSPASSKP**ISINYRT (SEQ ID NO: 1) (the AB, CD and EF loops are underlined, and the BC, FG, and DE loops are emphasized in bold).

[0058] In SEQ ID NO: 1, the AB loop corresponds to residues 15-16, the BC loop corresponds to residues 21-30, the CD loop corresponds to residues 39-45, the DE loop corresponds to residues 51-56, the EF loop corresponds to residues 60-66, and the FG loop corresponds to residues 76-87. (Xu et al., *Chemistry & Biology*, 9:933-942 (2002)). The BC, DE and FG loops align along one face of the molecule and the AB, CD and EF loops align along the opposite face of the molecule. In SEQ ID NO: 1, beta strand A corresponds to residues 9-14, beta strand B corresponds to residues 17-20, beta strand C corresponds to residues 31-38, beta strand D corresponds to residues 46-50, beta strand E corresponds to residues 57-59, beta strand F corresponds to residues 67-75, and beta

strand G corresponds to residues 88-94. The strands are connected to each other through the corresponding loop, *e.g.*, strands A and B are connected via loop AB in the formation strand A, loop AB, strand B, etc. The first 8 amino acids of SEQ ID NO:1 (italicized above) may be deleted while still retaining binding activity of the molecule. Residues involved in forming the hydrophobic core (the "core amino acid residues") include the amino acids corresponding to the following amino acids of SEQ ID NO: 1: L8, V10, A13, L18, I20, W22, Y32, I34, Y36, F48, V50, A57, I59, L62, Y68, I70, V72, A74, I88, I90 and Y92, wherein the core amino acid residues are represented by the single letter amino acid code followed by the position at which they are located within SEQ ID NO: 1. See *e.g.*, Dickinson et al., *J. Mol. Biol.*, 236:1079-1092 (1994).

[0059] ^{10}Fn3 are structurally analogous to antibodies, specifically the variable region of an antibody. While ^{10}Fn3 domains may be described as "antibody mimics" or "antibody-like proteins", they do offer a number of advantages over conventional antibodies. In particular, they exhibit better folding and thermostability properties as compared to antibodies, and they lack disulphide bonds, which are known to impede or prevent proper folding under certain conditions.

[0060] The BC, DE, and FG loops of ^{10}Fn3 are analogous to the complementary determining regions (CDRs) from immunoglobulins. Alteration of the amino acid sequence in these loop regions changes the binding specificity of ^{10}Fn3. ^{10}Fn3 domains with modifications in the AB, CD and EF loops may also be made in order to produce a molecule that binds to a desired target. The protein sequences outside of the loops are analogous to the framework regions from immunoglobulins and play a role in the structural conformation of the ^{10}Fn3. Alterations in the framework-like regions of ^{10}Fn3 are permissible to the extent that the structural conformation is not so altered as to disrupt ligand binding. Methods for generating ^{10}Fn3 ligand specific binders have been described in PCT Publication Nos. WO 00/034787, WO 01/64942, and WO 02/032925, disclosing high affinity TNFα binders, PCT Publication Nos. WO 2005/56764 and WO 2008/097497, disclosing high affinity VEGFR2 binders, and PCT Publication No. WO 2008/066752, disclosing high affinity IGFIR binders. Additional references discussing ^{10}Fn3 binders (which may benefit from the methods described herein) and methods of selecting binders include PCT Publication Nos. WO 98/056915, WO 02/081497, WO 2008/031098, U.S. Publication No. 2003/186385, PCT Publication Nos. WO

2009/102421, WO 2009/142773, WO2010/060095, U.S. Patent Nos. 6,818,418, 6,673,901, 7,115,396, PCT Publication Nos. WO 2010/0273261, WO 2011/103105, WO 2011/130354, WO 2011/140086, WO 2011/150133, WO 2010/051274, WO 2010/051310, WO 2009/086116, WO 2009/086116, WO 2010/093627, WO 2011/137319, WO 2012/016245, WO 98/056915, WO 02/081497, WO 2008/031098, U.S. Publication No. 2003/186385, PCT Publication Nos. WO 2011/130324, WO 2011/130328, WO 2009/083804, WO 2009/133208, WO 2010/093627, WO 2011/051333, WO 2011/051466, and WO 2011/092233.

[0061] As described above, amino acid residues corresponding to residues 21-30, 51-56, and 76-87 of SEQ ID NO: 1 define the BC, DE and FG loops, respectively. However, it should be understood that not every residue within the loop region needs to be modified in order to achieve a ^{10}Fn3 binder having strong affinity for a desired target. For example, in many cases, only residues corresponding to amino acids 23-30 of the BC loop and 52-55 of the DE loop are modified and result in high affinity ^{10}Fn3 binders. Accordingly, in certain embodiments, the BC loop may be defined by amino acids corresponding to residues 23-30 of SEQ ID NO: 1, and the DE loop may be defined by amino acids corresponding to residues 52-55 of SEQ ID NO: 1. Additionally, insertions and deletions in the loop regions may also be made while still producing high affinity ^{10}Fn3 binders.

[0062] Accordingly, in some embodiments, one or more loops selected from BC, DE, and FG may be extended or shortened in length relative to the corresponding loop in wild-type human ^{10}Fn3. In some embodiments, the length of the loop may be extended by from 2-25 amino acids. In some embodiments, the length of the loop may be decreased by 1-11 amino acids. In particular, the FG loop of ^{10}Fn3 is 12 residues long, whereas the corresponding loop in antibody heavy chains ranges from 4-28 residues. To optimize antigen binding, therefore, the length of the FG loop of ^{10}Fn3 may be altered in length as well as in sequence to cover the CDR3 range of 4-28 residues to obtain the greatest possible flexibility and affinity in antigen binding. In some embodiments, the integrin-binding motif "arginine-glycine-aspartic acid" (RGD), located at residues 79-81 of SEQ ID NO: 1, may be modified in order to disrupt integrin binding. For example, the RGD sequence may be replaced with SGE.

[0063] The non-ligand binding sequences of ^{10}Fn3, *i.e.*, the "^{10}Fn3 scaffold", may be altered provided that the ^{10}Fn3 retains ligand binding function and/or structural stability. In some embodiments, one or more of Asp 7, Glu 9, and Asp 23 are replaced by another amino acid, such as, for example, a non-negatively charged amino acid residue (*e.g.*, Asn, Lys, etc.). These mutations have been reported to have the effect of promoting greater stability of the mutant ^{10}Fn3 at neutral pH as compared to the wild-type form (See, PCT Publication No. WO 02/04523). A variety of additional alterations in the ^{10}Fn3 scaffold that are either beneficial or neutral have been disclosed. See, for example, Batori et al., *Protein Eng.*, 15(12):1015-1020 (2002); Koide et al., *Biochemistry*, 40(34):10326-10333 (2001).

[0064] Residues involved in forming the hydrophobic core (the "core amino acid residues") in SEQ ID NO: 1 include the amino acids corresponding to the following amino acids of SEQ ID NO: 1: L8, V10, A13, L18, I20, W22, Y32, I34, Y36, F48, V50, A57, I59, L62, Y68, I70, V72, A74, I88, I90 and Y92, wherein the core amino acid residues are represented by the single letter amino acid code followed by the position at which they are located within SEQ ID NO: 1. See *e.g.*, Dickinson et al., *J. Mol. Biol.*, 236:1079-1092 (1994). In some embodiments, the hydrophobic core amino acids are not modified relative to the wild-type sequence. In other embodiments, the following hydrophobic amino acids may be mutated: W22 and/or L62.

[0065] The ^{10}Fn3 scaffold may be modified by one or more conservative substitutions. As many as 5%, 10%, 20% or even 30% or more of the amino acids in the ^{10}Fn3 scaffold may be altered by a conservative substitution without substantially altering the affinity of the ^{10}Fn3 for a ligand. In certain embodiments, the scaffold may comprise anywhere from 0-15, 0-10, 0-8, 0-6, 0-5, 0-4, 0-3, 1-15, 1-10, 1-8, 1-6, 1-5, 1-4, 1-3, 2-15, 2-10, 2-8, 2-6, 2-5, 2-4, 5-15, or 5-10 conservative amino acid substitutions. In certain embodiments, the substitutions in the scaffold do not include substitutions of the hydrophobic core amino acid residues. Preferably, the scaffold modification reduces the binding affinity of the ^{10}Fn3 binder for a ligand by less than 100-fold, 50-fold, 25-fold, 10-fold, 5-fold, or 2-fold. It may be that such changes will alter the immunogenicity of the ^{10}Fn3 *in vivo*, and where the immunogenicity is decreased, such changes will be desirable. As used herein, "conservative substitutions" refers to replacement of one amino acid with another amino acid that is physically or functionally similar to the amino

acid being replaced. That is, a conservative substitution and its reference residue have similar size, shape, electric charge, chemical properties including the ability to form covalent or hydrogen bonds, or the like. Preferred conservative substitutions are those fulfilling the criteria defined for an accepted point mutation in Dayhoff et al., *Atlas of Protein Sequence and Structure*, 5:345-352 (1978 & Supp.). Examples of conservative substitutions are substitutions within the following groups: (a) valine, glycine; (b) glycine, alanine; (c) valine, isoleucine, leucine; (d) aspartic acid, glutamic acid; (e) asparagine, glutamine; (f) serine, threonine; (g) lysine, arginine, methionine; and (h) phenylalanine, tyrosine.

[0066] In some embodiments, a fibronectin based scaffold protein comprises a ^{10}Fn3 domain having at least 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, or 90% identity to the human ^{10}Fn3 domain having the amino acid sequence of SEQ ID NO: 1. Much of the variability will generally occur in one or more of the loops. Each of the beta or beta-like strands of a ^{10}Fn3 domain in a fibronectin based scaffold protein may comprise, consist essentially of, or consist of an amino acid sequence that is at least 80%, 85%, 90%, 95% or 100% identical to the sequence of a corresponding beta or beta-like strand of SEQ ID NO: 1, provided that such variation does not disrupt the stability of the polypeptide in physiological conditions. In exemplary embodiments, the ^{10}Fn3 domain binds to a desired target with a K_D of less than 500 nM, 100 nM, 10 nM, 1 nM, 500 pM, 100 pM or less. In exemplary embodiments, the fibronectin based scaffold protein binds specifically to a target that is not bound by a wild-type ^{10}Fn3 domain, particularly the wild-type human ^{10}Fn3 domain.

[0067] In some embodiments, the fibronectin based scaffold protein comprises a ^{10}Fn3 domain having an amino acid sequence at least 80, 85, 90, 95, 98, or 100% identical to the non-loop regions of SEQ ID NO: 1, wherein at least one loop selected from BC, DE, and FG is altered. In some embodiments, the altered BC loop has up to 10 amino acid substitutions, up to 4 amino acid deletions, up to 10 amino acid insertions, or a combination thereof. In some embodiments, the altered DE loop has up to 6 amino acid substitutions, up to 4 amino acid deletions, up to 13 amino acid insertions, or a combination thereof. In some embodiments, the FG loop has up to 12 amino acid substitutions, up to 11 amino acid deletions, up to 25 amino acid insertions, or a combination thereof.

[0068] In some embodiments, the disclosure provides polypeptides comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain comprises a loop, AB; a loop, BC; a loop, CD; a loop, DE; a loop, EF; and a loop, FG; and has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain. In some embodiments, the BC and FG loops are altered. In some embodiments, the BC, DE, and FG loops are altered, *i.e.*, the ^{10}Fn3 domain comprises non-naturally occurring loops. By "altered" is meant one or more amino acid sequence alterations relative to a template sequence (*i.e.*, the corresponding human fibronectin domain) and includes amino acid additions, deletions, and substitutions. Altering an amino acid sequence may be accomplished through intentional, blind, or spontaneous sequence variation, generally of a nucleic acid coding sequence, and may occur by any technique, for example, PCR, error-prone PCR, or chemical DNA synthesis.

[0069] In certain embodiments, antibody-like proteins based on the ^{10}Fn3 scaffold can be defined generally by the following core amino acid sequence:

EVVAAT$(X)_a$SLLI$(X)_x$YYRITYGE$(X)_b$QEFTV$(X)_y$ATI$(X)_c$DYTITVYAV$(X)_z$ISINYR T (SEQ ID NO: 2)

[0070] In SEQ ID NO: 2, the AB loop is represented by X_a, the CD loop is represented by X_b, the EF loop is represented by X_c, the BC loop is represented by X_x, the DE loop is represented by X_y, and the FG loop is represented by X_z. X represents any amino acid and the subscript following the X represents an integer of the number of amino acids. In particular, *a* may be anywhere from 1-15, 2-15, 1-10, 2-10, 1-8, 2-8, 1-5, 2-5, 1-4, 2-4, 1-3, 2-3, or 1-2 amino acids; and *b, c, x, y* and *z* may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. In preferred embodiments, *a* is 2 amino acids, *b* is 7 amino acids, *c* is 7 amino acids, *x* is 9 amino acids, *y* is 6 amino acids, and *z* is 12 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In an exemplary embodiment, the sequences of the beta strands may

have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In certain embodiments, the hydrophobic core amino acid residues are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues. In exemplary embodiments, the BC, DE, and FG loops as represented by $(X)_x$, $(X)_y$, and $(X)_z$, respectively, are replaced with polypeptides comprising BC, DE and FG loop sequences that bind to specific targets.

[0071] In certain embodiments, Antibody-like proteins based on the ^{10}Fn3 scaffold can be defined generally by the sequence:

EVVAATPTSLLI$(X)_x$YYRITYGETGGNSPVQEFTV$(X)_y$ATISGLKPGVDYTITVYAV $(X)_z$ISINYRT (SEQ ID NO: 3)

[0072] In SEQ ID NO: 3, the BC loop is represented by X_x, the DE loop is represented by X_y, and the FG loop is represented by X_z. X represents any amino acid and the subscript following the X represents an integer of the number of amino acids. In particular, x, y and z may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. In preferred embodiments, x is 9 amino acids, y is 6 amino acids, and z is 12 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In an exemplary embodiment, the sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In certain embodiments, the core amino acid residues are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues. In exemplary embodiments, the BC, DE, and FG loops as represented by $(X)_x$, $(X)_y$, and $(X)_z$, respectively, are replaced with polypeptides comprising BC, DE and FG loop sequences that bind to specific targets.

[0073] A ^{10}Fn3 domain as described herein may optionally contain a modified N- and/or C-terminal sequence. For example, with reference to SEQ ID NO: 2 or 3, the ^{10}Fn3 domain may comprise an N-terminal extension and/or a C-terminal tail as described further below.

[0074] In certain embodiments, the ^{10}Fn3 domain as shown in SEQ ID NO: 2 or 3 may optionally comprise an N-terminal extension of from 1-20, 1-15, 1-10, 1-8, 1-5, 1-4, 1-3, 1-2, or 1 amino acids in length. Exemplary N-terminal extensions include (represented by the single letter amino acid code) M, MG, G, MGVSDVPRDL (SEQ ID NO: 17), VSDVPRDL (SEQ ID NO: 18), and GVSDVPRDL (SEQ ID NO: 19), or N-terminal truncations of any one of SEQ ID NOs: 17, 18 or 19. Other suitable N-terminal extensions include, for example, X_nSDVPRDL (SEQ ID NO: 20), X_nDVPRDL (SEQ ID NO: 21), X_nVPRDL (SEQ ID NO: 22), X_nPRDL (SEQ ID NO: 23), X_nRDL (SEQ ID NO: 24), X_nDL (SEQ ID NO: 25), or X_nL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly. When a Met-Gly sequence is added to the N-terminus of a ^{10}Fn3 domain, the M will usually be cleaved off, leaving a G at the N-terminus.

[0075] In certain embodiments, the ^{10}Fn3 domain as shown in SEQ ID NO: 2 or 3 may optionally comprise a C-terminal tail of from 1-20, 1-15, 1-10, 1-8, 1-5, or 1-4 amino acids in length. Specific examples of tail sequences include, for example, polypeptides comprising, consisting essentially of, or consisting of, EIEK (SEQ ID NO: 5), EGSGC (SEQ ID NO: 10), EIEKPCQ (SEQ ID NO: 11), EIEKPSQ (SEQ ID NO: 26), EIEKP (SEQ ID NO: 27), EIEKPS (SEQ ID NO: 28), EIEKPC (SEQ ID NO: 12), EIDKPSQ (SEQ ID NO: 14), or EIDKPSQLE (SEQ ID NO: 16). In certain embodiments, the ^{10}Fn3 domain comprises a C-terminal tail comprising a sequence $X(ED)_n$, wherein n is an integer from 2-10, 2-8, 2-5, 3-10, 3-8, 3-7, 3-5, 4-7, or wherein n is 2, 3, 4, 5, 6, 7, 8, 9 or 10, and X is optional, and when present is an E, I or EI. Such ED repeat tails may enhance solubility and/or reduce aggregation of the ^{10}Fn3 domain. In exemplary embodiments, the C-terminal tail comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO: 11. In preferred embodiments, the C-terminal sequences lack DK sequences. In exemplary embodiments, the C-terminal tail comprises a residue that facilitates modification by PEG, *i.e.*, a lysine or cysteine residue. In

preferred embodiments, the C-terminal tail lacks a DK sequence and comprises a cysteine residue.

[0076] In certain embodiments, the fibronectin based scaffold proteins comprise a ^{10}Fn3 domain having both an N-terminal extension and a C-terminal tail.

Multivalent Fibronectin Based Scaffold Proteins

[0077] In certain embodiments, the fibronectin based scaffold protein is a multivalent protein that comprises two or more ^{10}Fn3 domains as described herein. For example, a multivalent fibronectin based scaffold protein may comprise 2, 3 or more ^{10}Fn3 domains that are covalently associated. In exemplary embodiments, the fibronectin based scaffold protein is a bispecific or dimeric protein comprising two ^{10}Fn3 domains. In certain embodiments, a multivalent fibronectin based protein scaffold comprises a first ^{10}Fn3 domain that binds to a first target molecule and a second ^{10}Fn3 domain that binds to a second target molecule. The first and second target molecules may be the same or different target molecules. When the first and second target molecules are the same, the ^{10}Fn3 domains, *i.e.*, the binding loops, may be the same or different. Furthermore, when the first and second ^{10}Fn3 domains bind to the same target, they may bind to the same or different epitopes on the target.

[0078] In exemplary embodiments, each ^{10}Fn3 domain of a multivalent fibronectin based protein scaffold binds to a desired target with a K_D of less than 500 nM, 100 nM, 10 nM, 1 nM, 500 pM, 100 pM or less. In exemplary embodiments, each ^{10}Fn3 domain of a multivalent fibronectin based protein scaffold binds specifically to a target that is not bound by a wild-type ^{10}Fn3 domain, particularly the wild-type human ^{10}Fn3 domain.

[0079] The ^{10}Fn3 domains in a multivalent fibronectin based scaffold protein may be connected by a polypeptide linker. Exemplary polypeptide linkers include polypeptides having from 1-20, 1-15, 1-10, 1-8, 1-5, 1-4, 1-3, or 1-2 amino acids. Suitable linkers for joining the ^{10}Fn3 domains are those which allow the separate domains to fold independently of each other forming a three dimensional structure that permits high affinity binding to a target molecule. The application provides that suitable linkers that meet these requirements comprise glycine-serine based linkers, glycine-proline based linkers, proline-alanine based linkers as well as the linker SEQ ID NO: 31. The Examples described in WO 2009/142773 demonstrate that Fn3 domains joined via these linkers

retain their target binding function. In some embodiments, the linker is a glycine-serine based linker. These linkers comprise glycine and serine residues and may be between 8 and 50, 10 and 30, and 10 and 20 amino acids in length. Examples of such linkers include SEQ ID NOs: 32-36. In some embodiments, the linker is a glycine-proline based linker. These linkers comprise glycine and proline residues and may be between 3 and 30, 10 and 30, and 3 and 20 amino acids in length. Examples of such linkers include SEQ ID NOs: 37, 38 and 39. In some embodiments, the linker is a proline-alanine based linker. These linkers comprise proline and alanine residues and may be between 3 and 30, 10 and 30, 3 and 20 and 6 and 18 amino acids in length. Examples of such linkers include SEQ ID NOs: 40, 41 and 42. It is contemplated, that the optimal linker length and amino acid composition may be determined by routine experimentation based on the teachings provided herein. In exemplary embodiments, the linker does not contain any DK sequences. In certain embodiments, the linker may be a C-terminal tail polypeptide as described herein, an N-terminal extension polypeptide as described herein, a linker polypeptide as described herein, or any combination thereof.

[0080] In the case of multivalent fibronectin based scaffold proteins, preferably none of the ^{10}Fn3 domains comprise a C-terminal tail containing a DK sequence. In exemplary embodiments, a multivalent fibronectin based scaffold protein comprises two or more ^{10}Fn3 domains, wherein each domain comprises a C-terminal tail that does not contain a DK sequence. In certain embodiments, a multivalent fibronectin based scaffold protein comprises two or more ^{10}Fn3 domains, wherein each domain comprises a C-terminal tail that does not contain a DK sequence and at least one of the domains comprises a residue suitable for addition of a PEG moiety, such as a lysine or cysteine residue.

PEGylation

[0081] PEG is a well-known, water soluble polymer that may be obtained commercially or prepared by ring-opening polymerization of ethylene glycol according to methods well known in the art (Sandler et al., *Polymer Synthesis*, Vol. 3, pp. 138-161, Academic Press, NY). The term "PEG" is used broadly to encompass any polyethylene glycol molecule, without regard to size or to modification at an end of the PEG, and can be represented by the formula:

[0082] X—O(CH_2CH_2O)$_{n-1}$$CH_2CH_2OH$ (1), where n is 20 to 2300 and X is H or a terminal modification, *e.g.*, a C_{1-4} alkyl. In one embodiment, the PEG of the invention terminates on one end with hydroxy or methoxy, *i.e.*, X is H or CH_3 ("methoxy PEG"). A PEG can contain further chemical groups which are necessary for binding reactions; which results from the chemical synthesis of the molecule; or which is a spacer for optimal distance of parts of the molecule. In addition, such a PEG can consist of one or more PEG side-chains which are linked together. PEGs with more than one PEG chain are called multiarmed or branched PEGs. Branched PEGs can be prepared, for example, by the addition of polyethylene oxide to various polyols, including glycerol, pentaerythriol, and sorbitol. For example, a four-armed branched PEG can be prepared from pentaerythriol and ethylene oxide. Branched PEG are described in, for example, European Published Application No. 473084A and U.S. Patent No. 5,932,462. One form of PEGs includes two PEG side-chains (PEG2) linked via the primary amino groups of a lysine (Monfardini, C. et al., *Bioconjugate Chem.*, 6:62-69 (1995)).

[0083] PEG conjugation to peptides or proteins generally involves the activation of PEG and coupling of the activated PEG-intermediates directly to target proteins/peptides or to a linker, which is subsequently activated and coupled to target proteins/peptides (see Abuchowski, A. et al., *J. Biol. Chem.*, 252:3571 (1977) and *J. Biol. Chem.*, 252:3582 (1977), Zalipsky et al. and Harris et al., in: *Poly(ethylene glycol) Chemistry: Biotechnical and Biomedical Applications*, Chapters 21 and 22, Harris, J.M., ed., Plenum Press, NY (1992)). It is noted that a polypeptide containing a PEG molecule is also known as a conjugated or PEGylated protein, whereas the protein lacking an attached PEG molecule can be referred to as unconjugated or free.

[0084] The size of PEG utilized will depend on several factors including the intended use of the polypeptide. Larger PEGs are preferred to increase half life in the body, blood, non-blood extracellular fluids or tissues. For *in vivo* cellular activity, PEGs of the range of about 10 to 60 kDa are preferred, as well as PEGs less than about 100 kDa and more preferably less than about 60 kDa, though sizes greater than about 100 kDa can be used as well. For *in vivo* imaging applications, smaller PEGs, generally less than about 20 kDa, may be used that do not increase half life as much as larger PEGs so as to permit quicker distribution and less half life. A variety of molecular mass forms of PEG can be selected, *e.g.*, from about 1,000 Daltons (Da) to 100,000 Da (n is 20 to 2300), for conjugating to

polypeptides of the invention. The number of repeating units "n" in the PEG is approximated for the molecular mass described in Daltons. It is preferred that the combined molecular mass of PEG on an activated linker is suitable for pharmaceutical use. Thus, in one embodiment, the molecular mass of the PEG molecules does not exceed 100,000 Da. For example, if three PEG molecules are attached to a linker, where each PEG molecule has the same molecular mass of 12,000 Da (each n is about 270), then the total molecular mass of PEG on the linker is about 36,000 Da (total n is about 820). The molecular masses of the PEG attached to the linker can also be different, *e.g.*, of three molecules on a linker two PEG molecules can be 5,000 Da each (each n is about 110) and one PEG molecule can be 12,000 Da (n is about 270). In some embodiments, one PEG moiety is conjugated to the polypeptide. In some embodiments, the PEG moiety is about 30, 40, 50, 60, 70, 80, or 90 KDa.

[0085] In some embodiments, PEGylated polypeptides contain one, two or more PEG moieties. In one embodiment, the PEG moiety(ies) are bound to an amino acid residue which is on the surface of the protein and/or away from the surface that contacts the target ligand. In one embodiment, the combined or total molecular mass of PEG in a PEGylated polypeptide is from about 3,000 Da to 60,000 Da, from about 10,000 Da to 36,000 Da, or from about 35,000 Da to 45,000 Da, or about 40,000 Da. In a one embodiment, the PEG in a PEGylated polypeptide is a substantially linear, straight-chain PEG.

[0086] One skilled in the art can select a suitable molecular mass for PEG, *e.g.*, based on how the pegylated polypeptide will be used therapeutically, the desired dosage, circulation time, resistance to proteolysis, immunogenicity, and other considerations. For a discussion of PEG and its use to enhance the properties of proteins, see Katre, N.V., *Advanced Drug Delivery Reviews*, 10:91-114 (1993).

[0087] In some embodiments, a polypeptide is covalently linked to one poly(ethylene glycol) group of the formula: —CO— $(CH_2)_x$— $(OCH_2CH_2)_m$—OR, with the —CO (*i.e.*, carbonyl) of the poly(ethylene glycol) group forming an amide bond with one of the amino groups of the polypeptide; R being lower alkyl; x being 2 or 3; m being from about 450 to about 950; and n and m being chosen so that the molecular weight of the conjugate minus the polypeptide is from about 10 to 40 kDa. In one embodiment, a polypeptide's ε-amino group of a lysine is the available (free) amino group.

[0088] In one specific embodiment, carbonate esters of PEG are used to form the PEG- polypeptide conjugates. N,N′-disuccinimidylcarbonate (DSC) may be used in the reaction with PEG to form active mixed PEG-succinimidyl carbonate that may be subsequently reacted with a nucleophilic group of a linker or an amino group of a polypeptide (see U.S. Patent Nos. 5,281,698 and 5,932,462). In a similar type of reaction, 1,1′-(dibenzotriazolyl)carbonate and di-(2-pyridyl)carbonate may be reacted with PEG to form PEG-benzotriazolyl and PEG-pyridyl mixed carbonate (U.S. Patent No. 5,382,657), respectively.

[0089] PEGylation of a polypeptide can be performed according to the methods of the state of the art, for example by reaction of the polypeptide with electrophilically active PEGs (supplier: Shearwater Corp., USA, www.shearwatercorp.com). Preferred PEG reagents of the present invention are, *e.g.*, N-hydroxysuccinimidyl propionates (PEG-SPA), butanoates (PEG-SBA), PEG-succinimidyl propionate or branched N-hydroxysuccinimides such as mPEG2-NHS (Monfardini, C., et al., *Bioconjugate Chem.*, 6:62-69 (1995)). Such methods may used to pegylate at an ε-amino group of a polypeptide lysine or the N-terminal amino group of the polypeptide.

[0090] In another embodiment, PEG molecules may be coupled to sulfhydryl groups on a polypeptide (Sartore, L. et al., *Appl. Biochem. Biotechnol.*, 27:45 (1991); Morpurgo et al., *Bioconjugate Chem.*, 7:363-368 (1996); Goodson et al., *Bio/Technology*, 8:343 (1990); U.S. Patent No. 5,766,897). U.S. Patent Nos. 6,610,281 and 5,766,897 describe exemplary reactive PEG species that may be coupled to sulfhydryl groups.

[0091] In some embodiments, the pegylated polypeptide is produced by site-directed PEGylation, particularly by conjugation of PEG to a cysteine moiety at the N- or C-terminus. In some embodiments, the polypeptide is an Fn3 domain covalently bound to a PEG moiety, wherein at least one of the loops of said Fn3 domain participates in binding to a target. The PEG moiety may be attached to the Fn3 polypeptide by site directed PEGylation, such as by attachment to a Cys residue, where the Cys residue may be positioned at the N-terminus of the Fn3 polypeptide or between the N-terminus and the most N-terminal beta or beta-like strand or at the C-terminus of the Fn3 polypeptide or between the C-terminus and the most C-terminal beta or beta-like strand. A Cys residue may be situated at other positions as well, particularly any of the loops that do not

participate in target binding. A PEG moiety may also be attached by other chemistry, including by conjugation to amines.

[0092] In some embodiments where PEG molecules are conjugated to cysteine residues on a polypeptide, the cysteine residues are native to the polypeptide, whereas in other embodiments, one or more cysteine residues are engineered into the polypeptide. Mutations may be introduced into a polypeptide coding sequence to generate cysteine residues. This might be achieved, for example, by mutating one or more amino acid residues to cysteine. Preferred amino acids for mutating to a cysteine residue include serine, threonine, alanine and other hydrophilic residues. Preferably, the residue to be mutated to cysteine is a surface-exposed residue. Algorithms are well-known in the art for predicting surface accessibility of residues based on primary sequence or a protein. Alternatively, surface residues may be predicted by comparing the amino acid sequences of polypeptides, given that the crystal structure of the framework based on which polypeptides are designed and evolved has been solved (see Himanen et al., *Nature*, 414(6866):933-938 (Dec. 20-27, 2001)) and thus the surface-exposed residues identified. In one embodiment, cysteine residues are introduced into polypeptides at or near the N- and/or C-terminus, or within loop regions. PEGylation of cysteine residues may be carried out using, for example, PEG-maleimide, PEG-vinylsulfone, PEG-iodoacetamide, or PEG-orthopyridyl disulfide. In exemplary embodiments, polypeptides are PEGylated on a cysteine residue using a maleimide linker.

[0093] In some embodiments, the pegylated polypeptide comprises a PEG molecule covalently attached to the alpha amino group of the N-terminal amino acid. Site specific N-terminal reductive amination is described in Pepinsky et al., *J. Pharmacol. Exp. Ther.*, 297:1059 (2001), and U.S. Patent No. 5,824,784. The use of a PEG-aldehyde for the reductive amination of a protein utilizing other available nucleophilic amino groups is described in U.S. Patent No. 4,002,531, in Wieder et al., *J. Biol. Chem.*, 254:12579 (1979), and in Chamow et al., *Bioconjugate Chem.*, 5:133 (1994).

[0094] In another embodiment, pegylated polypeptide comprises one or more PEG molecules covalently attached to a linker, which in turn is attached to the alpha amino group of the amino acid residue at the N-terminus of the polypeptide. Such an approach is disclosed in U.S. Publication No. 2002/0044921 and PCT Publication No. WO 94/01451.

[0095] In one embodiment, a polypeptide is PEGylated at the C-terminus. In a specific embodiment, a protein is pegylated at the C-terminus by the introduction of C-terminal azido-methionine and the subsequent conjugation of a methyl-PEG-triarylphosphine compound via the Staudinger reaction. This C-terminal conjugation method is described in Cazalis et al., "C-Terminal Site-Specific PEGylation of a Truncated Thrombomodulin Mutant with Retention of Full Bioactivity", *Bioconjugate Chem.*, 15(5):1005-1009 (2004).

[0096] In exemplary embodiments, a fibronectin based scaffold protein is pegylated in a C-terminal tail region as described further herein. Exemplary C-terminal tails include, for example, a polypeptide having any one of SEQ ID NOs: 10, 11, or 12.

[0097] In some embodiments, a branched PEG moiety may be conjugated to a protein via a lone cysteine residue on the protein. The chemistry of this conjugation may be, for example, highly selective maleimide chemistry in which free electrons on the sulfhydryl group on the protein attach to the maleimide group on the PEG via Michael Addition (Figure 1, where the protein is represented by R′ and PEG molecule is represented by R). Specifically, the maleimide moiety forms a thioether bond with a sulfhydryl group on the protein. The Michael Addition reaction may be performed at a pH between pH 5.0 and pH 5.5 inclusive, or between pH 6.0 and 8.0 inclusive.

[0098] Conventional separation and purification techniques known in the art can be used to purify PEGylated polypeptides, such as size exclusion (*e.g.*, gel filtration) and ion exchange chromatography. Products may also be separated using SDS-PAGE. Products that may be separated include mono-, di-, tri-, poly- and un- pegylated polypeptides, as well as free PEG. The percentage of mono-PEG conjugates can be controlled by pooling broader fractions around the elution peak to increase the percentage of mono-PEG in the composition. About ninety percent mono-PEG conjugates represents a good balance of yield and activity. Compositions in which, for example, at least ninety-two percent or at least ninety-six percent of the conjugates are mono-PEG species may be desired.

[0099] In certain embodiments, the pegylated polypeptides will preferably retain at least about 25%, 50%, 60%, 70%, 80%, 85%, 90%, 95% or 100% of the biological activity associated with the unmodified protein. In one embodiment, biological activity refers to its ability to bind to its target, as assessed by K_D, k_{on} or k_{off}.

[00100] The serum clearance rate of PEG-modified polypeptides may be decreased by about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or even 90%, relative to the clearance rate of the unmodified polypeptide. The PEG-modified polypeptide may have a half-life ($t_{1/2}$) which is enhanced relative to the half-life of the unmodified protein. The half-life of the PEG- polypeptide may be enhanced by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400% or 500%, or even by 1000% relative to the half-life of the unmodified polypeptide. In some embodiments, the protein half-life is determined *in vitro*, such as in a buffered saline solution or in serum. In other embodiments, the protein half-life is an *in vivo* half life, such as the half-life of the protein in the serum or other bodily fluid of an animal.

[00101] In certain embodiments, a PEGylated polypeptide has a shelf-life of at least 6 months, 1 year, 2 years, 3 years, 4 years, 5 years or more when formulated at a pH between pH 2.0 and pH 6.0 (*e.g.*, a pH between pH 3.0 and 5.0).

EXAMPLES

[00102] The invention now being generally described will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention in any way.

Example 1

Effects of pH on DePEGylation of FBSP-P

[00103] An exemplary fibronectin-based scaffold protein is FBSP-P, which is a mono-ADNECTIN™ having high affinity binding to PCSK9. FBSP-P is conjugated to a 40 kDa branched PEG via a lone cysteine residue on the protein. During formulation development of FBSP-P, an initial pH range of 6.0 to 7.5 was examined since, at the time, a neutral pH was thought to be desirable for the subcutaneous administration of the product. An example of the RP-HPLC results can be seen in Figure 2. Samples were run on a Polymer Labs PLRP-S column, 2.0*150 mm, with a column temperature of 40 °C and an H_2O/ACN/TFA gradient. Dual detection was performed with UV and Evaporative Light Scattering (ELS), which measures a relative quantification of protein-related

impurities by UV signal and quantifies free PEG species by ELS signal using a PEG calibration curve.

[00104] From the preliminary data of the pH screen, an increase in the level of free PEG and protein fragments was observed as a function of increasing pH. Characterization of the protein fragments was performed by LC-MS, which identified these species to be that of the intact, free (unPEGylated) FBSP-P ADNECTIN™ and its covalent dimer (Figure 3 and Table 1).

[00105] Unlike previous ADNECTIN™ molecules, FBSP-P showed no clipping along its protein backbone due to the substitution of the aspartic acid in the C-terminal tail region with a glutamic acid at the position corresponding to amino acid residue 97 of SEQ ID NO: 47 (*i.e.*, a DK- construct). Although several other aspartic acid residues exist in the protein sequence, these did not lead to clipping and only the fragment peaks identified in Figure 3 and Table 1 were consistently observed during formulation development and stability.

[00106] With the fragmented species characterized, and no other clipped species observed, this was the first occasion where dePEGylation could be clearly identified in ADNECTINS™. Based on these preliminary data, a lower pH range of 4 to 6 was examined for dePEGylation, and the complete set of results covering the entire pH range of 4 to 7.5 can be seen in Figure 4 and Figure 5, where the mole % of free PEG detected is plotted as % increase since T=0. In Figures 4 and 5, data have been normalized for more direct comparison since two different batches of FBSP-P drug substance were used in the experiments, with the earlier lot showing a higher initial level of free PEG and free ADNECTIN™. The negative values were likely a result of assay variability and the low level of free PEG in these samples.

[00107] From the data presented above, a clear pH dependency can be seen in the level of dePEGylation. In the lower pH formulations, some instances of decreased levels of free PEG can be seen, which was likely attributed to the very low levels of free PEG detected along with variability with the ELS detection. Since the balance of dePEGylation is the free (unPEGylated) ADNECTIN™, the pH effect on the formation of that species is also evaluated and this is presented in Figure 6 and Figure 7.

[00108] Increased levels of free PEG and free (unPEGylated) ADNECTIN™ correlate very well to each other, at two elevated temperatures, with both showing a pH dependency.

Example 2

Long-Term Stability and Formulation Study of FBSP-V

[00109] Following the discovery of dePEGylation with certain formulations of FBSP-P, other ADNECTINS™ were examined to determine if they were subject to the same degradation. FBSP-V is an ADNECTIN™ that binds to VEGFR2 with high affinity and having the sequence of SEQ ID NO: 48. FBSP-V is conjugated to a 40 kDa branched PEG moiety via a lone cysteine residue at position 93 of SEQ ID NO: 48. DePEGylation of FBSP-V was evaluated using a set of formulations ranging from pH 4.5 to 6.5. Similar to FBSP-P, the free (unPEGylated) FBSP-V_{free} ADNECTIN™ was evident in these samples and its relative level also increased as a function of increasing pH. The LC-MS results of the most degraded sample at pH 6.5 are shown in Figure 8 and Table 2. Relative quantification of these fragmented species can be seen in

[00110] Table 3.

[00111] With FBSP-V containing a DK in the C-terminal tail region (*i.e.*, the aspartic acid at position 90 of SEQ ID NO: 48), two additional clips were also observed which represented cleavage at the aspartic acid at position 90. As previously established with other ADNECTIN™ molecules, formulations at lower pH leads to higher level of DK cleavages. The data in

[00112] Table 3 indicates this trend in regard to total pre-peaks; however, as the pH increases, the % of intact free ADNECTIN™ increases, which was the same trend as that observed in FBSP-P as described in Example 1.

[00113] Analysis of the same FBSP-V stability samples by SDS-PAGE revealed similar information in a qualitative manner (Figure 9). For stressed samples at the lowest pH (pH 4.5, in lanes 5 and 6), a clipped species can be seen above the 6kD MW marker, corresponding to the dominant clip (G2-D91, corresponding to residues 1-90 of SEQ ID NO: 48). The presence of sodium chloride in the sample showed a higher level of this clip as compared to the sample formulated without sodium chloride at the same pH. As the pH of the formulation increased, this clip decreased in intensity but another band at

slightly higher molecular weight now appeared, corresponding in molecular weight to the free FBSP-V_{free} ADNECTIN™ at just above 10kD. Moreover, the new band (indicated with an arrow) appeared to increase in intensity as the formulation pH increased from 5.5 to 6.5. These observations are consistent with those described in Figure 8, Table 2 and Table 3.

[00114]

Example 3

Characterization of FBSP-V/I

[00115] Another exemplary fibronectin-based scaffold protein is FBSP-V/I, a multivalent polypeptide with high affinity to VEGFR2 and IGF-IR. FBSP-V/I comprises the amino acid sequence of SEQ ID NO: 9, and contains a single 40 kDa branched PEG conjugated to the cysteine at position 203 of SEQ ID NO:9.

[00116] Characterization of a stressed FBSP-V/I sample is shown in Figure 10. The results demonstrate, among various protein clips, the existence of the intact free (unPEGylated) FBSP-V/I ADNECTIN™ in the des Met form with oxidation (+32). The dimeric form of the same species can also be seen.

[00117] For a sample with the following sequence (SEQ ID NO: 9):

MGVSDVPRDL EVVAATPTSL LISWSARLKV ARYYRITYGE TGGNSPVQEF
TVPKNVYTAT ISGLKPGVDY TITVYAVTRF RDYQPISINY RTEI***D***KPSTS
TSTVS***D***VPRD LEVVAATPTS LLISWRHPHF PTRYYRITYG ETGGNSPVQE
FTVPLQPPTA TISGLKPGVD YTITVYAVT***D*** GRNGRLLSIP ISINYRTEI***D*** KPCQ

Several D residues are involved in fragmentation (in bold, italic font), with D95 and D200 (underlined) being the primary sites. With heat stress, cleavage also occurs at the maleimide bond of the PEG conjugation, resulting in the release of free FBSP-V/I (shown as "VI des Met").

[00118] Figure 11 shows a comparison of dePEGylation of several ADNECTINS™, as a measure of free PEG over the course of 1-4 weeks. The exemplary ADNECTINS™ are FBSP-P (samples F1, F2, and F3) stored at pH 6.0; FBSP-V/I stored at pH 5.5; FBSP-V stored at pH 5.0; and FBSP-E/I stored at pH 4.0. FBSP-E/I is a multivalent polypeptide comprising two ^{10}Fn3 domains with the BC, DE and FG loops altered such that one ^{10}Fn3

domain binds with high affinity to EGFR and the other ^{10}Fn3 domain binds with high affinity to IGF-IR.

Example 4

Characterization of Free PEG

[00119] A question arose as to the exact structure and functionality of the free PEG lost from the ADNECTINS™ during stability. Based on elution time by RP-HPLC, the free PEG peak appeared to closely resemble the unstressed PEG in terms of hydrophobicity, which would imply that the liberated free PEG remained largely intact and was close in molecular weight and size to the unstressed PEG.

[00120] The preferred pH range for conjugation through maleimide chemistry is 6.5 to 7.5, and in the past the PEGylation step for ADNECTINS™ has been conducted at pH 5 to 5.5 using the PEG in solid form. To address functionality, PEG solutions were prepared using MILLI-Q® water (pH ~5.5) and 50 mM Tris (pH 7.0). The solutions were stressed at 37 °C for one week, and their functionality was assessed through a PEGylation reaction with the FBSP-V_{free} ADNECTIN™. The pH 7 solution was pH adjusted to ~5.5 prior to the reaction for a more direct comparison to the PEG in water. The data in Table 4 shows that, after stress, some of the maleimide functional group on the PEG was lost in the pH 5.5 solution and that the functionality was completely lost in the pH 7.0 solution.

TABLES

[00121] Table 1: Summary of MS results on the protein fragments shown in Figure 3. The molecular weight of FBSP-P cannot be determined due to the heterogeneity associated with the PEGylation.

Peak Retention Time (min)	Observed MW (Da)	Theoretical MW (Da)	% Difference from Theoretical MW	Structure
5.7	11337.3	11338.72	-0.01	Des Met form of FBSP-P_{free} (G2-A104)

Peak Retention Time (min)	Observed MW (Da)	Theoretical MW (Da)	% Difference from Theoretical MW	Structure
6.0	22670.1	22675.44	-0.02	Des Met form of FBSP-P_{free} dimer (disulfide linked)

[00122] Table 2: Summary of MS results on the protein fragments shown in Figure 8.

Peak Retention Time (min)	Observed MW (Da)	Theoretical MW (Da)	% Difference from Theoretical MW	Structure
4.6	6866	6868.7	-0.04	I28-D91
5.3	10361	10362.7	-0.02	FBSP-V_{free} ADNECTIN™ (des Met form)
5.5	20723	20723.4	0.00	FBSP-V_{free} ADNECTIN™ dimer (des Met form)
5.7	9888	9888.2	0.00	(G2 to D91)-water (DK cleavage product)

[00123] Table 3: Relative quantification of protein fragments in FBSP-V stressed samples. Quantification is based on total UV area at 280 nm including the FBSP-V product peak. "Total pre-peaks" refers to all pre-peaks detected before the elution of FBSP-V product including all clips and intact FBSP-V_{free} species; "free FBSP-V_{free} ADNECTIN™" refers to the sum of free (unPEGylated) FBSP-V_{free} ADNECTIN™ and FBSP-V_{free} dimer.

FBSP-V Formulation	Total % Pre-peaks (Clips + FBSP-V_{free} ADNECTIN™)	% Free FBSP-V_{free} ADNECTIN™ Only	Mol % Free PEG
10 mM Sodium Acetate, 5% mannitol, pH 4.5; 5 mg/mL	7.0%	0.0%	0.63

FBSP-V Formulation	Total % Pre-peaks (Clips + FBSP-V_{free} ADNECTIN™)	% Free FBSP-V_{free} ADNECTIN™ Only	Mol % Free PEG
10 mM Sodium Acetate, 5% mannitol, pH 5.5; 5 mg/mL	2.9%	1.7%	1.01
10 mM Sodium Acetate, 5% mannitol, pH 6.5; 5 mg/mL	2.7%	1.9%	1.60
10 mM Sodium Acetate, 5% mannitol, pH 6.5; 10 mg/mL	3.3%	2.4%	1.56

[00124] Table 4: Conjugation efficiency of 40k PEG maleimide after heat and pH stresses

	% Unconjugated FBSP-V_{free} ADNECTIN™	
Stress Conditions	PEG in MQ water (pH ~5.5)	PEG in 50 mM Tris (pH 7.0)
T=0	15.9%	15.9%
T=1 week, 37C	33.1%	100%

Materials and Methods

Materials

[00125] FBSP-P. Two lots of FBSP-P (lots 1 and 2) were used in two separate pH studies covering the range of pH 4 to 7.5, at half pH unit intervals. The samples were formulated using the high throughput formulation format on a TECAN® robot. The drug substance (10 mg/mL, in 10 mM succinate, pH 6.0) was mixed with concentrates of succinate buffers (from pH 4 to 7.5) and sorbitol, which resulted in a final protein concentration of 1 mg/mL or 10 mg/mL in the excipients and pH described in the results section. The samples were put on stability in 96-well plate format and tested directly out of the plates.

[00126] FBSP-V/I. The FBSP-V/I sample was formulated using tangential flow filtration (TFF), filled in vials and subject to stability testing as described herein.

[00127] FBSP-V. The samples were formulated by TFF into the buffers indicated, filled in vials and subject to stability testing as described herein.

Analytical Methods

[00128] RP-UV-ELSD. A PLRP-S column (4.6*150 mm, Polymer Labs) was used for the analysis of FBSP-P samples. The protein fragments were analyzed on a relative percent basis at 280 nm using UV detection, and the free PEG moiety was quantified on a mole % basis using a 5-point PEG calibration curve with evaporative light scattering (ELS) detection. The method utilizes a water/acetonitrile/trifluoroacetic acid gradient.

[00129] RP-UV. A Jupiter C18 column (4.6*250 mm, PHENOMENEX®) was used for the analysis of FBSP-V and FBSP-V/I samples. The protein fragments were analyzed on a relative percent basis at 280 nm using UV detection. The method utilizes a water/acetonitrile/trifluoroacetic acid gradient.

[00130] LC-MS. The HPLC method using the Jupiter C18 column was coupled to a Thermo LTQ ion trap mass spectrometer, and the flow was split after the UV detector with 0.2 mL/min introduced into the ionization source of the MS. The MS data obtained was deconvoluted using the MagTran software, and structures were assigned to the detected masses using the PAWS software.

Expression, PEGylation and Purification of Fibronectin Based Scaffold Proteins (FBSP)

[00131] For expression of FBSP, a nucleotide sequence encoding the construct is cloned into an inducible expression vector and is expressed in *E. coli* cells (either as a soluble fraction or into intracellular inclusion bodies). Cell bank vials generated from a culture of a single plated colony are used to inoculate a shake flask culture as an inoculum for a large-scale fermentor. Alternatively, a seed fermentor is used for an inoculum culture, depending on the final fermentation volume. The large-scale fermentation contains a growth phase to accumulate biomass and a production phase to generate the FBSP.

[00132] For insoluble FBSP, intracellular inclusion bodies are released from harvested cells using a MICROFLUIDIZER® and recovered by centrifugation, followed by washes with buffer and water. The purification process for insoluble FBSP uses a Guanidine-HCl based resolubilization of inclusion bodies, followed by refolding the protein.

[00133] For soluble FBSP, cells were pelleted and lysed using a MICROFLUIDIZER® and the soluble fraction was recovered by centrifugation, and the supernatant was clarified by filtration.

[00134] The protein is then purified using one or more columns, such as a HISTRAP® column, a cation exchange chromatography column, and/or a hydrophobic interaction column. The resulting purified FBSP is then covalently linked to a PEG via maleimide chemistry at a single cysteine residue to produce PEGylated protein.

[00135] The PEGylated protein may then be purified over one or more additional columns, such as a cation exchange chromatography column. The elution is concentrated to a target protein concentration and then exchanged into the formulation buffer using ultrafiltration/diafiltration (UF/DF). The UF/DF product is filtered using a final 0.22 μm filter. The filtered product is then filled into vials to produce the final product.

Example 5

DePEGylation of Short PEGylated Peptides

[00136] This Example shows that dePEGylation at neutral or alkaline pH occurs not only with polypeptides and proteins, but also with smaller peptides. This Example also shows that dePEGylation occurs regardless of the type of linker connecting the PEG moiety to the peptide and regardless of the type of PEG.

[00137] A synthetic peptide, TEIEKPCQ (SEQ ID NO: 47), bearing the same C-terminal sequence as wildtype ^{10}FN3 proteins, was utilized as a model peptide for conjugation to three different 40kD PEG-MALs at its penultimate cysteine residue. The structures of the three PEG-MALs are described below:

2-Branched PEG-MAL, with a C2 alkyl linker (NOF p/n Sunbright GL2-400MA; Figure 12)

2-Branched PEG-MAL, with a C5 alkyl linker (NOF p/n Sunbright GL2-400MA3)

Linear PEG-MAL, with a C2 alkyl linker (NOF p/n Sunbright ME-400MA)

[00138] The PEG conjugated peptides were purified using PD-10 columns and formulated into 1x PBS at pH 8.3. The formulated peptides were analyzed at T=0 and then at 1 week after heat stress at 37 °C for level of dePEGylation.

[00139] The samples were analyzed for dePEGylation by RP-HPLC. A Polaris C8-A column (2.1*150 mm, VARIAN®) was used for the analysis of PEGylated peptide samples. The free peptide was quantified on a relative percent basis to the intact sample at 214 nm using UV detection. The method utilizes a water/acetonitrile/trifluoroacetic acid gradient. For peak identification, LC-MS was conducted.

[00140] The results, which are shown in Figures 13, 14 and 15, indicate that a higher level of dimerized free peptide was observed in each of the 3 stressed samples relative to the level in each of the samples at T=0. The bar graph in Figure 15 demonstrates an increase in the relative level of the free peptide, in the form of a covalent dimer, for all three conjugated peptides after heat stress. The free peptide generated formed a covalent dimer due to the free cysteine now available as a result of dePEGylation, which was confirmed by MS and MS/MS analysis. The fact that the level of the covalent dimer increased after heat stress further indicates that the dePEGylation event regenerated an intact free peptide containing a free cysteine residue. A low level of the free peptide was present at T0 for all three samples due to its incomplete removal with the PD-10 column purification. However, a measurable increase in the level of the free peptide was still observed.

[00141] Thus, the results indicate that dePEGylation can also occur with a short peptide (*i.e.*, not only with a larger polypeptide or protein). Moreover, the results show that dePEGylation is not greatly affected by the length of the alkyl linker, nor by the branching structure in the PEG-MAL, as all three samples underwent dePEGylation to a similar extent.

Example 6

Reduced DePEGylation of Small Peptide at Lower pH

[00142] This Example shows that less dePEGylation of a small PEGylated peptide occurs at lower pH relative to higher pH.

[00143] A synthetic peptide consisting of the amino acid sequence TEIDKPCQ (SEQ ID NO: 48) was conjugated to a 2kPEG-MAL. Briefly, the peptide was solubilized in NaOAc at pH 5.5. PEG in water was added to the peptide and the conjugation reaction occurred overnight. The sample was cleaned up via buffer exchange over PD-10 columns

into pH 8.0 Tris or pH 5.5 NaOAc. The two samples were stressed at 37 °C for one week, followed by analysis using RP-HPLC, as described in Example 5.

[00144] The results, which are shown in Figure 16, indicate that, similarly to larger polypeptides, smaller peptides are subject to less dePEGylation at lower pH, compared to higher pH.

Example 7

Reduced DePEGylation of PEGylated Proteins

at Lower pH Regardless of Type of PEG

[00145] This Example shows that reducing the pH reduces dePEGylation of proteins regardless of whether they contain a large PEG, a small PEG, a branched PEG or a linear PEG.

[00146] C7 protein (SEQ ID NO: 48), was conjugated to a variety of PEG-MALs with different molecular weights, including 2k, 5k, 10k, 12k, 20k, 20k bis (bi-functional), 30k and 40k branched (NOF America Corp.). Each sample was purified over an ion-exchange column, then formulated in 50 mM sodium acetate at pH 4.5 or 50 mM Tris at pH 8.0. The samples were heat stressed at 37 °C for one week and the results were measured by RP-HPLC using a Jupiter C18 column (4.6*250 mm, PHENOMENEX®). The protein fragments were quantified on a relative percent basis to the intact sample at 280 nm using UV detection. The method utilizes a water/acetonitrile/trifluoroacetic acid gradient. For peak identification, LC-MS was conducted.

[00147] The results, which are shown in Figure 17, indicate a substantially higher level of dePEGylation after the heat stress in the samples at pH 8.0 relative to the samples at pH 5.5. In addition, the results also indicate no difference in the level of degradation among the different sizes of PEG-MALs used in the conjugation.

Incorporation by Reference

[00148] The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, GENBANK® Accession numbers, SWISS-PROT® Accession numbers, or other disclosures) in the Background, Detailed Description, Brief Description of the Drawings, and Examples is hereby incorporated herein by reference in their entirety.

[00149] The present invention is not to be limited in scope by the embodiments disclosed herein, which are intended as single illustrations of individual aspects of the invention, and any that are functionally equivalent are within the scope of the invention. Various modifications to the models and methods of the invention, in addition to those described herein, will become apparent to those skilled in the art from the foregoing description and teachings, and are similarly intended to fall within the scope of the invention. Such modifications or other embodiments can be practiced without departing from the true scope and spirit of the invention.

SEQUENCES

Naturally occurring human ^{10}Fn3 (SEQ ID NO: 1)

*VSDVPRDL*EVVAATPTSLLI**SWDAPAVTVR**YYRITYGETGGNSPVQEFTV**PGSKS T** ATISGLKPGVDYTITVYAV**TGRGDSPASSKP**ISINYRT

Full length wild-type human ^{10}Fn3 domain (SEQ ID NO: 47)

*VSDVPRDL*EVVAATPTSLLI**SWDAPAVTVR**YYRITYGETGGNSPVQEFTV**PGSKS T** ATISGLKPGVDYTITVYAV**TGRGDSPASSKP**ISINYRTEIDKPSQ

Antibody-like protein based on the ^{10}Fn3 scaffold (SEQ ID NO:2)

EVVAAT$(X)_a$SLLI$(X)_x$YYRITYGE$(X)_b$QEFTV$(X)_y$ATI$(X)_c$DYTITVYAV$(X)_z$ISINYR T

Antibody-like protein based on the ^{10}Fn3 scaffold (SEQ ID NO: 3)

EVVAATPTSLLI$(X)_x$YYRITYGETGGNSPVQEFTV$(X)_y$ATISGLKPGVDYTITVYAV $(X)_z$ISINYRT

V core (SEQ ID NO: 4)

EVVAATPTSLLISWRHPHFPTRYYRITYGETGGNSPVQEFTVPLQPPTATISGLKPG VDYTITVYAVTDGRNGRLLSIPISINYRT

Full length FBSP-V (SEQ ID NO: 48)

GEVVAATPTSLLISWRHPHFPTRYYRITYGETGGNSPVQEFTVPLQPPTATISGLKP
GVDYTITVYAVTDGRNGRLLSIPISINYRTEIDKPCQ

Short Tail (SEQ ID NO: 5)
EIEK

VEGFR2 BC Loop (SEQ ID NO: 6)
RHPHFPT

VEGFR2 DE Loop (SEQ ID NO: 7)
LQPP

VEGFR2 FG Loop (SEQ ID NO: 8)
DGRNGRLLSI

DK+ VEGFR2/IGF-IR Binder (SEQ ID NO: 9)
MGVSDVPRDLEVVAATPTSLLISWSARLKVARYYRITYGETGGNSPVQEFTVPKN
VYTATISGLKPGVDYTITVYAVTRFRDYQPISINYRTEIDKPSTSTSTVSDVPRDLE
VVAATPTSLLISWRHPHFPTRYYRITYGETGGNSPVQEFTVPLQPPTATISGLKPG
VDYTITVYAVTDGRNGRLLSIPISINYRTEIDKPCQ

Modified Cys Tail (SEQ ID NO: 10)
EGSGC

Cys Tail (SEQ ID NO: 11)
EIEKPCQ

EIEKPC (SEQ ID NO: 12)

(SEQ ID NO: 13)
*VSDVPRDL*EVVAATPTSLLI**SWDAPAVTVR**YYRITYGETGGNSPVQEFTV**PGSKS**
TATISGLKPGVDYTITVYAV**TGRGDSPASSKP**ISINYRT

Extension sequence (SEQ ID NO: 14)
EIDKPSQ

I core (SEQ ID NO: 15)
EVVAATPTSLLISWSARLKVARYYRITYGETGGNSPVQEFTVPKNVYTATISGLKP
GVDYTITVYAVTRFRDYQPISINYRT

Extension sequence (SEQ ID NO: 16)
EIDKPSQLE

MGVSDVPRDL (SEQ ID NO: 17)

VSDVPRDL (SEQ ID NO: 18)

GVSDVPRDL (SEQ ID NO: 19)

X_nSDVPRDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 20)

X_nDVPRDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 21)

X_nVPRDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 22)

X_nPRDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 23)

X_nRDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 24)

X_nDL, wherein n = 0, 1 or 2 amino acids, wherein when n = 1, X is Met or Gly, and when n = 2, X is Met-Gly (SEQ ID NO: 25)

EIEKPSQ (SEQ ID NO: 26)

EIEKP (SEQ ID NO: 27)

EIEKPS (SEQ ID NO: 28)

EIDK (SEQ ID NO: 29)

EIDKPCQ (SEQ ID NO: 30)

Fn linker (SEQ ID NO: 31)
PSTSTST

GS_5 linker (SEQ ID NO: 32)
GSGSGSGSGS

GS_{10} linker (SEQ ID NO: 33)
GSGSGSGSGSGSGSGSGSGS

$(GGGGS)_3$ (SEQ ID NO: 34)
GGGGS GGGGS GGGGS

$(GGGGS)_5$ (SEQ ID NO: 35)
GGGGS GGGGS GGGGS GGGGS GGGGS

$G_4SG_4SG_3SG$ (SEQ ID NO: 36)
GGGGSGGGGSGGGSG

GPG (SEQ ID NO: 37)

GPGPGPG (SEQ ID NO: 38)

GPGPGPGPGPG (SEQ ID NO: 39)

PA3 linker (SEQ ID NO: 40)
PAPAPA

PA6 linker (SEQ ID NO: 41)
PAPAPAPAPAPA

PA9 linker (SEQ ID NO: 42)
PAPAPAPAPAPAPAPAPA

E Core (SEQ ID NO: 43)
EVVAATPTSLLISWWAPVDRYQYYRITYGETGGNSPVQEFTVPRDVYTATISGLK
PGVDYTITVYAVTDYKPHADGPHTYHESPISINYRT

IGF-IR BC Loop (SEQ ID NO: 44)
SARLKVA

IGF-IR DE Loop (SEQ ID NO: 45)
KNVY

IGF-IR FG Loop (SEQ ID NO: 46)
RFRDYQ

TEIEKPCQ (SEQ ID NO: 47)

TEIDKPCQ (SEQ ID NO: 48)

We claim:

1. A composition comprising a polypeptide conjugated to a PEG moiety through a maleimide linker, wherein the composition has a pH between pH 2.0 and pH 6.0.

2. The composition of claim 1, wherein the composition has a pH between pH 3.0 and pH 5.0.

3. The composition of claim 2, wherein the composition has a pH between pH 3.5 and pH 4.5.

4. The composition of claim 2, wherein less than 5% of the maleimide linkers are cleaved over a four week storage period.

5. The composition of any one of claims 1-4, wherein the polypeptide comprises a tenth fibronectin type III (^{10}Fn3) domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM.

6. The composition of claim 5, wherein the ^{10}Fn3 domain comprises at least one loop region that differs from the naturally occurring loop region and at least one beta strand that differs from the naturally occurring beta strand.

7. The composition of claim 6, wherein the ^{10}Fn3 domain does not contain a DK sequence in the C-terminal tail region.

8. The composition of claim 7, wherein the C-terminal tail of the ^{10}Fn3 domain comprises a cysteine residue, to which the PEG moiety is linked.

9. The composition of claim 8, wherein less than 1% of the maleimide linkers are cleaved over a four week storage period.

10. The composition of claim 7, wherein the polypeptide further comprises a second ^{10}Fn3 domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM.

11. The composition of claim 10, wherein the first and second ^{10}Fn3 domains bind to different targets.

12. The composition of claim 11, wherein the first and second ^{10}Fn3 domains are connected by a polypeptide linker comprising 1-30 amino acids.

13. The composition of claim 12, wherein the polypeptide linker is selected from the group consisting of: a glycine-serine linker, a glycine-proline linker, a proline-alanine linker and an Fn linker.

14. The composition of claim 8, wherein the maleimide linker forms a thioether bond with a sulfhydryl group on the polypeptide.

15. The composition of claim 8, wherein the ^{10}Fn3 domain comprises at least two loop regions that differ from the corresponding naturally occurring loop regions.

16. The composition of claim 2, wherein (i) the polypeptide comprises a ^{10}Fn3 domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM; (ii) the ^{10}Fn3 domain comprises at least one loop region that differs from the naturally occurring corresponding loop region and at least one beta strand that differs from the naturally occurring corresponding beta strand; (iii) the ^{10}Fn3 domain does not contain a DK sequence in the C-terminal tail region; and the ^{10}Fn3 domain comprises a cysteine residue, to which the PEG moiety is linked.

17. The composition of claim 16, wherein less than 5% of the maleimide linkers are cleaved over a four week storage period.

18. A method for maintaining PEGylation of polypeptides during storage, comprising storing the polypeptides in a solution buffered to a pH between pH 2.0 and pH 6.0, wherein the polypeptides are conjugated to a polyethylene glycol (PEG) moiety through a maleimide linker, and wherein less than 5% of the maleimide linkers are cleaved over a four week storage period.

19. The method of claim 18, wherein less than 5% of the maleimide linkers are cleaved over an eight week storage period.

20. The method of claim 19, wherein less than 5% of the maleimide linkers are cleaved over a six month storage period.

21. The method of claim 20, wherein less than 5% of the maleimide linkers are cleaved over a one year storage period.

22. The method of claim 21, wherein less than 2% of the maleimide linkers are cleaved over the storage period.

23. The method of any one of claims 18-22, wherein the polypeptides comprise a tenth fibronectin type III (^{10}Fn3) domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM.

24. The method of claim 23, wherein the ^{10}Fn3 domain does not contain a DK sequence in the C-terminal tail region.

25. The method of claim 24, wherein the C-terminal tail of the ^{10}Fn3 domain comprises a cysteine residue.

26. The method of claims 24, wherein the polypeptides further comprise a second ^{10}Fn3 domain having an altered amino acid sequence relative to the wild-type sequence that binds to a target molecule with a K_D of less than 500 nM.

27. The method of claim 26, wherein the first and second ^{10}Fn3 domains bind to different targets.

28. The method of claim 27, wherein the first and second ^{10}Fn3 domains are connected by a polypeptide linker comprising 1-30 amino acids.

29. The method of claim 28, wherein the polypeptide linker is selected from the group consisting of: a glycine-serine linker, a glycine-proline linker, a proline-alanine linker and an Fn linker.

30. The method of claim 18, wherein the maleimide linker forms a thioether bond with a sulfhydryl group on the polypeptides.

31. The method of claim 24, wherein the pH of the solution is between 3.0 and 4.0.

32. The method of claim 24, wherein the pH of the solution is between 3.5 and 4.5.

33. The method of claim 24, wherein the pH of the solution is between 4.0 and 5.0.

34. The method of claim 24, wherein the pH of the solution is between 4.5 and 5.5.

35. The method of claim 24, wherein the pH of the solution is between 5.0 and 6.0.

36. The method of claim 24, wherein the concentration of the PEGylated polypeptides in the solution is from 1-10 mg/mL.

37. The method of claim 24, wherein the PEGylated polypeptides are stored at a temperature from 4 °C to 30 °C.

38. A method for improving the stability of PEGylated polypeptides in a solution, wherein the polypeptides are conjugated to a polyethylene glycol (PEG) moiety through a maleimide linker, comprising the steps of:

(a) determining the amount of PEG cleaved from the polypeptides over a fixed storage period in the solution; and

(b) if PEG is cleaved from more than 5% of the polypeptides over the storage period, reformulating the PEGylated polypeptides in a storage solution buffered to a pH of between 2.0-6.0.

FIG. 1

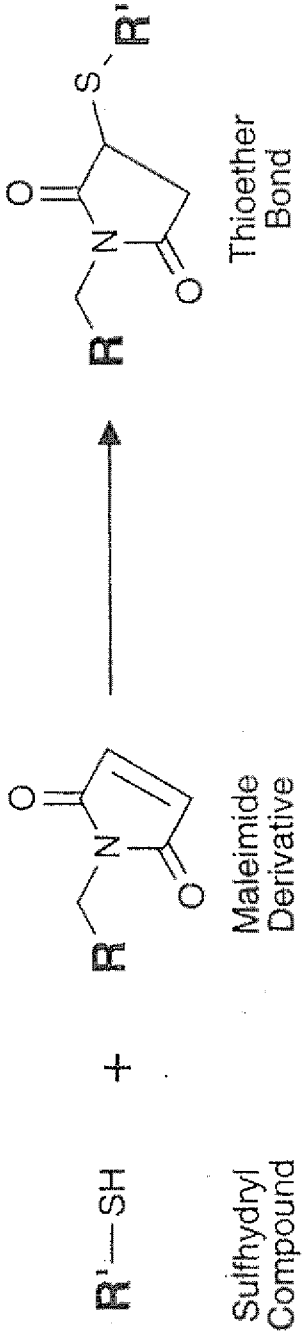
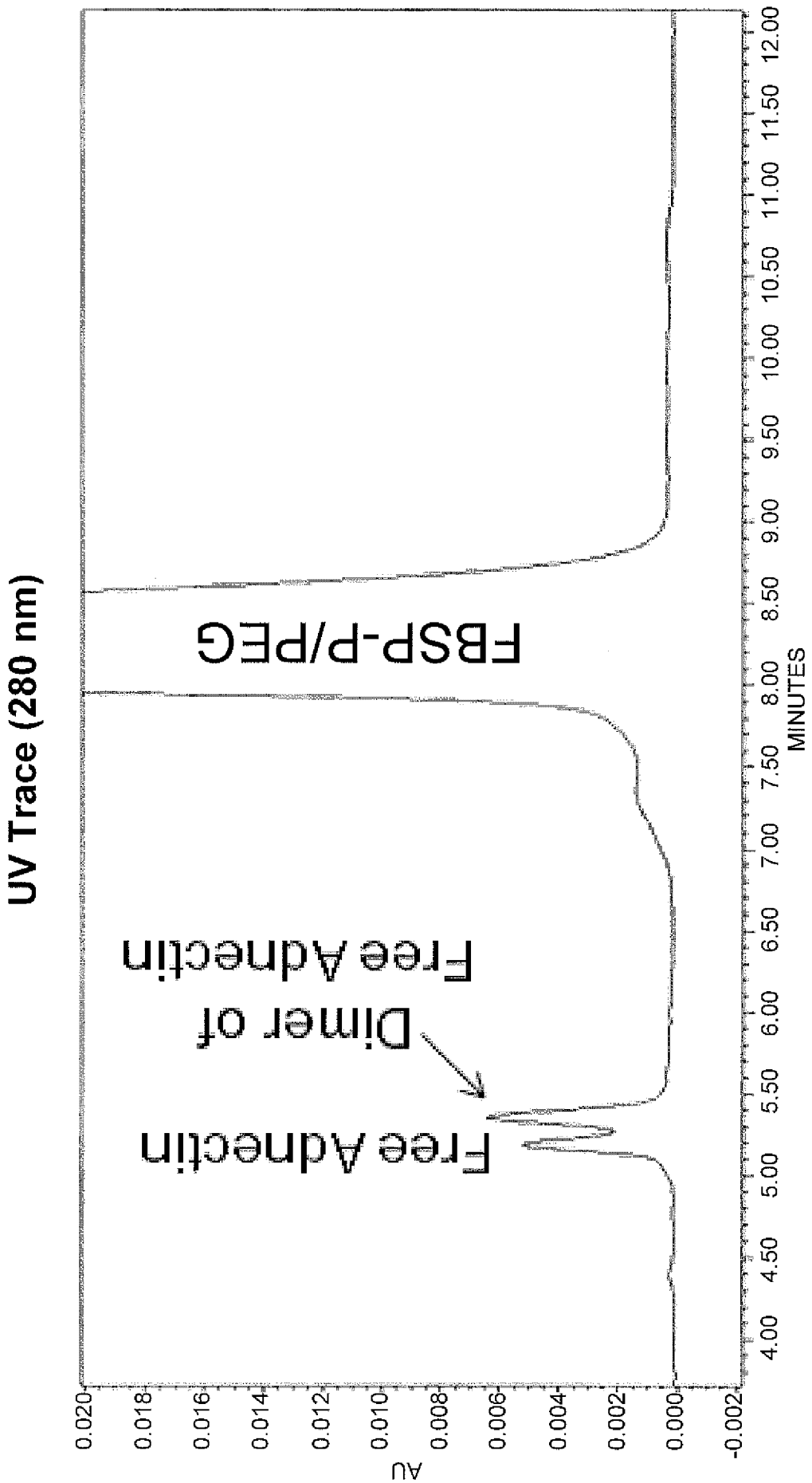

R'—SH
Sulfhydryl Compound
+
Maleimide Derivative
Thioether Bond

FIG. 2A


UV Trace (280 nm)
Free Adnectin
Dimer of
Free Adnectin
FBSP-P/PEG
AU
MINUTES
0.020
0.018
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
-0.002
4.00
4.50
5.00
5.50
6.00
6.50
7.00
7.50
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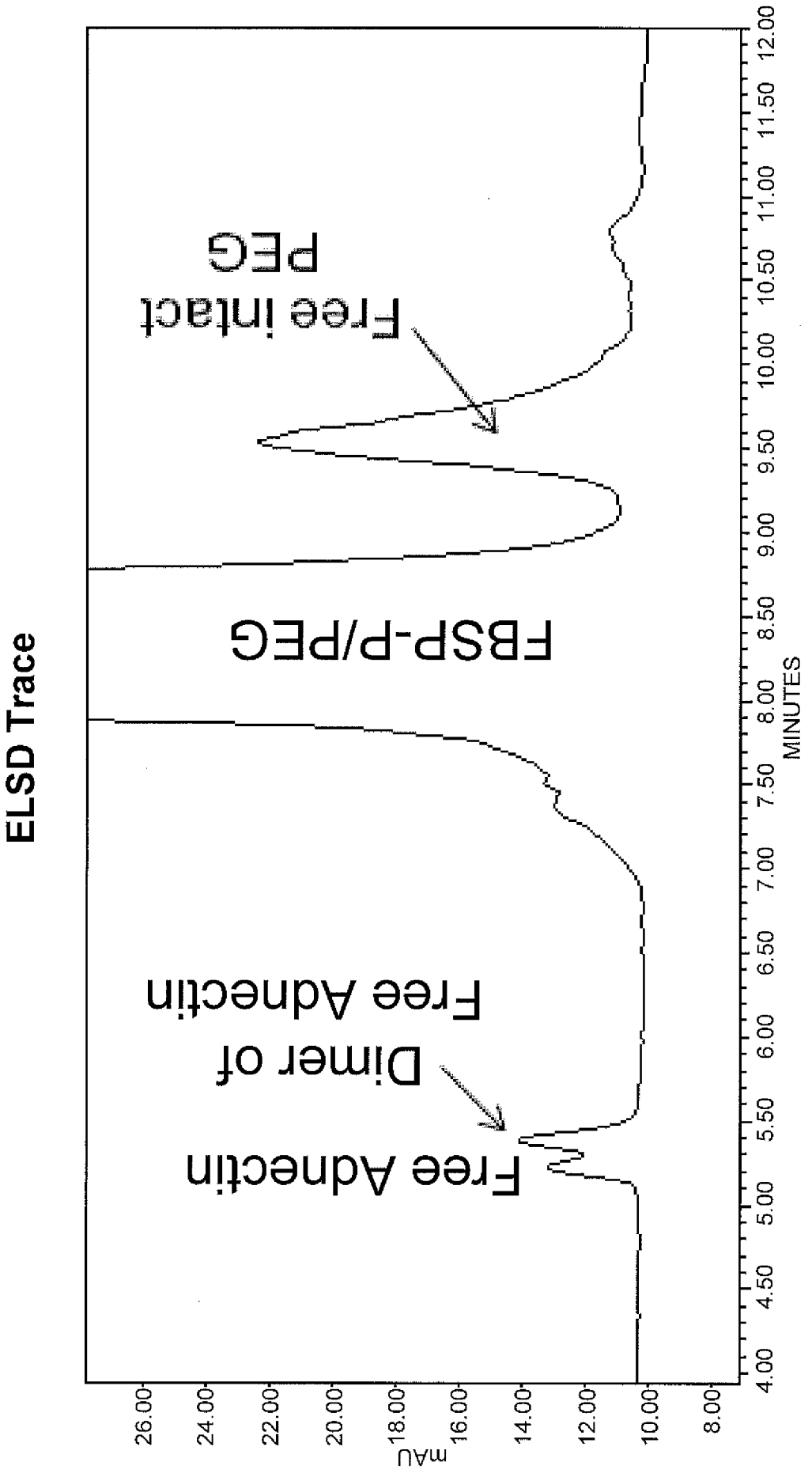
8.50
9.00
9.50
10.00
10.50
11.00
11.50
12.00

FIG. 2B


ELSD Trace
Free Adnectin
Dimer of
Free Adnectin
FBSP-P/PEG
Free intact
PEG
mAU
MINUTES
4.00
4.50
5.00
5.50
6.00
6.50
7.00
7.50
8.00
8.50
9.00
9.50
10.00
10.50
11.00
11.50
12.00
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12.00
14.00
16.00
18.00
20.00
22.00
24.00
26.00

FIG. 3

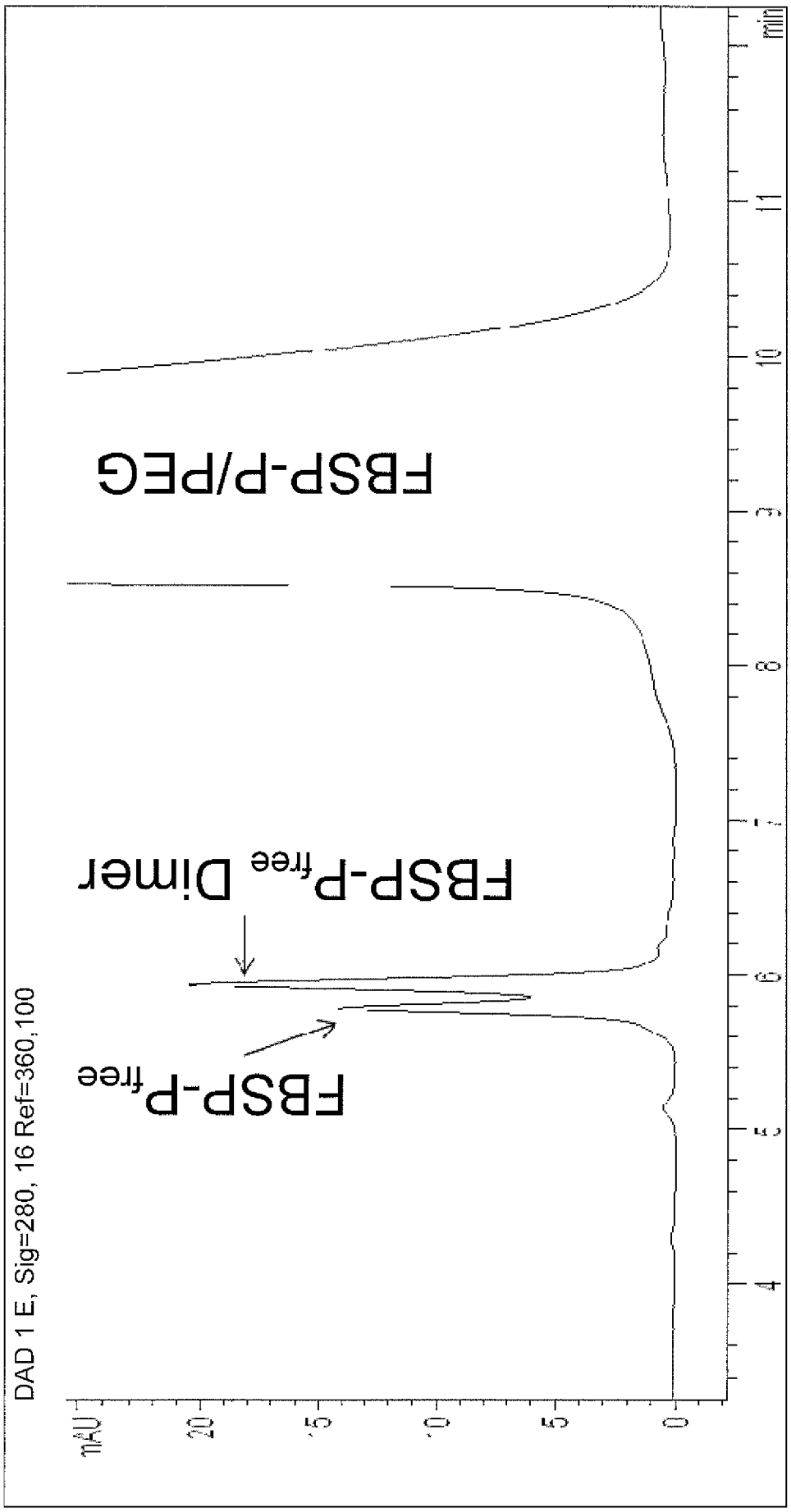

DAD 1 E, Sig=280, 16 Ref=360,100
mAU
min
FBSP-P/PEG
FBSP-P free Dimer
FBSP-P free

FIG. 4

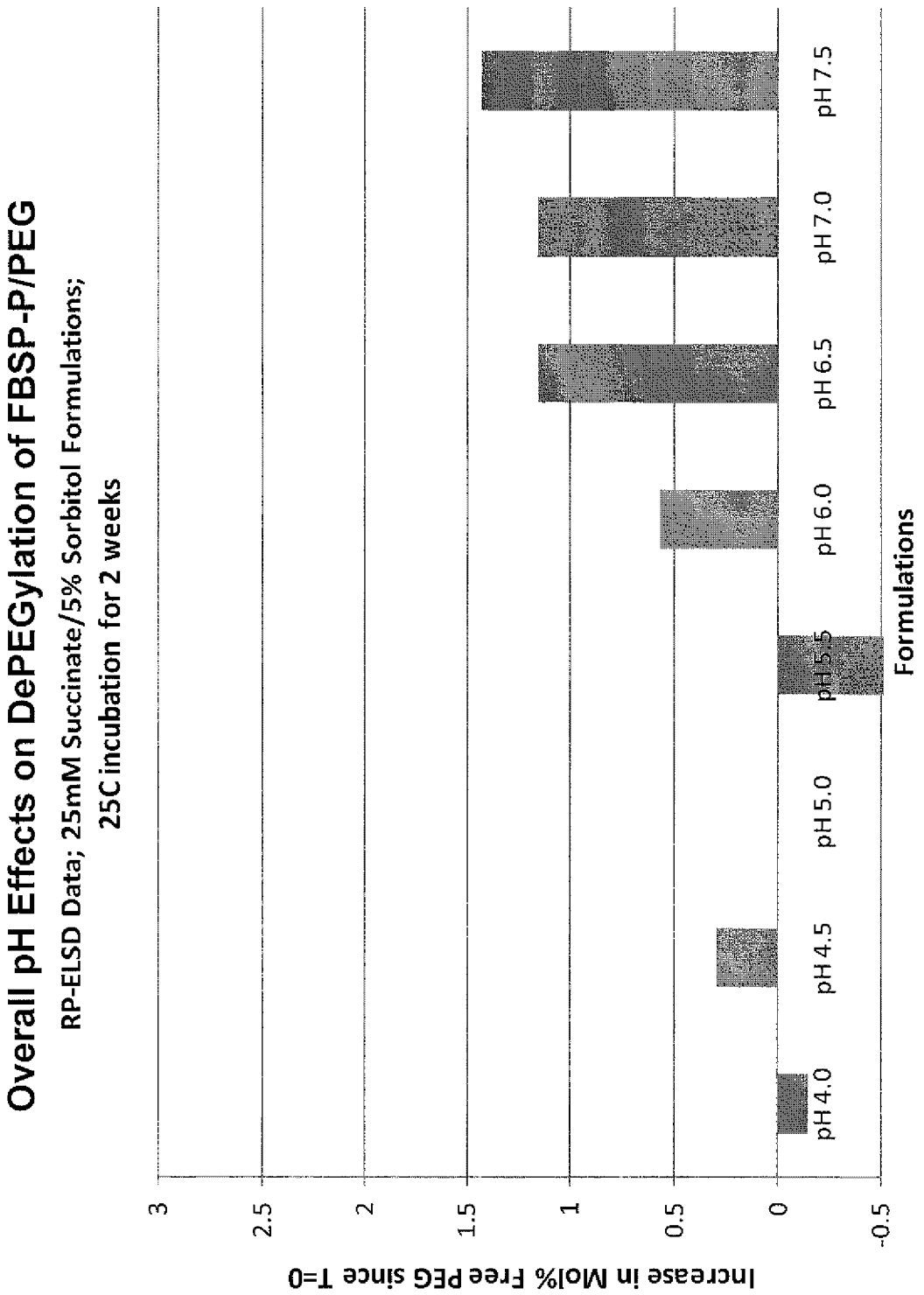

Overall pH Effects on DePEGylation of FBSP-P/PEG
RP-ELSD Data; 25mM Succinate/5% Sorbitol Formulations;
25C incubation for 2 weeks
Increase in Mol% Free PEG since T=0
3
2.5
2
1.5
1
0.5
0
-0.5
pH 4.0
pH 4.5
pH 5.0
pH 5.5
pH 6.0
pH 6.5
pH 7.0
pH 7.5
Formulations

FIG. 5

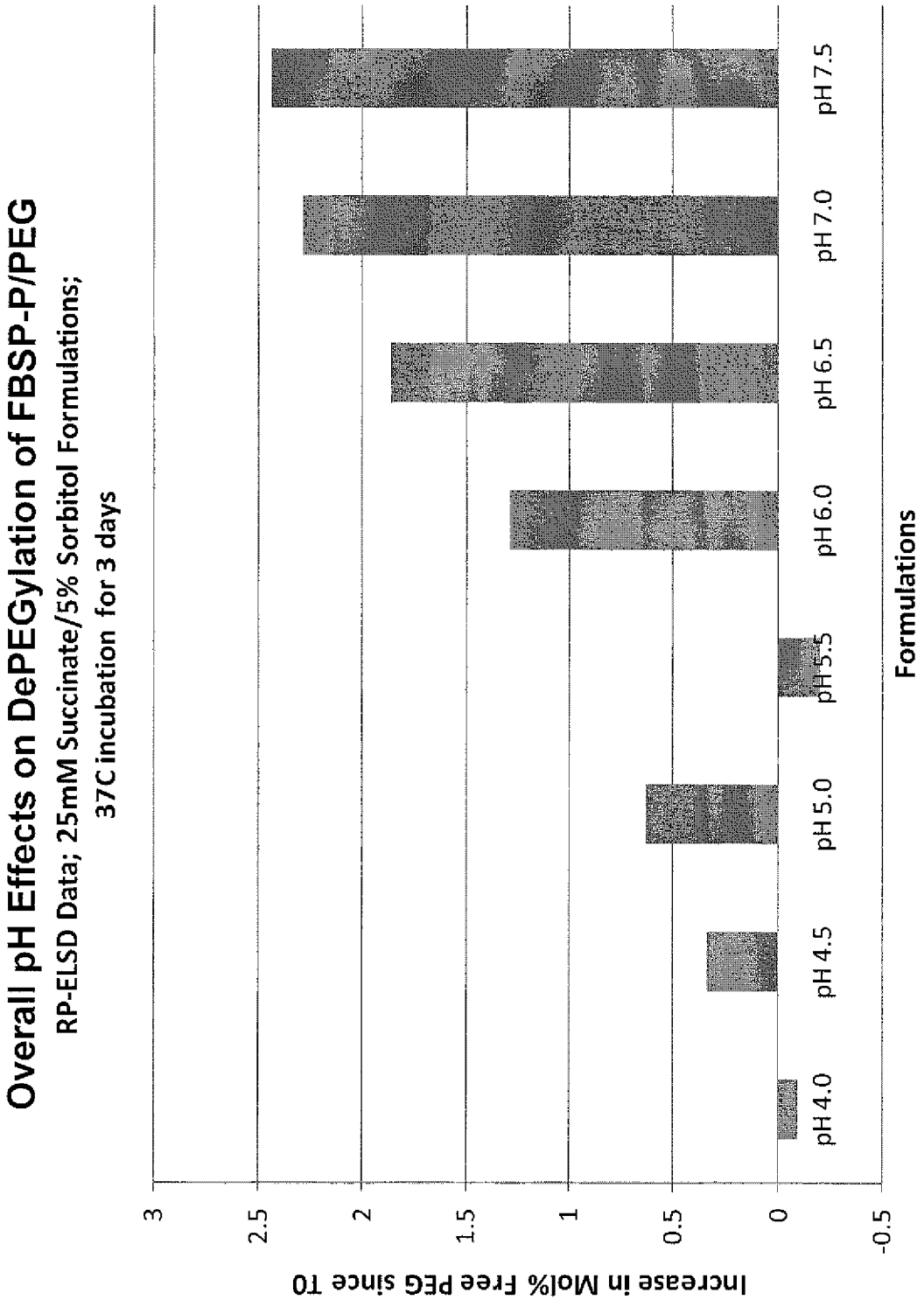

Overall pH Effects on DePEGylation of FBSP-P/PEG
RP-ELSD Data; 25mM Succinate/5% Sorbitol Formulations;
37C incubation for 3 days
Increase in Mol% Free PEG since T0
3
2.5
2
1.5
1
0.5
0
-0.5
pH 4.0
pH 4.5
pH 5.0
pH 5.5
pH 6.0
pH 6.5
pH 7.0
pH 7.5
Formulations

FIG. 6A

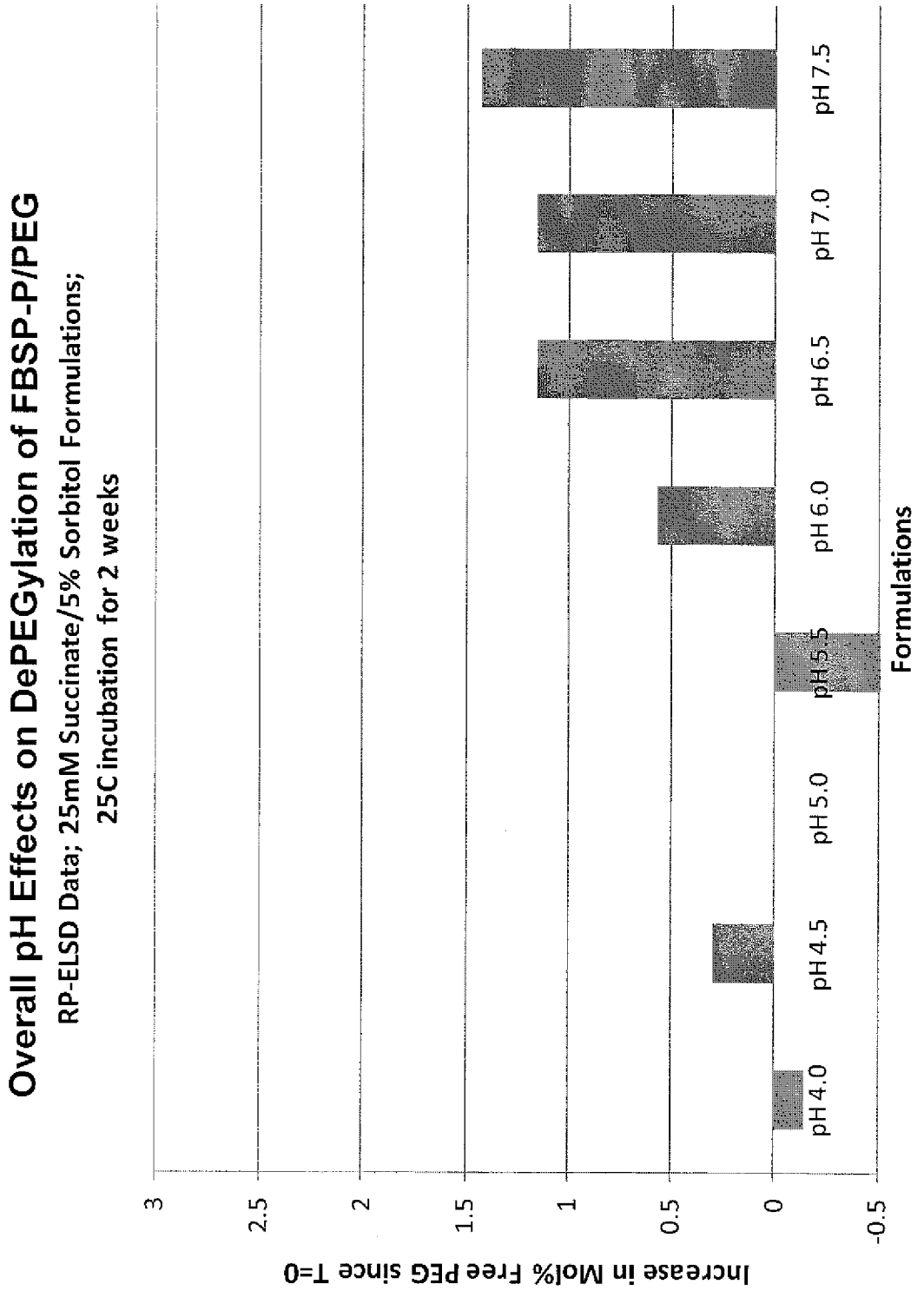

Overall pH Effects on DePEGylation of FBSP-P/PEG
RP-ELSD Data; 25mM Succinate/5% Sorbitol Formulations;
25C incubation for 2 weeks
Increase in Mol% Free PEG since T=0
3
2.5
2
1.5
1
0.5
0
-0.5
pH 4.0
pH 4.5
pH 5.0
pH 5.5
pH 6.0
pH 6.5
pH 7.0
pH 7.5
Formulations

FIG. 6B

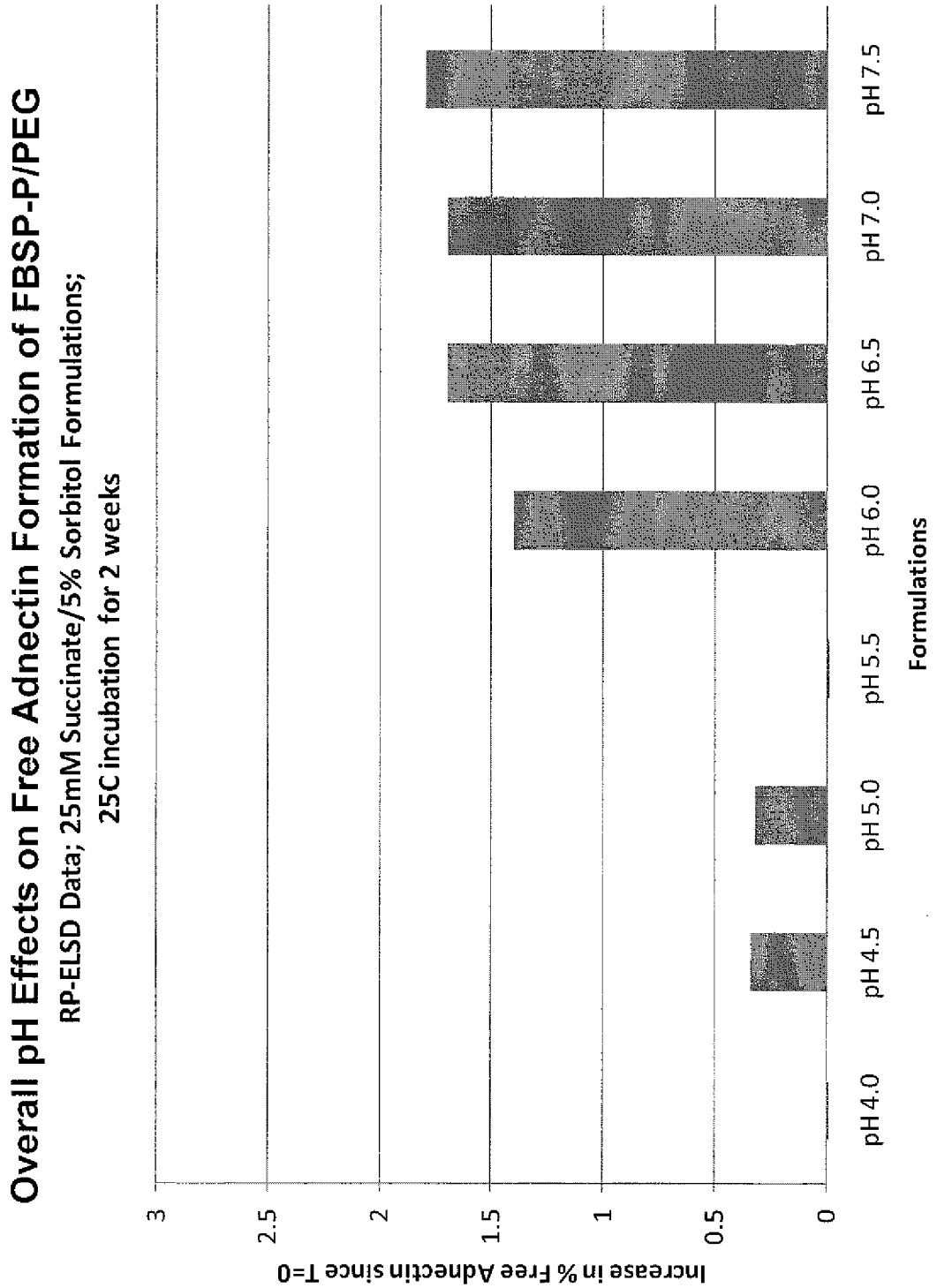

Overall pH Effects on Free Adnectin Formation of FBSP-P/PEG
RP-ELSD Data; 25mM Succinate/5% Sorbitol Formulations;
25C incubation for 2 weeks
Increase in % Free Adnectin since T=0
0
0.5
1
1.5
2
2.5
3
pH 4.0
pH 4.5
pH 5.0
pH 5.5
pH 6.0
pH 6.5
pH 7.0
pH 7.5
Formulations

FIG. 7

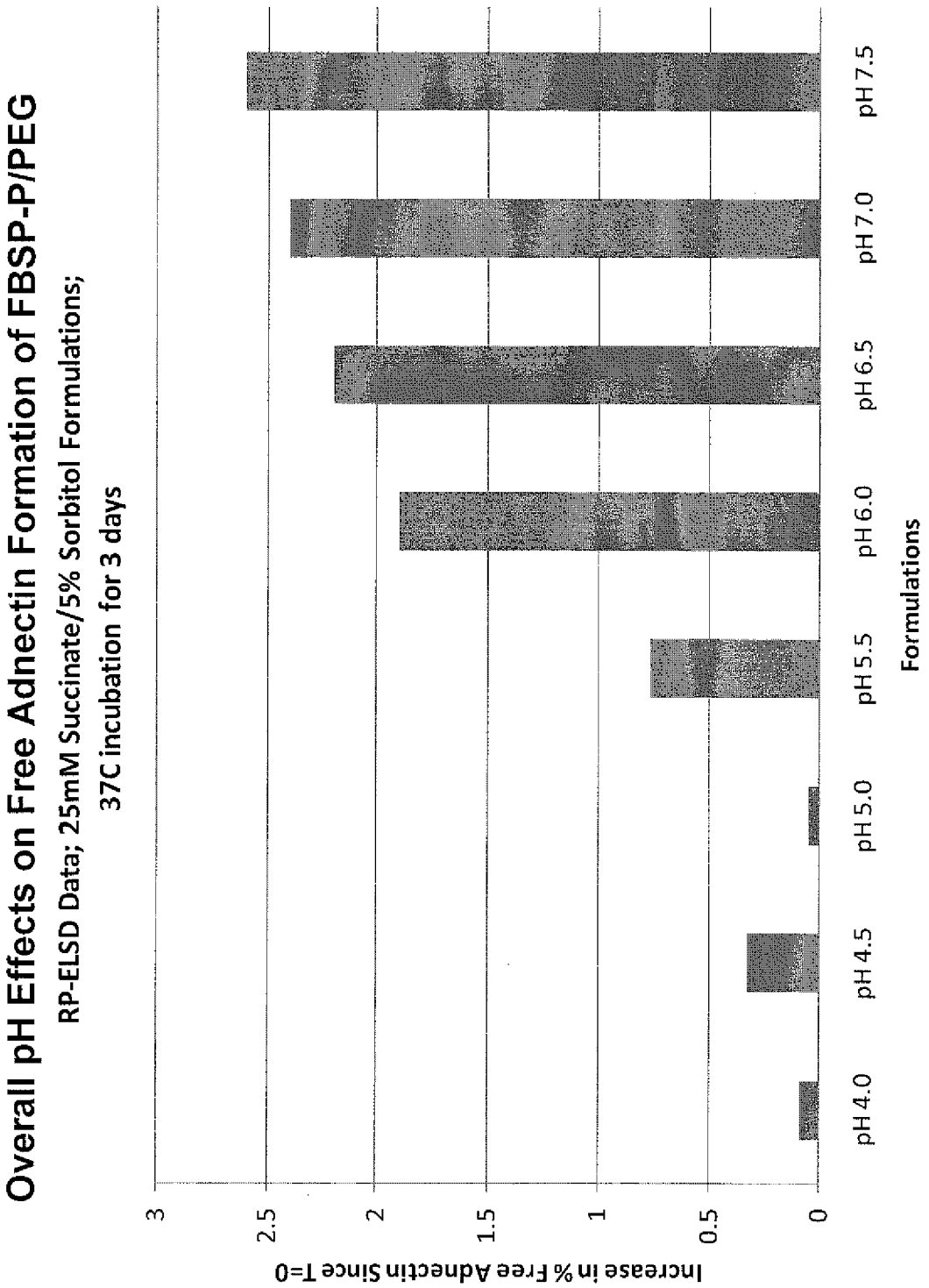

Overall pH Effects on Free Adnectin Formation of FBSP-P/PEG
RP-ELSD Data; 25mM Succinate/5% Sorbitol Formulations;
37C incubation for 3 days
Increase in % Free Adnectin Since T=0
0
0.5
1
1.5
2
2.5
3
pH 4.0
pH 4.5
pH 5.0
pH 5.5
pH 6.0
pH 6.5
pH 7.0
pH 7.5
Formulations

FIG. 8A

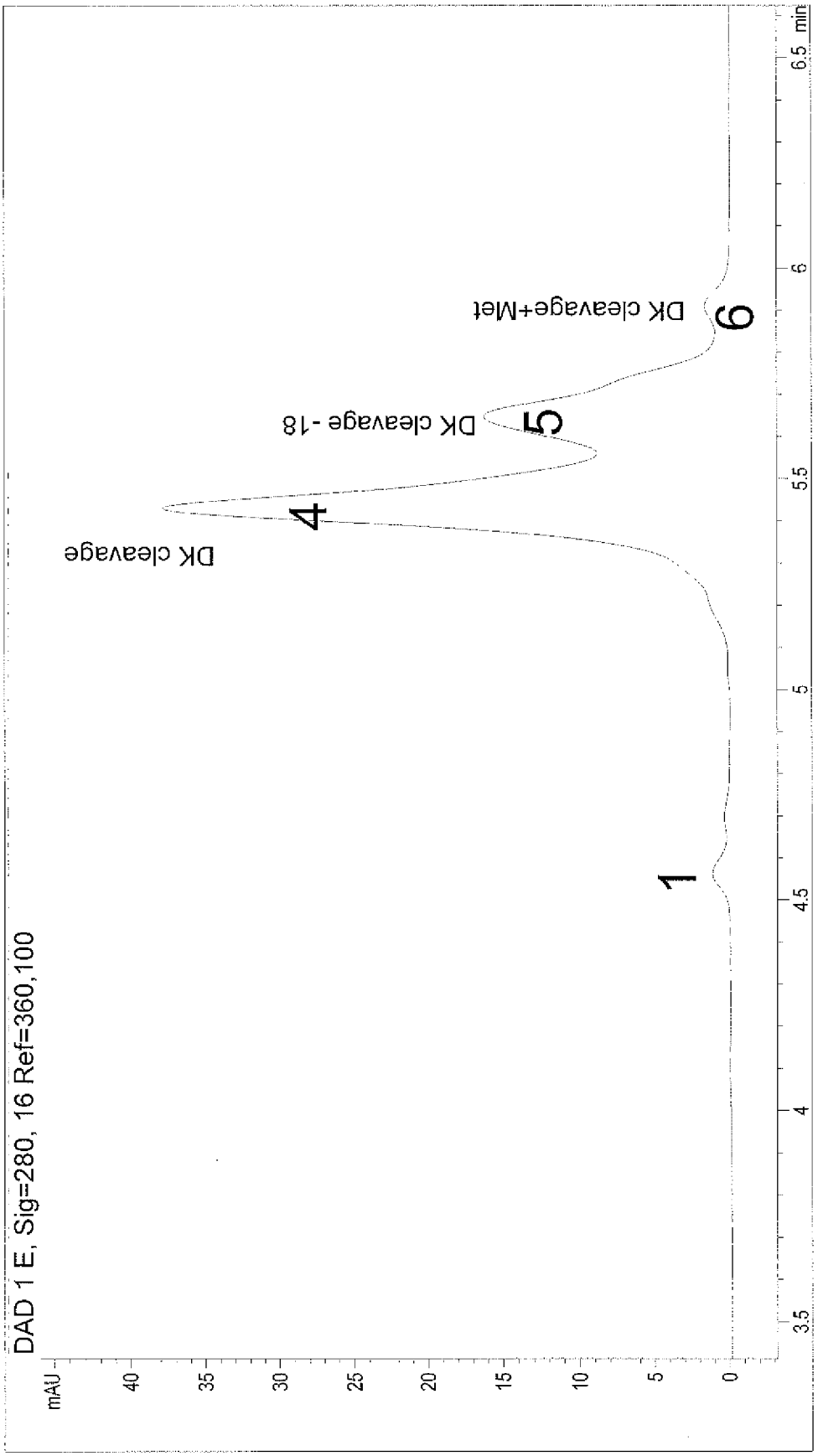

5 mg/mL, 10 mM NaOAc, 5% mannitol,pH 4.5
DAD 1 E, Sig=280, 16 Ref=360,100
mAU
0
5
10
15
20
25
30
35
40
3.5
4
4.5
5
5.5
6
6.5 min
1
4
5
6
DK cleavage
DK cleavage -18
DK cleavage+Met

FIG. 8B

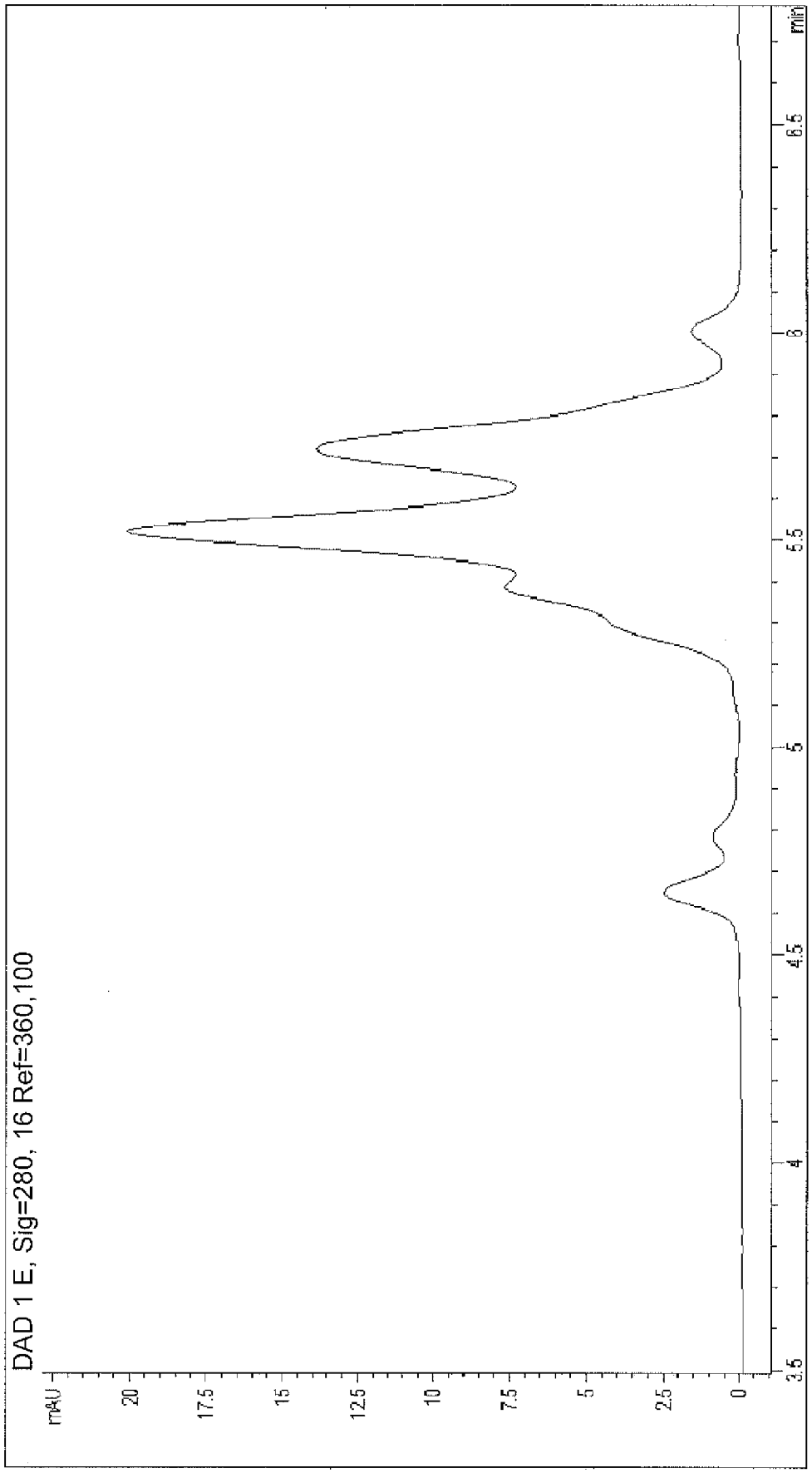

5 mg/mL, 10 mM NaOAc, 5% mannitol,pH 5.5
DAD 1 E, Sig=280, 16 Ref=360,100
mAU
20
17.5
15
12.5
10
7.5
5
2.5
0
3.5
4
4.5
5
5.5
6
6.5
min

FIG. 8C

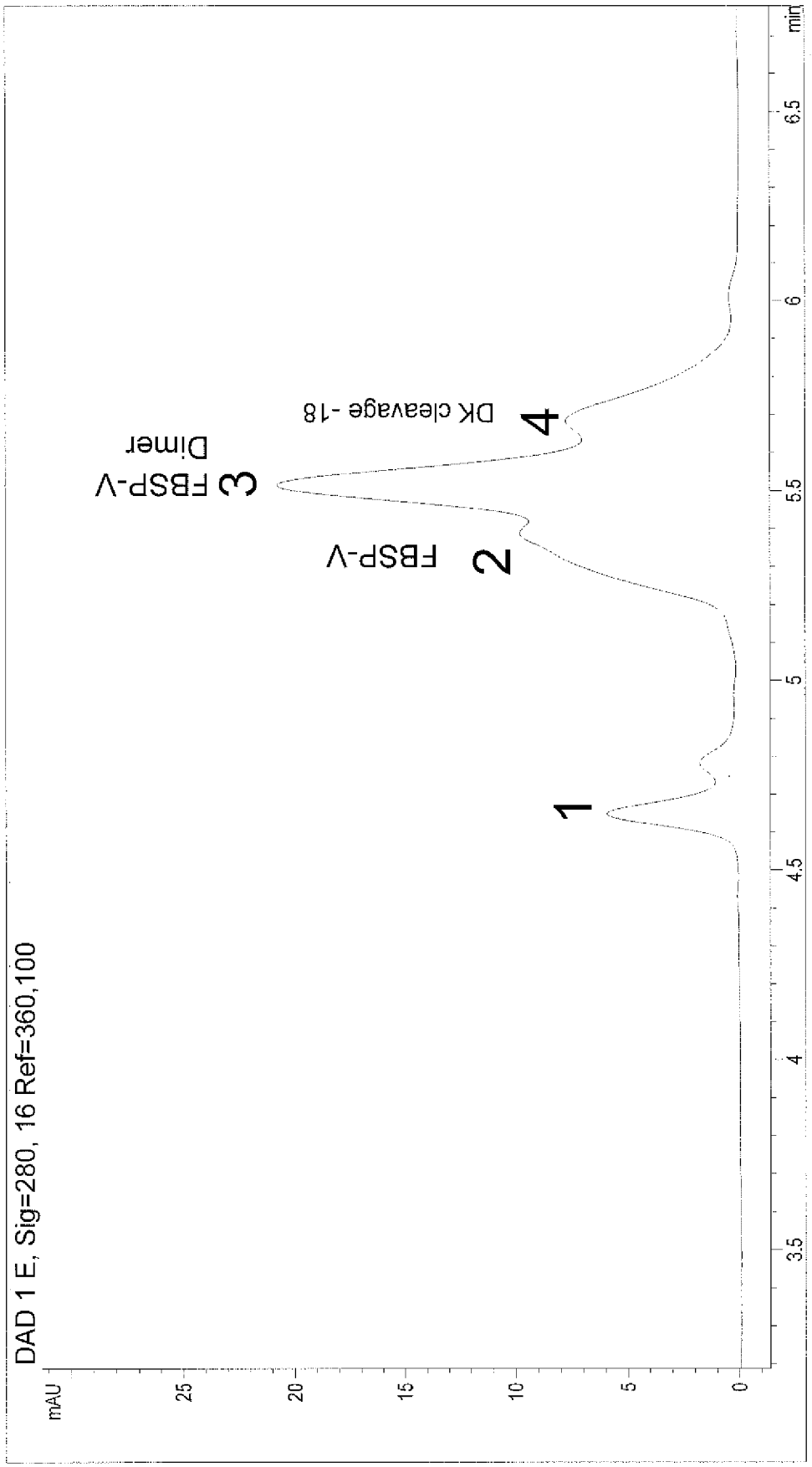

5 mg/mL, 10 mM NaOAc, 5% mannitol,pH 6.5
DAD 1 E, Sig=280, 16 Ref=360,100
mAU
25
20
15
10
5
0
3.5
4
4.5
5
5.5
6
6.5
min
1
2
FBSP-V
3
FBSP-V
Dimer
4
DK cleavage -18

FIG. 8D

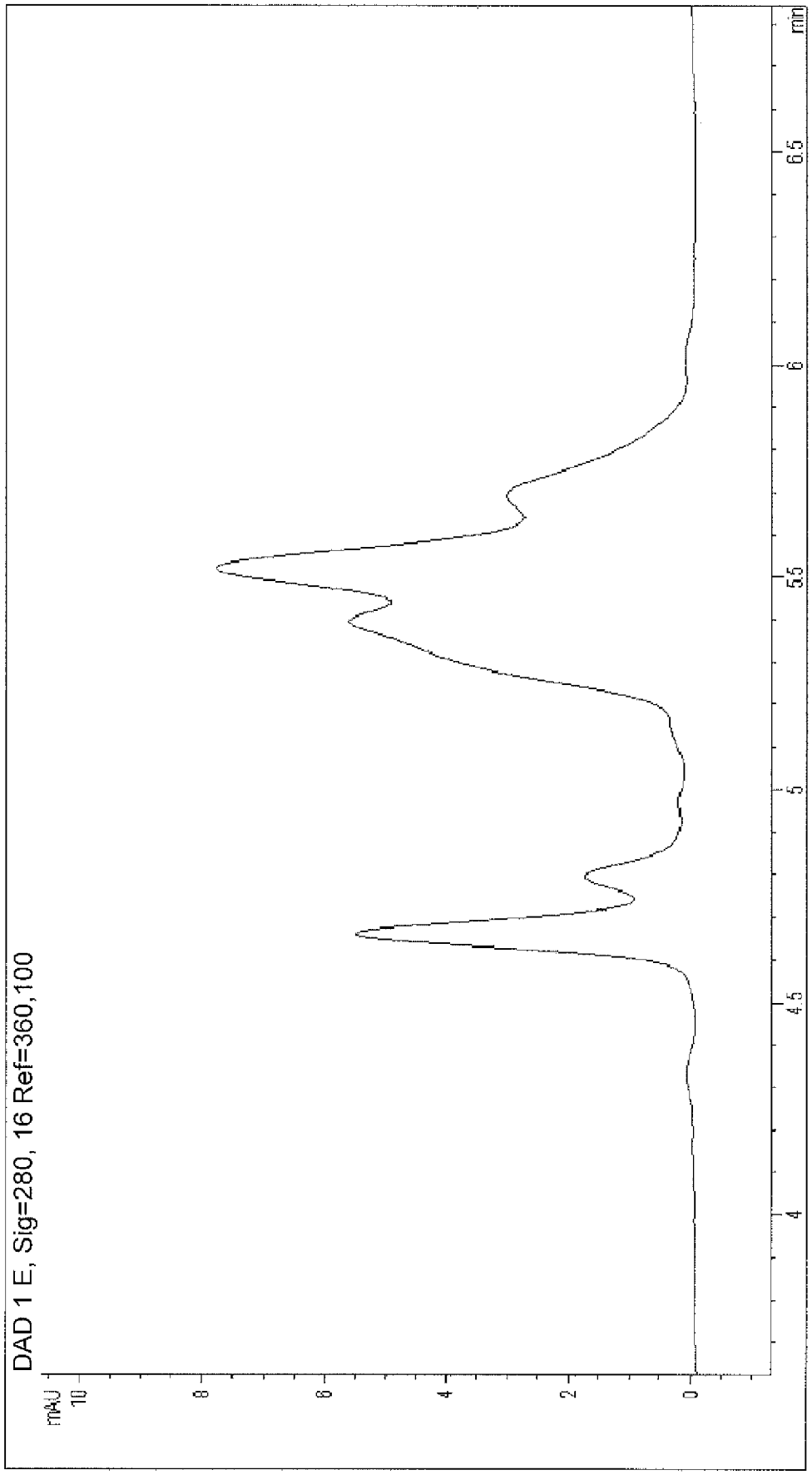

10mg/mL, 10 mM NaOAc, 5% mannitol, pH 6.5
DAD 1 E, Sig=280, 16 Ref=360,100
mAU
10
8
6
4
2
0
4
4.5
5
5.5
6
6.5
min

FIG. 9

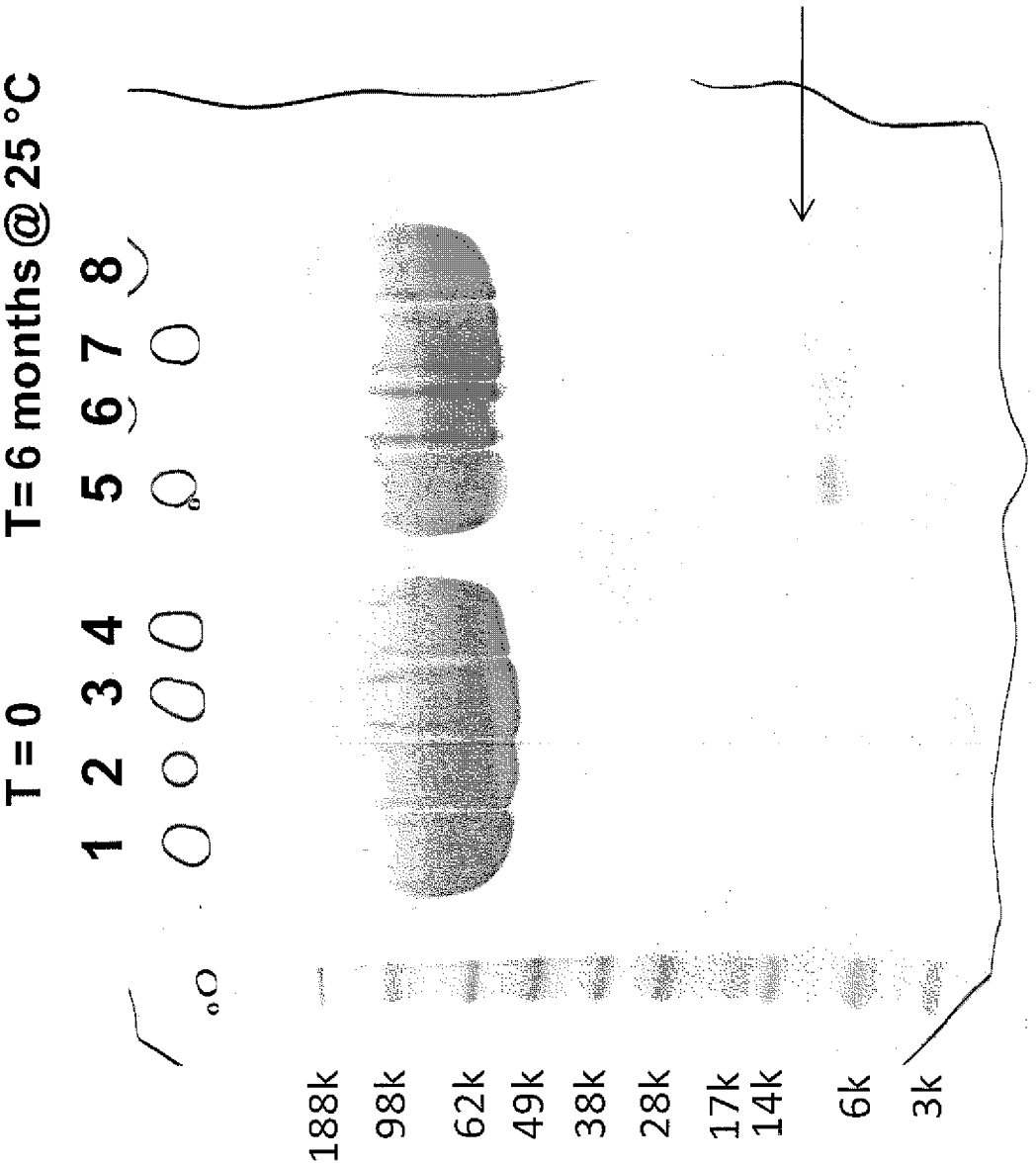

T=0
1 2 3 4
T=6 months@25 °C
5 6 7 8
188k
98k
62k
49k
38k
28k
17k
14k
6k
3k

FIG. 10

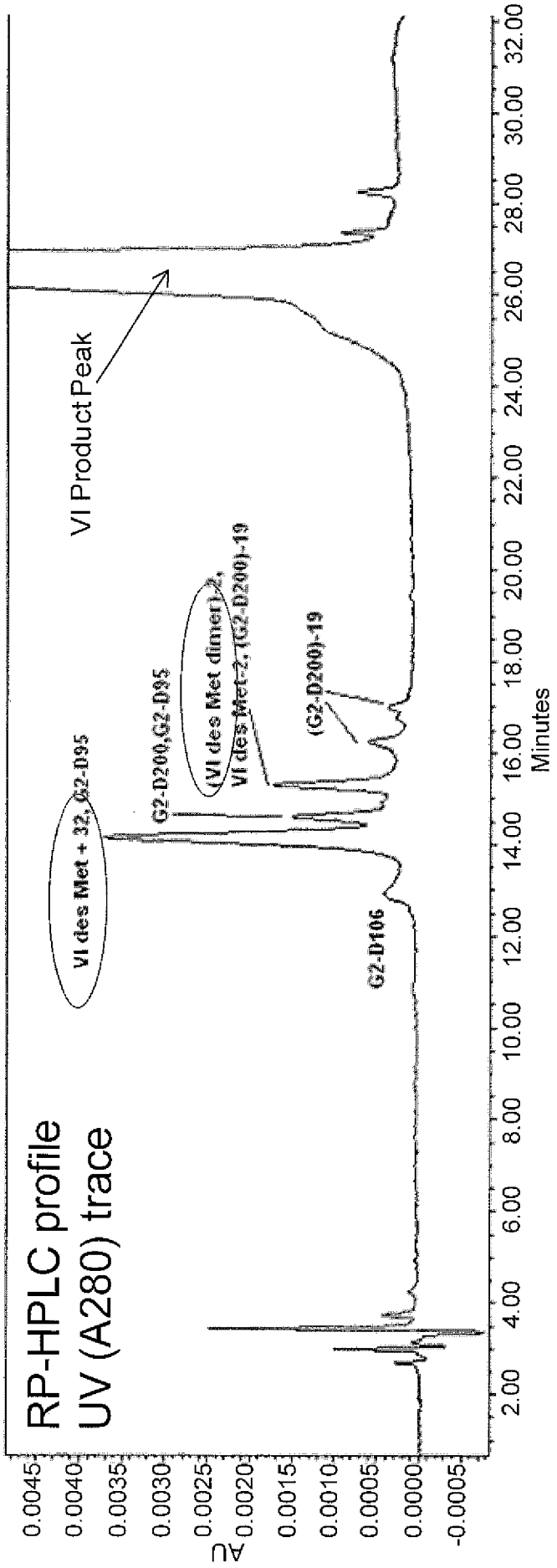

RP-HPLC profile
UV (A280) trace
VI Product Peak
VI des Met + 32, G2-D95
G2-D200,G2-D95
(VI des Met dimer)-2,
VI des Met-2, (G2-D200)-19
(G2-D200)-19
G2-D106
AU
Minutes
0.0045
0.0040
0.0035
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
-0.0005
2.00
4.00
6.00
8.00
10.00
12.00
14.00
16.00
18.00
20.00
22.00
24.00
26.00
28.00
30.00
32.00

FIG. 11

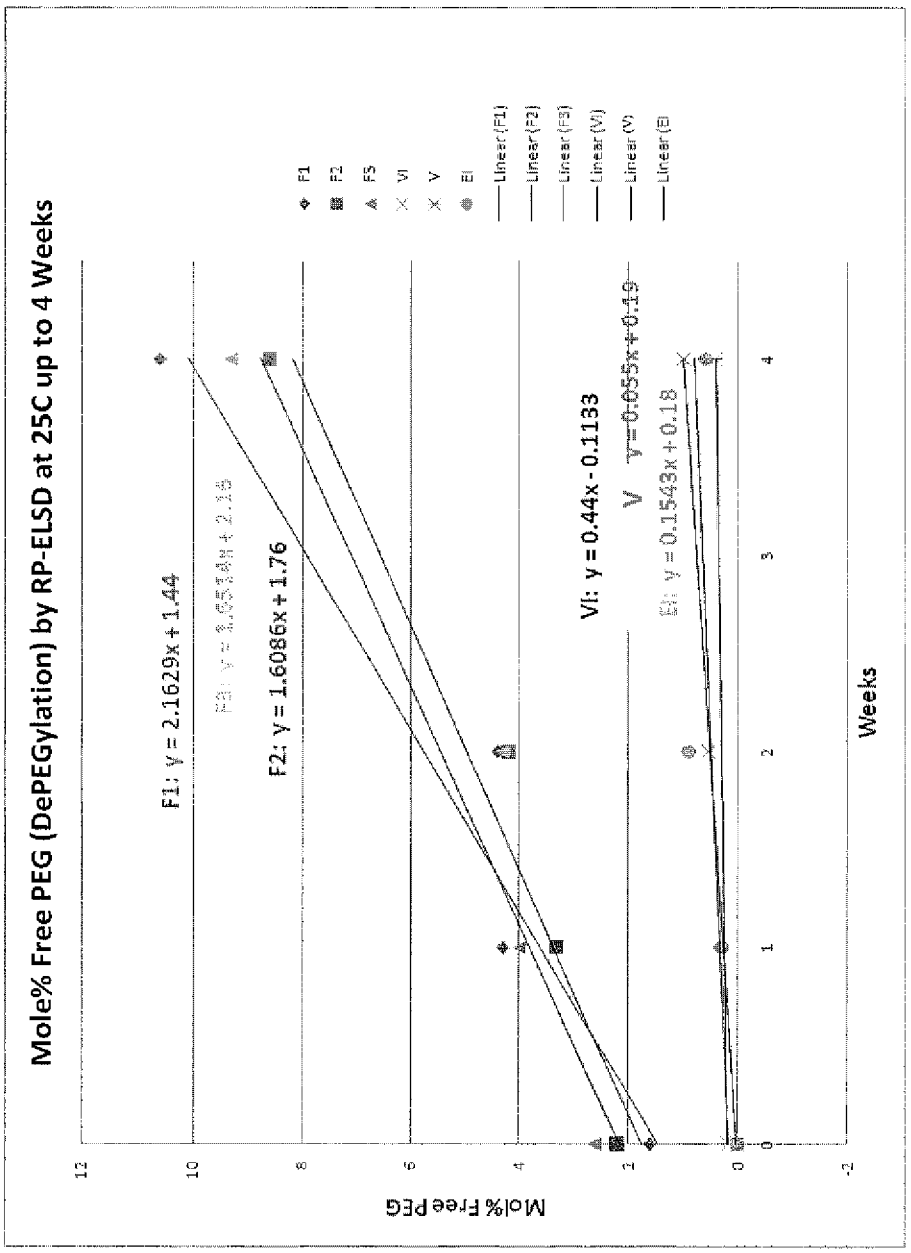

Mole% Free PEG (DePEGylation) by RP-ELSD at 25C up to 4 Weeks
F1: y = 2.1629x + 1.44
F2: y = 1.6086x + 1.76
Vi: y = 0.44x - 0.1133
V y=0.055x+0.19
Ei: y = 0.1543x + 0.18
Mol% Free PEG
Weeks
F1
F2
F5
Vi
V
Ei
Linear (F1)
Linear (F2)
Linear (F5)
Linear (Vi)
Linear (V)
Linear (Ei)

FIG. 12

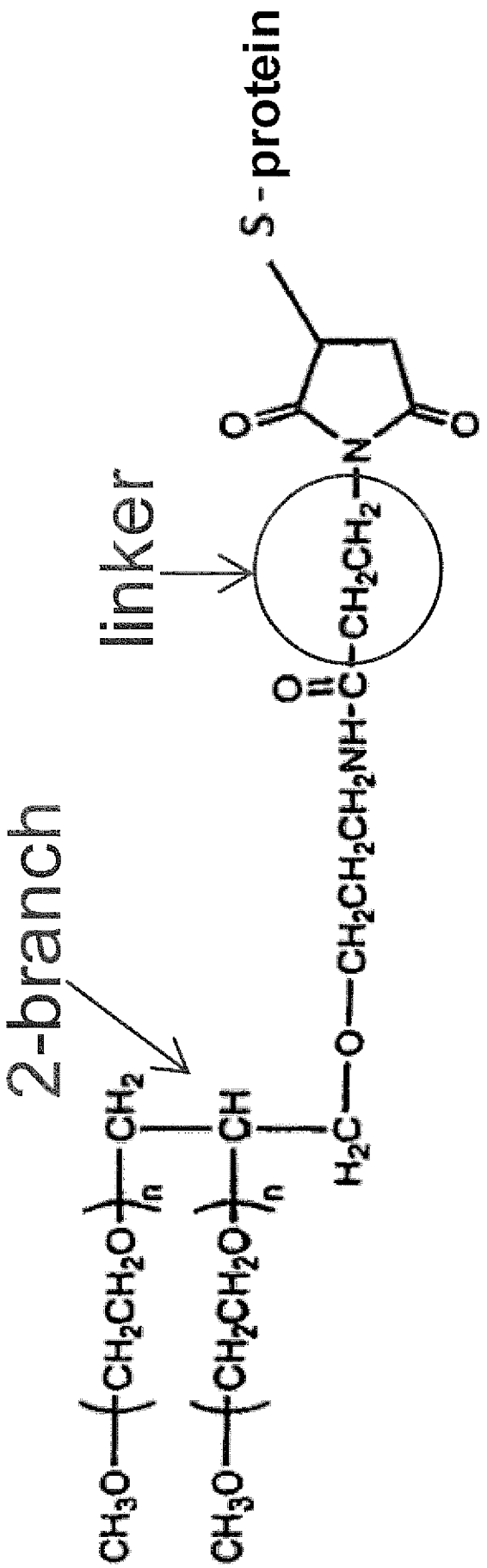

S - protein
linker
2-branch
CH_3O
CH_2CH_2O
n
CH
CH_2
H_2C
O
$CH_2CH_2CH_2NH$
C
CH_2CH_2
N

FIG. 13

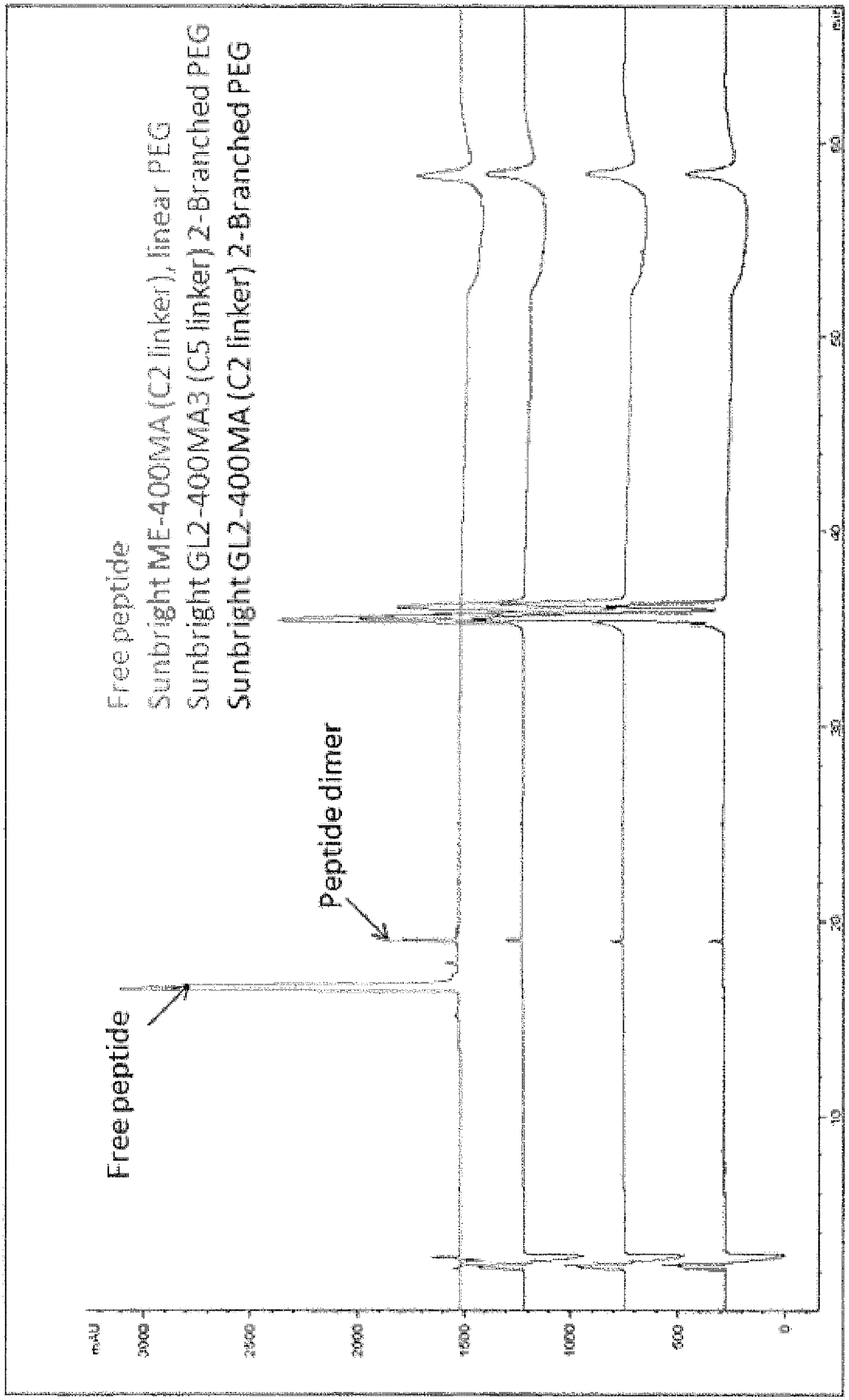

Free peptide
Sunbright ME-400MA (C2 linker), linear PEG
Sunbright GL2-400MA3 (C5 linker) 2-Branched PEG
Sunbright GL2-400MA (C2 linker) 2-Branched PEG
Free peptide
Peptide dimer
mAU
3000
2500
2000
1500
1000
500
0
min
10
20
30
40
50
60

FIG. 14

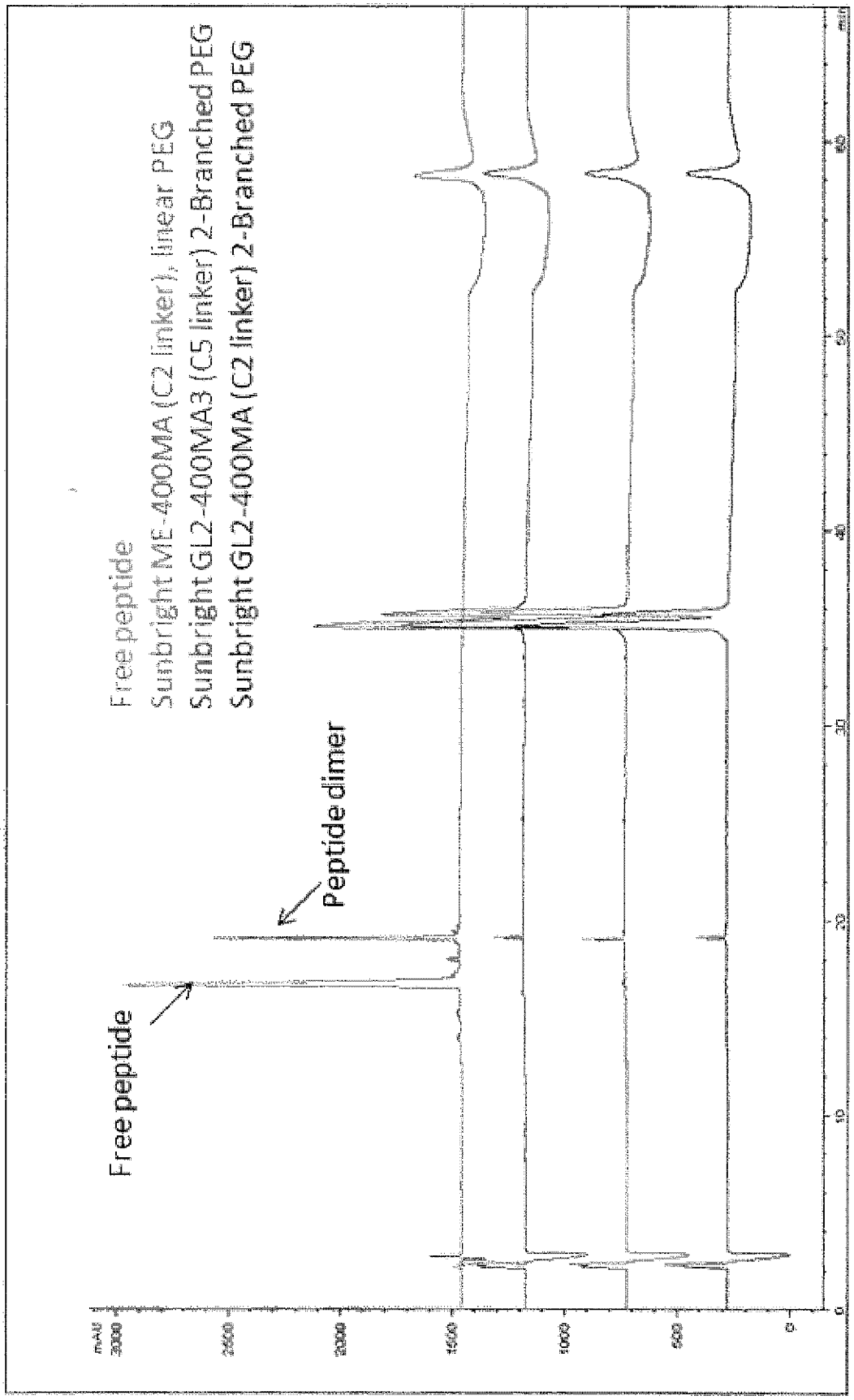

Free peptide
Sunbright ME-400MA (C2 linker), linear PEG
Sunbright GL2-400MA3 (C5 linker) 2-Branched PEG
Sunbright GL2-400MA (C2 linker) 2-Branched PEG
Free peptide
Peptide dimer
mAU
3000
2500
2000
1500
1000
500
0
0
10
20
30
40
50
min

FIG. 15

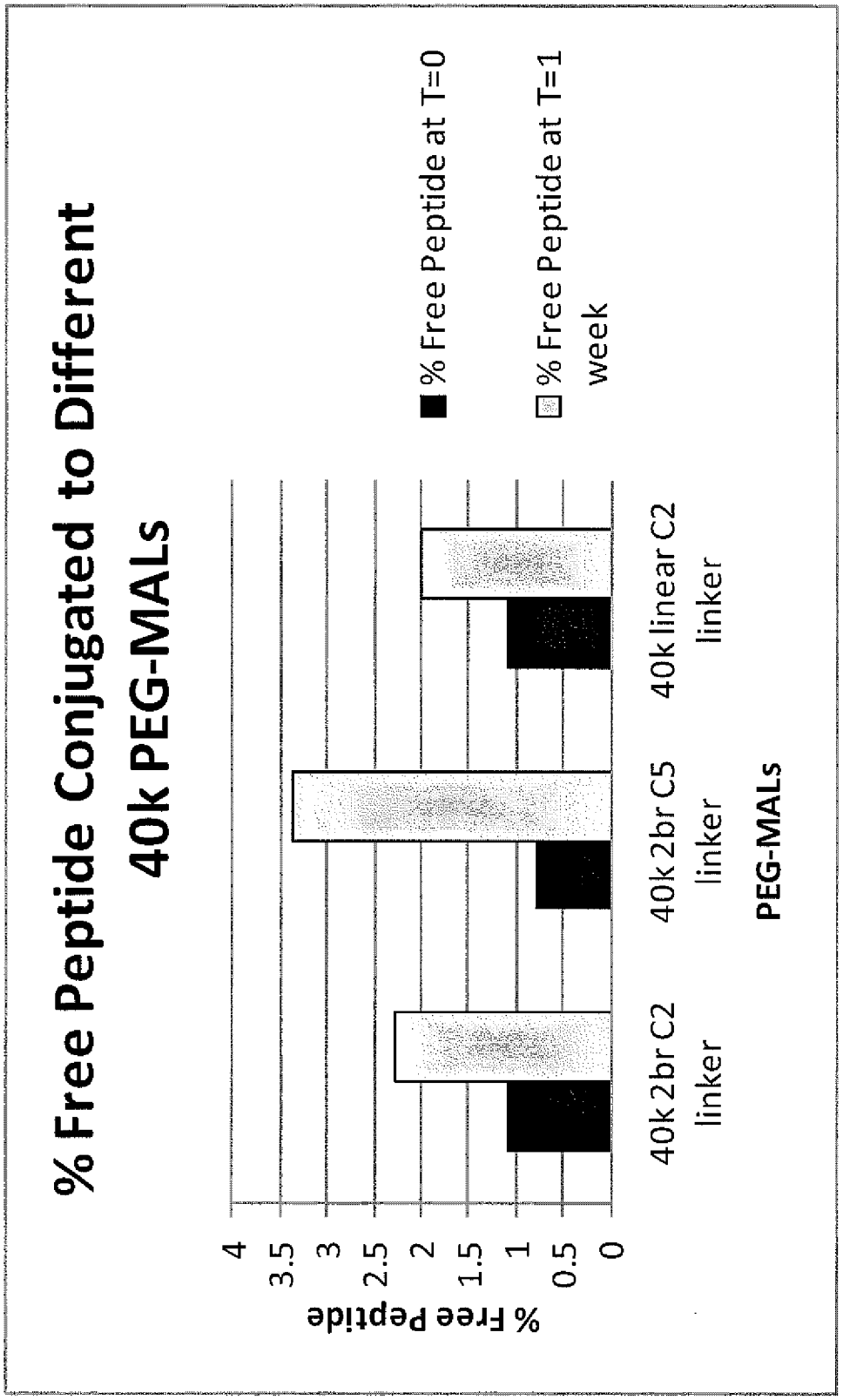

% Free Peptide Conjugated to Different 40k PEG-MALs
% Free Peptide at T=0
% Free Peptide at T=1 week
% Free Peptide
4
3.5
3
2.5
2
1.5
1
0.5
0
40k 2br C2 linker
40k 2br C5 linker
40k linear C2 linker
PEG-MALs

FIG. 16

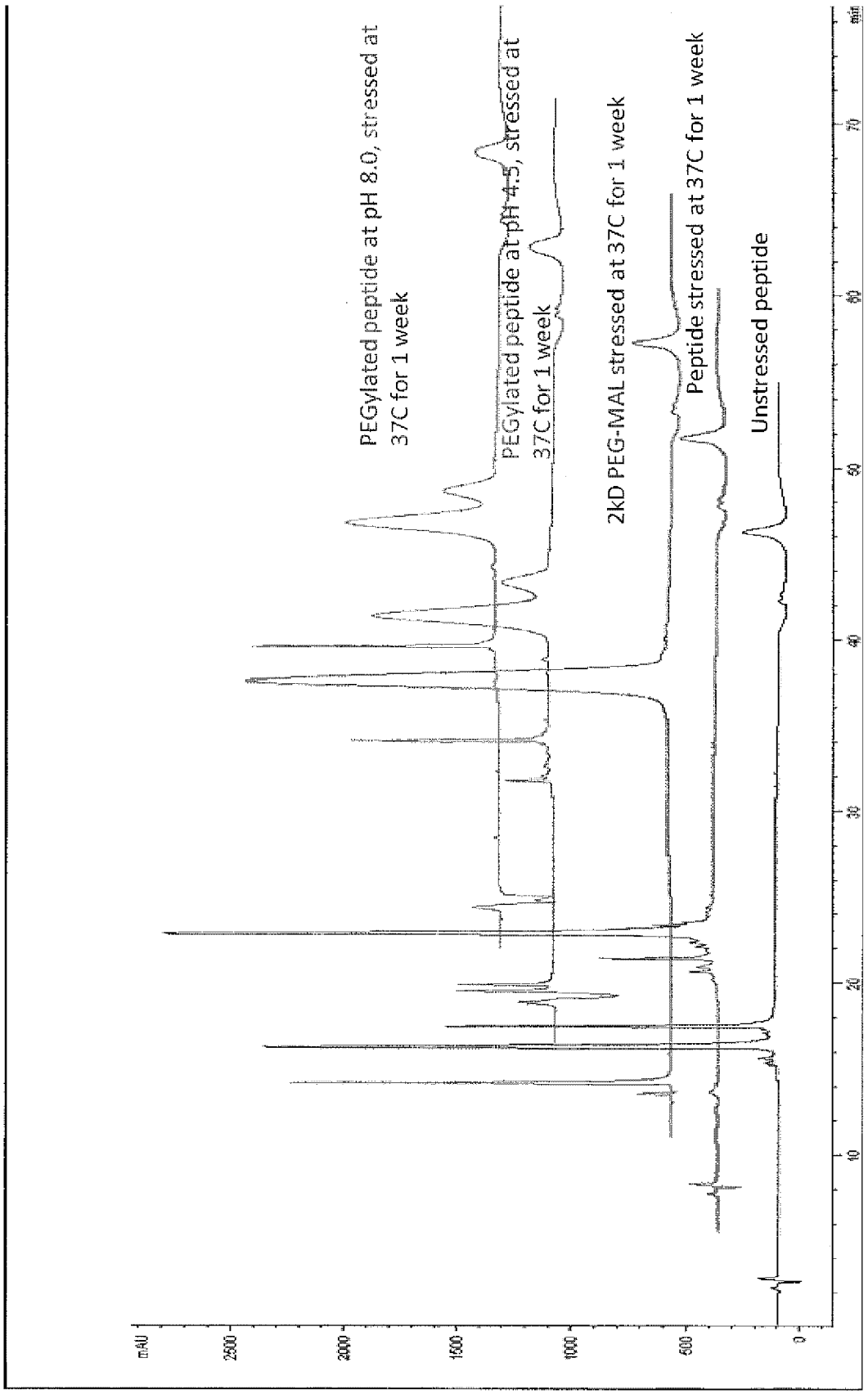
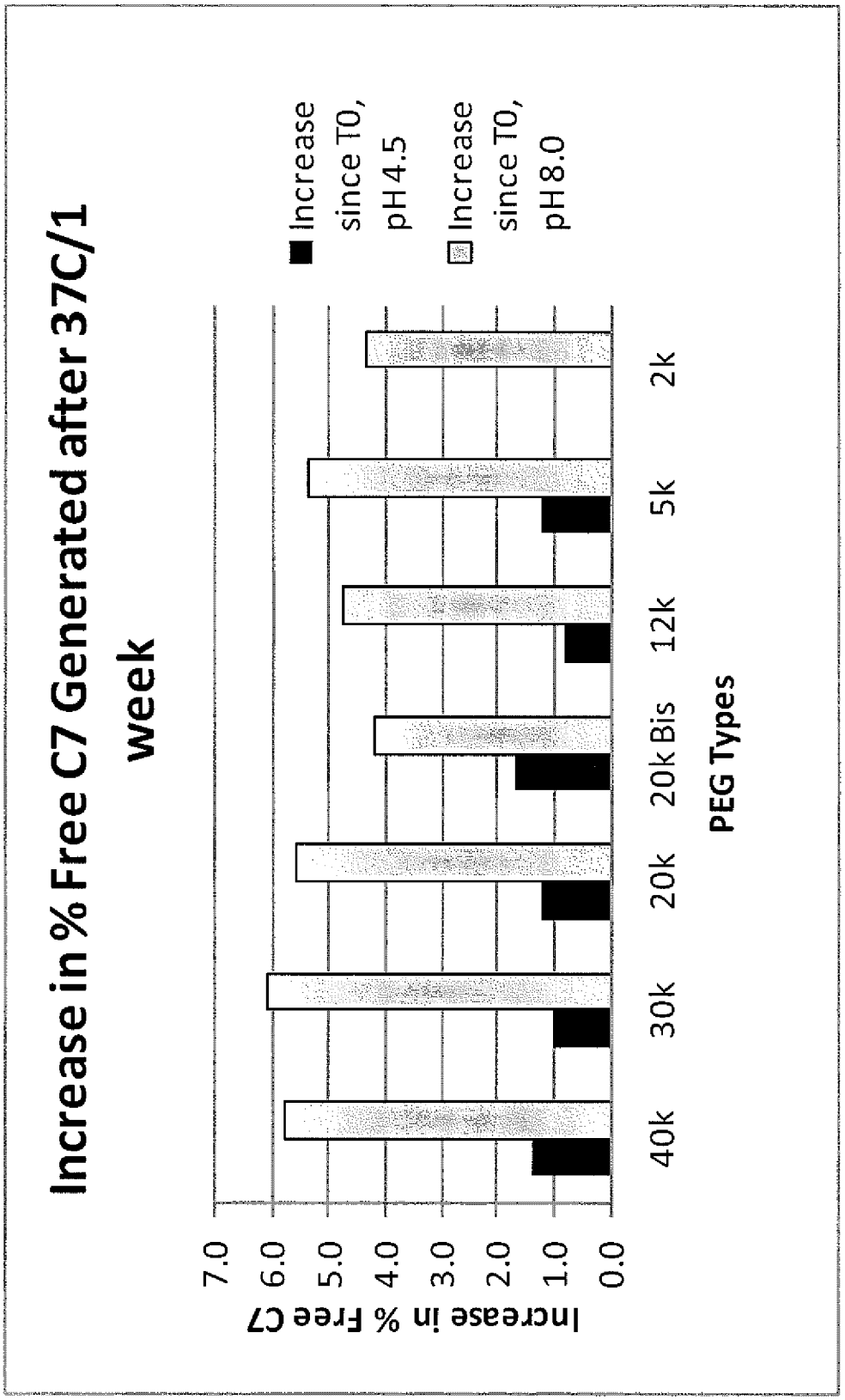

PEGylated peptide at pH 8.0, stressed at 37C for 1 week
PEGylated peptide at pH 4.5, stressed at 37C for 1 week
2kD PEG-MAL stressed at 37C for 1 week
Peptide stressed at 37C for 1 week
Unstressed peptide
mAU
2500
2000
1500
1000
500
0
10
20
30
40
50
60
70
min

FIG. 17


Increase in % Free C7 Generated after 37C/1 week
Increase since T0, pH 4.5
Increase since T0, pH 8.0
Increase in % Free C7
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
40k
30k
20k
20k Bis
12k
5k
2k
PEG Types

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/037908

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K47/48
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2004/019861 A2 (PHARMACIA CORP [US]; JOHNSON ROBERT E [US]; QI HONG [US]; BORGMEYER JE) 11 March 2004 (2004-03-11)	1-4, 18-22, 30,38
Y	paragraph [0028] - paragraph [0031] examples 1-2	1-38

X	WO 2009/142773 A2 (SQUIBB BRISTOL MYERS CO [US]; CAMPHAUSEN RAY [US]; FUFINE ERIC [US]; C) 26 November 2009 (2009-11-26) cited in the application	1-17
Y	page 103, line 3 - line 8 page 104, line 8 - line 13 sequences 9, 28	1-38

X	US 2010/273216 A1 (MORIN PAUL [US] ET AL) 28 October 2010 (2010-10-28)	1-17
Y	example 1 sequences 1-2	1-38

	-/--	

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

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

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

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

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

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

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 September 2012	01/10/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Monami, Amélie

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/037908

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   [X] on paper

   [X] in electronic form

   b. (time)

   [ ] in the international application as filed

   [ ] together with the international application in electronic form

   [X] subsequently to this Authority for the purpose of search

2. [X] In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/037908

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2007/011166 A1 (MOGAM BIOTECH RES INST [KR]; KANG KWAN-YUB [KR]; HONG JEONG-WOON [KR]) 25 January 2007 (2007-01-25) page 13, paragraph 75 - paragraph 76 page 14, paragraph 85 - paragraph 87	1-4

X,P	WO 2011/150133 A2 (SQUIBB BRISTOL MYERS CO [US]; CAMPHAUSEN RAY [US]; O'LOUGHLIN JOHN [US) 1 December 2011 (2011-12-01) cited in the application	1-17
Y,P	examples 1-7 sequence 22	1-38

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2012/037908

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2004019861 A2	11-03-2004	AR 041067 A1	27-04-2005
		AU 2003265361 A1	19-03-2004
		US 2004091490 A1	13-05-2004
		WO 2004019861 A2	11-03-2004
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		CN 102099373 A	15-06-2011
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		JP 2011520961 A	21-07-2011
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		TW 201000118 A	01-01-2010
		US 2009299040 A1	03-12-2009
		WO 2009142773 A2	26-11-2009
US 2010273216 A1	28-10-2010	NONE	
WO 2007011166 A1	25-01-2007	AT 551361 T	15-04-2012
		CN 101213208 A	02-07-2008
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		EP 2174951 A2	14-04-2010
		ES 2381256 T3	24-05-2012
		JP 4782834 B2	28-09-2011
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		KR 20070010817 A	24-01-2007
		US 2008200657 A1	21-08-2008
		WO 2007011166 A1	25-01-2007
WO 2011150133 A2	01-12-2011	NONE	