MULTILAYER FILMS, COATINGS, AND MICROCAPSULES COMPRISING POLYPEPTIDES

Inventor: Donald T. Haynie, New Haven, CT (US)
Assignee: Louisiana Tech Foundation, Inc., Ruston, LA (US)

Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

Filed: Oct. 25, 2006
Prior Publication Data

Related U.S. Application Data
Continuation-in-part of application No. 10/652,364, filed on Aug. 29, 2003.
Provisional application No. 60/729,828, filed on Oct. 25, 2005.

Int. Cl. C07K 17/00 (2006.01)
C07K 2/00 (2006.01)

U.S. Cl. 530/300
Field of Classification Search None
See application file for complete search history.

References Cited
U.S. PATENT DOCUMENTS
5,686,113 A 11/1997 Speaker et al.
6,022,500 A 2/2000 John et al.
6,107,084 A 8/2000 Onda et al.
6,208,222 B1 7/2001 Chandler et al.
6,309,701 B 10/2001 Barbera-Guillem
6,316,084 B 11/2001 Claus et al.
6,437,095 B1 8/2002 Lilie et al. 530/345
6,479,146 B1 11/2002 Cusano et al.
6,485,003 B1 1/2002 Cote et al.
6,833,192 B1 12/2004 Caruso et al.
6,989,267 B2 1/2008 Kim et al.
7,064,146 B2 5/2006 Caruso et al.

FOREIGN PATENT DOCUMENTS
EP 0 667 148 198/1985
EP 0 415 273 8/1990
EP 0 433 428 8/1991
EP 0 472 990 8/1991
EP 0 823 331 11/2001
GB 2 135 954 9/1994
WO WO 99/47252 9/1999
WO WO 99/47253 9/1999
WO WO 00/03797 1/2000
WO WO 00/77281 A1 12/2000
WO WO 02/09864 2/2002
WO WO 02/09865 2/2002
WO WO 02/17888 A2 2/2002

OTHER PUBLICATIONS
Lebaron (“Extracellular Matrix Cell Adhesion Peptides: Functional Applications in Orthopedic Materials,” Tissue Engineering, 2000, 6, 80-103)*
Mann et al. (“Modification of surfaces with cell adhesion peptides alters extracellular matrix deposition,” Biomat., 1999, 20, 2281-6).*

Primary Examiner—Cecilia Tsang
Assistant Examiner—Christina Marchetti Bradley
Attorney, Agent, or Firm Cantor Colburn LLP

ABSTRACT

Disclosed herein is a multilayer film comprising two or more layers of polyelectrolytes, wherein adjacent layers comprise oppositely charged polyelectrolytes. A first layer polyelectrolyte comprises a composite polypeptide comprising one or more surface adsorption regions covalently linked to one or more functional regions forming a single polyelectropeptide chain. The surface adsorption regions comprise one or more amino acid sequence motifs consisting of 5 to 15 amino acid residues. The one or more functional regions comprise 3 to 250 amino acid residues.

23 Claims, 17 Drawing Sheets

http://www.chem.fsu.edu/multilayers/ "Polyelectrolyte Multilayers Home Page."


* cited by examiner
FIGURE 2
Identification of Negatively-charged Motifs in Sequences Involving Usual Amino Acids Only

1. Select an amino acid sequence.

2. Locate an uncharged or a negatively-charged residue in this sequence (Asp or Glu).

4a. If this 7-residue sequence contains at least 4 negatively-charged residues (Asp or Glu), then this entire 7-residue sequence is a motif; record the sequence of the motif; return to step 2 if further motifs are sought.

3. Examine the next 6 residues for at least one occurrence of a positively-charged residue (Arg, Lys, or His).

N

Yes

4b. Return to step 2.

FIG. 5
Available Non-Redundant Sequence Motifs

FIG. 6
FIG. 7
FIG. 8
FIG. 10
FIG. 11(a)
FIG. 11(b)
Layer by layer assembly of poly-L-lysine and poly-L-glutamate

10 mM Tris, pH 7.4

FIG. 12
MULTILAYER FILMS, COATINGS, AND MICROCAPSULES COMPRISING POLYPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATION

This application is a Continuation-In-Part of U.S. Nonprovisional application Ser. No. 10/652,364 filed Aug. 29, 2003, and also claims the benefit of U.S. 60/739,828 filed Oct. 25, 2005, which are incorporated by reference herein.

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to the fabrication of ultrathin multilayered films on suitable surfaces by electrostatic layer-by-layer self assembly ("ELB."). More specifically, the present invention relates to a method for designing polypeptides for the nanofabrication of thin films, coatings, and microcapsules by ELBI for applications in biomedicine and other fields.

2. Description of Related Art

ELBI is an established technique in which ultrathin films are assembled by alternating the adsorption of oppositely charged polyelectrolytes. The process is based on the reversal of the surface charge of the film at the deposition of each layer. FIG. 1 shows a schematic diagram of the general ELBI process. Films of oppositely charged polyanions (catanic polyelectrolytes 10 and anionic polymers 11) are assembled in successive layers on a negatively charged planar surface 12; the surface charge is reversed after the deposition of each layer. This process is repeated until a film of desired thickness is formed. The physical basis of association is electrostatics—gravitation and nuclear forces play effectively no role—and the increase in entropy on release of counterions into solution. Because of the generality and relative simplicity of the process, ELBI allows for the deposition of many different types of materials onto many different types of surface. There are, therefore, a vast number of possible useful combinations of materials and surfaces. For a general discussion of ELBI, including its history, see Yuri I. Vov, "Electrostatic Layer-by-Layer Assembly of Proteins and Polyelectrolytes" in Protein Architecture: Interface Molecular Assembly and Immobilization Biotechnology, Y. I. Vov & R. Mithuland (eds. (New York: Marcel Dekker, 1999), pp. 125-167, which is incorporated herein by reference in its entirety.

ELBI has recently become a focus area in the field of nanotechnology because it can be used to fabricate films substantially less than 1 micron in thickness. Moreover, ELBI permits exceptional control over the film fabrication process, enabling the use of nanoscale materials and permitting nanoscale structural modifications. Because each layer has a thickness on the order of a few nanometers or less, depending on the type of material used and the specific adsorption process, multi-layer assemblies of precisely repeatable thickness can be formed.

A number of synthetic polyelectrolytes have been employed in ELBI applications, including sodium poly(styrene sulfonate) ("PSS"), polyallylamine hydrochloride ("PAH"), poly(diallyldimethylammonium chloride) ("PDADMA"), poly(acrylamide-co-diallyldimethylammonium chloride), poly(ethyleneimine) ("PEI"), poly(acrylic acid) ("PAA"), poly(methacrylic acid), poly(vinyl sulfate) ("PVS"), and poly(vinylsulfonic acid). Such materials, however, are not generally useful for biomedical applications because they are antigenic or toxic.

Proteins, being polymers with side chains having ionizable groups, can be used in ELBI for various applications, including biotechnological ones. Examples of proteins that have been used in ELBI include cytochrome c, hen egg white lysozyme, immunoglobulin G, myoglobin, hemoglobin, and serum albumin (ibid.). There are, however, difficulties with using proteins for this purpose. These include limited control over multilayer structure (because the surface of the protein is highly irregular and proteins will not ordinarily adsorb on a surface in a regular pattern), restrictions on pH due to the pH-dependence of protein solubility and structural stability, lack of biocompatibility when using exogenous proteins, and the cost of scaling up production if the gene has not been cloned; unless the protein were identical in a readily available source, e.g., a cow, the protein would have to be obtained from the organism in which it was intended for use, making the cost of large-scale production of the protein prohibitive.

By contrast polypeptides, which are generally smaller and less complex than proteins, constitute an excellent class of material for ELBI assembly, and polypeptide film structures formed by ELBI will be useful in a broad range of applications. The present invention provides a method for designing polypeptides for the nanofabrication of thin films, coatings, and microcapsules by ELBI. Polypeptides designed using the method of the present invention should exhibit several useful properties, including, without limitation, completely determined primary structure, minimal secondary structure in aqueous solution, monodispersity, completely controlled net charge per unit length, ability to form cross-links on demand, ability to reverse cross-link formation, ability to form more organized thin films than is possible with proteins, and relatively inexpensive large-scale production cost (assuming gene design, synthesis, cloning, and host expression in E. coli or yeast, or peptide synthesis).

Polypeptides designed using the method of the present invention have been shown useful for ELBI of thin film structures with targeted or possible applications in biomedical technology, food technology, and environmental technology. Such polypeptides could be used, for example, to fabricate artificial red blood cells, drug delivery devices, and antimicrobial films.

BRIEF SUMMARY OF THE INVENTION

Disclosed herein is a multilayer film comprising two or more layers of polyelectrolytes, wherein adjacent layers comprise oppositely charged polyelectrolytes. A first layer polyelectrolyte comprises a copolymeric polypeptide comprising one or more surface adsorption regions covalently linked to one or more functional regions forming a single polypeptide chain, wherein the covalent polypeptide and the one or more surface adsorption regions have the same polarity. The surface adsorption regions comprise one or more amino acid sequence motifs, the one or more amino acid sequence motifs consisting of 5 to 15 amino acid residues and having a magnitude of net charge per residue of greater than or equal to 0.4. The one or more functional regions comprise 3 to about 250 amino acid residues. The composite polypeptide is not a homopolymer, is at least 15 amino acids long, and has an aqueous solubility at pH 4 to 10 of greater than 50 μg/mL. Further, a second layer comprises a second layer polyelectrolyte comprising a polycationic material or a polycationic material having a molecular weight of greater than 1,000 and at least 5 charges per molecule, and a charge opposite that of the first layer polypeptide.

A method of manufacturing a multilayer film, said film comprising a first layer and a second layer, wherein adjacent
layers comprise oppositely charged polyelectrolytes, the method comprises covalently joining one or more surface adsorption regions and one or more functional regions to form a composite polypeptide, wherein the composite polypeptide and the one or more surface adsorption regions have the same polarity, and depositing the composite polypeptide onto a substrate or the second layer to form a first layer. When depositing comprises depositing the composite polypeptide onto a substrate, the method further comprises depositing the second layer polyelectrolyte onto the first layer.

The present invention also provides a novel method for identifying “sequence motifs” of a defined length and net charge at neutral pH in amino acid sequence information for use in ELBL, and recording a desired number of the motifs. The method comprises the steps of: (a) Obtaining an amino acid sequence for a peptide or a protein from a particular organism; (b) Locating a starter amino acid in the amino acid sequence; and (c) Examining the starter amino acid and the following n amino acids to determine the number of charged amino acids having a polarity opposite the certain polarity; (d) If the number of the charged amino acids having a polarity opposite the certain polarity is one or more, continuing the method at step g; (e) Examining the starter amino acid and the following n amino acids to determine the number of charged amino acids having the certain polarity; (f) If the number of charged amino acids having the certain polarity is equal to or greater than x, recording the amino acid sequence motif consisting of the starter amino acid and the following n amino acids; (g) Locating another starter amino acid in the amino acid sequence; and (h) Repeating the method beginning at step c until the desired number of amino acid sequence motifs have been identified or all of the amino acids in the amino acid sequence have been used as the starter amino acid in step c, wherein x is greater than or equal to approximately one-half of n.

The present invention also provides a novel method for designing a polypeptide for use in ELBL, comprising the steps of: (a) Identifying and recording one or more amino acid sequence motifs with a net charge of a certain polarity using the steps mentioned in the preceding paragraph and (b) Joining a plurality of said recorded amino acid sequence motifs to form a polypeptide.

The present invention also provides a novel method for designing a polypeptide for use in ELBL, comprising the following steps: (a) Designing de novo a plurality of amino acid sequence motifs, wherein said amino acid sequence motifs consist of n amino acids, at least x of which are positively charged and none is negatively charged, or at least x of which are negatively charged and none is positively charged, wherein x is greater than or equal to approximately one-half of n, and (b) Joining said plurality of said amino acid sequence motifs. The amino acid sequence motif can comprise the 20 usual amino acids or non-natural amino acids, and the amino acids can be either left-handed (L-amino acids) or right handed (D-amino acids).

The present invention also provides a thin film, the film comprising a plurality of layers of polypeptides, the layers of polypeptides having alternating charges, wherein the polypeptides comprise at least one amino acid sequence motif consisting of n amino acids, at least x of which are positively charged and none is negatively charged, or at least x of which are negatively charged and none is positively charged, wherein x is greater than or equal to approximately one-half of n. The motifs in these polypeptides may be selected using either of the methods described above.

The present invention also provides a novel process for using cysteine and other sulfhydryl-containing amino acids.
FIG. 12 shows adsorption data for polyelectrolytes of different lengths, illustrating that long polyelectrolytes adsorb better than short ones. FIG. 13 illustrates an embodiment of a "composite" polypeptide (4) comprising two surface adsorption (1,2) regions and one functional region (3). Each surface adsorption region (1,2) comprises one or more motifs. FIG. 14 illustrates independent preparation of the three different regions (1,2,3) of a composite polypeptide (4) by solution-phase synthesis, solid-phase synthesis, or recombinant polypeptide production.

FIG. 15 illustrates joining of three regions (1,2,3) of the composite polypeptide (4) by peptide synthesis to form a single polypeptide chain. Other approaches to joining the three regions of this example are possible. FIG. 16 illustrates the average extent of proliferation of 3T3 fibroblasts after 3 days on coverslips with different surface coatings. PL denotes 15 layers of poly(-glutamic acid) (PLGA) and poly(-lysine) (PLL). PLL/PEG denotes 10 layers of PLGA/PLL followed by 5 layers of RGD-containing peptides, and RGD denotes 15 layers of RGD-containing peptides. The coatings were prepared by layer-by-layer assembly, the terminal layer had a net positive charge in each case, and control coverslips were included as a control. Coated surfaces showed a greater extent of cell proliferation than uncoated surfaces, and surfaces coated with PLL/PEG showed the greatest proliferation.

FIG. 17 illustrates an embodiment of a "composite" polypeptide comprising two surfact (adsorption) regions (120 and 130) and one functional region (110). FIG. 18 (200) illustrates an embodiment of a "composite" polypeptide comprising two surfact (adsorption) regions (120 and 130) and one functional region (111), attached to a surface (150).

DETAILED DESCRIPTION OF THE INVENTION

Explanations of Terms

For convenience in the ensuing description, the following explanations of terms are adopted. However, these explanations are intended to be exemplary only. They are not intended to limit the terms as they are described or referred to throughout the specification. Rather, these explanations are meant to include any additional aspects and/or examples of the terms as described and claimed herein.

As used herein, "layer" means a film thickness increment, e.g., on a template for film formation, following an adsorption step. "Multilayer" means multiple (i.e., two or more) thickness increments. A "polyelectrolyte multilayer film" is a film comprising one or more thickness increments of polyelectrolytes. After depositions, the layers of a multilayer film may not remain as discrete layers. In fact, it is possible that there is significant intermingling of species, particularly at the interfaces of the thickness increments.

As used herein, "biocompatibility" means causing no adverse health effect upon ingestion, contact with the skin, or introduction to the bloodstream.

As used herein, "immune response" means the response of the human immune system to the presence of a substance in the bloodstream. An immune response can be characterized in a number of ways, for example, by an increase in the bloodstream of the number of antibodies that recognizes a certain antigen. (Antibodies are proteins made by the immune system, and an antigen is an entity that generates an immune response.) The human body fights infection and inhibits reinfection by increasing the number of antibodies in the bloodstream. The specific immune response depends somewhat on the individual, though general patterns of response are the norm.

As used herein, "epitope" means the structure of a protein that is recognized by an antibody. Ordinarily, an epitope will be on the surface of a protein. A "continuous epitope" is one that involves several amino acids in a row, not one that involves amino acid residues that happen to be in contact in a folded protein.

As used herein, "sequence motif" and "motif" mean a contiguous amino acid sequence of a given number of residues identified using the method of the present invention. In a preferred embodiment, the number of residues is 7.

As used herein, "amino acid sequence" and "sequence" mean any length of polypeptide chain that has at least two amino residues long.

As used herein, "residue" means an amino acid in a polypeptide, it is the residue of the amino acid monomer from which the polymer was formed. Polypeptide synthesis involves dehydration, that is, a single water molecule is "lost" on addition of the amino acid to a polypeptide chain.

As used herein, "designed polypeptide" means a polypeptide designed using the method of the present invention, and the terms "peptide" and "polypeptide" are used interchangeably.

As used herein, "primary structure" means the linear sequence of amino acids in a polypeptide chain, and "secondary structure" means the more or less regular types of structure stabilized by non-covalent interactions, usually hydrogen bonds-examples include α-helix, β-sheet, and β-turn.

As used herein, "amino acid" is not limited to the 20 usual naturally occurring L-α-amino acids; the term also refers to other L-α-amino acids, D-amino acids, and other non-natural amino acids, as the context permits.

As used herein, "non-natural amino acids" means amino acids other than the 20 naturally occurring ones.

A "peptoid," or N-substituted glycine, means an analog of the corresponding amino acid monomer, with the same side chain as the corresponding amino acid but with the side chain appended to the nitrogen atom of the amino group rather than to the α-carbons of the residue. Consequently, the chemical functionalities between monomers in a polypeptide may not be peptide bonds, which can be useful for limiting proteolytic digestion.

"Substrate" means a solid material with a suitable surface for adsorption of polyelectrolytes from aqueous solution. The surface of a substrate can have essentially any shape, for example, planar, spherical, rod-shaped, etc. A substrate surface can be regular or irregular. A substrate can be a crystal. Substrates range in size from the nanoscale to the macroscale. Moreover, a substrate optionally comprise a collection of colloidal particles. A substrate can be made of organic material, inorganic material, bioactive material, or a combination thereof. Non-limiting examples of substrates include silicon wafers; charged colloidal particles, e.g., micro-particles of CaCO3, or of melamine formaldehyde; biological cells such as erythrocytes, hepatocytes, bacterial cells, or yeast cells; organic polymer lattices, e.g., polysiloxane or styrene copolymer lattices; liposomes; organelles; and viruses. In one embodiment, a substrate is a medical device such as an artificial pacemaker, a cochlear implant, or a stent.

When a substrate is disintegrated or otherwise removed during or after film formation, it is called a "template" (for film formation). Template particles can be dissolved in appropriate solvents or removed by thermal treatment. If, for example, partially cross-linked melamine formaldehyde template particles are used, the template can be disintegrated by mild chemical methods, e.g., in dimethylformamide.
(DMSO), or by a change in pH value. After dissolution of the template particles, hollow multilayer shells remain which are composed of alternating polyelectrolyte layers.

A "microcapsule" is a polyelectrolyte film in the form of a hollow shell or a coating surrounding a core. The core comprises a variety of different encapsulants, for example, a protein, a drug, or a combination thereof.

"Bioactive molecule" means a molecule, macromolecule or a macromolecular assembly having a biological effect. The specific biological effect can be measured in a suitable assay for measuring the biological effect and normalizing per unit weight or per molecule of the bioactive molecule. A bioactive molecule can be encapsulated or retained behind a polypeptide film. Nonlimiting examples of a bioactive molecule are a protein, a functional fragment of a protein, a complex of proteins, an oligopeptide, an oligonucleotide, a nucleic acid, a ribosome, an active therapeutic agent, a phospholipid, a polysaccharide. As used herein, "bioactive molecule" further encompasses biologically active structures, such as, for example, a functional membrane fragment, a membrane structure, a virus, a pathogen, a cell, an aggregate of cells, and an organ. Examples of a protein that can be encapsulated or retained within a polypeptide film are hemoglobin, enzymes, such as for example glucose oxidase, urease, lysozyme and the like, extracellular matrix proteins, such as for example fibronectin, laminin, vitronectin and collagen, and an antibody. Examples of a cell that can be encapsulated or retained within a polypeptide film is a transplanted islet cell, a eukaryotic cell, a bacterial cell, a plant cell, and a yeast.

As used herein, a soluble polypeptide has a solubility in aqueous solution at pH 7.0 of greater than 50 μg/mL. In another embodiment, a soluble polypeptide has an aqueous solubility at pH 7.0 of greater than or equal to about 1 mg/mL.

The following three-letter abbreviations are used herein for the 20 usual amino acids:

\[
\begin{align*}
\text{Aa} & \rightarrow \text{alanine} \\
\text{Glu} & \rightarrow \text{glutamic acid} \\
\text{His} & \rightarrow \text{histidine} \\
\text{Leu} & \rightarrow \text{leucine} \\
\text{Pro} & \rightarrow \text{proline} \\
\text{Ser} & \rightarrow \text{serine} \\
\text{Tyr} & \rightarrow \text{tryptophan} \\
\text{Cys} & \rightarrow \text{cysteine} \\
\text{Tyr} & \rightarrow \text{tyrosine} \\
\text{Gln} & \rightarrow \text{glutamine} \\
\text{Thr} & \rightarrow \text{threonine} \\
\text{Val} & \rightarrow \text{valine} \\
\text{Asp} & \rightarrow \text{aspartic acid} \\
\text{Gly} & \rightarrow \text{glycine} \\
\text{Lys} & \rightarrow \text{lysine} \\
\text{Arg} & \rightarrow \text{arginine} \\
\end{align*}
\]

A. Description of the Invention

The present invention includes multilayer films comprising alternating layers of oppositely charged polyelectrolytes, wherein a first layer of the films comprises a designed polypeptide. "Designed polypeptide" means a polypeptide comprising one or more amino acid sequence motifs, wherein the polypeptide is at least 15 amino acids in length and the ratio of the number of charged residues of the same sign minus the number of residues of the opposite sign to the total number of residues in the polypeptide is greater than or equal to 0.4 at pH 7.0. In other words, the magnitude of the net charge per residue is greater than or equal to 0.4. In one embodiment, the ratio of the number of charged residues of the same sign minus the number of residues of the opposite sign to the total number of residues in the polypeptide is greater than or equal to 0.5 at pH 7.0. In other words, the magnitude of the net charge per residue is greater than or equal to 0.5. In one embodiment, a designed polypeptide is not a homopolymer.

In one embodiment, a polyelectrolyte comprises a polycationic material or a polyanionic material having a molecular weight of greater than 1,000 and at least 5 charges per molecule. In one embodiment, the polycationic material comprises a polyanion such as, for example, a polyelectrolyte, poly(vinyl amine), poly(aminoester), poly(amineacrylate), poly(N-methyl aminoacrylate), poly(N,N-dimethyl aminoacrylate), poly(N,N-cro- mermaleic diethylaminomethacrylate), poly(amineomethacrylate), poly(N-methyl amino-methacrylate), poly(N,N-dimethyl ammoniomethacrylate), poly(N,N-diethyl amionomethacrylate), poly(ethylene), poly(diallyl dimethylammonium chloride), poly(N,N,N-trimethylamionomethacrylate), poly(N,N,N-trimethylammoniomethacrylate), poly(N,N,N-trimethylammoniomethacrylate), chitosan and combinations comprising one or more of the foregoing polycationic materials. In another embodiment, the polyanionic material comprises a polypeptide, a nucleic acid, an antigen, a curranogen, a furcillan, a pectin, a xanthan, a hyaluronan acid, a heparin, a heparan sulfate, a chondroitin sulfate, a dextran sulfate, a dextran sulfate, poly(ethylene), a hydroxyl cellulose, a carboxymethyl cellulose, acidic polysaccharides, a croscarmellose, synthetic polymers and copolymers containing pendant carboxyl groups, and combinations comprising one or more of the foregoing polyanionic materials.

The present invention also provides a method for designing polypeptides for the nanofabrication by E.I. of thin films, coatings, and microcapsules for applications in biomedicine and other fields. The method involves 5 primary design concerns: (1) the electrostatic properties of the polypeptides; (2) the physical structure of the polypeptides; (3) the physical stability of the films formed from the polypeptides; (4) the biocompatibility of the polypeptides and films; and (5) the bioactivity of the polypeptides and films. The first design concern, electrostatics, is perhaps the most important because it is the basis of E.I. Without suitable charge properties, a polypeptide will not be soluble in aqueous solution and cannot be used for the intended purpose of nanofabrication. We have devised a novel process for identifying in amino acid sequence information amino acid sequence motifs having electrostatic properties suitable for E.I.

The secondary structure of the polypeptides used for E.I. is also important, because the physical properties of the film, including its stability, will depend on how the secondary structure of the peptide translates into its structure in the film. FIG. 11 illustrates how the solution structure of certain polypeptides correlates with film assembly. Panel (a) shows how the assembly behavior of polyl-glutamate and poly-l-lysine depends on pH. It is clear that the α-helix conformation correlates with a greater extent of deposited material than the β-sheet conformation. The precise molecular interpretation of this behavior remains to be elucidated. Panel (b) shows how the solution structure of these peptides depends on pH. At pH 4.2, poly-l-glutamate is largely α-helical, as is poly-l-lysine at pH 10.5. Both polypeptides are in a largely unstructured coil-like conformation at pH 7.3.

The remaining concerns relate to the applications of the polypeptide films. In practicing the invention, more or less...
weight will be placed on these other concerns depending on the design requirements of a particular application.

By using the selection process of the present invention to identify in amino acid sequence information the amino acid sequence motifs having suitable charge characteristics, and using the other design concerns to select particular motifs, one can design polypeptides suitable for use in ELiBL. The approach to de novo design is essentially the same as identifying motifs in existing amino acid sequence information, except that each residue in an amino acid sequence motif is selected by the practitioner rather than an entire motif being identified in the genomic or proteomic information of a specific organism. It must be emphasized that the fundamental polypeptide design principles enunciated in the present invention are independent of whether the amino acids involved are the 20 usually naturally-occurring ones, non-natural amino acids, or some novel combination of these, in the case of de novo polypeptide design. Further, other L-amino acids and D-amino acids could be used.

The design concerns of the present invention are discussed in more detail below.

1. Electrostatics

We have devised a novel process for identifying in amino acid sequence information amino acid sequence motifs having electrostatic properties suitable for use in ELiBL. Using this process, we have identified 85,315 non-redundant amino acid sequence motifs in human proteome data—the translation of the portion of the genome that encodes all known proteins in the human body. This information is publicly available at the National Center for Biotechnology Information's (NCBI) Web site: http://www.ncbi.nlm.nih.gov, among other places. Such information is constantly being updated as the human genome is further analyzed. As the amount of such information increases, the number of amino acid sequence motifs that could be identified in human sequence information by the selection process of the present invention as having suitable electrostatic properties for ELiBL will also increase. The same is true for any organism. Accepted biochemical and physics principles, as well as the experimental results described below, indicate that the identified sequence motifs will be useful for the design of polypeptides for the nanofabrication of ELiBL structures.

The key selection criterion is the average charge per unit length at neutral pH (pH 7, close to the pH of human blood). In addition, there are several structural preferences. First, it is preferred that each amino acid sequence motif consist of only 7 residues.

a. Total Number of Residues in the Motif

In one exemplary embodiment, a motif length of 7 was chosen in an effort to optimize biocompatibility, physical structure, and the number of non-redundant sequence motifs in available amino acid sequence data.

As discussed below, the magnitude of the net charge on the amino acid sequence motif per residue is greater than or equal to 0.4. In one embodiment, at least half of the amino acid residues in each sequence motif are charged, such that the magnitude of the net charge on the amino acid sequence motif per residue is greater than or equal to 0.5. Moreover, it is preferred, but not required, that all of the charged residues in each motif be of the same charge. These requirements ensure that each motif will be sufficiently soluble in aqueous solvent and have sufficient charge at neutral pH to be useful for ELiBL. Because only a relatively small percentage of amino acid types are charged, as the length of a given amino acid sequence increases, the odds decrease that the sequence will have a sufficient percentage of appropriately charged amino acids for ELiBL. Charged amino acids is the preferred minimum for a motif size of 7, because fewer than 4 charges yields substantially decreased peptide solubility and decreased control over ELiBL.

Regarding biocompatibility (discussed further below), each identified sequence motif is long enough at 7 residues to constitute a continuous epitope (relevant to the possible immune response of an organism into which a designed peptide might be introduced), but not so long as to correspond substantially to residues both on the surface of a protein and in its interior; the charge requirements help to ensure that the sequence motif occurs on the surface of the folded protein; a charged residue cannot be forced in the core of a folded protein. By contrast, a very short motif could appear to the body to be a random sequence, or one not specifically "well," and therefore elicit an immune response. Although the ideal length of a peptide for generating antibodies is a point of some dispute, most peptide antigens range in length from 12 to 16 residues. Motifs that are 5 residues or shorter can be effective antigens; peptides longer than 12 to 16 amino acids may contain multiple epitopes (Angeletti, R. H. (1999) Design of Useful Peptide Antigens, J. Biomol. Tech. 10:2-10, which is hereby incorporated by reference in its entirety). Thus, to minimize antigenicity one would prefer a motif shorter than 12 and, better yet, shorter than 9 residues.

The preferred motifs should not be too long for another reason: to minimize secondary structure formation. Secondary structure decreases control of the physical structure of the polypeptides (see below) and the films made from them. Thus, an amino acid sequence motif should contain 5 to 15 contiguous amino acids.

Furthermore, the maximum number of non-redundant motifs in the human genome is found when the number of residues in each motif is 7. FIG. 6 shows the number of non-redundant sequence motifs in available human amino acid sequence information. The greatest number of positive motifs is for a 5-residue length, while the greatest number of negative motifs is for a 7-residue length. The greatest number of positive and negative motifs is about the same for 5 and 7. Thus, a motif length of 7 residues would appear to maximize the number of non-redundant motifs.

For all of the above reasons, 7 residues is the preferred length of motif to optimize polypeptide design for ELiBL. Nevertheless, it is possible that in some cases either slightly shorter or slightly longer motifs will work equally as well. For example, motifs 5 or 6 residues long may be employed, and motifs on the order of 8 to 15 residues in length could also be useful. Thus, an amino acid sequence motif is defined as having 5 to 15 amino acid residues.

b. Number of Charged Residues

Second, it is preferred that at least 4 positively-charged (basic) amino acids (Arg, His, or Lys) or at least 4 negatively-charged (acidic) amino acids (Glu or Asp) are present in each 7-residue motif at neutral pH. Combinations of positive and negative charges are disfavored in an effort to ensure a sufficiently high charge density at neutral pH. It is possible, however, that a motif containing both positive and negative amino acids could be useful for ELiBL. For example, a slightly longer motif, say of 9 residues, could have 6 positively charged amino acids and 3 negatively charged amino acid. It is the magnitude of the net charge (i.e., the absolute value of
The net charge of each amino acid is important—the overall peptide must be either sufficiently positively charged or sufficiently negatively charged at neutral pH. Preferred embodiments of the motifs, however, will contain only Glu or Asp of only Arg, His, or Lys as the charged amino acids (although other non-charged amino acids could, and ordinarily do, form part of the motif(s)), unless the charged amino acids are admitted as acidic or basic amino acids.

Fig. 5 is a flowchart showing the steps involved in an exemplary selection process for identifying amino acid sequences having suitable electrostatic properties. It is assumed that only the 20 usual amino acids are involved. If searching for negatively-charged motifs, the process begins by locating an amino acid in the sequence data. This amino acid will be called the "starter amino acid" because it is the starting point for the analysis of the surrounding amino acids (i.e., it will be the motif). Next, the starter amino acid and the following 6 residues are examined for occurrences of Arg, His, or Lys. If one or more Arg, His, or Lys is located in these 7 amino acids, the process is begun anew at a different starter amino acid. If no Arg, His, or Lys is found, the 7 amino acids are examined to determine the number of occurrences of Glu and/or Asp. If there are at least 4 occurrences of Glu and/or Asp in the 7 residues, the sequence motif is cataloged. The selection process is essentially the same for positively charged amino acids, except that Glu and Asp are replaced by Arg, His, and Lys, and Arg, His, and Lys are replaced by Glu and Asp, respectively. Obviously, one could also begin the method at the beginning of the amino acid sequence (amino terminus) and proceed to the end (carboxyl terminus), or, alternatively, one could begin at a random point and work through all of the amino acids in the sequence, randomly or systematically in either direction. Moreover, one could use the methodology to identify motifs in sequence information containing natural amino acids. In such a case, one would search for natural acidic or basic amino acids instead of Glu and Asp, and Arg, Lys, and His, respectively.

In one embodiment, the one or more first amino acid sequence motifs consists of 5 to 15 amino acids, wherein the magnitude of the net charge on the first amino acid sequence motif per residue is greater than or equal to 0.4. In another embodiment, the one or more first amino acid sequence motifs consists of a amino acids, wherein the magnitude of the net charge in the first amino acid sequence motif at pH 7 is greater than or equal to approximately one-half of n, and wherein n is 5 to 15.

The remaining design concerns, namely, physical structure, physical stability, biocompatibility, and biofunctionality, deal primarily with the particular application for which the designed peptides will be used. As noted above, more or less weight will be placed on these concerns during the design process, depending on the desired peptide properties for a particular application.

2. Physical Structure

A design concern regarding the amino acid sequence motif is its propensity to form secondary structures, notably α-helix or β-sheet. We have sought in several ways to control, notably minimize, secondary structure formation of designed polypeptides in an aqueous medium in order to maximize coating of thin film layer formation. First, it is preferred that the sequence motifs be relatively short, because long motifs are more likely to adopt a stable three-dimensional structure in solution. Second, we place a glycine residue between each motif in preferred embodiments of the polypeptide designs. Glycine has a very low α-helix propensity and a very low β-sheet propensity, making it energetically very unfavorable for a glycine and its neighboring amino acids to form regular secondary structure in aqueous solution. Polypeptide has similar properties in some respects and could be used as an alternative to glycine to join motifs. Third, we have sought to minimize the α-helix and β-sheet propensity of the designed polypeptides themselves by focusing on motifs for which the summed α-helix propensity is less than 7.5 and the summed β-sheet propensity is less than 8. ("Summed" propensity means the sum of the α-helix or β-sheet propensities of all amino acids in a motif.) It is possible, however, that amino acid sequences having a somewhat higher summed α-helix propensity and/or summed β-sheet propensity would be suitable for ELBL under some circumstances, as the Gly (or Pro) residues between motifs will play a key role in inhibiting stable secondary structure formation in the designed polypeptide. In fact, it may be desirable in certain applications for the propensity of a polypeptide to form secondary structure to be relatively high, as a specific design feature of thin film fabrication; the necessary electrostatic charge requirements for ELBL must still be met, as discussed above.

In order to be able to select amino acid sequences with desired secondary structure propensities, we first calculated the secondary structure propensities for all 20 amino acids using the method of Chou and Fasman (see P. Chou and G. Fasman, Biochemistry, 13:211 (1974), which is incorporated by reference herein in its entirety) using structural information from more than 1,800 high-resolution X-ray crystallographic structures (1, 334 containing α-helices and 1,221 containing β-strands). Structures were selected from the Protein Data Bank (a publicly-accessible repository of protein structures) based on: (a) method of structure determination (X-ray diffraction); (b) resolution (better than 2.0 Å); “resolution” in this context refers to the minimum size of a structure one can resolve, as in the Rayleigh criterion; and (c) structural diversity (less than 50% sequence identity between the protein crystallographic structures used to compute the helix and sheet propensities of the various amino acids). The rationale was to choose high resolution structures determined by the most reliable methodology and not to bias the propensity calculation by having similar structures. Next, for comparison, 100,000 non-redundant random sequences were produced using a random number generator in a personal computer. We then calculated the secondary structure propensities for the 88,315 amino acid sequences identified using the selection process described in part (A)(1) above (9,385 non-redundant basic sequence motifs and 28,930 non-redundant acidic sequence motifs). The propensities for the random sequences were then compared to the propensities of the selected sequences. Fig. 2 shows the distribution of secondary structure formation propensities in these sequence motifs. The rectangle in Fig. 2 highlights the sequence motifs we have identified as least likely to form secondary structure on the basis of secondary structure propensities.

3. Physical Stability

Another design concern is control of the stability of the polypeptide ELBL films. Ionic bonds, hydrogen bonds, van der Waals interactions, and hydrophobic interactions provide some, albeit relatively limited, stability to ELBL films. By contrast, covalent disulfide bonds could provide exceptional structural strength. We have devised a novel process for using cysteine (or some other type of sulfhydryl-containing amino acid) to "lock" and "unlock" adjacent layers of polypeptide ELBL films. This process enables a polypeptide nanofibers to remain stable at extremes of pH, giving greater control over its mechanical stability and diffusive properties (for discussions of porosity of multilayer films made of non-polypeptide polyelectrolytes, see Caruso, F., Niihara, X., Fur-
long, N. and Ohashita (1997) Langmuir 13:547 and Caruso, F., Furong, N., Aigia, K., Ichinose, I., and Kunii, K. (1998) Langmuir 14:4559, both of which are incorporated herein by reference (as their entirety). Also, the incorporation of cysteine (or some other type of thiol-containing amino acid) in a sequence motif of a designed polypeptide enables the use of relatively short peptides in thin film fabrication, by virtue of in situ molecular disulfide bond formation. Without cysteine, such peptides would not generally yield sufficiently stable films (see FIG. 12, discussed below). Thus, our novel use of cysteine will obviate the need to produce expensive long versions of the designed polypeptides in a substituting percentage of possible applications. This will be particularly advantageous in situations where the thin film is to be fabricated over material to be encapsulated, for example a small crystal of a drug, a small spherical hemoglobin crystal, or a solution containing hemoglobin.

For applications in which the physical stability of the films is important, amino acid sequence motifs containing cysteine (or some other type of thiol-containing amino acid) may be selected from the library of motifs identified using the methods discussed above, or designed de novo using the principles described above. Polypeptides can then be designed and fabricated based on the selected or designed amino acid sequence motifs. Once the polypeptides have been synthesized chemically or produced in a host organism, ELBL assembly of cysteine-containing peptides is done in the presence of a reducing agent, to prevent premature disulfide bond formation. Following assembly, the reducing agent is removed and an oxidizing agent is added. In the presence of the oxidizing agent disulfide bonds form between cysteine residues, thereby “locking” together the polypeptide layers that contain them.

This “locking” method may be further illustrated using the following example of microcapsule fabrication. First, designed polypeptides containing cysteine are used to form multilayers by ELBL on a suitably charged spherical surface, normally in aqueous solution at neutral pH and in the presence of dithiothreitol (“DTT”), a reducing agent. Next, DTT is removed by filtration, diffusion, or some other similar method known in the art, causing cysteine to form from pairs of cysteine side chains and thereby stabilizing the film. If the peptide multilayers are constructed on a core particle containing the materials one wishes to encapsulate, for instance a crystalline material, the fabrication process is complete and the core particle can thereafter be made to dissolve in the encapsulated environment, for example by a change of pH. If, however, the multilayers are constructed on a “dummy” core particle, the core must be removed. In the case of melamine formaldehyde particles (“MF”), for example, the core is ordinarily dissolved by decreasing the pH—is acid-catalyzed. Following dissolution of the core, the pH of solution is adjusted to 4, where partial charge on the peptide polyanions makes the microcapsules semi-permeable (compare Lov et al. 2001 Nano Letters 1:125, which is hereby incorporated herein in its entirety). Next, 10 mM DTT is added to the microcapsule solution to reduce cysteine to cysteine. The microcapsules may then be “loaded” by transferring them to a concentrated solution of the material to be encapsulated, for example a protein (ibid.). The protein enters the microcapsules by moving down its concentration gradient. The encapsulated protein is “locked in” by removal of reductant and addition of oxidant, thereby promoting the reformation of disulfide bonds.

A schematic of the cysteine “locking” and “unlocking” method of the present invention is shown in FIG. 4. Cysteine can form both intra- and inter-molecular disulfide bonds. Further, disulfide bonds can be formed between molecules in the same layer or adjacent layers, depending on the location of cysteine-containing peptides in the film. Referring to FIG. 4(a), basic polypeptides 2 are linked by disulfide bonds 3 in all layers in which the basic peptides contain cysteine. The acidic peptides of the intervening layer (represented in the figure by a translucent layer 4) do not contain cysteine. However, alternating layers continue to attract each other electrostatically, if the acidic and basic side chains are charged at the pH of the surrounding environment. Referring to FIG. 4(b), disulfide bonds are shown between layers. Such structures will form when both the acidic and basic polypeptide layers (i.e., alternating polypeptide layers) used for ELBL contain cysteine and the procedure used has been suitable for disulfide bond formation. Referring to FIG. 4(c), reduction and oxidation reactions are used to regulate the release of encapsulated compounds 5 by breaking and forming disulfide bonds 3, respectively, and thereby regulating the diffusion of particles through the capsule wall.

The cysteine “locking” and “unlocking” is a novel way of regulating the structural integrity and permeability of ELBL films. It is known in the art that glutaraldehyde can be used to cross-link proteins, and this chemical could therefore be used to stabilize polypeptide films. Glutaraldehyde cross-linking, however, is irreversible. In contrast, the cysteine “locking” and “unlocking” method of the present invention is reversible and, therefore, offers better control over structure formation and, importantly, use of the films and capsules that can be fabricated using the present invention. Blood is an oxidizing environment. Thus, in certain biomedical applications, for example artificial red blood cells or drug delivery systems fabricated from designed polypeptides, exposing Cys-crosslinked polypeptide film to the blood or some other oxidizing environment after the formation of disulfide bonds is not expected to cause these bonds to be broken. Finally, it should also be noted that applications involving non-natural amino acids would replace Cys with other sulfhydryl-containing amino acid type. For example, a sulfhydryl could be added to ω-amino acids such as D.L-ω-aminobutyric acid and D.L-ω-aminobutyric acid, or 5-methyl-ω-aminobutyric acid (see http://www.synthetex.com).

4. Biocompatibility

Biocompatibility is a major design concern in biomedical applications. In such applications, the practitioner of the present invention will aim to identify genomics or proteomics information that will yield “immune inert” polypeptides, particularly if the fabricated or coated object will make contact with circulating blood. For purposes of the present invention, it is preferred that the selection process discussed in Part (A)(1) above be used to analyze the amino acid sequences of blood proteins. This will maximize the odds of minimizing the immune response of an organism.

Computer algorithms exist for predicting the antigenicity of an amino acid sequence. Such methods, however, are known in the art to be semi-reliable at best. In the present invention, the sequence motifs identified using the selection method discussed above in Part (A)(1) are highly polar. The motifs must therefore occur on the surface of the native state of the proteins of which they are part of the sequence. The “surface” is that part of a folded protein that is in contact with the solvent or inaccessible to the solvent solely because of the granular nature of water. The “interior” is that part of a folded protein that is inaccessible to solvent for any other reason. A folded globular soluble protein is like an organic crystal, the interior being as densely packed as in a crystal lattice and the exterior being in contact with the solvent, water. Because of
15 their charge properties, the polypeptide sequence motifs identified using the method of the present invention must occur mostly, if not exclusively, on the surface of a protein. Thus, all of the sequence motifs identified in human blood proteins using the selection process of the current invention are effectively always in contact with the immune system while the protein is in the blood. This holds for all conformations of the protein that might become populated in the bloodstream, including denatured states, because it is highly energetically unfavorable to transfer a charge from an aqueous medium to one of low dielectric (as occurs in a protein interior). Accepted biochemical principles indicate, therefore, that the polypeptides designed from blood proteins using the method of the present invention will either not illicit an immune response or will elicit a minimal immune response. For the same reasons, polypeptides designed using the method of the present invention should be biocompatible. All sequence motifs identified from genomic data using the selection process of the current invention, not only those in blood proteins, should be biocompatible, though the extent of immune response or any other type of biological response may well depend on specific details of a sequence motif. (Because the polypeptide sequence on which the motifs are based actually occurs in the organism for which the film as been fabricated, this approach will, at least in principle, work equally well for any type of organism. For instance, the approach may be of significant value to veterinary science.) Both immune response and biocompatibility are important regardless the use of the designed peptides in biomedical applications, including, without limitation, the manufacture of artificial red blood cells, drug delivery systems, or polypeptides for fabrication of biocompatible films to coat implants for short-term or long-term introduction into an organism.

5. Bioactivity

In some applications of polypeptide thin films, coatings, or microcapsules, it is desirable to modify the design of the polypeptides to include a functional domain for use in some layer of the structure, often the outermost. A functional domain in this context is an independently thermostable region of a protein that has specific biofunctionality (e.g., binding phosphotyrosine). It is well known in the art that such biofunctionality may be integrated with other functionalities in a multi-domain protein, as for example in the protein tensin, which encompasses a phosphotyrosine binding domain and a protein tyrosine phosphatase domain. The inclusion of such a domain in a designed polypeptide could function in a number of ways, including without limitation specific ligand binding, targeting in vivo, biosensing, or biocatalysis.

In one embodiment, a multilayer film comprises a first layer composite polypeptide comprising one or more surface adsorption regions covalently linked to one or more functional regions, wherein the first layer composite polypeptide and the one or more surface adsorption regions have the same polarity. The surface adsorption regions comprise one or more amino acid sequence motifs. The first layer composite polypeptide is at least 15 amino acids long, and has a solubility in aqueous solution at pH 4 to 10 of greater than 50 μg/mL. In one embodiment, the one or more surface adsorption regions and the one or more functional regions have the same polarity. In another embodiment, the solubility of the first layer composite polypeptide at pH 4 to 10 is greater than or equal to about 1 mg/mL. The solubility is a practical limitation to facilitate deposition of the polypeptides from aqueous solution. A practical upper limit on the degree of polymerization of a composite polypeptide is about 1,000 residues. It is conceivable, however, that longer composite polypeptides could be realized by an appropriate method of synthesis.

In one embodiment, a composite polypeptide comprises one functional region and one surface adsorption region, wherein the surface adsorption region comprises two amino acid sequence motifs. In another embodiment, a composite polypeptide (4) comprises one functional region (3) and two surface adsorption regions (1,2), one attached to the N-terminus of the functional region and one attached to the C-terminus of the functional region, wherein each surface adsorption region comprises one or more amino acid sequence motifs and the two surface adsorption regions are the same or different and have the same polarity. (FIG. 13) The purpose of the surface adsorption region(s) is to enable adsorption of the polypeptide onto an oppositely charged surface in order to build a multilayer film. The purpose of the functional region(s) is to provide specific functionality to the film, such as, for example, a biological function. Other types of function are possible. For example, in one embodiment, the functional region confers on the polypeptide multilayer film the ability to bind calcium divalent cations with a high degree of specificity, as in the case where the functional region is a calcium binding motif from a protein, e.g., the calcium binding loop of human milk protein α-lactalbumin. There is nothing fundamentally biological about the ability of a multilayer film to bind calcium ions with high specificity, even if some biological macromolecules do exhibit such ability and the peptide structure which enables such binding has been engineered into a multilayer film.

The number of surface adsorption regions in a composite polypeptide relative to the number and/or length of the functional regions is related to the solubility requirement. For example, if the functional region is a short amino acid sequence such as "RGGY," that is, arginine-glycine-aspartic acid, only one amino acid sequence motif of at least 12 amino acid residues will be required to adsorb the composite polypeptide onto a suitably charged surface. If, by contrast, the functional region is a soluble folded structural domain of a protein comprising, for example, 120 amino acid residues, two amino acid sequence motifs will typically be sufficient to impart enough charge for the composite polypeptide to be water soluble and suitable for adsorption. The motifs could be contiguous and located at the N-terminus of the domain, contiguous and located at the C-terminus of the domain, or noncontiguous with one at the N-terminus and one at the C-terminus.

The combined length of the surface adsorption regions is related more to the dissipation due to thermal energy, which must be overcome for composite polypeptide adsorption to occur spontaneously, than to the number amino acid residues in the functional region of the composite polypeptide. Therefore, increasing the degree of polymerization of the functional region by a factor of two does not necessarily require surface adsorption regions twice as long for effective binding of the surface adsorption regions of the composite polypeptide. The physical basis of adsorption of a composite polypeptide to a surface is electrostatic attraction (and release of counterions to bulk solution), the precise mass of the domain is of secondary importance on the length scale of nanometers, and the main “force” counteracting composite polypeptide adsorption is thermal energy. In view of this, use of skill in the art can readily design surface adsorption regions that are suitable for physical adsorption to a surface of the particular functional region of interest.

A functional region comprises to about 250 amino acid residues. The term functional region includes both functional
motifs and functional domains. Functional motifs comprise relatively few amino acid residues and therefore generally do not have a compact or persistent threedimensional structure; Nevertheless, they can exhibit specific functionality, as with some peptide hormones and neuropeptides, and they can comprise elements of secondary structure such as α-helices and β-sheets. An example of a functional motif is provided by the RGDF sequence of the extracuticular matrix protein fibronectin. When the functional unit is a functional motif, it will typically comprise 3 to about 50 amino acid residues. When the functional region is a domain, it will typically comprise about 50 to about 250 amino acid residues.

A functional domain is defined herein as at least a portion of a polypeptide which, when folded, creates its own hydrophobic core. A native protein, for example, may contain a plurality of structural domains, each of which acts as an independent unit of structure and function. The biological function of one domain can be completely independent of the function of another, as in the case of a catalytic domain and a binding domain in the same polypeptide chain, and the two domains do not interact with each other at all. Structural interactions between domains in a native protein are not possible, but relatively common, in such cases the interaction between one structural domain and another structural domain can be viewed as a type of quaternary structure.

As used herein, a functional domain typically has a minimum of about 50 amino acid residues and a maximum of about 250 amino acid residues. In principle, any functional domain from a protein can be employed in a composite peptide as outlined herein so long as the composite polypeptide has the appropriate aqueous solubility for ELISA deposition. In one embodiment, the functional domain has a water solubility at pH 4 to 10 of greater than 50 μg/mL. In another embodiment, the functional domain has a water solubility at pH 4 to 10 of greater than or equal to 1 mg/mL. In yet another embodiment, the first layer composite polypeptide comprises at least two amino acid sequence motifs when the functional unit comprises a functional domain.

The composite polypeptide, when it comprises a functional motif instead of a functional domain, will typically have a net charge per residue of greater than or equal to 0.4. If, however, the functional motif has a net charge per residue of less than 0.4, the one or more surface adsorption regions will typically have a net charge per residue of greater than 0.4 to compensate and give the composite polypeptide the appropriate charge properties for solubility and physical adsorption.

Suitable functional regions for inclusion in composite polypeptides include cystein-containing motifs or a protease recognition sites to control film stability and/or the release of encapsulated materials from films/capsules, T-cell epitopes, HLA-class I epitopes, or a cytotoxic T lymphocyte epitope for control of immunoreactivity; sequences suitable for attachment of a saccharide or polysaccharide by enzymatic catalysis, for example, as in N-linked or O-linked glycosylation; peptide recognition sequences in extracellular matrix proteins for control of surface functionality and tissue engineering; sequences from antibacterial peptides for control of antimicrobial properties; extracellular domains of transmembrane receptors for specific targeting in vivo; and cation binding motifs such as E3d hand motifs for control of divalent cation binding.

In one non-limiting embodiment, the functional region of a composite peptide comprises a recognition sequence. Suitable protease recognition sequences include, for example, the factor Xa recognition sequence Lle-Glu/Asp-Gly-Arg (SEQ ID NO:42), the proteinase K recognition sequence Asp-Asp-Asp-Lys (SEQ ID NO:43), the thrombin recognition sequence Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO:44), the TEV protease recognition sequence Glu-Asp-Leu-Tyr-Phen-Gln-Gly (SEQ ID NO:45), the PreScission™ protease recognition sequence Leu-Glu-Val-Leu-Pro-Phen-Gln-Gly-Pro (SEQ ID NO:46), and the like.

In another non-limiting embodiment, the functional region of composite peptide comprises a T-cell epitope, a B-cell epitope, or a cytotoxic T-cell epitope. As used herein, "T-cell epitope" refers to any peptide antigenic determinant which is recognized by T-cells. As used herein, "B-cell epitope" refers to any antigenic determinant which is recognized by B-cell immunoglobulin receptors and is capable of eliciting the production of antibodies with appropriate help from T cells when administered to an animal. As used herein, "cytotoxic T lymphocyte epitope" refers to an antigenic epitope which is recognized by cytotoxic T lymphocytes. The epitopes are polypeptides produced by viruses, bacteria, fungi, or parasites. In some cases, the epitopes may be polypeptides to which saccharides or oligosaccharides are attached or could be attached, e.g., by N-linked or O-linked glycosylation.

Glycosylation is a common and highly diverse protein modification reaction which occurs in most eukaryotic cells. This modification can be divided into two general categories, N-linked and O-linked. In the former, the carbohydrate moiety is attached to the amide nitrogen of the side chain of asparagine, when asparagine is part of the consensus sequence Asn-X-Ser/Thr. This signal is necessary but not sufficient for glycosylation, e.g., X cannot be Pro, and if Pro occurs shortly downstream of Ser/Thr glycosylation is inhibited. In O-linked glycosylation, the carbohydrate moiety is attached to the hydroxyl oxygen of Ser or Thr; it also occurs as a primary modification of tyrosine and a secondary modification of SN-hydroxylsine and 4-hydroxyproline. There is a high frequency of occurrence of Pro, Ser, Thr, and Ala residues around O-linked glycosylation sites.

Linear epitopes are segments composed of a continuous string of amino acid residues along the polymer chain. Typical linear epitopes have a length of about 5 to about 20 amino acids. Conformational epitopes, by contrast, are constituted by two or more sequentially discontinuous segments that are brought together by the folding of the antigen into its native structure. Conformational epitopes generally correspond to longer peptide chains than do linear epitopes. Either type of epitope could serve as the functional region of a composite polypeptide for LB.

In another non-limiting embodiment, the functional region of a composite peptide comprises a sequence from an antibacterial peptide. Antimicrobial peptides include, for example, inhibitory peptides that slow the growth of a microbe, microbicidal peptides that are effective to kill a microbe (e.g., bacteriocidal and virucidal peptide drugs, sterilants, and disinfectants), and peptides effective for interfering with microbial reproduction, host toxicity, or the like. Examples of antimicrobial peptides include nisin, cecropins B2 and BM1, leucocin A, mesentericin Y105, sakacin P and A, and curvacin A.

In another non-limiting embodiment, the functional region of a composite peptide is a peptide recognition sequence for extracellular matrix (ECM) recognition. One such sequence, RGDF, occurs in various extracellular matrix proteins and is a key recognition sequence for integrin transmembrane receptor molecules. Another ECM recognition sequence is 5GFOG (SEQ ID NO:47), GSFOG (SEQ ID NO:48), or GASGER (SEQ ID NO:49), wherein 'O' represents hydroxyproline. These are recognition sequences in collagen for
hybrid approach has been applied to the synthesis of T20, a 36-amino acid residue peptide, but it has not been widely exploited.

FIG. 17 illustrates an embodiment of a “composite” polypeptide comprising 2 surface adsorption regions (120 and 130) and 1 functional region (110). 120 is the N-terminal surface adsorption region. 130 is the C-terminal absorptive region. Each surface adsorption region comprises one or more motifs. A “composite” polypeptide is a unique combination of surface adsorption region(s) and functional region(s) in a single polypeptide chain. Linker polypeptide sequences (140) can be used to generate a composite polypeptide comprising multiple functional regions in a single polypeptide chain. In one embodiment, functional region 110 can be a small functional region comprising from about 50 to about 139 amino acid residues, and having a diameter of about 2 nm. In an alternate embodiment, functional region 110 can be a large functional region comprising about 250 amino acid residues, and having a diameter of about 4 nm. The length of 16 amino acid residues in extended conformation is approximately 5.5 nm.

FIG. 18 (200 and 300) illustrate embodiments of a “composite” polypeptide comprising 2 surface adsorption regions (120 and 130) and 1 functional region (111, 112), attached to a surface (150). Embodiment 200 of FIG. 18 illustrates a “composite” polypeptide comprising 2 surface adsorption regions (120 and 130) and 1 functional region (111), attached to a surface (150), wherein functional region 111 represents a small functional region comprising from about 50 to about 139 amino acid residues, and having a diameter of about 2 nm. Small functional region 111 can be a short peptide sequence, e.g., RGD. 120 is the N-terminal surface adsorption region. 130 is the C-terminal absorptive region.

FIG. 18 (300) further illustrates an alternate embodiment of a “composite” polypeptide comprising 2 surface adsorption regions (120 and 130) and 1 functional region (110), wherein functional region 112 represents a large functional region comprising about 250 amino acid residues and having a diameter of about 4 nm. Large functional domain 112 can be the domain of a protein, e.g., the PTP domain of tensin. 120 is the N-terminal surface adsorption region. 130 is the C-terminal absorptive region.

An advantage of a modular approach to building composite polypeptides includes taking advantage of the previously described amino acid sequence motif technology, minimizing risk. Other advantages include generality of the approach for nearly any conceivable functional region; and chemically distinct peptides containing identical or different functional regions and identical or different surface adsorption regions of the same sign of electronic charge can be adsorbed simultaneously, creating a multifunctional or a multifunctional surface as desired. Advantages of synthesizing the surface adsorption regions and the functional regions as individual building blocks include: the ability to pm-make and store practically indefinitely (by lyophilization) the individual building blocks for ready availability; the low cost of production, and use of circumstances peptides of specific functionality by use of warehoused building blocks prepared in large quantities; rapid preparation of the composite peptide in comparison to straight solid-phase, solution-phase or biotic synthesis; rapid response to new developments concerning functional regions due to the modular synthetic approach; and the use of completely synthetic peptides and polypeptide multilayer-based materials as a means of minimizing contamination by microbes and simplifying approval of products by the US Food and Drug Administration.
C. Uses for Polypeptides Designed Using the Method of the Present Invention

As noted above, polypeptides of suitable design are excellent materials for ELBL and polypeptide film structures formed using ELBL will be useful in a large number of different types of applications. Polypeptides designed using the method of the present invention have been shown to be useful for ELBL of film structures for possible applications in biomedical technology, food technology, and environmental technology. For example, such polypeptides could be used to fabricate artificial red blood cells.

6. Artificial Red Blood Cells

A number of different approaches have been taken to red blood cell substitute development. One approach involves the use of perfluorocarbons. Perfluorocarbon emulsions contain synthetic fluorinated hydrocarbons capable of binding oxygen and delivering it to tissues. This approach however, increases reticuloendothelial cell blockage. The perfluorocarbons can become trapped in the reticuloendothelial system, which may result in adverse consequences.

Another approach focuses on antigen camouflaging, which involves coating red blood cells with a bio-compatible polymer called polyethylene glycol (PEG). The PEG molecules form permanent covalent bonds on the surface of the cell. The coating effectively hides the antigenic molecules on the surface of the red blood cells, so that the blood recipient's antibodies do not recognize the cells as foreign. For example, the immune system of a normal person who has type A blood will naturally have antibodies that recognize antigen A on the surface of type B red blood cells, leading to cell destruction. The attachment of PEG to the surface of a type B red blood cell "camouflages" the surface of the cell, so that its surface antigens can no longer be recognized by the immune system and the antigenically foreign red blood cells will not be destroyed as quickly (see Fargenkar, N., A., G. Sharma, and K. K. Vistakova. 2001 "Artificial Blood: Current Research Report," which is hereby incorporated by reference in its entirety).

A number of diseases, including thalassemia, that require repeated blood transfusions are often complicated by the development of antibodies to "minor" red cell antigens. This "alloantigenization" can render these patients almost impossible to transfuse, rendering the situation life-threatening. In in vitro testing, the PEG-modified red cells appear not to trigger alloantigenization and may also be useful in clinical situations where alloantigenization has already occurred (see Scott, M.D. et al. 1997) "Chemical camouflage of antigenic determinants: Stealth erythrocytes," Proc. Natl. Acad. Sci. USA, 94 (14): 7566-7571, which is hereby incorporated by reference in its entirety.

Other approaches involve purified hemoglobin. Unmodified cell-free hemoglobin has known limitations. These include oxygen affinity that is too high for effective tissue oxygenation, a half-life within the intravascular space that is too short to be clinically useful, and a tendency to undergo dissociation into dimers with resultant renal tubular damage and toxicity. Because of these limitations, hemoglobin used to make a cell-free red blood cell substitute must be modified. A number of modification techniques have been developed. Hemoglobin can be cross-linked (a covalent bond between two molecules is made by chemical modification) and polymerized using reagents such as gluteraldehyde. Such modifications result in a product that has a higher 0_2 (partial pressure of oxygen at which 50% of all oxygen-binding sites are occupied) than that of normal hemoglobin, and an increase in the plasma half-life of up to 30 hours. The source of the hemoglobin for this purpose can be human ( outdated donated blood), bovine, or human recombinant. The solution of modified hemoglobin is prepared from highly purified hemoglobin and taken through various biochemical processes, to eliminate phospholipids, endotoxins, and viral contaminants. (see Nettleton, D., M. J. Arnold, and M. (2000) "Transfusion Medicine Update." Blood Substitutes, which is hereby incorporated by reference in its entirety). Biopure Corporation (Cambridge, Mass.) has been using modified hemoglobin for their product, Hemopure.

The main potential adverse effect of modified hemoglobin solutions is an increase in systemic and pulmonary vascular resistance that may lead to a decrease in cardiac index. Decreases in the cardiac index may impair optimum oxygen delivery and outweigh the advantage of an oxygen-carrying solution (see Kasper S. M. et al. 1998) "The effects of increased doses of bovine hemoglobin or hemodxamines and oxygen transport in patients undergoing hepatic hemodialysis for elective abdominal aortic surgery," Anesthes. Analg. 87: 284-91, which is hereby incorporated by reference in its entirety). One study has examined the utility of these solutions in the acute resuscitation phase of unstable trauma patients. Design of the study, however, was poor, and any role of the solutions in influencing ultimate patient outcome was unclear (see Koenigsberg D. et al. 1999) "The efficacy trial of diaspirin cross-linked hemoglobin in the treatment of severe traumatic hemorrhagic shock," Acad. Emerg. Med. 6: 379-80, which is hereby incorporated by reference in its entirety).

Many of the problems of cell-free hemoglobin can be overcome by encapsulating it with an artificial membrane. Liposomes are being used to encapsulate hemoglobin for use as a blood substitute. The approach is technically challenging because not only must the hemoglobin be prepared, it must be encapsulated in relatively high concentration and yield. The final products must be sterile and the liposomes must be relatively uniform in size and shape. Encapsulated hemoglobin has several advantages over cell-free hemoglobin. Firstly, the artificial cell membrane protects hemoglobin from degradative and oxidative forces in the plasma. Secondly, the membrane protects the vascular endothelium from toxic effects of hemoglobin. These relate to homeostatic loss, the production of free radicals and vasocostrictor effects of NO binding. Third, encapsulation greatly increases the circulating persistence of the hemoglobin. Moreover, encapsulated hemoglobin can be freeze-dried for convenient storage.

Liposomal encapsulation involves phospholipids, as in cell membranes. One major problem associated with liposomal encapsulation, however, is that it is very difficult to regulate the average size and distribution of liposomes. Another is that unlike red blood cells, liposomes are often not very stable, as they readily lack an organized cytoskeleton. Yet another problem is that liposomes often consist of multiple layers of phospholipid. (A recent review of blood substitute development is presented in Stowell et al. 2001) Progress in the development of RBC substitutes, Transfusion 41:287-299, which is hereby incorporated by reference in its entirety. See also Chang, T. 1998 "Modified hemoglobin-based blood substitutes: cross-linked, recombinant and encapsulated hemoglobin," Artificial Cell 74 Suppl 2:233-41, which is hereby incorporated by reference in its entirety.)

Red blood cell substitutes employing polypeptides designed using the method of the present invention should offer several advantages over approaches to the development of red blood cell substitutes known in the art, including, without limitation, superior oxygen and carbon dioxide binding functionality, lower production cost (large-scale and therefore low-cost production is possible because bacteria
can be used to mass-produce the peptides and because peptide ELBL can be automated, the possibility of using suitable preparations of hemoglobin as a template for ELBL, polypeptide biodegradability, the immune “innocence” of designed polypeptides based on blood protein structure, and the structural stability exhibited by designed polypeptide films, which exceeds that of liposomes. Polypeptide ELBL assembly yields semi-porous films, minimizing the amount of materials required for fabricating a means of encapsulation and enabling glucose, oxygen, carbon dioxide, and various metabolites to diffuse freely through the films as a lipid bilayer. In contrast, other polymers potentially suitable for this purpose have undesirable side effects for example, polylactide degrades into lactic acid, the substance that causes muscle cramps, and poly(ethylene sulfonate) is not biocompatible.

Microcapsules could be formed of designed polypeptides to encapsulate hemoglobin to serve as a red blood cell substitute. Hemoglobin polypeptide microcapsules could also be engineered to incorporate enzymes, including superoxide dismutase, catalase, and methemoglobin reductase, which are ordinarily important for red blood cell function. Moreover, the nanofabricated microcapsules can predictably be dehydrated, suggesting that artificial red blood cells made as described herein could be dehydrated, without loss of function, particularly because hemoglobin can be lyophilized (i.e., freeze-dried) and reconstituted without loss of function, and polystyrene films are stable to dehydration. This will be important for long-term storage, transport of blood substitutes, battlefield applications (particularly in remote locations), and space exploration.

Polypeptides designed using the method of the present invention could also be used for drug delivery.

7. Drug Delivery

Microencapsulation “cores” of a suitable therapeutic material in “crystalline” form can be encapsulated by designed polypeptides, and the resulting microcapsules could be used for drug delivery. The core must be insoluble under some conditions, for instance high pH or low temperature, and soluble under the conditions where controlled release will occur. The surface charge on the crystals can be determined by C-potential measurements (used to determine the charge in electrostatic units on colloidal particles in a liquid medium). The rate at which microcapsule contents are released from the interior of the microcapsule to the surrounding environment will depend on a number of factors, including the thickness of the encapsulating shell, the polypeptides used in the shell, the presence of disulfide bonds, the extent of cross-linking of peptides, temperature, ionic strength, and the method used to assemble the peptides. Generally, the thicker the capsule, the longer the release time—the principle resembles that of gel filtration chromatography.


Polypeptides designed using the method of the present invention should offer a number of advantages in the context of drug delivery, including without limitation control over the physical, chemical, and biological characteristics of the microcapsule; the ability to make capsules with a diameter of less than 1 mm, making the capsules suitable for injection; low likelihood of eliciting an immune response; generally high biocompatibility of capsules; control over the diffusive properties of the microcapsules by varying the thickness of the layers and using cysteine, as discussed below; the ability to target specific locations by modification of the microcapsule surface using the highly reactive sulfhydryl groups in cysteine (as is well known in the art, free sulfhydryl groups, free amino groups, and free carboxyl groups are sites to which molecules for specific targeting could be attached), or by incorporation of a specific functional domain in the design of the polypeptide; and the ability of microstructures to be taken up by cells using either endocytosis or pinocytosis.

Polypeptides designed using the method of the present invention could also be used for antimicrobial coatings.

8. Antimicrobial Coatings

The method of the present invention could be used to manufacture films encompassing antimicrobial peptides. For example, one suitable sequence might be Histrin 5, which occurs in humans:

```
Amp Ser His Ala Lys Arg His His Gly (SEQ ID NO: 8)
```

The presence of positive charge at slightly basic pH makes this sequence quite suitable for ELBL. It could be appended to a peptide designed using the method of the present invention, resulting in an antimicrobial peptide suitable for use in ELBL. This peptide could be used as an anti-biofouling coating. For instance, the peptide could be used to form a coating on devices used for implantation.

There are also a number of other areas in which polypeptides designed using the method of the present invention could be useful.

9. Other Uses

Other possible uses for peptides designed using the method of the present invention include without limitation food covers, wraps, and separation layers; food casings, pouches, bags, and labels; food coatings; food ingredient microcapsules; drug coatings, capsules, and microcapsules; disposable food service items (plates, cups, cutlery); trash bags; water-soluble bags for fertilizer and pesticides; microcapsules for fertilizer and pesticides; agricultural mulches; paper coatings; loose-fill packaging; disposable medical products (e.g. gloves and gowns); and disposable diapers.

B. Fabrication

Once amino acid sequence motifs have been selected from those identified using the method discussed in Part A(1) above or designed de novo, the designed polypeptide is synthesized using methods well known in the art, such as solid phase synthesis and F-moc chemistry or heterologous expression following gene cloning and transformation. Designed polypeptides may be synthesized by a peptide synthesis company, for example SynPeptide Corp. (Dublin, Calif.), produced in the laboratory using a peptide synthesizer, or produced by recombinant methods.

In one embodiment, a designed polypeptide, e.g., a first layer polypeptide, comprises a plurality of individual amino acid sequence motifs joined in tandem to form a single polypeptide chain. The same motif may be repeated, or different motifs may be joined in designing a polypeptide for ELBL. Moreover, functional domains may be included, as discussed above. Amino acids such as glycine or proline could be used to link the sequence motifs, so long as the overall charge properties of the polypeptide are maintained, that is, the magnitude of the net charge on the polypeptide per residue is 0.4. In one embodiment, a linker comprises 1-4 amino acid residues, for example, 1-4 glycine or proline residues. In addition, amino acids other than the 20 usual ones
could be included in the motifs themselves, depending on the properties desired of the polypeptide. Other properties could likewise be specified by design requirements, using methods known in the art. For example, proline could be included for stretch formation, glycine for chain flexibility, and histidine for pI-sensitive charge properties near neutral pI. “Hydrophobic” amino acids could also be included—hydrophobic residue content could play a role in assembly behavior and contribute to layer stability in a way resembling the hydrophobic stabilization of globular proteins.

In one embodiment, a first layer polypeptide comprises one or more amino acid sequence motifs, wherein the polypeptide is at least 15 amino acids in length and the ratio of the number of charged residues of the same sign minus the number of residues of the opposite sign to the total number of residues in the polypeptide is greater than or equal to 0.4 at pH 7.8. In other words, the magnitude of the net charge on the polypeptide per residue is greater than or equal to 0.4. In another embodiment, the ratio of the number of charged residues of the same sign minus the number of residues of the opposite sign to the total number of residues in the polypeptide is greater than or equal to 0.5 at pH 7.0. In other words, the magnitude of the net charge on the polypeptide per residue is greater than or equal to 0.5.

In one embodiment, a designed polypeptide is greater than or equal to 15 amino acid residues long. In other embodiments, a designed polypeptide is greater than 18, 20, 25, 30, 32 or 35 amino acids long. The reason for this is that the entropy loss per molecule is thermodynamically unfavorable for short polypeptides with a high probability of adsorption to an oppositely charged surface is inhibited, even if the polypeptide has a charge per unit length of 1; long polypeptides adsorb better than short ones. This is illustrated in FIG. 12. The average molecular masses of the peptides utilized for the length-dependence studies were 1,500-3,000 Da (poly-L-glutamate, “small”), 3,800 Da (poly-L-lysine, “small”), 32,000 Da (poly-L-glutamate, “medium”), 48,100 Da (poly-L-lysine, “medium”), 50,300 Da (pol-glycylglutamate, “large”), and 222,400 Da (poly-L-glutamate, “large”). The data shows in FIG. 12 clearly indicate that ELBL depends on length of peptide. Inclusion of Cys enables the use of relatively small peptides for ELBL, because the sulphydryl group can be used to form disulfide linkages between polypeptides.

C. Film Assembly

A method of making a designed polypeptide multilayer film comprises depositing a plurality of layers of oppositely charged chemical species on a template, wherein at least one layer comprises a designed polypeptide. Subsequently deposited polyelectrolytes will have opposite net charges. In one embodiment, deposition of a designed polypeptide (or other polyelectrolyte) comprises exposing the substrate to an aqueous solution comprising a designed polypeptide (or other polyelectrolyte) at a pH at which it has a suitable net charge for ELBL. In other embodiments, the deposition of designed polypeptide or other polyelectrolyte on the substrate is achieved by sequential spraying of solutions of oppositely charged polypeptides. In yet other embodiments, deposition on the substrate is by simultaneous spraying of solutions of oppositely charged polyelectrolytes.

In the ELBL method of forming a multilayer film, the opposing charges of the adjacent layers and the gain in entropy on release of counterions to solution together provide the driving force for assembly. It is not critical that polyelectrolytes in opposing layers have the same net linear charge density, only that opposing layers have opposite charges. The standard film assembly procedure includes forming aqueous solutions of the polyelectrolytes at a pH at which they are ionized (i.e., pH 4-10), providing a substrate bearing a surface charge, and alternating immersion of the substrate into the charged polyelectrolyte solutions. The substrate is optionally washed between deposition of alternating layers.

The concentration of polyelectrolyte suitable for deposition of the polypeptide can readily be determined by one of ordinary skill in the art. An exemplary concentration is 0.1 to 10 mg/mL. Typically, the thickness of the layer produced is substantially independent of the solution concentration of the polypeptide during deposition in the stated range. For typical non-polypeptide polyelectrolytes such as poly(acrylic acid) and poly(allylamine hydrochloride), typical layer thicknesses are about 3 to about 5 Å, depending on the ionic strength of solution. Short polyelectrolytes typically form thinner layers than long polyelectrolytes. Regarding film thickness, polyelectrolyte film thickness depends on humidity as well as the number of layers and composition of the film. For example, PLL/PFA films 50 nm thick shrink to 1.6 nm upon drying with nitrogen.

In general, films of 1-2 nm to 100 nm or more in thickness can be formed depending on the hydration state of the film and the molecular weight of the polyelectrolytes employed in the assembly. In addition, the number of layers required to form a stable polyelectrolyte multilayer film will depend on the polyelectrolytes in the film. For films comprising only low molecular weight polyelectrolyte layers, a film will typically have 4 or more bilayers of oppositely charged polypeptides. For films comprising high molecular weight polyelectrolytes such as poly(acrylic acid) and poly(allylamine hydrochloride), films comprising a single bilayer of oppositely charged polyelectrolyte can be stable.

D. Experiments

EXAMPLE 1

Design of Polypeptides Based on Human Blood Protein Sequences and their Use in Polypeptide Film Fabrication

For this work, amino acid sequences were selected using the process described in Part (A)(1) above to identify sequence motifs in the primary structure of human blood proteins: Complement C3 (gi:69766) was the source of the anionic sequence motifs, and lactotransferrin (gi:4505043) the source of the cationic sequence motifs. As discussed above, blood protein sequences were used to minimize the immune response of patients. In whom devices involving the polypeptides might be introduced (including, e.g., artificial red blood cells). In principle, this approach should be applicable for any organism having an immune system; it is not limited to humans. Polypeptides were synthesized by SynPep Corp. (Dublin, Calif.). The polypeptide sequences were:

```
PGG FLV GLU ASP GLU CYS GLN AEP GLY
SEQ ID No.: 1
```

```
Tyr Glu Gln Asp Glu Cys Gin Asp Gly
SEQ ID No.: 2
```

```
Arg Arg Arg Arg Ser Val Gin Gly
SEQ ID No.: 3
```

```
Tyr Gln Asp Glu Cys Gin Asp Gln
SEQ ID No.: 4
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 5
```

```
Tyr Arg Asp Arg Arg Ser Val Gin Gly
SEQ ID No.: 6
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 7
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 8
```

```
Tyr Arg Asp Arg Arg Ser Val Gin Gly
SEQ ID No.: 9
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 10
```

```
Tyr Arg Asp Arg Arg Ser Val Gin Gly
SEQ ID No.: 11
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 12
```

```
Tyr Glu Asp Glu Cys Gin Asp Gln
SEQ ID No.: 13
```

US 7,544,770 B2

sodium azide, pH 7.4. All chemicals other than polypeptides were purchased from Sigma-Aldrich (USA).

ii. Procedures

Experiments were done using pairs of designed polypeptides, one negative and one positive. Multilayer films consisting of at least 5 bi-layers of the above-identified SP2, SN1, LP4, and LN3 were deposited onto the QCM resonators using standard ELBL techniques (a bi-layer consists of one layer of polycation and one layer of polyanion). The polypeptide concentration for layer adsorption was 2 mg mL⁻¹. It is known that dependence of polyion layer thickness on polyelectrolyte concentration is not strong (see Lvoev, Y. and Decher, G. (1994) Crystallog Rep. 39:628, which is incorporated herein by reference in its entirety); in the concentration range 0.1 to 5 mg mL⁻¹, bilayer thickness was approximately independent of concentration for PSS/PAH. By contrast, polypeptide thin films appear substantially less thick than those fabricated using high molecular weight PSS/PAH (mass calculated using Δf data using the well-known Sauerbrey equation); see Lvoev, Y. and Decher, G. (1994) Crystallog Rep. 39:628. This follows from calculating film thickness on the basis of mass deposited, as is ordinarily done in the art for proteins. The calculated thickness for the designed polypeptide assembly shown in Fig. 3(c) is greater than the end-to-end length of the peptides used to make the film. DTT was included at 1 mM to inhibit disulfide bond formation. The adsorption time was 20 minutes.

Resonators were rinsed for 1 min in pure water between subsequent adsorption cycles (removing perhaps 10-15% of weakly adsorbed material) and dried in a stream of gaseous N₂. Then the mass of the deposited peptide was measured indirectly by QCM. The mass measurement includes some water, despite drying, and low mass ions like K⁺, Na⁺, and Cl⁻. Partial interpenetration of neighboring layers of peptide is probable (see Decher, G. (1997) Science 272:1323; Schmitt et al. (1993) Macromolecules 26:7058; and Komech et al. (1995) Physica B 214:954); this could be important for the efficiency of disulfide "locking."

iii. Results

After adsorption of the polypeptide and rinsing and drying the QCM resonator, the resonant frequency of the resonator was measured. This enabled calculation of the frequency shift on adsorption and change in adsorbed mass. A decrease in frequency indicates an increase in adsorbed mass. The results are provided in Figs. 3(a) and 3(b). Fig. 3(a) shows a comparison of adsorption data for LP4 and LN3 in different buffers (10 mM sodium phosphate, pH 7.4, 1 mM DTT and 10 mM Tris-HCl, pH 7.4, 1 mM DTT). It is clear from these data that adsorption depends more on the properties of the peptides than the specific properties of the buffer used. Fig. 3(b) shows resonator frequency versus adsorbed layer for different combinations of SP2, SN1, LP4, and LN3 (namely, SP2/SN1, SP2/LN3, LP4/SN1, and LN4/LN3) in 10 mM sodium phosphate, pH 7.4 and 1 mM DTT (the lines merely connect experimental data points). Each of these combinations involved one negative polypeptide and one positive polypeptide, as required by ELBL. Fig. 3(c) shows a graph of calculated adsorbed mass versus layer number for SN1/LP4 in 10 mM Tris-HCl, pH 7.4 and 1 mM DTT (calculated from experimental data using the Sauerbrey equation). The total adsorbed mass, approximately 5 μg, corresponds approximately to 1 amol of peptide. The equation used for this calculation was Δf = -0.87×10⁻⁷ Δf, where m is mass in

The amino acid residues are represented by the three-letter code given above. One glycine was introduced between each 7-residue motif to inhibit secondary structure formation. Glycine was selected for this purpose because it allows the greatest variability in combination of dihedral angles (see Ramachandran, G. N. and Sasisekharan, V. (1968) Adv. Protein Chemistry 23:285, which is incorporated by reference in its entirety) and has a low helix propensity (0.677) and low sheet propensity (0.766). Alternatively, proline could be substituted for glycine between motifs on the basis of calculated structure propensities. Additionally, a single tyrosine was included at the N-terminus of each peptide for concentration determination by UV absorption at 260 nm. SEQ ID NO: 2 has a magnitude of the net charge of 203 (0.625) at pH 7; SEQ ID NO: 1 has a magnitude of the net charge of 16 (0.5); SEQ ID NO: 1 has a magnitude of the net charge of 30 (0.625) at pH 7; and SEQ ID NO: 3 has a magnitude of the net charge of 24 (0.5) at pH 7. In all cases, the magnitude of the net charge is greater or equal to approximately one-half of the length of the first layer polypeptide at pH 7.

The polypeptides were named SN1 (SEQ ID NO: 2), SP2 (SEQ ID NO: 1), LN3 (SEQ ID NO: 4), and LP4 (SEQ ID NO: 3), respectively, meaning short negative, short positive, long negative, and long positive. These sequences are quite different from polylsine (commonly used in the art as a polycation) and polystyrene (commonly used in the art as a polyanion) which, though available commercially and inexpensive, have a high α-helix propensity under conditions of mild pH and, crucially, are immunoreactive. The calculated charge per unit length on the designed peptides at neutral pH is 0.5 electrostatic units for SP and LP and 0.6 electrostatic units for SN and LN. The positive peptides are somewhat more hydrophobic than the negative ones, owing to the presence of valine and the long hydrocarbon side chain of arginine. (As mentioned above, hydrophobic interactions between polypeptide layers could stabilize films to some extent.) The lengths are consistent with published studies showing that polyions must have greater than 20 charged groups (i.e. aspartic acid and glutamic acid; lysine, arginine, and histidine) to be suitable for ELBL (see Kabarov, V. and Zerzin, L. (1984) Pure Appl. Chem. 56:343 and Kabarov, V. (1994) Polym. Sci. 36:143, both of which are incorporated by reference herein in their entireties).

a. Experimental Demonstration

i. Materials

QCM electrodes (UTI-System, Japan) coated with evaporated silver had a surface area of 0.66±0.01 cm² on each side, a resonant frequency of 9 MHz (±0.01), and a long-term stability of ±1 Hz. The polypeptide molecular weight was verified by electrospray mass spectrometry. Peptide purity was greater than 70%. The polypeptide buffer was 10 mM sodium phosphate or 10 mM Tris-HCl, 1 mM DTT, 0.1 mM

b. Experimental Procedure

Experiments were done using pairs of designed polypeptides, one negative and one positive. Multilayer films consisting of at least 5 bi-layers of the above-identified SP2, SN1, LP4, and LN3 were deposited onto the QCM resonators using standard ELBL techniques (a bi-layer consists of one layer of polycation and one layer of polyanion). The polypeptide concentration for layer adsorption was 2 mg mL⁻¹. It is known that dependence of polyion layer thickness on polyelectrolyte concentration is not strong (see Lvoev, Y. and Decher, G. (1994) Crystallog Rep. 39:628, which is incorporated herein by reference in its entirety); in the concentration range 0.1 to 5 mg mL⁻¹, bilayer thickness was approximately independent of concentration for PSS/PAH. By contrast, polypeptide thin films appear substantially less thick than those fabricated using high molecular weight PSS/PAH (mass calculated using Δf data using the well-known Sauerbrey equation); see Lvoev, Y. and Decher, G. (1994) Crystallog Rep. 39:628. This follows from calculating film thickness on the basis of mass deposited, as is ordinarily done in the art for proteins. The calculated thickness for the designed polypeptide assembly shown in Fig. 3(c) is greater than the end-to-end length of the peptides used to make the film. DTT was included at 1 mM to inhibit disulfide bond formation. The adsorption time was 20 minutes.

Resonators were rinsed for 1 min in pure water between subsequent adsorption cycles (removing perhaps 10-15% of weakly adsorbed material) and dried in a stream of gaseous N₂. Then the mass of the deposited peptide was measured indirectly by QCM. The mass measurement includes some water, despite drying, and low mass ions like K⁺, Na⁺, and Cl⁻. Partial interpenetration of neighboring layers of peptide is probable (see Decher, G. (1997) Science 272:1323; Schmitt et al. (1993) Macromolecules 26:7058; and Komech et al. (1995) Physica B 214:954); this could be important for the efficiency of disulfide "locking."

After adsorption of the polypeptide and rinsing and drying the QCM resonator, the resonant frequency of the resonator was measured. This enabled calculation of the frequency shift on adsorption and change in adsorbed mass. A decrease in frequency indicates an increase in adsorbed mass. The results are provided in Figs. 3(a) and 3(b). Fig. 3(a) shows a comparison of adsorption data for LP4 and LN3 in different buffers (10 mM sodium phosphate, pH 7.4, 1 mM DTT and 10 mM Tris-HCl, pH 7.4, 1 mM DTT). It is clear from these data that adsorption depends more on the properties of the peptides than the specific properties of the buffer used. Fig. 3(b) shows resonator frequency versus adsorbed layer for different combinations of SP2, SN1, LP4, and LN3 (namely, SP2/SN1, SP2/LN3, LP4/SN1, and LN4/LN3) in 10 mM sodium phosphate, pH 7.4 and 1 mM DTT (the lines merely connect experimental data points). Each of these combinations involved one negative polypeptide and one positive polypeptide, as required by ELBL. Fig. 3(c) shows a graph of calculated adsorbed mass versus layer number for SN1/LP4 in 10 mM Tris-HCl, pH 7.4 and 1 mM DTT (calculated from experimental data using the Sauerbrey equation). The total adsorbed mass, approximately 5 μg, corresponds approximately to 1 amol of peptide. The equation used for this calculation was Δf = -0.87×10⁻⁷ Δf, where m is mass in

http://www.patentquest.net/

iv. Conclusions

The results show that polyamides designed using the method of the present invention are suitable for ELBL, despite significant qualitative differences from PSS and PAH, flexible homopolymers having 1 charge per unit length at pH 7.4. The charge per unit length on poly-L-lysine and poly-L-glutamic acid is 1 at pH 7.4, as with PSS and PAH, but both of these polyamides have a marked propensity to form \( \alpha \)-helical structure under various conditions, making them substantially less suitable for multilayer assembly when control over thin film structure is desired. The monodispersed polyamides of the present invention, however, enable the practitioner to fine-tune precisely the structure of the material being used for ELBL. Moreover, usual commercial preparations of poly-L-lysine and poly-L-glutamic acid are polydispersed, and poly-L-lysine, poly-L-glutamic acid, PSS, and PAH evoke an immune response (i.e. are immunogenic) in humans.

Because the designed polyamides are readily adsorbed on an oppositely charged surface, as demonstrated by experiment, there is no need for a "precursor" layer. As is known in the art, "precursor" layers are deposited on a substrate to enhance adsorption of less adsorptive substances. The lack of a precursor layer enhances the biocompatibility of the polyion films because polyamides are used as precursors are immunogenic or allow less precise control over polymer structure or thin film structure than designed polyamides.

Multilayers of the designed polyamides were stable at the pH of human blood, 7.4. Thus, the multilayers should be useful for a broad range of biological applications. Adsorption of the designed polyamides, each of less than 1 charge per residue, was essentially complete in less than 10 min. at 2 mg/mL and low ionic strength. This implies that these polyamides can be used to form multilayer films quickly and with relative ease. Drying the peptide film with \( 10 \) after deposition of each layer did not impair assembly. Drying is done to get an accurate QCM frequency measurement, but it is not required for assembly.

The film assembly experiments were done at a lower ionic strength than that of blood, but the process gives a qualitatively similar result at higher ionic strength. The chief difference is the amount of peptide deposited per adsorption layer; the higher the ionic strength, the greater the amount of peptide deposited. This is illustrated by the graph in FIG. 7, which shows the amount of material deposited as a function of ionic strength—the peptides used were poly-L-glutamic acid and poly-L-lysine. QCM resonant frequency is plotted against adsorption layer. The average molecular mass of poly-L-glutamate was 84,600 Da, while that of poly-Lys was 84,000 Da. The peptide concentration used for assembly was 2 mg/mL. The data indicate salt concentration (ionic strength of solution) influences thin film assembly. In general, the amount of material deposited per layer increases with ionic strength in the range 0-100 mM NaCl. As the essential character of ELBL, with designed polyamides appears not to depend on the choice of buffer under conditions of relatively high net charge per unit length and low ionic strength, qualitatively similar results are expected at the ionic strength of human blood. Thus, the choice of buffer should not fundamentally alter the stability of the multilayers in their target environment. However, even if the choice of buffer did affect the stability of the multilayers, the "locking" mechanism would be available as a design feature to stabilize the capsule.

The greater apparent deposition of positive polyamides than negative ones may result from the higher charge per unit length on the positive polyamides at pH 7.4. The material deposited in each layer probably corresponds to that required for neutralization of the charge of the underlying surface. Hydrophobic interactions could also help to explain this feature of adsorption behavior.

The usual thin film thickness calculation for proteins and other polymers is probably invalid for short polyamides (calculated thickness is 60-90 nm, but scanned length of 10 polyamides is approximately 120 nm). This probably results from a high density of packing of the relatively short polyamides onto the adsorption surface; the result is also consistent with finding that film thickness varies with ionic strength, as changes in structural properties of a polymer will occur and screening of charges by ions will reduce intra-layer charge repulsion between adsorbed peptides. The thickness of the designed polyamide thin film discussed here is estimated at 20-50 nm.

Many aspects of the design and fabrication cycles could be automated. For example, a computer algorithm could be used to optimize the primary structure of peptides for ELBL by comparing predicted peptide properties with observed physical properties, including structure in solution, adsorption behavior, and film stability at extremes of pH. Moreover, the polyamide film assembly process can be mechanized, once the details of the various steps have been sufficiently determined.

EXAMPLE 2

Experiments Involving De-Noxo-Designed Polyamides Containing Cysteine

b. Polyamides

The polyamides used were:

```plaintext
  Tyr Lys Cys Lys Gly Lys Val Lys Val (SEQ ID NO: 5)  
  Lys Cys Gly Lys Lys Val Lys Val Lys  
  Cys Lys Gly Lys Val Lys Cys  
  Gly Lys Gly Val Lys  
  Lys Cys Gly Gly Gly Val Gly Val  
  Gly Gly Gly Gly Gly Gly Gly  
  Cys Gly Gly Gly Gly Gly Val Gly  
  Gly Gly Gly Gly Gly Gly Lys  
```

Unlike the other polyamides used in the experiments described herein, these two were not designed using human genome information; they were designed de novo for the sole purpose of assessing the role of disulfide bond formation in...
polypeptide film stabilization, SEQ ID NO:5 has a magnitude of the net charge of 1632 (0.5) at pH 7; and SEQ ID NO:6 has a magnitude of the net charge of 1632 (0.5) at pH 7. In both cases, the magnitude of the net charge is greater than, or equal to approximately one-half of the total length of the first layer polypeptide at pH 7.

c. Procedures

All experiments were conducted at ambient temperature. All assembly experiments using QCM were conducted in the same conditions, except that the samples to undergo oxidation were dried using air instead of nitrogen gas. The assembly conditions were 10 mM Tris-Cl, 18 mM DTT, pH 7.4. The nominal peptide concentration was 2 mg/mL. The number of layers formed was 14.

Disulfide locking conditions for the oxidizing samples were 10 mM Tris-Cl, 1% DMSO, saturation of water with air, pH 7.5. The duration of the "locking" step was 6 hours. Conditions for the reducing samples were 10 mM Tris-Cl, 18 mM DTT, saturation of water with nitrogen, pH 7.5. The duration of this step was 6 hours.

All disassembly experiments using QCM were conducted in the same conditions, except that the oxidizing samples were dried using air instead of nitrogen. Disassembly conditions were 10 mM KCl, pH 2.0. Samples were rinsed with DI water for 30 seconds prior to drying.

Three different types of experiments were conducted: (1) Reducing—no treatment; disassembly was conducted immediately after assembly; (2) Reducing—6 hours, as described above for reducing samples; and (3) Oxidizing—6 hours, as described above for oxidizing samples.

d. Results

The results are illustrated in FIG. 10 in the first two experiments (both reducing), all of the deposited material (100%) disassembled within 50 minutes. By contrast, in the oxidizing experiment, a substantial amount of material remained after substantial incubation of the peptide film-coated QCM resonator at pH 2 for over 5 hours. The stability of the polypeptide films at acidic pH is determined by the conditions of assembly; in this way, film or capsule stability is a design feature that becomes possible by using polypeptides as the polyelectrolytes for ELBL.

e. Conclusions

Electrostatic forces play a key role in holding together oppositely-charged layers of designed polypeptides. At acidic pH, the net charge on one of the peptides is neutralized and the polypeptide film disassembles due to electrostatic repulsion. Reducing conditions prevent disulfide bond formation. Therefore, the electrostatic attraction between the layers is the only binding force for stabilizing the layers under these conditions. By contrast, under oxidizing conditions disulfide bonds are formed. At acidic pH, disulfide bonds inhibit film disassembly. The results indicate that layer stability at acidic pH is directly affected by the formation of intra- and/or inter-layer disulfide bonds—i.e., between molecules in the same layer, between molecules in adjacent layers, or both. This is illustrated by the results shown in FIG. 10 due to disulfide locking, more than 30% of the film remained stable at acidic pH, despite electrostatic repulsion at relatively low ionic strength. Peptides with more cysteine residues are anticipated to further improve disulfide locking efficiency. Moreover, adjustment of the conditions of peptide assembly will be an important aspect of engineering films to have the desired physical as well as chemical and biological properties.

EXAMPLE 3

Experiments involving Designed Polypeptides Containing Cysteine

f. Materials

The essential elements of this experiment were a quartz crystal microbalance instrument; silver-coated resazurin (9 MHz resonant frequency); the negative 48-residue peptide (L3N) (SEQ ID NO: 4); and a positive 48-residue peptide named "SPS" of the following sequence:

[Sequence]

Like the other designed peptides described above in Part (1)(1), SPS was designed using the process described above in Part (3)(1) to analyze the amino acid sequence of the human blood protein lactoferrin (gi4505045). The ELBL buffer was 10 mM Tris, pH 7.4, 10 mM NaCl, and 1 mM DTT. The disassembly buffer was 10 mM KCl, pH 2.2. 2 mL peptide solutions were prepared for SPS and LN3 by adding 4 mg of each peptide to 2 mL of the above buffer solution and adjusting the pH of each solution to 7.4; the peptide concentration was 2 mg/mL.

g. Procedure for Monitoring Assembly of Polypeptide Layers on QCM Resonators

Reducing procedures were as follows: (1) The frequency of the resonator was measured and recorded prior to peptide adsorption; (2) The resonator was dipped into the SPS peptide solution for 20 min; (3) The resonator was dipped into the SPS rinse solution for 30 sec; (4) The resonator was removed from the rinse solution and dried using nitrogen gas; (5) The QCM resonant frequency of the resonator was recorded; (6) The resonator was dipped into the LN3 peptide solution for 20 min; (7) The resonator was dipped into the LN3 rinse solution for 30 sec; (8) The resonator was removed from the rinse solution and dried using nitrogen gas; (9) The QCM resonant frequency of the resonator was recorded; (10) Steps 2 through 9 were repeated until 16 layers were adsorbed onto the resonator.

Oxidizing procedures were the same as the reducing procedures, except that the resonator was rinsed in DI water instead of the SPS buffer or the LN3 buffer and dried with air instead of nitrogen before each measurement.

h. Locking Procedures

Reducing procedures were as follows: The resonator was placed in an aqueous solution containing 1 mM DTT for 6 hours. DTT, a reducing agent, inhibited disulfide bond formation.

Oxidizing procedures were as follows: The resonator was placed in an air-saturated aqueous solution containing 1% DMSO for 6 hours. DMSO, an oxidizing agent, promoted disulfide bond formation.
US 7,544,770 B2

33

i. Disassembly on Resonator

i. Solutions

Reducing conditions were as follows: 10 mM KCl, 1 mM DTT, pH 2.

Oxidizing conditions were as follows: 10 mM KCl, 20% DMSO, pH 2.

ii. Procedure for Disassembly

Reducing procedures were as follows: (1) The initial resonant frequency of the resonator was measured by QCM and recorded. (2) The resonator was dipped into the reducing disassembly solution for 5 min. (3) The resonator was rinsed in reducing buffer solution for 30 sec. (4) The resonator was dried with gaseous N₂. (5) The resonant frequency of the resonator was measured by QCM and recorded. (6) Steps 2 through 5 were repeated for reading times of 5, 10, 15, 20, 30, 60, and 90 min.

Oxidizing procedures were the same as for reducing procedures, except that raising of the resonator was done in D.I. water saturated with air instead of reducing buffer.

j. Results

FIG. 8 shows approximately linear increase in mass deposited during thin film assembly of Sp5 and L23. Both resonators show almost identical deposition of mass throughout the process of assembly, despite differences in assembly conditions.

FIG. 9 shows the percentage of material remaining during film disassembly. The layers subjected to oxidizing conditions showed a minimal loss of material at acidic pH with almost 90 to 95% of mass retention. By contrast, layers subjected to reducing conditions lost almost all the film material within the first 5 minutes of exposure to acidic pH.

k. Conclusions

The results demonstrate that at acidic pH, disulfide bonds prevent layer degeneration and hold the layers firmly together. Layer stability at acidic pH is directly affected by the formation of intra- and/or inter-layer disulfide bonds. Disulfide bond formation is dependent on the concentration and proximity of cysteine residues to each other. Increasing the concentration per unit chain length of the polyamide would therefore directly influence disulfide bond formation and film stability. Increasing the ionic strength of the buffer solutions used for film assembly influences the concentration of cysteine in the film by increasing the amount of material deposited per adsorption cycle and the thickness of each layer. The increased number of cysteine amino acids in a single layer would in this way increase the number of disulfide bonds formed, and, on oxidation, increase film stability.

EXAMPLE 5

Films With Polypeptides Comprising an RGD Functional Domain Wherein the Magnitude of the Linear Charge Density Per Residue is About 0.4

In one embodiment, the functional region of a composite polypeptide comprises an RGD sequence wherein the charge density of the composite peptide is about 0.4. Sample peptide designs are the following:

KAKAKAAK (SEQ ID NO:14)

KAKAKAKK (SEQ ID NO:15)

In this example, the polypeptide of SEQ ID NO:14 is a positively charged polypeptide having a functional region of RGD, a first surface adsorption region of AAAKAKAKK (SEQ ID NO:16) and a second surface adsorption region of AAAKAKAKK (SEQ ID NO:17). The magnitude of the net charge per residue at neutral pH of the composite peptide is +14/35 or +0.4. The polypeptide of SEQ ID NO:15 is a negatively charged polypeptide having a functional region of RGD, a first surface adsorption region of AAAAFAFGEAF (SEQ ID NO:18).
US 7,544,770 B2

Composite Polypeptide Comprising a Single Functional Region and a Single Surface Adsorption Region at the N-terminus of the Polypeptide

In this example, the functional region is a known functional domain from a protein, e.g., the protein tyrosine phosphatase (PTP) domain of human axillin:

**EXAMPLE 7**

Composite Polypeptide Comprising a Single Functional Region and a Single Surface Adsorption Region at the N-terminus of the Polypeptide

In this example, the functional region is a known functional domain from a protein, e.g., the protein tyrosine phosphatase (PTP) domain of human axillin:

**EXAMPLE 8**

Composite polypeptide comprising two functional regions, wherein there are three surface adsorption regions, one at the N-terminus and one at the C-terminus of the composite peptide and one between the two functional regions, and wherein there are two different functional regions for glycosylation.

A representative peptide structure is the following:

**SAR-functional region:SAR-functional region:SAR**

where, as before, the SAR is a motif and therefore suitable for surface adsorption, e.g., RRRARR (SEQ ID NO:25), and one functional region contains a recognition site for N-linked glycosylation, e.g., GGNVSAG (SEQ ID NO:26), and the other for O-linked glycosylation, e.g., PPSSPP (SEQ ID NO:27). The amino acid sequence of a representative composite peptide is:

RRARRGQVQGRARRARRPPSSPPRARR

The magnitude of the net charge per residue at pH 7 of the composite polypeptide +18.35+0.5. The multilayer film in this case is built of the indicated positive peptide and a suitable negative peptide, e.g.,

EERARKHEGKEAEGERAEAEKAEKAEKAEKAEKAEK
US 7,544,770 B2

composite peptide with one functional region, wherein there is one surface adsorption region at the C-terminus of the composite peptide, and wherein there is one functional region which comprises a peptide sequence known to have antimicrobial activity.

A representative peptide structure is the following:

**Functional region-SAR**

where, as before, SAR is a suitable surface adsorption region, e.g., KKKAKKXGKXKAKAKK (SEQ ID NO: 1), and the functional region contains the sequence of histatin 5, viz., DSHAKRHFFYKRFHFKHSHHYQY (SEQ ID NO: 30). The amino acid sequence of a representative composite peptide is:

**KRAARKRGQVQSGRAAGKRPPPSPPRRRR** (SEQ ID NO: 31)

The magnitude of the net charge per residue at pH 5.5 per residue of the amino acid sequence of this representative composite peptide is +24/39 ≈ 0.6. The multilayer film in this case is built of the indicated positive peptide and a suitable negative peptide, e.g., SEQ ID NO: 29.

**EXAMPLE 10**

Composite peptide with a single functional region, wherein there are two surface adsorption regions, one at the N-terminus and one at the C-terminus of the functional region, and wherein the functional region comprises two specific protease recognition sites and two linkers, each of which is a single glycine residue.

In one embodiment, the protease recognition sites are for enterokinase and thrombin:

**SAR-Enterokinase recognition-linker-Thrombin recognition-linker-SAR**

where in each instance SAR represents a suitable surface adsorption region, e.g., SEQ ID NO: 10 and SEQ ID NO: 11. The functional region is encoded, e.g., as DDDXGLVPRGS (SEQ ID NO: 32), wherein DDDX (SEQ ID NO: 33) is a recognition site for enterokinase, G is a linker, LVPGRS (SEQ ID NO: 34) is a recognition site for thrombin, and G is a linker. The amino acid sequence of a representative composite peptide is:

**KKXAKKXGKXKAKAKKDDXGLVPRGSXKXKAKAKKXGKXKAKAKK** (SEQ ID NO: 35)

The magnitude of the net charge per residue at neutral pH of the composite peptide is +22/46 ≈ 0.5. The multilayer film in this case is built of the indicated positive peptide and a suitable negative peptide, e.g., SEQ ID NO: 29.

**EXAMPLE 11**

Composite peptide with two functional regions, wherein there are three surface adsorption regions, one at the N-terminus and one at the C-terminus of the composite peptide and one between the two functional regions, and wherein there are two identical functional regions for formation of natural peptide crosslinks.

A representative peptide structure is the following:

**SAR-Functional region-SAR-functional region-SAR**

where, as before, SAR is a suitable surface adsorption region, e.g., EFEAEEF (SEQ ID NO: 36), and the functional region contains a specific number of Cys residues, e.g., GCGG-GCGG (SEQ ID NO: 37). The amino acid sequence of a representative composite peptide is:

**EFEAEEF-EFEAEEF-EFEAEEF** (SEQ ID NO: 38)

The magnitude of the net charge per residue at pH 7 of the composite peptide is ≈ 0.5. The multilayer film in this case is built of the indicated negative peptide and a suitable positive peptide, e.g.,

**KKXAKKXGKXKAKAKKDDXGLVPRGSXKXKAKAKKDDXGLVPRGS** (SEQ ID NO: 39)

**EXAMPLE 12**

Composite Polypeptide Comprising a Single Functional Region and a Single Surface Adsorption Region at the C-terminus of the Polypeptide in this example, the functional region is a known functional domain from a protein, e.g., the BAG domain of National Center for Biotechnology Information accession AAP06461:

**BAG sequence-FFEAEEF** (SEQ ID NO: 40)

where "BAG sequence" represents the amino acid sequence of the BAG domain of a hypothetical protein from Schistosoma japonicum:

**BAG sequence**

**KIQSPKIPGSPFHPKIECLMHEQLEQLIGVLLL** (SEQ ID NO: 41)

**STQWHRFRFTDQAVRIGQIAEMLYEVLNL** (SEQ ID NO: 42)

The surface adsorption region is the same as SEQ ID NO: 13.

The use of the terms "a" and "an" and "the" and similar referents (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms first, second etc. as used herein are not meant to denote any particular order, but simply for convenience to denote a plurality of, for example, layers. The terms "comprising", "having", "including", and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to") unless otherwise noted. Recitation of ranges of values are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. The endpoints of all ranges are included within the range and independently combinable. All methods described herein can be performed in a suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as"), is intended merely to better illustrate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any nonclaimed element as essential to the practice of the invention as used herein.

Other embodiments of the invention are possible and modifications may be made without departing from the spirit and scope of the invention. Therefore, the detailed description above is not meant to limit the invention. Rather, the scope of the invention is defined by the appended claims.
SEQ ID NO: 1
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: The sequence was designed de novo and synthesized.

1 Tyr Arg Arg Arg Ser Val Gln Gly Arg Arg Arg Ser Val Gln
   5                     10                   15
   Gly Arg Arg Arg Ser Val Gln Gly Arg Arg Arg Ser Val Gln
   20                  25                  30

SEQ ID NO: 2
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: The sequence was designed de novo and synthesized.

1 Tyr Glu Glu Asp Glu Gln Asp Gly Glu Glu Asp Glu Cyc Gly Glu Asp
   5                     10                   15
   Gly Glu Glu Asp Glu Gln Asp Gly Glu Asp Glu Cyc Gly Glu Asp
   20                  25                  30

SEQ ID NO: 3
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: The sequence was designed de novo and synthesized.

1 Tyr Arg Arg Arg Arg Ser Val Gln Gly Arg Arg Arg Ser Val Gln
   5                     10                   15
   Gly Arg Arg Arg Ser Val Gln Gly Arg Arg Arg Ser Val Gln
   20                  25                  30
   Gly Arg Arg Arg Ser Val Gln Gly Arg Arg Arg Ser Val Gln
   35                40                45

SEQ ID NO: 4
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: The sequence was designed de novo and synthesized.

1 Tyr Glu Glu Asp Glu Cyc Gln Asp Gly Glu Glu Asp Glu Cyc Gly Glu Asp
   5                     10                   15
   Gly Glu Glu Asp Glu Cyc Gln Asp Gly Glu Glu Asp Glu Cyc Gly Glu Asp
   20                  25                  30
   Gly Glu Glu Asp Glu Cyc Gln Asp Gly Glu Glu Asp Glu Cyc Gly Glu Asp
   35                40                45
<210> SEQ ID NO 5
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 5
Tyr Cys Lys Gly Lys Val Lys Val Lys Cys Lys Gly Lys Val Lys
1 5 10 15
Val Lys Cys Lys Gly Lys Val Lys Val Lys Cys Lys Gly Lys Val Lys
20 25 30

<210> SEQ ID NO 6
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 6
Glu Cys Glu Gly Glu Val Glu Val Glu Cys Glu Gly Glu Val Glu
1 5 10 15
Val Glu Cys Glu Gly Glu Val Glu Val Glu Cys Glu Gly Glu Val Glu
20 25 30

<210> SEQ ID NO 7
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 7
Tyr Lys Gly Lys Lys Ser Cys His Gly Lys Gly Lys Lys Ser Cys His
1 5 10 15
Gly Lys Gly Lys Lys Lys Ser Cys His Gly Lys Gly Lys Lys Ser Cys His
20 25 30

<210> SEQ ID NO 8
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 8
Lys Lys Ala Lys Lys Gly Lys Lys Lys Lys Ala Lys Lys Lys Lys
1 5 10 15
Arg Gly Arg Lys Lys Lys Lys Lys Gly Lys Lys Lys Lys Lys
20 25 30
Lys Lys Tyr
35

<210> SEQ ID NO 9
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.
**US 7,544,770 B2**

---

**SEQUENCE: 9**

Glu Glu Glu Ala Glu Glu Gly Glu Glu Ala Glu Glu Glu Gly 1 5 10 15
Arg Gly Asp Glu Glu Ala Glu Glu Gly Glu Glu Ala Glu 20 25 30
Glu Glu Tyr 35

---

**SEQUENCE: 10**

Lys Lys Lys Ala Lys Lys Gly Lys Lys Lys Lys Lys Lys Gly 1 5 10 15

---

**SEQUENCE: 11**

Lys Lys Lys Ala Lys Lys Gly Lys Lys Lys Lys Lys Lys Tyr 1 5 10 15

---

**SEQUENCE: 12**

Glu Glu Glu Ala Glu Glu Gly Glu Glu Ala Glu Glu Glu Gly 1 5 10 15

---

**SEQUENCE: 13**

Glu Glu Glu Ala Glu Glu Gly Glu Glu Ala Glu Glu Glu Tyr 1 5 10 15

---

**SEQUENCE: 14**

Ala Ala Lys Ala Lys Lys Gly Lys Ala Lys Ala Lys Ala Lys Gly
<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5</td>
<td>10</td>
<td>15</td>
</tr>
<tr>
<td>Arg Gly Asp Lys Ala Lys Ala Lys Lys Gly Lys Ala Lys Ala Lys</td>
<td>25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala Ala Tyr</td>
<td>35</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 15
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 15
Ala Ala Glu Ala Glu Ala Glu Ala Glu Ala Glu Ala Lys Gly
1   5   10   15
Arg Gly Asp Lys Ala Glu Ala Glu Ala Gly Glu Ala Glu Ala Glu
26   30
Ala Ala Tyr
35

<210> SEQ ID NO 16
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 16
Ala Ala Lys Ala Lys Ala Lys Gly Lys Ala Lys Ala Lys Ala Lys Gly
1   5   10   15

<210> SEQ ID NO 17
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 17
Lys Ala Lys Ala Lys Lys Gly Lys Ala Lys Ala Lys Ala Ala Tyr
1   5   10   15

<210> SEQ ID NO 18
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 18
Ala Ala Glu Ala Glu Ala Glu Gly Glu Ala Glu Ala Glu Ala Glu Gly
1   5   10   15

<210> SEQ ID NO 19
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.
<400> SEQUENCE: 10
Glu Ala Glu Ala Glu Gly Glu Ala Glu Ala Glu Ala Tyr
1  5  10  15

<210> SEQ ID NO: 20
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURES:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 20
Lys Lys Lys Ala Lys Lys Gly Lys Lys Lys Lys Lys Lys Lys Gly
1  5  10  15
Lys Tyr Trp Tyr Lys Pro Glu Ile Ser Arg Glu Gin Ala Ile Ala Leu
20  25  30
Leu Lys Asp Gin Gin Pro Gly Ala Phe Ile Ile Arg Asp Ser His Ser
35  40  45
Phe Arg Gly Ala Tyr Gly Leu Ala Met Lys Val Ser Ser Pro Pro Pro
50  55  60
Thr Ile Met Gin Gin Asn Lys Lys Gly Asp Met Thr His Glu Leu Val
65  70  75  80
Arg His Phe Leu Ile Glu Thr Gly Pro Arg Gly Val Lys Leu Lys Gly
85  90  95
Cys Pro Asn Gin Pro Asn Phe Gin Gin Ser Leu Ser Ala Leu Val Tyr Gin
100 105 110
His Ser Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu Val Ile Lys Tyr
115 120 125
Trp Tyr Lys Pro Glu Ile Ser Arg Glu Gin Ala Ile Ala Leu Leu Lys
130 135 140
Asp Gin Glu Pro Gly Ala Phe Ile Ile Arg Asp Ser His Ser Phe Arg
145 150 155 160
Gly Ala Tyr Gly Lys Ala Met Lys Val Ser Ser Pro Pro Pro Thr Ile
165 170 175
Met Gin Gin Asn Lys Lys Gly Asp Met Thr Ile Gin Leu Val Arg His
180 185 190
Phe Leu Ile Glu Thr Gly Pro Arg Gly Val Lys Leu Lys Gly Cys Pro
195 200 205
Asn Gin Pro Asn Phe Gly Ser Leu Ser Ala Leu Val Tyr Gin His Ser
210 215 220
Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu Val Ile Lys Lys Lys Ala
225 230 235 240
Lys Lys Lys Gly Lys Lys Lys Leu Ala Lys Lys Lys Tyr
245 250

<210> SEQ ID NO: 21
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21
Lys Tyr Trp Tyr Lys Pro Glu Ile Ser Arg Glu Gin Ala Ile Ala Leu
1  5  10  15
Leu Lys Asp Gin Gin Pro Gly Ala Phe Ile Ile Arg Asp Ser His Ser
20  25  30
Phe Arg Gly Ala Tyr Gly Leu Ala Met Lys Val Ser Ser Pro Pro Pro

```
| Thr Ile Met Glu Gin Asn Lys Gly Asp Met Thr His Glu Leu Val | 60 65 | 49 |
| Arg His Phe Leu Ile Glu Thr Gly Pro Arg Gly Val Lys Leu Lys Gly | 45 70 | 50 |
| Cys Pro Asn Glu Pro Asn Phe Gly Ser Leu Ser Ala Leu Val Tyr Gin | 45 90 95 |
| His Ser Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu Val Ile | 100 105 110 |

<210> SEQ ID NO 22
<211> LENGTH: 135
<212> TYPE: PRT
<219> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Val Leu Phe Val Asn Val Asp Met Glu Ser Leu Thr Gly Pro Gln

| Ala Ile Ser Lys Ala Thr Ser Leu Ala Ala Asp Pro Thr Pro | 20 25 30 |
| Ala Ala Thr Ile Val His Phe Gly Val Ser Ala Gin Gly Ile Thr Leu | 35 40 45 |
| Thr Asp Asn Gin Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Leu Ala | 50 55 60 |
| Thr Val Thr Phe Cys Asp Leu Asp Pro Gin Arg Lys Trp Met Lys | 65 70 75 80 |
| Thr Gin Gly Cys Ala Pro Ala Lys Leu Phe Gly Phe Val Ala Arg Lys | 85 90 95 |
| Gin Gly Ser Thr Thr Asp Asn Ala Cys His Leu Phe Ala Gin Leu Asp | 100 105 110 |
| Pro Asn Gin Pro Ala Ser Ala Ile Val Asn Phe Val Ser Leu Val Met | 115 120 125 |

Leu Asn Ala Gin Gin Lys Gin Arg

| 130 135 |

<210> SEQ ID NO 23
<211> LENGTH: 195
<212> TYPE: PRT
<219> ORGANISM: Artificial

<500> FEATURE:
<23> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 23

Lys Lys Lys Ala Lys Lys Lys Gly Lys Lys Lys Lys Lys Gly

| Leu Lys Asp Thr Leu Lys Asp Thr Ser Ser Arg Val Ile Gin Ser Val | 10 15 20 |
| Thr Ser Tyr Thr Lys Gly Asp Leu Asp Phe Thr Tyr Val Thr Ser Arg | 35 40 45 |
| Ile Ile Val Met Ser Phe Pro Leu Asp Asn Val Ala Gin Gly Phe Arg | 50 55 60 |
| Asn Gin Val Asp Asp Ile Arg Ser Phe Leu Asp Ser Arg His Leu Asp | 65 70 75 80 |
| His Tyr Thr Val Tyr Asn Leu Ser Pro Lys Ser Tyr Arg Thr Ala Lys | 85 90 95 100 |

Phe His Ser Arg Val Ser Gin Cys Ser Trp Pro ile Arg Gin Ala Pro
```
Ser Leu His Asn Leu Phe Ala Val Cys Arg Asn Met Tyr Arg Tyr Leu
Leu Gin Asn Pro Pro Asn Val Cys Val Val His Cys Leu Asp Gly Arg
Ala Ala Ser Ser Ile Leu Val Gly Ala Met Phe Ile Phe Cys Asn Leu
Tyr Ser Thr Pro Gly Pro Ala Ile Arg Leu Ser Tyr Ala Lys Arg Pro
Gly Ile Gly Leu Ser Pro Ser His Arg Tyr Leu Gly Tyr Met Cys Asp
Leu Leu Ala

<210> SEQ ID NO 24
<211> LENGTH: 180
<220> TYPE: PBT
<221> ORGANISM: Homo sapiens
<406> SEQUENCE: 24
Leu Lys Asp Thr Leu Lys Asp Thr Ser Ser Arg Val Ile Gin Ser Val
Thr Ser Tyr Thr Lys Gly Asp Leu Asp Phe Thr Tyr Val Ser Arg
Ile Ile Val Met Ser Phe Pro Leu Asp Asn Val Asp Ile Gly Phe Arg
Asn Gin Val Asp Ile Arg Ser Phe Leu Asp Ser Arg His Leu Asp
His Tyr Thr Val Tyr Asn Leu Ser Pro Lys Ser Tyr Arg Thr Ala Lys
The His Ser Arg Val Ser Glu Cys Ser Trp Pro Ile Arg Gin Ala Pro
Ser Leu His Asn Leu Phe Ala Val Cys Arg Asn Met Tyr Asn Trp Leu
Leu Gin Asn Pro Lys Asn Val Cys Val Val His Cys Leu Asp Gly Arg
Asn Asn Pro Val Val Cys Ala Val Cys Leu Asp Gly Arg
Ala Ala Ser Ser Ile Leu Val Gly Ala Met Phe Ile Phe Cys Asn Leu
Tyr Ser Thr Pro Gly Pro Ala Ile Arg Leu Ser Tyr Ala Lys Arg Pro
Gly Ile Gly Leu Ser Pro Ser His Arg Arg Tyr Leu Gly Tyr Met Cys
Asp Leu Leu Ala

<210> SEQ ID NO 25
<211> LENGTH: 7
<212> TYPE: PBT
<220> ORGANISM: Artificial
<222> FEATURES:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.
<406> SEQUENCE: 25
Arg Arg Arg Ala Arg Arg Arg

1 5
Arg Arg Arg Ala Arg Arg Gly Gly Aen Val Ser Gly Gly Arg Arg
1  5  10  15
Arg Ala Arg Arg Pro Pvo Ser Ser Ser Pro Pro Arg Arg Arg Ala
27  30
Arg Arg Arg
35

Asp Asp Asp Lys Leu Val Pro Arg Gly Ser Gly
1  5  10

Asp Asp Asp Lys
1  5

Leu Val Pro Arg Gly Ser
1  6

Lys Lys Lys Ala Lys Lys Lys Lys Lys Lys Lys
1  5  10  15
Asp Asp Asp Lys Gly Leu Val Pro Arg Gly Ser Gly Lys Lys
20  25  30
Ala Lys Lys Lys Gly Lys Lys Ala Lys Lys Tyr
<210> SEQ ID NO 36
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 36

Glu Glu Glu Ala Glu Glu Glu
1 5

<210> SEQ ID NO 37
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 37

Gly Gly Cys Gly Gly Cys Gly Gly
1 5

<210> SEQ ID NO 38
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 38

Glu Glu Glu Ala Glu Glu Glu Gly Cys Gly Gly Cys Gly Gly Cys Gly Glu
1 5 10 15

Glu Glu Ala Glu Glu Glu Gly Cys Gly Gly Cys Gly Gly Cys Gly Glu
20 25 30

Glu Ala Glu Glu Glu Tyr
35

<210> SEQ ID NO 39
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 39

Lys Lys Lys Ala Lys Lys Lys Gly Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Tyr
20 25 30

<210> SEQ ID NO 40
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: The sequence was designed de novo and synthesized.

<400> SEQUENCE: 40

Ser Leu Glu Pro Glu Ile Asp Arg Phe Asp Gly Thr Pro His Ser Lys
The invention claimed is:

1. A multilayer film, said film comprising two or more layers of polyelectrolytes, wherein adjacent layers comprise oppositely charged polyelectrolytes,

   wherein a first layer polyelectrolyte comprises a composite polypeptide comprising one or more non-homopolymer surface adsorption regions covalently linked to one or more functional regions forming a single polypeptide chain, wherein the composite polypeptide and the one or more non-homopolymer surface adsorption regions have the same polarity,

   wherein the one or more non-homopolymer surface adsorption regions comprise one or more amino acid sequence motifs consisting of 5 to 15 amino acid residues and having a magnitude of net charge per residue at neutral pH of greater than or equal to 0.4, and

   wherein the one or more functional regions comprise 3 to about 250 amino acid residues, and are selected from the group consisting of a cysteine-containing sequence, a sequence for extracellular matrix recognition, a phosphotyrosine binding domain, a Src homology 2 domain, a protein tyrosine phosphatase domain, an N-linked glycosylation substrate sequence, an O-linked glycosylation substrate sequence, a protease recognition site, an antimicrobial peptide sequence, and a BAG domain, and
wherein the composite polypeptide is an unbranched polypeptide, is not a homopolymer, is at least 15 amino acid residues long, and has an aqueous solubility at pH 4 to 10 of greater than 50 μg/mL; wherein a second layer comprises a second layer polyelectrolyte comprising a polycationic material or a polyanionic material having a molecular weight of greater than 1,000 and at least 5 charges per molecule, and a charge opposite that of the first layer polypeptide.

2. The multilayer film of claim 1, wherein the composite polypeptide has an aqueous solubility of greater than or equal to about 1 mg/mL.

3. The multilayer film of claim 1, wherein the one or more functional regions comprise 3 to about 50 amino acid residues, and wherein the composite polypeptide has a magnitude of net charge per residue at neutral pH of greater than or equal to 0.4.

4. The multilayer film of claim 1, wherein the one or more functional regions comprise about 50 to about 250 amino acid residues.

5. The multilayer film of claim 4, wherein the one or more functional regions have a water solubility at pH 4 to 10 of greater than 50 μg/mL.

6. The multilayer film of claim 5, wherein the one or more functional regions have a water solubility at pH 4 to 10 of greater than or equal to 1 mg/mL.

7. The multilayer film of claim 4, wherein polypeptide comprises at least two amino acid sequence motifs.

8. The multilayer film of claim 1, wherein the polycationic material comprises a polycation.

9. The multilayer film of claim 8, wherein the polypeptide comprises polyelectrolyte, poly(aminostyrene), poly(aminocarboxylate), poly(N-methyl aminoacrylate), poly(N,N-dimethyl aminoacrylate), poly(N,N-diethyl aminoacrylate), poly(N,N-dimethylaminoacrylate), poly(N,N,N-trimethylammonium chloride), poly(N,N,N,N-tetramethylammonium chloride), chitosan and combinations comprising one or more of the foregoing polycationic materials.

10. The multilayer film of claim 1, wherein the polycationic material comprises a nucleic acid, alginate, carrageenan, furcellaran, pectin, xanthan, hyaluronic acid, heparin, heparan sulfate, chondroitin sulfate, dermatan sulfate, dextran sulfate, poly(meth)acrylic acid, oxidized cellulose, carboxymethyl cellulose, acidic polysaccharides, and crossmethylcellulose, and combinations comprising one or more of the foregoing polyanionic materials.

11. The multilayer film of claim 1, wherein the film is in the form of a microcapsule.

12. The multilayer film of claim 11, wherein the microcapsule comprises a core, and the core comprises a protein, a drug, or a combination thereof.

13. The multilayer film of claim 12, wherein the protein or drug is in crystallized form.

14. The multilayer film of claim 12, wherein the protein or drug is in liquid form.

15. The multilayer film of claim 1, comprising at least 4 pairs of alternately charged layers.

16. The multilayer film of claim 1, having a thickness of 1 nm to 100 nm.

17. The multilayer film of claim 1, wherein the film is formed on a substrate.

18. The multilayer film of claim 17, wherein the substrate comprises a medical device.

19. The multilayer film of claim 1, wherein the polypeptide comprises at least one amino acid sequence motif that is present in the human proteome.

20. The multilayer film of claim 1, wherein the composite polypeptide comprises at least one amino acid sequence motif that is present in the human proteome.

21. The multilayer film of claim 1, wherein the second layer polyelectrolyte comprises a second layer polypeptide, wherein the second layer polypeptide is not a homopolymer, is at least 15 amino acids long, and has a magnitude of net charge per residue at neutral pH of greater than or equal to 0.4.

22. The multilayer film of claim 1, wherein the one or more functional regions comprise a cysteine-containing sequence, a sequence for extracellular matrix recognition, a phosphotyrosine binding domain, a Src homology 2 domain, an O-linked glycosylation substrate sequence, a protease recognition site, or an antimicrobial peptide sequence.