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(54) **BIOFUNCTIONAL COATINGS**

(75) Inventors: **Paul T. Hamilton**, Cary, NC (US);
Mark W. Grinstaff, Brookline, MA (US); **Daniel J. Kenan**, Chapel Hill, NC (US); **Dale J. Christensen**, Cary, NC (US)

Correspondence Address:
PASSE' INTELLECTUAL PROPERTY, LLC
1717 BRASSFIELD RD.
RALEIGH, NC 27614 (US)

(73) Assignee: **Affinergy, Inc.**, Research Triangle Park, NC

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(57) **ABSTRACT**

The present invention provides compositions and methods for an improved coating for medical devices. The coating is an interfacial biomaterial ("IFBM") which comprises at least one binding module that binds to the surface of a device ("surface-binding module") and at least one binding module that performs another function ("affector module") and which acts to inhibit biofilm formation.

BIOFUNCTIONAL COATINGS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 60/580,019, filed Jun. 16, 2004; U.S. Provisional Application No. 60/651,338, filed Feb. 9, 2005; and U.S. Provisional Application No. 60/651,747, filed Feb. 10, 2005, each of which is hereby incorporated by reference herein.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

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FIELD OF THE INVENTION

[0003] The present invention provides materials and methods for coating surfaces with a coating that reduces adsorption by, and/or biochemically interacts with, biological cells, viruses and/or macromolecules. Generally, the present invention finds use in providing improved medical implants, catheters, and similar items.

BACKGROUND OF THE INVENTION

[0004] The fouling of polymer surfaces by biological materials is a common problem that can compromise safety and hygiene as well as appearance. Often the fouling involves formation of a "biofilm." Particularly serious problems result when fouling occurs in the context of medicine or medical care. In the context of medical care, for example, every year over 5 million patients in United States hospitals are implanted with a "central line catheter." In these catheterizations, a polyurethane or polyvinylchloride hose is implanted into the patient's chest while the other end of the hose remains exposed to the hospital room environment and therefore to a variety of pathogens, including drug-resistant pathogens (McGee & Gould (2003) *N. Engl. J. Med.* 348: 1123-1133). Frequently, this catheterization results in the life-threatening complication of system-wide infection of the blood. Research suggests that up to 90% of such cases originate in films of bacteria that adhere to catheter walls (Donlan (2001) *Emerg. Infect. Dis.* 7: 277-281).

[0005] Pathogenic bacterial biofilms form on both outer and inner walls of catheters and may be detected on catheter surfaces within twenty four hours of catheter insertion. Bacteria in these biofilms are thickly embedded in a mostly polysaccharide substance known simply as "matrix" which protects the bacteria from administered antibiotics as well as the immune system. These biofilms also provide an environment in which bacteria can exchange drug-resistance genes. The selective pressures on bacteria in these environments give rise to bacteria which are resistant not only to commonly-used antibiotics but also to drugs which are treatments of "last resort."

[0006] Other types of catheters that are frequently used include urinary catheters, which are typically used with incontinent elderly patients and are typically made of sili-

cone and latex. Unfortunately, virtually all patients who have urinary catheters in place for 28 days or more develop urinary tract infections (Donlan (2001) *Emerg. Infect. Dis.* 7: 277-281). Nearly all hospital-acquired systemic infections that are not associated with central line catheters are associated with urinary catheters (Maki & Tambyah (2001) *Emerg. Infect. Dis.* 7: 342-347). Treatment of urinary catheter-associated infections alone costs an estimated \$1.8 billion annually (Platt et al. (1982) *N. Engl. J. Med.* 307: 637-642).

[0007] Polymer surfaces can also be "fouled" and their usefulness negated by the adherence of non-bacterial cells and/or protein. For example, receptacles that are used for collecting and storing blood for use in transfusion can be "fouled" and destroy the blood stored in them unless they deter the natural tendency of various blood components to clot and to adhere to surfaces. Similarly, receptacles that are used for storing proteins of interest are often made from synthetic polymers such as, for example, plastic tubes, syringes, etc. Once proteins begin to adhere to a receptacle wall, the process often continues until no protein remains in solution. Thus, these receptacles should ideally prevent adhesion of the proteins to the receptacle surface in order to preserve the quality of the proteins stored in them.

[0008] Similar problems currently exist with orthopedic implants. The long-term effectiveness of an implanted medical device is extremely dependent upon the appropriate integration of the implant with the patient's tissues. Nowhere is this more true than in the field of orthopedics, particularly for procedures such as total knee arthroplasty and total hip arthroplasty. According to the National Center for Health Statistics, currently there are over 150,000 new hip replacements and 300,000 knee replacements performed in the U.S. each year. These numbers are expected to continue to increase as the baby boom generation ages. With orthopedic implants, failure usually results in surgical removal of the faulty implant and replacement with a new implant, a process known as revision. The revision rate for total joint replacements remains a significant burden to the health care economies of Western countries and varies between 10-20% depending upon the country. See, e.g., Malchau et al. (2002) "Prognosis of total hip replacement: Update of results and risk-ratio analysis for revision and re-revision from the Swedish National Hip Arthroplasty Registry, 1979-2000," 69th Annual Meeting of the American Academy of Orthopaedic Surgeons, Scientific Exhibition; Fitzpatrick et al. (1998) *Health Technol. Assess.* 2: 1-64; Mahomed et al. (2003) *J. Bone Joint Surg. Am.* 85-A: 27-32).

[0009] In the United States, Medicare data for patients aged 65 years and older suggests that revision procedures occur at a yearly rate of about 18% relative to the number of primary surgeries (Mahomed et al. (2003) *J. Bone Joint Surg. Am.* 85-A: 27-32). Main causes of implant failure include host inflammation responses and infection due to the formation of bacterial biofilms on the surface of the implants. This has led to an increase in the failure of orthopedic implants. In a study by Charnley and Cupic ((1973) *Clin. Orthop.* 95: 9-25), it was reported that 4-6% of total hip arthroplasty revision surgeries were due to infection, typically as a result of the formation of bacterial biofilms on the surface of the implants. Once present, these infections are extremely difficult to treat and may lead to removal and

replacement of the implant, amputation, or even death. In contrast, the same study revealed that only 1-2% of the revision surgeries were performed due to mechanical loosening of the implant. With the use of prophylactic antimicrobial agents and improved operating room techniques, the rates of deep infection in total hip arthroplasty has dropped to approximately 1% over the last 20 years (Tang et al. (2003) *J. Arthroplasty* 18: 714-718; Gaine et al. (2000) *J. Bone Joint Surg. Br.* 82: 561-565; An and Friedman (1998) *J. Invest. Surg.* 11: 139-146). However, with over 450,000 new hip and knee arthroplasty surgeries each year, infections may affect 4000 to 5000 patients.

[0010] Furthermore, studies have shown that infections are very common at the site of pin insertion (Parameswaran et al. (2003) *J. Orthop. Trauma* 17: 503-507), and infection associated with external fixators may be as high as 85% (Sims and Saleh (1996) *Prof. Nurse* 11: 261-264). Because metal pins and wires are being used more often in the treatment of orthopedic trauma, primarily for external fixation of bone fractures (Davis (2003) *Nurs. Times.* 99: 46-48), any device improvements that decreased the rate of infections from joint prostheses or other metallic implants could have a significant impact on the quality of orthopedic healthcare.

[0011] The biofilm "life cycle" from the adhesion of bacteria to a surface to the maturation of a biofilm and subsequent release of cells has been the focus of many recent basic research studies. Using a variety of molecular genetic techniques, genes required for biofilm formation and maturation have been identified in a broad range of Gram-positive and Gram-negative microbes. While similar themes have been elucidated among microbes in terms of biofilm development (i.e., a role for surface adhesion and quorum sensing), no universal "biofilm genes" have yet been identified that are conserved among the many opportunistic pathogens.

[0012] Biofilm formation is-regulated via the exchange of chemical signals between cells in a process called quorum sensing. *Staphylococci* bacteria, which are a common cause of nosocomial infections related to biofilm formation on implanted catheters, use two peptide-based quorum sensing systems. The first system is composed of the autoinducer RNA-III activating protein (RAP) and its target receptor TRAP (target of RNA-III activating protein). When the concentration of RAP reaches a threshold concentration, it induces the phosphorylation of TRAP, which in turn leads to increased cell adhesion and the activation of the second quorum sensing system, agr. The agr system controls toxin production (Balaban et al. (2001) *J Biol Chem* 276: 2658-67). *S. aureus* virulence can be inhibited by the heptapeptide YSPWTNF, which is called RIP (RNA-III inhibiting peptide). RIP is a competitive inhibitor of RAP binding to TRAP, and thus inhibits TRAP phosphorylation, leading to reduced expression of the agr system, which leads in turn to suppression of the virulence phenotype (Gov et al. (2001) *Peptides* 22: 1609-1620; Vieira-da-Motta et al. (2001) *Peptides* 22: 1621-1627). Among Gram-negative bacteria, quorum sensing is accomplished using N-acyl-homoserine lactone signaling molecules (AHLs), LuxI-type signal synthetases and LuxR-type signal receptors. The AHL-dependent sensing system mediates the regulation of a number of genes, including those involved in biofilm for-

mation and production of virulence factors (Eberl (1999) *Syst. Appl. Microbiol.* 22(4): 493-506).

[0013] While research into the use of quorum sensing antagonists as a means of controlling biofilm formation appears promising, it has not yet been reduced to practice (Ehrlich (2004) *ASM News* 70(3): 127-133). Efforts to reduce the incidence of infection due to biofilms on medical devices, including implants and catheters, have focused on two approaches. The first is the development of antibacterial compounds that retain efficacy on bacteria in biofilms (Shih and Huang (2002) *J. Antimicrob. Chemother.* 49: 309-314). Unfortunately, it is not yet understood how bacteria within a biofilm become resistant to antibiotics, which makes development of antibiotics with efficacy for treatment of biofilms virtually unattainable. Due to the difficulties of this approach, the main strategy that has been used to combat this problem is to modify the surface or composition of the article to prevent biofilm formation.

[0014] Surface modification technologies that have been tested for use with medical devices include diffusion, laser and plasma processing, chemical grafting, and bombardment with high-energy particles. These treatments have traditionally been used to alter the physical or mechanical properties of materials but are not proving to be effective in reducing infection rates (Katz (1997) *Medical Device & Diagnostic Industry Magazine*, April 1997). More recently, new treatments designed to reduce infection rates have been investigated, including hydrogel encapsulation and impregnation of the catheter or other article surface with antimicrobial agents (Raad and Hanna (1999) *Support. Care Cancer* 7: 386-390; DiTizio et al. (1998) *Biomaterials* 19: 1877-1884; Maki et al. (1997) *Ann. Intern. Med.* 127: 257-266). This approach seeks to kill the bacteria prior to, or shortly after, adhesion to the surface of the article. Representative examples of patents involving articles that have been coated or impregnated with anti-microbial drugs include U.S. Pat. No. 5,520,664 ("Catheter Having a Long-Lasting Antimicrobial Surface Treatment"), U.S. Pat. No. 5,709,672 ("Silastic and Polymer-Based Catheters with Improved Antimicrobial/Antifungal Properties"), U.S. Pat. No. 6,361,526 ("Antimicrobial Tympanostomy Tubes"), U.S. Pat. No. 6,261,271 ("Anti-infective and antithrombotic medical articles and method for their preparation"), U.S. Pat. No. 5,902,283 ("Antimicrobial impregnated catheters and other medical implants") U.S. Pat. No. 5,624,704 ("Antimicrobial impregnated catheters and other medical implants and method for impregnating catheters and other medical implants with an antimicrobial agent") and U.S. Pat. No. 5,709,672 ("Silastic and Polymer-Based Catheters with Improved Antimicrobial/Antifungal Properties").

[0015] Some recent studies and review articles have suggested that impregnating catheters with antibiotics may help prevent colonization by killing organisms when they come in close proximity to the surface, before they can establish a biofilm. There are, however, several other limitations to that approach. For example, although chlorhexidine-impregnated catheters showed limited efficacy in preventing infections, they are also believed to cause hypersensitivity reactions (Knight et al. (2001) *Intern. Med. J.* 31: 436-437). Furthermore, impregnating catheters with antibiotics may be counter-productive because as the concentration of antibiotics released from the catheter inevitably falls, bacteria are exposed to sublethal levels of antibiotics, a condition that

promotes the development of antibiotic resistance (Rachid et al. (2000) *J. Bacteriol.* 182: 6824-6826; Rachid et al. (2000) *Antimicrob. Agents Chemother.* 44: 3357-3363; Rupp and Hamer (1998) *J. Antimicrob. Chemother.* 41: 155-161). Moreover, several studies have demonstrated that sublethal levels of antibiotics actually stimulate biofilm formation by *Staphylococcus* strains, one of the key organisms involved in implant infections.

[0016] Another alternative for preventing biofilm formation is the development of a coating that prevents adherence of bacterial cells to the catheter surface. Such coatings could be used alone or in combination with antibacterial impregnation of the catheter to further prevent biofilm formation. The most commonly used coatings to prevent biological fouling on surfaces include those generated using plasma treatment, biotin-avidin conjugation strategies, phospholipids, self-assembled monolayers on transition metal coatings, and chemically grafted poly(ethylene glycol) (Kingshott et al. (1999) *Anal. Biochem.* 273(2): 156-62; Ratner (1993) *J. Biomed. Mater. Res.* 27: 837-50).

[0017] Of these approaches, coating a surface with poly(ethylene glycol) has met with some success for preventing cell and protein adhesion (Dalsin et al. (2003) *J. Am. Chem. Soc.* 125(14): 4253-8). However, chemically grafting this macromolecule to a surface often requires special preparation of the surface and multi-step chemical procedures (Golander et al. (1992) *J. Biomater. Sci. Polym. Ed.* 4(1): 25-30). Investigators who have derivatized a percentage of PLL side chains with poly(ethylene glycol) ("PEG") report both that the polymer so modified retains affinity for surfaces and that surfaces coated with it inhibit adhesion by proteins (Tosatti et al. (2003) *Biomaterials* 24: 4949; Huang et al. (2001) *Langmuir* 17(2): 489) as well as bacteria (Harris et al. (2004) *Biomaterials* 25: 4135; Wagner et al. (2004) *Biomaterials* 25: 2247). In addition, Hubbell et al. have described a method to suppress the interaction, adsorption or attachment of proteins or cells to a biomaterial surface through a polymer coating comprised of a polyionic backbone with poly(ethylene glycol) (PEG) or poly(ethylene oxide) (PEO) side chains (U.S. Patent Application No. 20020128234). Still another non-covalent means of associating PEG with metal surfaces includes linkage to mussel adhesive protein (Dalsin et al. (2003) *J. Am. Chem. Soc.* 125: 4253-8). For negatively charged metal oxides (TiO_2 , Ta_2O_5 , Nb_2O_5 , SiO_2), an alternative method for coating the surface is the use of polycationic polymers such as poly-L-lysine. This type of polymer spontaneously adsorbs to metal oxides based on the interaction of the positively charged amino groups on the polymer with the negatively charged metal oxide surface (Huang et al. (2001) *Langmuir* 17(2): 489). Unfortunately, these current methods of coating surfaces also often require special preparation of the surface and multi-step chemical procedures.

[0018] Another disadvantage of current methods to coat medical device surfaces is that, in general, the conditions necessary for attachment of the coating threaten to modify the relatively labile chemical groups or macromolecular folds that are typical of bioactive agents such as antimicrobial compounds. The extra steps and costs necessary to preserve the function of bioactive agents in a surface coating often render the project cost-prohibitive. In principle, each new material and each new agent that is identified for use as a coating presents a different chemical engineering chal-

lenge that will require an unknown investment of time, money, personnel and infrastructure in order to obtain a final product.

[0019] Thus, existing methods to modify medical devices to prevent protein adsorption, cell adhesion, or biofilm formation suffer from various shortcomings: surface modification is often unreliable, incomplete, and requires specialized equipment; impregnating with traditional antibiotics can lead to increases in antibiotic resistance among bacteria and is often ineffective against bacteria in biofilms; and many of the surface coatings require multiple steps and are prohibitively expensive. Thus, the need remains in the art for a stable coating that can be applied simply, quickly, and in a cost-effective manner to the surface of a medical device.

SUMMARY OF THE INVENTION

[0020] The present invention provides materials and compositions for an improved coating for surfaces of medical devices, including implants and catheters. The coating is an interfacial biomaterial ("IFBM") which comprises at least one binding module that specifically binds to a surface ("surface-binding module") and at least one binding module that performs another function ("affector module"). The affector module can: inhibit binding to the polymer surface by an organism, cell, or protein ("adhesion-resistance module"); modify the behavior of cells and/or organisms which bind to it ("behavior modification module"); and/or bind to a moiety which is a compound or molecule of interest ("moiety-binding module"). The modules are connected by a linker. In some embodiments, the affector module inhibits biofilm formation. The compositions and methods of the invention improve the performance of medical devices, for example, by preventing unwanted adsorption and/or growth of bacterial cells on the surface of the device.

DETAILED DESCRIPTION OF THE INVENTION

[0021] The present invention provides compositions for an improved coating for medical devices and methods of coating medical devices using those compositions. The term "medical device" as used herein refers to any article used as an implant in the body of a patient (including both human and non-human patients), any article used as a conduit (e.g., a catheter) related to medical treatment or for biological materials, or any container used as a storage device for biological materials, for example, for proteins or solutions containing cells. Medical devices may be made of any material, including metal and/or polymers. The coating of the invention is an interfacial biomaterial ("IFBM") which comprises at least one binding module that specifically binds to a surface of a medical device ("surface-binding module") and at least one binding module that performs another function ("affector module"). The binding modules are connected by a linker. The affector module acts to inhibit formation of a biofilm by any suitable mechanism. For example, the affector module may inhibit formation of a biofilm by inhibiting binding of an organism, cell, or compound (e.g., a protein) to the surface of the medical device ("adhesion-resistance module"). Alternatively, the affector module inhibits formation of a biofilm by modifying the behavior of cells and/or organisms which come into contact with it or bind to it ("behavior modification module"); and/or it may function to specifically bind to a moiety which

is a compound or molecule of interest (“moiety-binding module”). Any effector module is suitable for use in an IFBM of the invention so long as an IFBM comprising it acts to inhibit formation of a biofilm. Effector modules may have more than one function; thus, for example, a single effector module may have both adhesion-resistance function and behavior modification function. Any effector module may be used in an IFBM of the invention so long as it accomplishes the objective of the invention to inhibit biofilm formation. In some embodiments, at least one binding module (i.e., surface-binding module or effector module) is a peptide or comprises a peptide. Exemplary binding modules are set forth in SEQ ID NOs: 1-10, 39-43, 95-96, and 97-558.

[0022] The compositions and methods of the invention improve the performance of medical devices including those made from polymeric materials. The term “polymer” or “polymeric material” as used herein refers to any of numerous natural and synthetic compounds of usually high molecular weight consisting of up to millions of repeated linked units, each a relatively simple molecule. Generally, wherever the surface of a medical device is to interface with biochemical solutions or biological tissue, such a surface is susceptible to microbial growth, attachment, and biofilm formation. In medical devices that are inserted into a patient’s body, said microbial organisms include non-pathogenic microbes that are ordinarily present in non-sterile areas as well as pathogenic microbes that are present as a result of extant disease or due to accidental introduction during the insertion of the device. The IFBM coatings of the invention are useful for improving the performance of medical devices such as, for example, implants, catheters, and endotracheal tubes. In some embodiments, these coatings prevent unwanted adsorption of and/or growth of bacterial cells to the surface of the device.

[0023] The surface-binding module of the IFBM of the invention is selected to specifically bind to the material of which the surface of the medical device is made. Typically, this binding is non-covalent. The effector module of the IFBM of the invention is chosen so as to confer to an IFBM-coated surface a desired property such as, for example, resistance to adhesion of bacteria. The IFBMs of the invention comprise at least one surface-binding module and at least one effector module which are connected by a linker. A linker may be chosen for particular properties, such as a specific susceptibility to modification and/or to allow effector modules flexibility of orientation at a distance from the binding modules so linked. In some embodiments, the linker itself may also have activities similar to those of the binding module or effector module; that is, the linker may act to enhance binding to a particular surface or to have anti-adhesive properties such as inhibiting cell attachment, etc. For example, an IFBM comprising a poly (ethylene glycol) (“PEG”) linker to join the surface-binding module to the effector module may help to prevent non-specific protein and/or cell adherence to the surface of the medical device coated with that IFBM.

[0024] In some embodiments, the effector module inhibits biofilm formation. In some embodiments, an effector module inhibits biofilm formation due to its anti-adhesive properties; that is, the effector module is a molecule or moiety that does not bind to biomolecules and/or biomolecular constituents of cells. In some embodiments, an effector module inhibits biofilm formation by damaging cells so that

they do not adhere to the surface or by affecting a regulatory mechanism of cells that is involved in biofilm formation. Any combination of effector modules may be linked to any combination of surface-binding modules to create an IFBM of the invention so long as the IFBM comprises at least one effector module and at least one surface-binding module.

[0025] A surface-binding module is a peptide that binds to the surface of a medical device. A surface-binding module may bind to any material which is used to make a medical device, including a metal, a metal oxide, a non-metal oxide, a ceramic, a polymer, such as, for example, a synthetic polymer such as a polyurethane, a rubber, a plastic, an acrylic, a silicone, and combinations thereof. Suitable materials are known in the art. Binding modules (i.e., surface-binding modules and/or effector modules) can be peptides, antibodies or antibody fragments, polynucleotides, oligonucleotides, complexes comprising any of these, or various molecules and/or compounds. Binding modules which are peptides may comprise sequences disclosed in this application or known in the art, such as the peptides described in pending U.S. patent application Ser. No. 10/300,694, filed Nov. 20, 2002 and published on Oct. 2, 2003 as publication number 20030185870. Binding modules can also be identified using the methods described in pending U.S. patent application Ser. No. 10/300,694 and/or other methods known in the art. In some embodiments, binding modules may be identified by screening phage display libraries for affinity to materials such as titanium, stainless steel, cobalt-chrome alloy, polyurethane, polyethylene, acrylic, latex or silicone. Exemplary binding modules which are peptides which exhibit specific binding to particular materials are set forth in SEQ ID NOs: 1-10 (showing specific binding to titanium), 39-43 (showing specific binding to stainless steel), 95-96 (showing specific binding to Teflon), and 97-558. By “binds specifically” or “specific binding” is intended that a binding module binds to a selected surface, material, or composition. In some embodiments, a binding module that binds specifically to a particular surface, material or composition binds at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500%, or a higher percentage more than the binding module binds to an appropriate control such as, for example, a different material or surface, or a protein typically used for such comparisons such as bovine serum albumin.

[0026] The term “antibody” as used herein with reference to a binding module encompasses single chain antibodies. Thus, an antibody useful as a binding module may be a single chain variable fragment antibody (scFv). A single chain antibody is an antibody comprising a variable heavy and a variable light chain that are joined together, either directly or via a peptide linker, to form a continuous polypeptide. The term “single chain antibody” as used herein encompasses an immunoglobulin protein or a functional portion thereof, including but not limited to a monoclonal antibody, a chimeric antibody, a hybrid antibody, a mutagenized antibody, a humanized antibody, and antibody fragments that comprise an antigen binding site (e.g., Fab and Fv antibody fragments).

[0027] In some embodiments, the IFBM comprises an effector module that is an anti-adhesive or that binds to a protein which is an anti-adhesive. In such embodiments, the surface-binding module of the IFBM binds to the surface of the device and the anti-adhesive forms a dense structure that

prevents the adsorption of biological cells, viruses and macromolecules onto that surface. Suitable anti-adhesives are “non-interactive” polymer and/or functional groups that resist adhesion to protein and/or to cells. The term “non-interactive” as used herein with regard to coating polymer articles means a polymer that reduces the amount of non-specific adsorption of molecules to a coated surface, such as, for example, inorganic ions, peptides, proteins, saccharides and cells such as mammalian cells, bacteria and fungi. In embodiments using non-interactive polymers, an IFBM may comprise an effector module which is a non-interactive polymer or an IFBM may comprise an effector module which binds to a non-interactive polymer. Suitable non-interactive polymers which have adhesion-resistant function are known in the art and include, for example: albumin, poly(ethylene glycol) (PEG) (see, e.g., Wagner et al. (2004) *Biomaterials* 25: 2247-2263; Harris et al. (2004) *Biomaterials* 25: 4135-4148); mixed polyalkylene oxides having a solubility of at least one gram/liter in aqueous solutions such as some poloxamer nonionic surfactants; neutral water-soluble polysaccharides; poly(vinyl alcohol); poly(N-vinyl pyrrolidone); non-cationic polymethacrylates such as poly(methacrylic acid); many neutral polysaccharides, including dextran, Ficoll™, and derivatized celluloses; non-cationic polyacrylates such as poly(acrylic acid); and esters, amides, and hydroxylalkyl amides thereof, and combinations thereof. For example, an IFBM can comprise an effector module that binds human serum albumin, a native protein present in the blood of people and animals which is known to reduce bacterial adherence to coated surfaces (see, e.g., Keogh and Eaton (1994) *J. Lab. Clin. Med.* 124: 537-545; U.S. Pat. No. 5,073,171; Sato et al. (2002) *Biotechnol. Prog.* 18: 182-192). IFBMs comprising an effector module which has affinity for albumin can be coated onto polymer surfaces such as catheters or containers for blood, serum or other tissue, or solutions containing bacteria; albumin present in physiological solutions will then bind to the effector module, effectively providing a coating of albumin to the polymer surface, e.g., of the catheter or container.

[0028] In other embodiments, the IFBM comprises an effector module that has anti-microbial activity. For example, the effector module can be a peptide which has anti-microbial activity such as, for example, cationic anti-microbial peptides such as a magainin, defensin, bacteriocin, or microcin, all of which are known in the art (see, e.g., Lin et al. (2001) *Medical Device Technology*, October 2001 issue; Zasloff (2002) *Nature* 415: 389-395). Lactoferrin is also known to inhibit biofilm formation and is therefore useful as an effector module. While the invention is not limited to a particular mechanism of action of biofilm inhibition, the mechanism of action for many anti-microbial peptides is through disruption of the integrity of the bacterial membrane; most of these peptides do not affect the membranes of plant or animal cells. Because this disruption is mechanical in nature, it is unlikely that bacteria would develop resistance to these peptides (Zasloff (2002) *Nature* 415: 389-395).

[0029] In other embodiments, an effector module has biofilm inhibitor activity due to its interference with a regulatory mechanism of cells that is involved in their establishment of or participation in a biofilm. Suitable biofilm inhibitors for use as an effector module include compounds that are known in the art to interfere with bacterial quorum sensing such as RNA III inhibiting peptide

(RIP), RIP analogs, antagonists of TRAP (Target for RNA III Activating Peptide), antagonists of N-acyl-homoserine lactone-based signaling, and furanone analogs.

[0030] The IFBMs of the invention can be coated onto a medical device and implanted into the body. The linkers used in such IFBMs can be, for example, a PEG linker which joins the binding module to the effector module and also may prevent non-specific protein and/or cell adherence to the surface of the medical device. When the IFBM-coated medical device is implanted in a patient, the effector module which has affinity for albumin will bind endogenous serum albumin, thereby specifically coating the surface of the medical device with albumin. A medical device coated with such IFBMs may also be coated with albumin by contacting the device with albumin-containing solutions *in vitro* prior to implantation of the device in a patient (see, e.g., Wagner et al. (2004) *Biomaterials* 25: 2247-2263; Harris et al. (2004) *Biomaterials* 25: 4135-4148).

[0031] Phage display technology is well-known in the art and can be used to identify additional peptides for use as binding modules in IFBMs of the invention. Using phage display, a library of diverse peptides can be presented to a target substrate, and peptides that specifically bind to the substrate can be selected for use as binding modules. Multiple serial rounds of selection, called “panning,” may be used. As is known in the art, any one of a variety of libraries and panning methods can be employed to identify a binding module that is useful in the methods of the invention. For example, libraries of antibodies or antibody fragments may be used to identify antibodies or fragments that bind to particular cell populations or to viruses (see, e.g., U.S. Pat. Nos. 6,174,708, 6,057,098, 5,922,254, 5,840,479, 5,780, 225, 5,702,892, and 5,667,988). Panning methods can include, for example, solution phase screening, solid phase screening, or cell-based screening. Once a candidate binding module is identified, directed or random mutagenesis of the sequence may be used to optimize the binding properties of the binding module. The terms “bacteriophage” and “phage” are synonymous and are used herein interchangeably. The term “bacteriophage” is defined as a bacterial virus containing a nucleic acid core and a protective shell built up by the aggregation of a number of different protein molecules.

[0032] A library can comprise a random collection of molecules. Alternatively, a library can comprise a collection of molecules having a bias for a particular sequence, structure, or conformation. See, e.g., U.S. Pat. Nos. 5,264,563 and 5,824,483. Methods for preparing libraries containing diverse populations of various types of molecules are known in the art, and numerous libraries are also commercially available. Methods for preparing phage libraries can be found, for example, in Kay et al. (1996) *Phage Display of Peptides and Proteins* (San Diego, Academic Press); Barbas (2001) *Phage Display: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

[0033] A binding module that is a peptide comprises about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 50, 60, 70, 80, 90, 100, 200, or up to 300 amino acids. Exemplary binding modules that are peptides are set forth in SEQ ID NOs: 1-10, 39-43, and 95-558. Peptides that are useful as binding modules in IFBMs of the invention may differ from these exemplary peptides so long

as the desired property of the binding module is retained. Peptides useful as a binding module can be linear, branched, or cyclic, and can include non-peptidyl moieties. The term "peptide" broadly refers to an amino acid chain that includes naturally occurring amino acids, synthetic amino acids, genetically encoded amino acids, non-genetically encoded amino acids, and combinations thereof. Peptides can include both L-form and D-form amino acids. A peptide of the present invention can be subject to various changes, substitutions, insertions, and deletions where such changes provide for certain advantages in its use. Thus, the term "peptide" encompasses any of a variety of forms of peptide derivatives including, for example, amides, conjugates with proteins, cyclone peptides, polymerized peptides, conservatively substituted variants, analogs, fragments, chemically modified peptides, and peptide mimetics. Any peptide that has desired binding characteristics can be used in the practice of the present invention.

[0034] Representative non-genetically encoded amino acids include but are not limited to 2-amino adipic acid; 3-amino adipic acid; β -aminopropionic acid; 2-aminobutyric acid; 4-aminobutyric acid (piperidinic acid); 6-aminocaproic acid; 2-aminoheptanoic acid; 2-aminoisobutyric acid; 3-aminoisobutyric acid; 2-aminopimelic acid; 2,4-diaminobutyric acid; desmosine; 2,2'-diaminopimelic acid; 2,3-diaminopropionic acid; N-ethylglycine; N-ethylasparagine; hydroxylysine; allo-hydroxylysine; 3-hydroxyproline; 4-hydroxyproline; isodesmosine; allo-isoleucine; N-methylglycine (sarcosine); N-methylisoleucine; N-methylvaline; norvaline; norleucine; and ornithine. Representative derivatized amino acids include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups can be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups can be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine can be derivatized to form N-im-benzylhistidine.

[0035] The term "conservatively substituted variant" refers to a peptide having an amino acid residue sequence substantially identical to a sequence of an exemplary peptide in which one or more residues have been conservatively substituted with a functionally similar residue such that the "conservatively substituted variant" will bind to the same binding partner with substantially the same affinity as the parental variant and will prevent binding of the parental variant. In one embodiment, a conservatively substituted variant displays a similar binding specificity when compared to the exemplary reference peptide. The phrase "conservatively substituted variant" also includes peptides wherein a residue is replaced with a chemically derivatized residue.

[0036] Examples of conservative substitutions include the substitution of one non-polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another; the substitution of one aromatic residue such as tryptophan, tyrosine, or phenylalanine for another; the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine; the substitution of one basic residue such as lysine, arginine or histidine for another; or the substitution of one acidic residue such as aspartic acid or glutamic acid for another.

[0037] Peptides which are useful as binding modules of the present invention also include peptides having one or more substitutions, additions and/or deletions of residues relative to the sequence of an exemplary peptide sequence as disclosed herein, so long as the binding properties of the original exemplary peptide are retained. Thus, binding modules of the invention include peptides that differ from the exemplary sequences disclosed herein by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids but that retain the ability of the corresponding exemplary sequence to bind to a particular material or to act as an effector module. A binding module of the invention that differs from an exemplary sequence disclosed herein will retain at least 25%, 50%, 75%, or 100% of the activity of a binding module comprising an entire exemplary sequence disclosed herein as measured using an appropriate assay. That is, binding modules of the invention include peptides that share sequence identity with the exemplary sequences disclosed herein of at least 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity. Sequence identity may be calculated manually or it may be calculated using a computer implementation of a mathematical algorithm, for example, GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package of Genetics Computer Group, Version 10 (available from Accelrys, 9685 Scranton Road, San Diego, Calif., 92121, USA). The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89: 10915). Alignments using these programs can be performed using the default parameters.

[0038] A peptide can be modified, for example, by terminal-NH₂ acylation (e.g., acetylation, or thioglycolic acid amidation) or by terminal-carboxylamidation (e.g., with ammonia or methylamine). Terminal modifications are useful to reduce susceptibility by proteinase digestion, and to therefore prolong a half-life of peptides in solutions, particularly in biological fluids where proteases can be present. Peptide cyclization is also a useful modification because of the stable structures formed by cyclization and in view of the biological activities observed for such cyclic peptides. Methods for cyclizing peptides are described, for example, by Schneider & Eberle (1993) *Peptides. 1992: Proceedings of the Twenty-Second European Peptide Symposium, Sep. 13-19, 1992, Interlaken, Switzerland*, Escom, Leiden, The Netherlands.

[0039] Optionally, a binding module peptide can comprise one or more amino acids that have been modified to contain one or more halogens, such as fluorine, bromine, or iodine, to facilitate linking to a linker molecule. As used herein, the term "peptide" also encompasses a peptide wherein one or more of the peptide bonds are replaced by pseudopeptide bonds including but not limited to a carba bond (CH₂—CH₂), a depsipeptide bond (CO—O), a hydroxyethylene bond (CHOH—CH₂), a ketomethylene bond (CO—CH₂), a methylene-oxo bond (CH₂—O), a reduced bond (CH₂—NH), a thiomethylene bond (CH₂—S), an N-modified bond (—NRCO—), and a thiopeptide bond (CS—NH). See e.g., Garbay-Jaureguiberry et al. (1992) *Int. J. Pept. Protein Res.* 39: 523-527; Tung et al. (1992) *Pept. Res.* 5: 115-118; Urge et al. (1992) *Carbohydr. Res.* 235: 83-93; Corringer et al. (1993) *J. Med. Chem.* 36: 166-172; Pavone et al. (1993) *Int. J. Pept. Protein Res.* 41: 15-20.

[0040] In some embodiments, IFBMs of the invention comprise binding modules which comprise peptides that specifically bind to materials used in medical implants, such as peptides having an amino acid sequence as set forth in SEQ ID NOS:1-10, 39-43, and 95-558. While these exemplary peptide sequences are disclosed herein, one of skill will appreciate that the binding properties conferred by those sequences may be attributable to only some of the amino acids comprised by the sequences. Thus, a peptide which comprises only a portion of an exemplary amino acid sequence disclosed herein may have substantially the same binding properties as a peptide comprising the full-length exemplary sequence; thus, also useful as binding modules in IFBMs of the present invention are peptides that comprise only 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 of the amino acids in a particular exemplary sequence provided herein. Such amino acids may be contiguous or non-contiguous so long as the desired property of the binding module is retained as determined by an appropriate assay. Such amino acids may be concentrated at the amino-terminal end of the exemplary peptide (for example, 4 amino acids may be concentrated in the first 4, 5, 6, 7, 8, 9, 10, 11, or 12 amino acids of the peptide) or they may be dispersed throughout the exemplary peptide.

[0041] Binding modules of the present invention that are peptides can be synthesized by any of the techniques that are known to those skilled in the art of peptide synthesis. Representative techniques can be found, for example, in Stewart & Young (1969) *Solid Phase Peptide Synthesis*, (Freeman, San Francisco, Calif.); Merrifield (1969) *Adv. Enzymol. Relat. Areas Mol. Biol.* 32:221-296; Fields & Noble (1990) *Int. J. Pept. Protein Res.* 35:161-214; and Bodanszky (1993) *Principles of Peptide Synthesis*, 2nd Rev. Ed. (Springer-Verlag, Berlin). Representative solid phase synthesis techniques can be found in Andersson et al. (2000) *Biopolymers* 55: 227-250, references cited therein, and in U.S. Pat. Nos. 6,015,561; 6,015,881; 6,031,071; and 4,244,946. Peptide synthesis in solution is described in Schröder & Lübke (1965) *The Peptides* (Academic Press, New York, N.Y.). Appropriate protective groups useful for peptide synthesis are described in the above texts and in McOmie (1973) *Protective Groups in Organic Chemistry* (Plenum Press, London). Peptides, including peptides comprising non-genetically encoded amino acids, can also be produced in a cell-free translation system, such as the system described by Shimizu et al. (2001) *Nat. Biotechnol.* 19: 751-755. In addition, peptides having a specified amino acid sequence can be purchased from commercial sources (e.g., Biopeptide Co., LLC of San Diego, Calif., and PeptidoGenics of Livermore, Calif.).

[0042] The linker that joins the binding module to at least one other module to form an IFBM can be any suitable linker. Linkers may be peptides or non-peptides. Suitable linkers are known in the art and can comprise, for example, a polymer, including a synthetic polymer or a natural polymer. In some embodiments, an IFBM is synthesized as a single continuous peptide comprising sequences originally identified as separate binding modules; in such embodiments, the linker is simply one of the bonds in the peptide. Representative synthetic polymers include but are not limited to polyethers (e.g., poly(ethylene glycol) ("PEG")), polyesters (e.g., polylactic acid (PLA) and polyglycolic acid (PGA)), polyamines, polyamides (e.g., nylon), polymethacrylates (e.g., polymethylmethacrylate; PMMA),

polyacrylic acids, polyurethanes, polystyrenes, flexible chelators such as EDTA, EGTA and other synthetic polymers having a molecular weight of about 200 daltons to about 1000 kilodaltons. Representative natural polymers include but are not limited to hyaluronic acid, alginate, chondroitin sulfate, fibrinogen, fibronectin, albumin, collagen, calmodulin EF-hand domains and other natural polymers having a molecular weight of about 200 daltons to about 20,000 kilodaltons. Polymeric linkers can comprise a diblock polymer, a multi-block copolymer, a comb polymer, a star polymer, a dendritic polymer, a hybrid linear-dendritic polymer, or a random copolymer. A linker can also comprise a mercapto(amido)carboxylic acid, an acrylamidocarboxylic acid, an acrylamido-amidotriethylene glycolic acid, and derivatives thereof. See, for example, U.S. Pat. No. 6,280,760. Linkers are known in the art and include linkers that can be cleaved and linkers that can be made reactive toward other molecular moieties or toward themselves, for cross-linking purposes. Fluorescent linkers are also known in the art.

[0043] Methods for linking a linker molecule to a ligand, binding module, or to a non-binding domain will vary according to the reactive groups present on each molecule. Protocols for linking using reactive groups and molecules are known to one of skill in the art. See, e.g., Goldman et al. (1997) *Cancer Res.* 57: 1447-1451; Cheng (1996) *Hum. Gene Therapy* 7: 275-282; Neri et al. (1997) *Nat. Biotechnol.* 19: 958-961; Nabel (1997) *Current Protocols in Human Genetics*, vol. on CD-ROM (John Wiley & Sons, New York); Park et al. (1997) *Adv. Pharmacol.* 40: 399-435; Pasqualini et al. (1997) *Nat. Biotechnol.* 15: 542-546; Bauminger & Wilchek (1980) *Meth. Enzymol.* 70: 151-159; U.S. Pat. Nos. 6,280,760 and 6,071,890; and European Patent Nos. 0 439 095 and 0 712 621.

[0044] The compositions and methods of the invention find particular use in coating any implantable or insertable medical device that is susceptible to microbial growth on and around the surfaces of the device. Implantable medical devices that can be improved with the compositions and methods of the invention include those adapted to remain implanted for a relatively long-term, i.e., for period of from about 30 days to about 12 months or greater, such as, for example, orthopedic implants. However, devices intended to remain implanted for about 30 days or less such as, for example, certain catheters, are also included within the scope of the present invention. "Medical device" as used herein refers to devices used in human patients as well as to devices used in non-human animals.

[0045] Examples of medical devices that are conduits and vessels made of polymers or that have polymeric surfaces include but are not limited to: medical conduits for insertion into a human or animal body, such as catheters and endotracheal tubes; vessels such as blood collection tubes, specimen containers and storage jars; vessels and conduits for the storage and transport of biochemical reagents in biomedical research or manufacturing; and tubing and containers for waste, water or combinations thereof. The polymer may be any suitable kind, including for example a synthetic polymer such as a plastic, rubber, a silicone material and combinations thereof. Suitable materials are known in the art and include polyurethane, polyethylene, polyvinylchloride, acrylic and latex. Examples of implantable medical devices include but are not limited to: prosthetic joints, plates,

screws, pins, nails, rivets, bone fixation implants and artificial ligaments and tendons. Medical devices may be made of any suitable material, including for example a synthetic polymer, a plastic, a metal (such as titanium, stainless steel, or cobalt-chrome alloy), a metal oxide, a non-metal oxide, a silicone material, a ceramic material, and combinations thereof. Suitable materials are known in the art and include polyurethane, polyethylene, and silicone.

[0046] Medical devices that are coated with IFBMs of the invention will exhibit at least one superior property in comparison to an appropriate control, such as a similar medical device that is not coated with at least one IFBM; for example, a medical device coated with IFBMs of the invention will exhibit reduced formation of bacterial biofilms or show resistance to adhesion of protein or cells. Thus, an IFBM is considered to act to inhibit formation of a biofilm if a surface coated with that IFBM exhibits a detectable decrease in the tendency for a biofilm to form on that surface when compared to a suitable control surface or if a surface coated with that IFBM shows a detectable increase in resistance to adhesion of protein or cells when compared to a suitable control surface. An IFBM also acts to inhibit formation of a biofilm if a surface coated with that IFBM becomes coated with a biofilm which exhibits a detectable reduction in any of the characteristics of a biofilm. That is, an IFBM acts to inhibit formation of a biofilm if it decreases the frequency of biofilm formation or if it reduces a characteristic of a biofilm or resists adhesion of protein or cells by at least 5%, 10%, 15%, 20%, 30%, 40%, 50%, 100% when a surface coated with that IFBM is compared to a surface that is uncoated or that is not coated with that IFBM. In this manner, a medical device which is coated with at least one IFBM has a superior property where that medical device has a measurable characteristic which differs in a statistically significant way from the same characteristic of an appropriate control medical device (such as, for example, a medical device that is not coated with at least one IFBM). Thus a property of a medical device which is coated with at least one IFBM will have a property which is superior to a property of an appropriate control medical device by at least

5%, 10%, 15%, 20%, 30%, 40%, 50%, 100%, or more. Such a property may result from the performance of the IFBM or of its component modules. One of skill in the art is familiar with techniques that can be used to compare the performance of coated and uncoated medical devices or materials. For example, such techniques are described in the American Society of Testing and Materials (ASTM) Standard Method E-2196-02, entitled "Standard Test Method for the Quantification of *Pseudomonas aeruginosa* Biofilm Grown with Shear and Continuous Flow using a Rotating Disk reactor" and E1427-OOel, entitled "Standard Guide for Selecting Test Methods to Determine the Effectiveness of Antimicrobial Agents and Other Chemicals for the Prevention, Inactivation and Removal of Biofilm." Thus, for example, a medical device which is coated with at least one IFBM will inhibit biofilm formation by at least 5% when compared to a comparable uncoated medical device.

[0047] A medical device that is coated with at least one IFBM is coated by any suitable method, for example, by dipping or spraying the IFBM onto the device. The coating may be stabilized, for example, by air drying or by lyophilization. However, these treatments are not exclusive, and other coating and stabilization methods may be employed; one of skill in the art will be able to select the compositions and methods used to fit the needs of the particular device and purpose.

[0048] All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[0049] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claim(s).

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<220> FEATURE:

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Ala Val Val Ser Arg
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Leu Ala Ala Ser Arg
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Gly Ala Gly Ser Arg
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<223> OTHER INFORMATION: isolated from phage display libraries
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Leu Ser Ser Ser Arg
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Arg

<210> SEQ ID NO 27
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<223> OTHER INFORMATION: Xaa can be any amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa at this position can be Ser, Thr, Ala, or Gly

<400> SEQUENCE: 27

Xaa Xaa Xaa Phe Xaa Xaa Leu
1 5

<210> SEQ ID NO 28
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides isolated from phage display libraries
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(1)
<223> OTHER INFORMATION: Xaa at this position can be Leu or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: Xaa can be any amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)...(6)
<223> OTHER INFORMATION: Xaa at this position can be Lys or Arg

<400> SEQUENCE: 28

Xaa Xaa Phe Pro Leu Xaa Gly
1 5

<210> SEQ ID NO 29
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 29

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

-continued

Arg Gly Ser Ser Gly Lys Asp Val Asn Ser Ile Trp Met Ser Arg Val
20 25 30

Ile Glu Trp Thr Tyr Asp Ser
35

<210> SEQ ID NO 30
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 30

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

Ser Gly Ser Ser Gly Lys Ser Ser Phe Glu Pro Leu Arg Phe Pro Leu
20 25 30

Lys Gly Val Pro Val Ser Arg
35

<210> SEQ ID NO 31
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 31

Ser Arg Ser Ser Asp Ser Ala Phe Ser Ser Phe Ser Ala Leu Glu Gly
1 5 10 15

Ser Val Val Ser Arg Gly Ser Ser Gly Lys Asp Val Asn Ser Ile Trp
20 25 30

Met Ser Arg Val Ile Glu Trp Thr Tyr Asp Ser
35 40

<210> SEQ ID NO 32
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 32

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

Ser Gly Ser Ser Gly Lys Ser Arg Ser Ser Asp Ser Ala Phe Ser Ser
20 25 30

Phe Ser Ala Leu Glu Gly Ser Val Val Ser Arg
35 40

<210> SEQ ID NO 33
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 33

Ser Ser Ser Val Asp Leu Tyr Phe Pro Leu Lys Gly Asp Val Val Ser
1 5 10 15

-continued

Arg Gly Ser Ser Gly Lys Asp Val Asn Ser Ile Trp Met Ser Arg Val
20 25 30

Ile Glu Trp Thr Tyr Asp Ser
35

<210> SEQ ID NO 34
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 34

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

Ser Gly Ser Ser Gly Lys Ser Ser Ser Val Asp Leu Tyr Phe Pro Leu
20 25 30

Lys Gly Asp Val Val Ser Arg
35

<210> SEQ ID NO 35
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 35

Ser Arg Gly Gly Glu Ala Ala Ala Gly Ala Trp Val Ser Phe Ser Ala
1 5 10 15

Leu Glu Ser Ser Arg Gly Ser Ser Gly Lys Asp Val Asn Ser Ile Trp
20 25 30

Met Ser Arg Val Ile Glu Trp Thr Tyr Asp Ser
35 40

<210> SEQ ID NO 36
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 36

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

Ser Gly Ser Ser Gly Lys Ser Arg Gly Gly Glu Ala Ala Ala Gly Ala
20 25 30

Trp Val Ser Phe Ser Ala Leu Glu Ser Ser Arg
35 40

<210> SEQ ID NO 37
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 37

Ser Ser Asp Trp Gly Val Val Ala Ser Ala Trp Asp Ala Phe Glu Ala
1 5 10 15

-continued

Leu Asp Ala Ser Arg Gly Ser Ser Gly Lys Asp Val Asn Ser Ile Trp
20 25 30

Met Ser Arg Val Ile Glu Trp Thr Tyr Asp Ser
35 40

<210> SEQ ID NO 38
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IFBM

<400> SEQUENCE: 38

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

Ser Gly Ser Ser Gly Lys Ser Ser Asp Trp Gly Val Val Ala Ser Ala
20 25 30

Trp Asp Ala Phe Glu Ala Leu Asp Ala Ser Arg
35 40

<210> SEQ ID NO 39
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 39

Ser Ser Ser Ser Tyr Phe Asn Leu Gly Leu Val Lys His Asn His Val
1 5 10 15

Arg His His Asp Ser Ser Arg
20

<210> SEQ ID NO 40
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 40

Ser Ser Cys His Asp His Ser Asn Lys Tyr Leu Lys Ser Trp Lys His
1 5 10 15

Gln Gln Asn Cys Ser Arg
20

<210> SEQ ID NO 41
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 41

Ser Ser Ser Cys Lys His Asp Ser Glu Phe Ile Lys Lys His Val His
1 5 10 15

Ala Val Lys Lys Cys Ser Arg
20

<210> SEQ ID NO 42

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<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 42

Ser Ser Ser Cys His His Leu Lys His Asn Thr His Lys Glu Ser Lys
1 5 10 15
Met His His Glu Cys Ser Arg
20

<210> SEQ ID NO 43
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 43

Ser Ser Val Asn Lys Met Asn Arg Leu Trp Glu Pro Leu Ser Arg
1 5 10 15

<210> SEQ ID NO 44
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 44

Ser Ser Ala Pro Leu Thr Glu Ser Glu Ala Trp Arg Gly Phe Ser Lys
1 5 10 15
Leu Glu Val Ser Arg
20

<210> SEQ ID NO 45
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 45

Ser Ser Ser Met Pro Val Gly Trp Asp Ser Trp Arg Gly Leu Glu Trp
1 5 10 15

Ser Asp Arg Ser Arg
20

<210> SEQ ID NO 46
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 46

Ser Ser Glu Gly Arg Gly Gly Trp Asn Ser Trp Glu Ala Phe Arg Glu
1 5 10 15
Leu Val Val Ser Arg
20

-continued

<210> SEQ ID NO 47
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 47

Ser Ser Gly Gly Gly Ala Trp Glu Ser Trp Arg Gly Leu Ser Gly
1 5 10 15

Val Glu Leu Ser Arg
20

<210> SEQ ID NO 48
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 48

Ser Arg Asn Val Glu Gly Ser Trp Glu Ser Phe Ala Gly Leu Ser His
1 5 10 15

Val Arg Glu Ser Arg
20

<210> SEQ ID NO 49
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 49

Ser Arg Glu Asp Gly Gly Arg Trp Glu Ser Phe Leu Gly Leu Ser Ala
1 5 10 15

Val Glu Val Ser Arg
20

<210> SEQ ID NO 50
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 50

Ser Ser Val Glu Gly Ser Ala Trp Ser Ala Phe Lys Ser Leu Ser Ser
1 5 10 15

Glu Gly Val Ser Arg
20

<210> SEQ ID NO 51
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 51

Ser Arg Val Glu Gly Gly Ala Trp Gln Ala Leu Ala Gly Leu Thr Val
1 5 10 15

-continued

Glu Arg Val Ser Arg
20

<210> SEQ ID NO 52
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 52

Ser Ser Pro Pro Lys His Ala Trp Gly Ser Phe Asp Ala Leu Gly Gly
1 5 10 15

Gln Val Val Ser Arg
20

<210> SEQ ID NO 53
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 53

Ser Ser Glu Arg Gly Val Gly Trp Glu Val Phe Leu Ala Met Glu Gly
1 5 10 15

Ala Arg Met Ser Arg
20

<210> SEQ ID NO 54
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 54

Ser Ser Ser Ser Ser Gly Thr Trp Gln Ala Phe Thr Gly Leu Ser Gly
1 5 10 15

Glu Arg Val Ser Arg
20

<210> SEQ ID NO 55
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 55

Ser Ser Ser Pro Gly Gly Ser Gly Gly Trp Asp Ala Phe Tyr Ser
1 5 10 15

Leu Val Gly Ser Arg
20

<210> SEQ ID NO 56
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 56

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Ser Ser Gly Gly Gly Gly Gly Glu Gly Phe Ser Ser Leu Ser Gly
1 5 10 15

Asn Gly Arg Ser Arg
20

<210> SEQ ID NO 57
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 57

Ser Ser Thr Gly Gly Ser Trp Glu Glu Phe Lys Ala Met Thr Pro
1 5 10 15

Ser Trp Thr Ser Arg
20

<210> SEQ ID NO 58
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 58

Ser Ser Glu Gly Ser Gly Leu Trp Asp Ser Phe Ser Ser Leu Ser Val
1 5 10 15

His Glu Val Ser Arg
20

<210> SEQ ID NO 59
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 59

Ser Ser Gly Val Thr Gln Glu Ser Ala Ser Trp Ser Ser Phe Arg Thr
1 5 10 15

Leu Ala Val Ser Arg
20

<210> SEQ ID NO 60
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 60

Ser Ser Ser Lys Val Ala Pro Ser Gly Glu Trp Arg Ser Phe Ala Thr
1 5 10 15

Leu Glu Val Ser Arg
20

<210> SEQ ID NO 61
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 61

Ser Ser Glu Ala Gly Arg Gly Trp Glu Gly Phe Lys Ala Leu Glu Gly
1 5 10 15

Tyr Gln Val Ser Arg
20

<210> SEQ ID NO 62
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 62

Ser Ser Leu Gly Gln Thr Gly Trp Glu Ala Phe Glu Ser Leu Ser Gly
1 5 10 15

Thr Arg Gly Ser Arg
20

<210> SEQ ID NO 63
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 63

Ser Ser Val Ala Trp Asp Ala Phe Thr Val Phe Glu Ser Leu Glu Gly
1 5 10 15

Val Ala Thr Ser Arg
20

<210> SEQ ID NO 64
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 64

Ser Ser Glu Val Val Glu Pro Trp Glu Trp Trp Val Ala Leu Glu Arg
1 5 10 15

Ala Gly Gly Ser Arg
20

<210> SEQ ID NO 65
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 65

Ser Arg Val Ala Ala Val Ser Trp Glu Phe Phe Gly Ser Leu Ser Ser
1 5 10 15

Ala Gly Val Ser Arg
20

-continued

<210> SEQ ID NO 66
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 66

Ser Ser Ala Asp Leu Gly Val Ser Gly Ser Trp Glu Gly Phe Ala Leu
1 5 10 15

Met Arg Gly Ser Arg
20

<210> SEQ ID NO 67
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 67

Ser Ser Val Gly Gln Met Gly Trp Glu Ala Phe Glu Ser Leu Ser Gly
1 5 10 15

Thr Gly Gly Ser Arg
20

<210> SEQ ID NO 68
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 68

Ser Ser Gly Gln Gly Glu Thr Trp Glu Trp Phe Ala Gly Met Arg Gly
1 5 10 15

Ser Val Ala Ser Arg
20

<210> SEQ ID NO 69
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 69

Ser Ser Tyr Phe Asp Val Phe Ser Ser Met Thr Gly Thr Arg Ala Ala
1 5 10 15

Gly Ser Trp Ser Arg
20

<210> SEQ ID NO 70
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 70

Ser Ser Ala Tyr Ser Val Phe Ser Ser Leu Arg Ala Asp Asn Ser Gly
1 5 10 15

-continued

Gly Ala Val Ser Arg
20

<210> SEQ ID NO 71
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 71

Ser Ser Gly Gly Ile Ala Ser Leu Lys Tyr Asp Val Val Lys Thr Trp
1 5 10 15

Glu Ser Arg

<210> SEQ ID NO 72
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries

<400> SEQUENCE: 72

Gly Gly Gly Ala Trp Glu Ala Phe Ser Ser Leu Ser Gly Ser Arg Val
1 5 10 15

<210> SEQ ID NO 73
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (0)...(0)
<223> OTHER INFORMATION: Xaa can be any amino acid

<400> SEQUENCE: 73

Trp Xaa Xaa Phe Xaa Xaa Leu
1 5

<210> SEQ ID NO 74
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries

<400> SEQUENCE: 74

Ser Ser Gly Ala Trp Glu Ser Phe Ser Ser Leu Ser Gly Ser Ser
1 5 10 15

<210> SEQ ID NO 75
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: encoding consensus sequence

<400> SEQUENCE: 75

tcgagtggtg cttggggagtcttttcgtca ctgagtggat

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<210> SEQ_ID NO 76
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: partial complement of SEQ_ID NO:75

<400> SEQUENCE: 76

caccacgaac cctcagaaaa agcagtgact cacctagatc 40

<210> SEQ_ID NO 77
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 77

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

Ala Trp Ala Ser Arg
20

<210> SEQ_ID NO 78
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (18)...(0)
<223> OTHER INFORMATION: Xaa can be any amino acid

<400> SEQUENCE: 78

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

Val Xaa Lys Ser Arg
20

<210> SEQ_ID NO 79
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries

<400> SEQUENCE: 79

Ser Ser Gly Gly Phe Val Pro Phe Pro Leu Arg Gly Glu Val Trp Asp
1 5 10 15

Gly Val His Ser Arg
20

<210> SEQ_ID NO 80
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 80

Ser Ser Glu Gly Ser Leu Ser Phe Pro Leu Lys Gly Gln Val Tyr Ser

-continued

1 5 10 15

Gly Trp Gly Ser Arg
20

<210> SEQ ID NO 81
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 81

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

Trp Pro Val Ser Arg
20

<210> SEQ ID NO 82
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 82

Ser Arg Gly Glu Ala Leu Gly Phe Pro Leu Thr Gly Gln Leu Met Glu
1 5 10 15

Ala Ala Glu Ser Arg
20

<210> SEQ ID NO 83
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 83

Ser Ser Met Trp Asp Val Gly Phe Pro Leu Lys Gly Arg Trp Ile Asp
1 5 10 15

Gly Ala Asp Ser Arg
20

<210> SEQ ID NO 84
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 84

Ser Ser Ser Asn Ser Leu Trp Phe Pro Leu Arg Gly Ser Thr Val Glu
1 5 10 15

Val Gly Ala Ser Arg
20

<210> SEQ ID NO 85
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 85
Ser Ser Gly Pro Ala Leu Arg Leu Pro Leu Arg Gly Thr Val Val Ser
1 5 10 15

Asp Val Pro Ser Arg
20

<210> SEQ ID NO 86
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 86
Ser Ser Ala Asp Arg Val Ala Trp Pro Leu Lys Gly Ala Pro Val Trp
1 5 10 15
Val Lys Glu Ser Arg
20

<210> SEQ ID NO 87
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 87
Ser Ser Gly Leu Ala Leu Gly Leu Pro Ile Lys Gly Trp Thr Val Ser
1 5 10 15
Gly Lys Asp Ser Arg
20

<210> SEQ ID NO 88
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 88
Ser Ser Gly Tyr Thr Leu Gly Phe Pro Leu Ser Gly Gln Thr Ile Lys
1 5 10 15
Asp Trp Pro Ser Arg
20

<210> SEQ ID NO 89
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 89
Ser Ser Glu Gly Trp Val His Phe Pro Leu Lys Gly Asp Val Met Gly
1 5 10 15
Gly Pro Phe Ser Arg
20

<210> SEQ ID NO 90
<211> LENGTH: 21

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 90

Ser Ser Gly Arg Tyr Val Ser Leu Pro Leu Lys Gly Glu Val Val Pro
1 5 10 15
Gln Thr Ala Ser Arg
20

<210> SEQ_ID NO 91
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 91

Ser Ser Glu Gly Gly Val Gly Phe Pro Leu Lys Gly Ile Pro Gln Glu
1 5 10 15
Ala Trp Ala Ser Arg
20

<210> SEQ_ID NO 92
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 92

Ser Arg Val Asp Ser Val Asn Phe Pro Leu Arg Gly Glu Thr Val Thr
1 5 10 15
Ser Met Val Ser Arg
20

<210> SEQ_ID NO 93
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries

<400> SEQUENCE: 93

Gly Gly Ala Leu Gly Phe Pro Leu Lys Gly Glu Val Val Glu Gly Trp
1 5 10 15

Ala

<210> SEQ_ID NO 94
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: consensus sequence from comparing peptides
isolated from phage display libraries

<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (2)...(0)
<223> OTHER INFORMATION: Xaa can be any amino acid

<400> SEQUENCE: 94

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Leu Xaa Phe Pro Leu Lys Gly
1 5

<210> SEQ ID NO 95
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 95

Ser Ser Cys Trp Ser Arg Phe Arg Leu Phe Met Leu Phe Cys Met Phe
1 5 10 15

Tyr Leu Val Ser Ser Arg
20

<210> SEQ ID NO 96
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 96

Ser Arg Cys Ile Lys Tyr Pro Phe Leu Tyr Cys Cys Leu Leu Ser Leu
1 5 10 15

Phe Leu Phe Ser Ser Arg
20

<210> SEQ ID NO 97
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 97

Cys Ala Glu Lys Trp Trp Trp Ile Gln Tyr Ala Trp Gly Gly Val
1 5 10 15

Leu Cys

<210> SEQ ID NO 98
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 98

Cys Asp Asp Ile Asp Tyr Ile Lys Glu Ala Pro Ile Asp Ala Met Met
1 5 10 15

Cys Cys

<210> SEQ ID NO 99
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 99

Cys Asp Phe Phe Asn Arg His Gly Tyr Asn Ser Gly Cys Glu His Ser

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1 5 10 15

Val Cys

<210> SEQ ID NO 100
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 100

Cys Asp Phe His Ser Asn Lys Tyr Tyr Ile Asn Gln Ile Ala Gly Ser
1 5 10 15

Asp Cys

<210> SEQ ID NO 101
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 101

Cys Asp Asn Gly Leu Asp Asp Cys Phe Glu Pro Cys Tyr Trp Ile Gln
1 5 10 15

Leu Cys

<210> SEQ ID NO 102
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 102

Cys Phe Glu Ile Ser Ser Ser Ser Thr Pro Ile Glu Leu Trp Glu Ser
1 5 10 15

Val Cys

<210> SEQ ID NO 103
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 103

Cys Phe Glu Ser Asp Phe Pro Asn Val Arg His His Val Leu Lys Gln
1 5 10 15

Ser Cys

<210> SEQ ID NO 104
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 104

Cys Phe Phe Phe Arg Arg Gln Ile Glu Ile Tyr Tyr Ala Arg Phe Gly
1 5 10 15

-continued

Phe Cys

<210> SEQ ID NO 105
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 105

Cys Phe Leu Phe Phe Ser Met Cys Asn Met Ala Cys Thr Lys Ala Lys
1 5 10 15

Glu Cys

<210> SEQ ID NO 106
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 106

Cys Phe Tyr Gln Asn Val Ile Ser Ser Phe Ala Gly Asn Pro Trp
1 5 10 15

Glu Cys

<210> SEQ ID NO 107
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 107

Cys Gly Asp His Met Thr Asp Lys Asn Met Pro Asn Ser Gly Ile Ser
1 5 10 15

Gly Cys

<210> SEQ ID NO 108
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 108

Cys His Arg Tyr Asp Arg Arg Trp Thr Met Tyr Thr Arg Ala Arg Leu
1 5 10 15

Arg Cys

<210> SEQ ID NO 109
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 109

Cys Ile Met Thr Ser Asp Met Val Asn Ala Ala Ile Trp Asn Glu Val
1 5 10 15

-continued

Gln Cys

```
<210> SEQ_ID NO 110
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 110
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Cys Leu Phe Phe Phe Ser Met Ile Met Asn Phe Asp Phe Pro Asn Phe
1 5 10 15

Glu Cys

```
<210> SEQ_ID NO 111
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 111
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Cys Leu Pro Pro Pro Tyr Glu Pro Lys Gln Leu Ala Glu Pro Cys Asp
1 5 10 15

Gly Cys

```
<210> SEQ_ID NO 112
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 112
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Cys Leu Pro Trp Tyr Tyr Tyr Lys Ala Gln Gln Leu Tyr Asp His
1 5 10 15

Tyr Cys

```
<210> SEQ_ID NO 113
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 113
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Cys Met Arg Arg Trp Asp Arg Trp Val Arg Trp Ala Trp Ser Arg Gln
1 5 10 15

Lys Cys

```
<210> SEQ_ID NO 114
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 114
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Cys Met Trp Trp Trp Gln Trp Gly Ser Tyr Ile Tyr Gly Glu Leu Trp
1 5 10 15

Ile Cys

-continued

<210> SEQ ID NO 115
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 115

Cys Asn Glu Asp Val Asn Asn Phe Pro Pro Arg Met Asn Thr Glu Leu
1 5 10 15

Gly Cys

<210> SEQ ID NO 116
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 116

Cys Asn Met Leu Leu Asn Ser Leu Pro Leu Pro Ser Glu Asp Trp Ser
1 5 10 15

Ala Cys

<210> SEQ ID NO 117
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 117

Cys Asn Asn Asn His Arg Asp Val Asn Trp Asn Leu Arg Asp Asn Thr
1 5 10 15

Ala Cys

<210> SEQ ID NO 118
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 118

Cys Asn Asn Asn Val Asn Trp Tyr His Tyr Met Phe Ile Pro Trp Ala
1 5 10 15

Lys Cys

<210> SEQ ID NO 119
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 119

Cys Asn Asn Val Asn Ala Cys Gln Asn His Glu Asn Asn Met His Asn
1 5 10 15

Asp Cys

-continued

<210> SEQ ID NO 120
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 120

Cys Asn Pro Gly Tyr Asn Asn Met Met Asn Asp Ser Met Val Met Trp
1 5 10 15

Arg Cys

<210> SEQ ID NO 121
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 121

Cys Pro Phe Thr His Ser Leu Ala Leu Asn Thr Asp Arg Ala Ser Pro
1 5 10 15

Gly Cys

<210> SEQ ID NO 122
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 122

Cys Pro His Trp Pro Pro Trp Cys Glu Trp Tyr Pro Glu Asn Trp
1 5 10 15

Cys Cys

<210> SEQ ID NO 123
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 123

Cys Pro Asn Pro Phe Pro Glu Pro Leu Asn His Asp Ala Ile Asp Trp
1 5 10 15

Cys Cys

<210> SEQ ID NO 124
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 124

Cys Pro Asn Val Pro Arg Pro Ala Gln Leu Ser Ile Cys Gly Asn Leu
1 5 10 15

Pro Cys

-continued

<210> SEQ ID NO 125
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 125

Cys Pro Pro Met Tyr Pro Gln Trp Glu Gly Asp Pro Asn Gln Arg Tyr
1 5 10 15

Asp Cys

<210> SEQ ID NO 126
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 126

Cys Pro Pro Pro Gly Gln Val Pro Pro Trp Pro Pro Ser Pro Pro Pro
1 5 10 15

Pro Cys

<210> SEQ ID NO 127
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 127

Cys Pro Arg Arg His Lys Arg Tyr Asn Trp Phe Ala His Asn Ala Arg
1 5 10 15

Met Cys

<210> SEQ ID NO 128
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 128

Cys Arg Gln Tyr Arg Phe Arg Pro Ile Val Arg Ala Arg Arg Leu Asn
1 5 10 15

Lys Cys

<210> SEQ ID NO 129
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 129

Cys Arg Arg Phe Arg Ser Arg Cys Pro Gly Glu Trp Arg Ser Trp Thr
1 5 10 15

Thr Cys

<210> SEQ ID NO 130

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<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 130

Cys Arg Val Gly Val Arg Arg Lys Glu Gly Gly Phe Arg Pro Trp Tyr
1 5 10 15

Lys Cys

<210> SEQ_ID NO 131
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 131

Cys Arg Val Arg Arg Glu Pro Arg Met Arg Lys Ile Lys Lys Met Ala
1 5 10 15

Leu Cys

<210> SEQ_ID NO 132
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 132

Cys Arg Tyr Ser Thr Ser Ser Trp Ser Asp Met Thr Cys Gly Cys Gly
1 5 10 15

Gln Cys

<210> SEQ_ID NO 133
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 133

Cys Ser Gly Trp Lys Trp Trp Val Phe His Val Cys Trp Lys Gln Val
1 5 10 15

His Cys

<210> SEQ_ID NO 134
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 134

Cys Ser Asn Ser Ser Cys Thr Ser His Thr Leu Tyr Ser Ser Val Met
1 5 10 15

Gly Cys

<210> SEQ_ID NO 135
<211> LENGTH: 18

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 135

Cys Ser Ser Phe Met Ser Met His His Trp His Val Val Val Asp Ser
1 5 10 15

Cys Cys

<210> SEQ_ID NO 136
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 136

Cys Ser Ser Ile Asn Ser Ser Tyr Val His Cys Leu Gly Cys Thr Glu
1 5 10 15

Ser Cys

<210> SEQ_ID NO 137
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 137

Cys Ser Ser Arg Tyr Ser Thr Ala Tyr His Met Ala Ser Asn Ser Ile
1 5 10 15

Phe Cys

<210> SEQ_ID NO 138
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 138

Cys Thr Glu Arg Arg Arg Arg Phe Asn Arg Asn Arg Pro Ala Lys Met
1 5 10 15

Arg Cys

<210> SEQ_ID NO 139
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 139

Cys Thr Pro Arg Pro Pro Val Pro Val Tyr Ile Pro Tyr Ser Ser Ser
1 5 10 15

Pro Cys

<210> SEQ_ID NO 140
<211> LENGTH: 18
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 140

Cys Val Asp Phe Lys Ser Lys Glu Lys Thr Glu Ile Met Leu Arg His
1 5 10 15

Ala Cys

<210> SEQ ID NO 141
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 141

Cys Val Phe Asp Ser Lys His Phe Ser Pro Thr His Ser Pro His Asp
1 5 10 15

Val Cys

<210> SEQ ID NO 142
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 142

Cys Val Tyr Lys Ile Tyr Tyr Leu Tyr Cys His Pro Tyr Leu Thr Phe
1 5 10 15

Pro Cys

<210> SEQ ID NO 143
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 143

Cys Trp Lys Ser Ser Ser Met Met Thr Ile Val Trp Trp Asn Lys
1 5 10 15

Met Cys

<210> SEQ ID NO 144
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 144

Cys Trp Met Trp Trp Pro Glu Trp Trp Trp Gln Cys Ala Val Gln Cys
1 5 10 15

Asn Cys

<210> SEQ ID NO 145
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 145

Cys Trp Tyr Thr Trp Trp Cys Gln Ala Ser Thr Met Gly Gln Ile Tyr
1 5 10 15

Glu Cys

<210> SEQ_ID NO 146
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 146

Cys Tyr Tyr Asp Ser Tyr Pro Ser Val Pro Tyr Tyr Gln Asn Pro
1 5 10 15

Ser Cys

<210> SEQ_ID NO 147
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 147

Cys Tyr Tyr Phe Tyr Gln Ala Leu Gln Gly Leu Ile Lys Asn His Trp
1 5 10 15

Ala Cys

<210> SEQ_ID NO 148
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 148

Cys Tyr Tyr Lys Pro Tyr Tyr Pro Cys Ser Ala Tyr Met Asn Phe Pro
1 5 10 15

Leu Cys

<210> SEQ_ID NO 149
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 149

Cys Tyr Tyr Asn Gly Leu Val Val His His Ser Asn Ser Gly His Lys
1 5 10 15

Asp Cys

<210> SEQ_ID NO 150
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 150

Cys Ala Asn Phe Leu Ser Phe Val Asn Asn Ser Tyr Cys Ile Asp Ser
1 5 10 15

Asn

<210> SEQ ID NO 151

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 151

Cys Ala Arg Arg Arg His His His His Pro Pro Met Pro His Phe Arg
1 5 10 15

Arg

<210> SEQ ID NO 152

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 152

Cys Cys Asp Gly Leu Ile Thr Ser Ser Trp Leu Asn Trp Phe Ala Arg
1 5 10 15

Gly

<210> SEQ ID NO 153

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 153

Cys Cys Glu Trp Trp Trp Cys Trp Lys Trp Trp Gln Cys Leu Trp Trp
1 5 10 15

Cys

<210> SEQ ID NO 154

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 154

Cys Cys Phe Asn Phe Phe Thr Ser Phe Asn Gln Gly Lys Asp Asn Phe
1 5 10 15

Val

<210> SEQ ID NO 155

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 155

Cys Cys Ser Ser Cys Glu Ser His Trp Lys Lys Phe Glu His Asn Arg
1 5 10 15

Gln

<210> SEQ_ID NO 156

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 156

Cys Asp Asp Phe Val Leu Asp Tyr Asp Asp Glu Tyr Met Val Met Asn
1 5 10 15

His

<210> SEQ_ID NO 157

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 157

Cys Asp Asp Met Gly Asp Asp Val Lys Asp Pro Glu Asp Tyr Ile Asp
1 5 10 15

Gln

<210> SEQ_ID NO 158

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 158

Cys Asp Phe Cys Phe Thr Asn Val Leu Phe Asp Ala Phe Gly Ser His
1 5 10 15

Val

<210> SEQ_ID NO 159

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 159

Cys Asp Tyr Phe Ser Phe Leu Glu Cys Phe Ser Asn Gly Trp Ser Gly
1 5 10 15

Ala

<210> SEQ_ID NO 160

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 160

Cys Phe Phe Phe Gly Gln Gly Asp Phe Met Cys Trp Ile Cys Leu Thr
1 5 10 15

Val

<210> SEQ ID NO 161
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 161

Cys Phe Phe Asn Ser Phe Asn Cys Thr Pro Asn Glu Met Trp Tyr Trp
1 5 10 15

Phe

<210> SEQ ID NO 162
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 162

Cys Phe Phe Ser Tyr Cys Phe Ser His Asp Val Ser Thr Tyr Asn Thr
1 5 10 15

Ala

<210> SEQ ID NO 163
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 163

Cys Phe Phe Ser Tyr Trp Asn Cys Leu Thr Asn Asn Ala Phe Val Lys
1 5 10 15

Pro

<210> SEQ ID NO 164
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 164

Cys Phe Gly Phe Ser Asp Cys Leu Ser Trp Phe Val Gln Pro Ser Thr
1 5 10 15

Ala

<210> SEQ ID NO 165
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 165

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Cys Phe Gly Asn Phe Leu Ser Phe Gly Phe Asn Cys Glu Ser Ala Leu
1 5 10 15

Gly

<210> SEQ_ID NO 166
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 166

Cys Phe Gly Asn Leu Gly Asn Leu Ile Tyr Thr Cys Asp Arg Leu Met
1 5 10 15

Pro

<210> SEQ_ID NO 167
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 167

Cys Phe Gly Asn Val Phe Cys Val Tyr Asn Gln Phe Ala Ala Gly Leu
1 5 10 15

Phe

<210> SEQ_ID NO 168
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 168

Cys Phe Thr Cys Phe Ser Phe Ala Phe Asn Phe Cys Phe Met Cys Trp
1 5 10 15

Met

<210> SEQ_ID NO 169
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 169

Cys Phe Thr Phe Phe Lys Ala Ser Trp Ser Trp Trp His His Ala Met
1 5 10 15

Met

<210> SEQ_ID NO 170
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 170

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Cys Phe Val His Asn Phe Phe Trp Phe Leu Gly Lys Asn Ser Asn Cys
1 5 10 15

Arg

<210> SEQ ID NO 171
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 171

Cys Phe Trp Tyr Ser Trp Leu Cys Ser Ala Ser Ser Ser Asp Ala Leu
1 5 10 15

Ile

<210> SEQ ID NO 172
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 172

Cys Gly Tyr Phe Cys Ser Phe Tyr Asn Tyr Leu Asp Ile Gly Thr Ala
1 5 10 15

Ser

<210> SEQ ID NO 173
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 173

Cys His Arg Cys Lys Arg Arg His Leu Leu Arg Arg Lys Gln Ala Asn
1 5 10 15

Arg

<210> SEQ ID NO 174
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 174

Cys Ile Phe Asn Ser Tyr Phe Cys Ser Phe Gln Leu Thr Ser Tyr Gly
1 5 10 15

Ser

<210> SEQ ID NO 175
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 175

Cys Lys Ala Phe Phe Asn Phe Gln Cys Phe Val Phe Val Phe His

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1 5 10 15

Phe

<210> SEQ ID NO 176
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 176

Cys Lys Phe Ser Phe Asp Phe Phe Ala Arg Phe Asn Arg His Phe Tyr
1 5 10 15

His

<210> SEQ ID NO 177
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 177

Cys Lys Ser Lys Lys Ser Ser His Ser Glu Ser Glu His Lys Lys Ser
1 5 10 15

Ser

<210> SEQ ID NO 178
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 178

Cys Leu Phe Asn Cys Ser Gly Glu Ser Trp Pro Met Ser Ile Val Pro
1 5 10 15

Ser

<210> SEQ ID NO 179
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 179

Cys Leu Lys Asp Tyr Tyr Ser Pro Cys Ser Tyr Ser Cys Asp Gln
1 5 10 15

His

<210> SEQ ID NO 180
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 180

Cys Leu Leu Lys Tyr Cys Tyr Ser Asp Leu Ala Ser Ser Ser Leu Ser
1 5 10 15

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Ile

<210> SEQ ID NO 181
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 181

Cys Leu Val Phe Met Arg Pro Tyr Phe Leu Leu Val Phe Leu Met Cys
1 5 10 15

Trp

<210> SEQ ID NO 182
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 182

Cys Leu Tyr Cys His Leu Asn Asn Gln Phe Leu Ser Trp Val Ser Gly
1 5 10 15

Asn

<210> SEQ ID NO 183
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 183

Cys Leu Tyr Cys Leu Asn Tyr Ala Asn Phe Ser Asp Pro Met Thr Met
1 5 10 15

Phe

<210> SEQ ID NO 184
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 184

Cys Asn His Leu Gly Phe Phe Ser Ser Phe Cys Asp Arg Leu Val Glu
1 5 10 15

Asn

<210> SEQ ID NO 185
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 185

Cys Asn Ser Phe Met Phe Ile Asn Gly Ser Phe Lys Glu Thr Gly Gly
1 5 10 15

-continued

Cys

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<210> SEQ_ID NO 186
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 186
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Cys Asn Ser Ser Ser Tyr Ser Trp Tyr Cys Trp Phe Gly Gly Ser Ser
1 5 10 15

Pro

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<210> SEQ_ID NO 187
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 187
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Cys Arg Asp Arg Gln Arg Trp Val Arg Ile Phe Asn Arg Arg Cys Val
1 5 10 15

Thr

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<210> SEQ_ID NO 188
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 188
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Cys Arg Met Lys Lys Arg Arg Arg Ala His Pro Pro Arg Asn Cys Met
1 5 10 15

Glu

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<210> SEQ_ID NO 189
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 189
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Cys Arg Arg Met Arg Cys Arg Asp His Thr Gln Lys Trp Arg Arg Glu
1 5 10 15

Arg

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<210> SEQ_ID NO 190
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 190
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Cys Arg Arg Arg Lys Asn Phe Gln Arg Cys Phe Arg Pro Leu Leu Tyr
1 5 10 15

Pro

-continued

<210> SEQ ID NO 191
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 191

Cys Arg Arg Arg Ser Gln Arg Arg Asn Arg Arg Gly Asn Asp Asp Ser
1 5 10 15

Ala

<210> SEQ ID NO 192
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 192

Cys Ser Phe Phe Met Pro Trp Cys Asn Phe Leu Asn Gly Glu Met Ala
1 5 10 15

Val

<210> SEQ ID NO 193
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 193

Cys Ser Phe Ser Val Ser Lys Ser Ser Gln Ile Phe Ala Val Ser Tyr
1 5 10 15

Ser

<210> SEQ ID NO 194
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 194

Cys Ser Leu Thr Gly Cys Leu Tyr Asp Tyr Val Ser Phe Gly Trp Gly
1 5 10 15

Ala

<210> SEQ ID NO 195
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 195

Cys Ser Ser Ser Met Thr Tyr Arg Thr Ser Ser Ser Trp His Leu Lys
1 5 10 15

Ile

-continued

<210> SEQ_ID NO 196
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 196

Cys Ser Thr Ser Tyr Ser Trp Asn Lys Trp Gln Ile Ser Ile Ser Ser
1 5 10 15

Tyr

<210> SEQ_ID NO 197
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 197

Cys Thr Cys Phe Asn Leu Phe Asp Met Lys Thr Cys Pro Ser Phe Cys
1 5 10 15

Thr

<210> SEQ_ID NO 198
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 198

Cys Thr Phe Gly Phe Pro Cys Val Met Ser Leu Val Asn His Val Pro
1 5 10 15

Ser

<210> SEQ_ID NO 199
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 199

Cys Thr Asn Ser Asn Leu Asn Ser Ser Ser Trp His Thr Met Val Asp
1 5 10 15

Arg

<210> SEQ_ID NO 200
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 200

Cys Thr Trp Trp Trp Trp Val Val Asn Arg Glu Pro Tyr Val Ala
1 5 10 15

Cys

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<210> SEQ ID NO 201
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 201

Cys Trp Asp Trp Met Thr Trp Gly Asn Asp Val Leu Val Asn Thr Asp
1 5 10 15

Trp

<210> SEQ ID NO 202
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 202

Cys Trp Leu Asp Asp Asp Ser Asp Asp Tyr Asp Asp Asp Asp Met Met
1 5 10 15

Ala

<210> SEQ ID NO 203
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 203

Cys Trp Met Gly Leu Phe Glu Cys Pro Asp Ala Trp Leu His Asp Trp
1 5 10 15

Asp

<210> SEQ ID NO 204
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 204

Cys Trp Asn Ile Ser Cys Met Phe Gly Phe Gly Trp Gly Gly Gly
1 5 10 15

Leu

<210> SEQ ID NO 205
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 205

Cys Tyr Ala Tyr Tyr Phe Phe Tyr Ser Ser Gly Arg Gly Tyr His
1 5 10 15

Gln

<210> SEQ ID NO 206

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<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 206

Cys Tyr Phe Pro Phe Tyr Cys Tyr Asn Thr Ser Ser Leu Ser Leu Asp
1 5 10 15

Phe

<210> SEQ ID NO 207
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 207

Ala Asp Arg Val Trp Pro Arg His Thr Ser Ser Pro Tyr His Arg His
1 5 10 15

<210> SEQ ID NO 208
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 208

Ala Phe Ile Ser Asn Leu His Ala Ala Cys Ser Val Gly Ser Cys Lys
1 5 10 15

<210> SEQ ID NO 209
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 209

Cys His Thr Pro Trp Pro Pro Met Asn Arg Tyr Ala Ser Val Leu Ile
1 5 10 15

<210> SEQ ID NO 210
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 210

Cys Thr Arg Arg Arg Arg Phe Cys Val Ile Ile Phe Arg Arg Glu Met
1 5 10 15

<210> SEQ ID NO 211
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 211

Cys Thr Ser Ser Ser Gln Lys His Cys Tyr His Gly His Ser Ser Asp

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1 5 10 15

<210> SEQ ID NO 212
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 212

Asp Cys Cys Cys Met Trp Asp Asp Gly Val Gly Asp Asp Val Asp Met
1 5 10 15

<210> SEQ ID NO 213
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 213

Asp Phe Cys Phe Met Met Asn Cys Thr Met Asn Ala His Tyr Phe
1 5 10 15

<210> SEQ ID NO 214
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 214

Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

<210> SEQ ID NO 215
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 215

Asp Trp Cys Asn Asn Ala Trp Asp Thr Tyr Ala Ile His Asn Asp Cys
1 5 10 15

<210> SEQ ID NO 216
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 216

Phe Leu Phe Phe Thr Asn Met Val Trp Tyr Phe Phe Ile Met Gly Ala
1 5 10 15

<210> SEQ ID NO 217
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 217

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Phe Thr Val Ser Ser His Ile Ile Glu Trp Ser Ala Asp Ser Val Val
1 5 10 15

<210> SEQ ID NO 218
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 218

Gly Ala Gly Gly Phe Phe Leu Pro Cys Leu Trp Asn Pro Asp Arg Thr
1 5 10 15

<210> SEQ ID NO 219
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 219

Gly Lys Cys Val Phe Arg Arg Glu Asp Cys Phe Trp Tyr Tyr Met His
1 5 10 15

<210> SEQ ID NO 220
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 220

Gly Ser Ser Ser Cys Gln Gly Val Ser Gly Ser Asp Tyr Val Met Lys
1 5 10 15

<210> SEQ ID NO 221
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 221

His Ala Ser Ile His His Cys Ser Tyr Gln Gly Tyr Gly Gln Ser Gly
1 5 10 15

<210> SEQ ID NO 222
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 222

His Cys Asn Asn Glu Asn Arg Trp His His Asn Gly Ala Ile Gly Val
1 5 10 15

<210> SEQ ID NO 223
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 223

His Ile Ser Ser Cys Gln Met Val Gln Ser Trp Ser Arg Pro Ala His
1 5 10 15

<210> SEQ ID NO 224

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 224

Ile Trp Glu Trp Phe Glu Leu Glu Met Leu Tyr Val Asn Arg Tyr Cys
1 5 10 15

<210> SEQ ID NO 225

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 225

Leu Ile His Arg Tyr Cys Arg Arg Val Pro Cys Arg Arg Glu Leu Lys
1 5 10 15

<210> SEQ ID NO 226

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 226

Met Ser Asn Phe Leu Ile Glu Phe Thr Tyr Asp Asn Val Gly Val Arg
1 5 10 15

<210> SEQ ID NO 227

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 227

Asn Phe Phe Val Glu Trp Ala Phe Asp Thr Gln Asp Arg Glu Glu Leu
1 5 10 15

<210> SEQ ID NO 228

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 228

Asn Gly Asn Glu Asn Asp Thr Ile Asn Asp Asn Asp Ile Asn Ala Ser
1 5 10 15

<210> SEQ ID NO 229

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 229

Asn Ile Asn Ile Val Glu Glu Arg Phe Met Val Glu Trp Asp Val Gln
1 5 10 15

<210> SEQ ID NO 230
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 230

Asn Pro Trp Ala Ser Ser Leu Val Ala Ala Cys Tyr Leu Asp Glu Ser
1 5 10 15

<210> SEQ ID NO 231
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 231

Asn Trp Trp Met Val Asn Leu Ile Pro Asp Glu Trp Cys Trp Asn Ser
1 5 10 15

<210> SEQ ID NO 232
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 232

Pro Phe Leu Phe Glu Ala Ser Asp Arg His Pro Ala Phe Asn His Met
1 5 10 15

<210> SEQ ID NO 233
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 233

Pro Gly Ser Ser Thr Phe Tyr Ser Ile Thr Met Thr Trp Asp Leu Pro
1 5 10 15

<210> SEQ ID NO 234
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 234

Pro Pro Ser Ser Asn Ser Asn Phe Met Leu Glu Phe Ser Trp Asp Ser
1 5 10 15

<210> SEQ ID NO 235
<211> LENGTH: 16

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 235

Pro Gln Ser Glu His Ser Lys Ser Tyr Met Ser Trp Ala Arg Ser Ser
1 5 10 15

<210> SEQ ID NO 236
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 236

Pro Ser Ala Cys Ser Arg Arg Ile Ile Gln Asp Thr Phe Phe Phe Met
1 5 10 15

<210> SEQ ID NO 237
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 237

Gln Glu Leu Arg Val Arg Lys Arg Arg Pro Lys Asp His Glu Arg
1 5 10 15

<210> SEQ ID NO 238
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 238

Gln Glu Met Leu Asn Phe Phe His Asn Gly Asn Phe Phe Phe Val
1 5 10 15

<210> SEQ ID NO 239
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 239

Gln His Arg Gln His His Asn Val Ile Tyr Ser Ala Val Cys Val Ala
1 5 10 15

<210> SEQ ID NO 240
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 240

Gln Met Asp Thr Ile Asp Asp Met Thr Trp Thr Gly Asp Asp Asp Cys
1 5 10 15

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<210> SEQ ID NO 241
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 241

Arg Gly Pro Tyr Ile Trp Trp Leu Glu Glu Gln Ser Arg Thr Trp Glu
1 5 10 15

<210> SEQ ID NO 242
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 242

Arg Arg Arg Asn Lys Leu Ala Arg Thr Leu Val Tyr Arg Arg Arg Val
1 5 10 15

<210> SEQ ID NO 243
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 243

Arg Arg Arg Pro Lys Pro Gly Pro His Ile Ile Phe Thr Ala Ile Asn
1 5 10 15

<210> SEQ ID NO 244
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 244

Arg Arg Tyr Ala Thr Trp Ser Val Ala Ser Ile Gln Glu Cys Pro Arg
1 5 10 15

<210> SEQ ID NO 245
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 245

Arg Tyr Pro Tyr Asp Met Asp Trp Asp Trp His His Gln Glu Arg Asp
1 5 10 15

<210> SEQ ID NO 246
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 246

Ser Phe Phe Phe Trp Asp Thr Phe Gly Glu Ser Asn Lys Phe Phe Met
1 5 10 15

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<210> SEQ ID NO 247
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 247

Ser Phe Met Phe Asn Asp Ser Ile Asp Asp Asp Asp Val Ser Glu
1 5 10 15

<210> SEQ ID NO 248
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 248

Ser Pro Gln Ala Arg Ser His Glu Asp Gln Val Met Gln Trp Trp Ile
1 5 10 15

<210> SEQ ID NO 249
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 249

Thr Phe Asp Asp Ala Met Leu Glu Trp Ser Leu Val Glu Trp Asp Ile
1 5 10 15

<210> SEQ ID NO 250
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 250

Thr Gly Gln Ser Ser Met Val Asn His Met Val Ser Glu Asn Gly Gly
1 5 10 15

<210> SEQ ID NO 251
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 251

Thr Met Gln Asp Phe Ser Ser Asp Glu Phe Tyr Thr Trp Thr Trp Asp
1 5 10 15

<210> SEQ ID NO 252
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 252

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Val Phe Gly Phe Ser Cys Phe Glu Lys Asp Lys Arg Phe Asp Glu Leu
1 5 10 15

<210> SEQ ID NO 253
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 253

Val Leu Gly Trp Lys Ser Trp Lys Ile Tyr Trp Ala Trp Leu Val Glu
1 5 10 15

<210> SEQ ID NO 254
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 254

Trp Leu Trp Thr Trp Gln Glu Thr Ala Glu His Pro Ile Trp Asn Ser
1 5 10 15

<210> SEQ ID NO 255
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 255

Trp Met Trp Gln Ile Cys Pro Cys Met Met His Trp Val Leu Asn Trp
1 5 10 15

<210> SEQ ID NO 256
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 256

Trp Asn Cys Asp Tyr Glu Thr Gly Ala Gly Trp Arg Cys Ser Glu Ala
1 5 10 15

<210> SEQ ID NO 257
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 257

Trp Asn Phe Tyr Phe Val Ala Phe Ile Ala Leu Pro Met Glu Phe Val
1 5 10 15

<210> SEQ ID NO 258
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 258

Trp Trp Phe Arg Phe Lys Arg Arg Arg Arg Trp Met Lys Ser Val Arg
1 5 10 15

<210> SEQ ID NO 259
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 259

Tyr Asp Met Met Met Asp Met Leu Lys Asn Asp Asp Lys Gly Phe Phe
1 5 10 15

<210> SEQ ID NO 260
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 260

Tyr Arg Met Ala Asp Arg Asp Val His Arg Trp Asp Lys Glu Tyr Glu
1 5 10 15

<210> SEQ ID NO 261
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 261

Tyr Arg Asn Met Glu Arg Ser Asn Met Ala Glu Thr Asn Ile Leu Ala
1 5 10 15

<210> SEQ ID NO 262
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 262

Tyr Tyr Phe Thr Glu Trp Ser Glu Asp Thr Ser Gly Gly Ser Ser Gly
1 5 10 15

<210> SEQ ID NO 263
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 263

Ala Lys Ile Leu Tyr Tyr Asp Met Gln Trp His Ile
1 5 10

<210> SEQ ID NO 264
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 264

Ala Pro Phe Leu Val Trp Tyr Ala Ser Thr Ser Asp Thr
1 5 10

<210> SEQ ID NO 265

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 265

Ala Val Ser Thr Ala Leu Tyr Asn Thr Trp Gln Val Leu
1 5 10

<210> SEQ ID NO 266

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 266

Cys Ala His Pro Pro Pro Tyr Lys Glu Asn Tyr Leu Tyr
1 5 10

<210> SEQ ID NO 267

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 267

Cys Cys Trp Thr Glu Ala Tyr Asp Ala His Pro Trp Arg
1 5 10

<210> SEQ ID NO 268

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 268

Cys Lys Phe Phe His Tyr His Ile Gly Phe Ala Thr
1 5 10

<210> SEQ ID NO 269

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 269

Cys Val Trp Cys Ser Glu Tyr Phe Arg Glu Asp Pro Pro
1 5 10

<210> SEQ ID NO 270

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 270

Cys Tyr Thr Ser Lys Tyr Tyr Arg Glu Lys Tyr Glu Leu
1 5 10

<210> SEQ ID NO 271
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 271

Asp Thr Ile Trp Trp Trp Tyr Met Trp Cys Trp His Tyr
1 5 10

<210> SEQ ID NO 272
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 272

Glu His Gly Pro Phe Val Asp Ser Glu Tyr Pro Gln Pro
1 5 10

<210> SEQ ID NO 273
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 273

Phe Ala Asp Asn Leu Gly Tyr Val Gly Ser Asp Val Ile
1 5 10

<210> SEQ ID NO 274
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 274

Phe Ala Pro Met Lys Ser Tyr Gly Val Ser Leu Pro Pro
1 5 10

<210> SEQ ID NO 275
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 275

Phe Glu Leu Ala Thr Gly Tyr Val Pro Ala Leu Leu Lys
1 5 10

<210> SEQ ID NO 276

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 276

Phe Phe Phe Ser Met Ser Tyr Phe Phe Phe Arg Ala Ala
1 5 10

<210> SEQ ID NO 277
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 277

Phe Phe Gly Phe Asp Val Tyr Asp Met Ser Asn Ala Leu
1 5 10

<210> SEQ ID NO 278
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 278

Phe Phe His Phe Cys Phe Tyr Thr Cys Met Phe His Leu
1 5 10

<210> SEQ ID NO 279
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 279

Phe Phe Leu Ser Pro Phe Tyr Phe Phe Asn Glu Phe Phe
1 5 10

<210> SEQ ID NO 280
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 280

Phe Phe Met Ala Ser Ser Tyr Ser Tyr Pro Val Ala Gly
1 5 10

<210> SEQ ID NO 281
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 281

Phe Phe Pro Ser Ser Trp Tyr Ser His Leu Gly Val Leu
1 5 10

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<210> SEQ ID NO 282
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 282

Phe Phe Val Leu Phe Leu Tyr Leu Trp Leu Gly Val Ser
1 5 10

<210> SEQ ID NO 283
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 283

Phe Gly Cys Glu Leu Pro Tyr Ser Gly Val Cys Ser Val
1 5 10

<210> SEQ ID NO 284
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 284

Phe Gly Ser Asp Val Phe Tyr Leu Arg Ser Ala Pro His
1 5 10

<210> SEQ ID NO 285
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 285

Phe His Glu Ala Pro Val Tyr Glu Thr Ser Glu Pro Pro
1 5 10

<210> SEQ ID NO 286
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 286

Phe Leu Gly Phe Gln Asp Tyr Lys Ser Ala Ala Met Met
1 5 10

<210> SEQ ID NO 287
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 287

Phe Leu Leu Thr Gly Glu Tyr Val Asp Val Val Ala Ala

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1 5 10

<210> SEQ ID NO 288
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 288

Phe Leu Ser Phe Ala Asn Tyr Glu Asp Glu Leu Leu Arg
1 5 10

<210> SEQ ID NO 289
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 289

Phe Met Phe Ile Phe Phe Tyr Pro Val Phe Cys Phe Gln
1 5 10

<210> SEQ ID NO 290
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 290

Phe Arg Phe Phe Asn His Tyr Arg Tyr Pro Ser Gly Gln
1 5 10

<210> SEQ ID NO 291
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 291

Phe Arg Met Asp Phe Asp Tyr Leu Tyr Pro Ser Leu Pro
1 5 10

<210> SEQ ID NO 292
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 292

Phe Arg Tyr Phe Tyr Phe Tyr Ser His Gly Phe Lys Phe
1 5 10

<210> SEQ ID NO 293
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 293

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Phe Ser Ala Leu Pro Thr Tyr Glu Val Asn Ser Tyr Lys
1 5 10

<210> SEQ ID NO 294
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 294

Phe Ser Asp Ser Ser Phe Tyr Ser Asp Leu Ser Val Val
1 5 10

<210> SEQ ID NO 295
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 295

Phe Ser Ser Val Asp Ser Tyr Ser Gly Pro Arg Pro Asp
1 5 10

<210> SEQ ID NO 296
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 296

Phe Ser Tyr Ser Val Ser Tyr Ala His Pro Glu Gly Leu
1 5 10

<210> SEQ ID NO 297
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 297

Phe Val Gly Phe Phe Leu Tyr Leu Thr Leu Leu Leu Pro
1 5 10

<210> SEQ ID NO 298
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 298

Gly Glu Asn Phe Cys Pro Tyr Ser Phe Phe Gly Cys Gly
1 5 10

<210> SEQ ID NO 299
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 299

Gly Phe Ala Trp Ser Ser Tyr Leu Gly Thr Thr Val His
1 5 10

<210> SEQ ID NO 300
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 300

Gly Phe Pro Phe Ile Phe Tyr Val Val Asp Trp Met Arg
1 5 10

<210> SEQ ID NO 301
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 301

Gly Phe Ser Glu Phe Leu Tyr Asp Leu Glu Val Gly Ile
1 5 10

<210> SEQ ID NO 302
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 302

Gly Phe Val Ala Tyr Asn Tyr Asp Lys Tyr Ser Gly Ala
1 5 10

<210> SEQ ID NO 303
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 303

Gly Val Ser Gln Phe Leu Tyr Asp Trp Val Lys Gly Gly
1 5 10

<210> SEQ ID NO 304
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 304

Gly Tyr Asn Ile Tyr Trp Tyr Ile Asn Asn Val Glu Tyr
1 5 10

<210> SEQ ID NO 305
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 305

His Tyr Lys Tyr Asn Val Tyr Cys Lys Tyr Asn Gly Tyr
1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 306

Ile Phe Leu Pro Trp His Tyr Asp Gly Tyr Thr Phe Ala
1 5 10

<210> SEQ ID NO 307
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 307

Ile Phe Ser Phe Leu Ser Tyr Val Pro Val Asp Lys Val
1 5 10

<210> SEQ ID NO 308
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 308

Ile Tyr Ala Ala Leu Tyr Tyr Arg Phe Pro Thr Met Asp
1 5 10

<210> SEQ ID NO 309
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 309

Lys Phe Phe Phe Trp Phe Tyr Ile Asn Phe Val Met Met
1 5 10

<210> SEQ ID NO 310
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 310

Leu Asp Pro Leu Val Pro Tyr Leu Tyr Glu Asn Leu Phe
1 5 10

<210> SEQ ID NO 311
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 311

Leu Phe Asp Ala Tyr Trp Tyr Ser Asp Thr Ala Met Ser
1 5 10

<210> SEQ ID NO 312
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 312

Leu Leu Phe Phe Asp Asp Tyr Phe Lys Ser Ala Gly Arg
1 5 10

<210> SEQ ID NO 313
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 313

Leu Asn Phe Met Ile Phe Tyr Leu Ser Leu Asn Pro Trp
1 5 10

<210> SEQ ID NO 314
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 314

Leu Pro His Leu Ile Gln Tyr Arg Val Leu Leu Val Ser
1 5 10

<210> SEQ ID NO 315
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 315

Leu Pro Ser Gln Phe Gly Tyr Gly Ser Val Pro Thr Asp
1 5 10

<210> SEQ ID NO 316
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 316

Leu Pro Ser Gln Phe Gly Tyr Gly Ser Val Pro Thr Asp
1 5 10

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<210> SEQ ID NO 317
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 317

Leu Ser Phe Ser Asp Phe Tyr Phe Ser Glu Gly Ser Glu
1 5 10

<210> SEQ ID NO 318
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 318

Leu Thr Asn Ser Gly Val Tyr Asp Gly Thr Pro Leu Pro
1 5 10

<210> SEQ ID NO 319
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 319

Leu Val Leu Leu Ile Leu Tyr Leu Phe Leu Ser Trp Pro
1 5 10

<210> SEQ ID NO 320
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 320

Leu Val Leu Leu Leu Phe Tyr Phe Leu Met Leu Ser Pro
1 5 10

<210> SEQ ID NO 321
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 321

Leu Tyr Leu Phe Tyr Pro Tyr Pro Asn Tyr Tyr Met Val
1 5 10

<210> SEQ ID NO 322
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 322

Asn Phe Ser Ser Ser Phe Tyr Ser Leu Val Ser Glu Gly
1 5 10

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<210> SEQ ID NO 323
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 323
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Asn Trp Tyr Ala Glu Tyr Tyr Val Tyr Asp Lys Gly
 1           5           10
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<210> SEQ ID NO 324
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 324
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Asn Tyr Phe Ser Ala Met Tyr Tyr Asp Gly Trp Met Ser
 1           5           10
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<210> SEQ ID NO 325
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 325
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Pro Ala Ser Leu Glu Leu Tyr Glu Asn Leu Val Ala Gly
 1           5           10
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<210> SEQ ID NO 326
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 326
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Pro Cys Trp Tyr Arg Tyr Tyr His Glu Phe Trp Ile Trp
 1           5           10
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<210> SEQ ID NO 327
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 327
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Pro Leu Tyr Tyr Glu Ser Tyr Arg Met Arg Thr Tyr Gln
 1           5           10
```

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<210> SEQ ID NO 328
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
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<400> SEQUENCE: 328
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Gln Tyr Ala Ser Tyr Met Tyr Tyr Cys Phe Pro Lys Tyr
1 5 10

<210> SEQ ID NO 329
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 329

Arg Ala Trp Trp Trp Trp Tyr Leu Asp Met Tyr Trp Thr
1 5 10

<210> SEQ ID NO 330
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 330

Arg Ala Tyr Asn Tyr Tyr Tyr Tyr Val Met Tyr Ala Cys
1 5 10

<210> SEQ ID NO 331
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 331

Arg Trp Ile Trp Trp Pro Tyr Val Asn Met Ile Trp Thr
1 5 10

<210> SEQ ID NO 332
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 332

Ser Asp Phe Leu Ser Pro Tyr Leu Ala Tyr Glu Arg Ser
1 5 10

<210> SEQ ID NO 333
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 333

Ser Phe Asp Val Arg Ser Tyr Val Leu Ala Gly Thr Glu
1 5 10

<210> SEQ ID NO 334
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 334

Ser Leu Phe Leu Asp Asp Tyr Ala Leu Gly Pro Arg Val
1 5 10

<210> SEQ ID NO 335
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 335

Ser Ser Val Leu Gly Phe Tyr Asp Pro Val Glu Val Ser
1 5 10

<210> SEQ ID NO 336
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 336

Ser Val Ala Phe Tyr Asp Tyr Leu Pro Thr Asp Leu Pro
1 5 10

<210> SEQ ID NO 337
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 337

Ser Val Leu Asp Phe Asn Tyr Gly His Asp Val Asn Val
1 5 10

<210> SEQ ID NO 338
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 338

Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> SEQ ID NO 339
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 339

Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> SEQ ID NO 340
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 340

Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> SEQ ID NO 341

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 341

Ser Trp Ser Trp Trp Arg Tyr Gly Pro Gln Asn Thr Val
1 5 10

<210> SEQ ID NO 342

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 342

Ser Tyr Gly Phe Pro Ile Tyr Asp Ala Leu Leu Glu Gln
1 5 10

<210> SEQ ID NO 343

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 343

Val Phe Asp Val Gly Leu Tyr Trp His Ala Ala Pro Pro
1 5 10

<210> SEQ ID NO 344

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 344

Val Gly Phe Trp Val Asp Tyr Asp Asn Ser Ser Val Met
1 5 10

<210> SEQ ID NO 345

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 345

Val Leu Asp Leu Pro Tyr Tyr Trp Pro Val Lys Tyr Thr
1 5 10

<210> SEQ ID NO 346

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 346

Val Leu Leu Ala Asp Ser Tyr Gln Arg Asp Glu His Met
1 5 10

<210> SEQ ID NO 347
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 347

Val Leu Leu Phe Asp Asp Tyr Gly Tyr Ala Glu Ser Ala
1 5 10

<210> SEQ ID NO 348
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 348

Val Ser Ala Ser Gly Met Tyr Asp Gly Val Asp Leu Met
1 5 10

<210> SEQ ID NO 349
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 349

Val Ser Leu Leu Phe Ser Tyr Ser Pro Ala Gly Tyr Asp
1 5 10

<210> SEQ ID NO 350
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 350

Val Ser Ser Glu Trp Thr Tyr Gly Ala Val Ala Asp Leu
1 5 10

<210> SEQ ID NO 351
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 351

Val Ser Val Leu Ser Asp Tyr Ser Ile Lys Ala Leu Leu
1 5 10

<210> SEQ ID NO 352

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 352

Trp Ala Asp Met Tyr Tyr Tyr Asp Trp Tyr Thr Met
1 5 10

<210> SEQ ID NO 353
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 353

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

<210> SEQ ID NO 354
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 354

Trp Asn Trp Trp Gly Val Tyr Leu Gly Ile Cys Trp Leu
1 5 10

<210> SEQ ID NO 355
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 355

Trp Trp Gln Thr Trp Trp Tyr Arg Thr Tyr Trp Glu Ile
1 5 10

<210> SEQ ID NO 356
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 356

Tyr Ala Gly Val Tyr Ser Tyr Phe Thr Gly Ser Thr Leu
1 5 10

<210> SEQ ID NO 357
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 357

Tyr Cys Gln Tyr Arg Glu Tyr Tyr Thr Met Tyr Val Cys
1 5 10

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<210> SEQ ID NO 358
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 358

Tyr Phe Val Glu Thr Tyr Tyr Asn Arg Tyr His Val Ser
1 5 10

<210> SEQ ID NO 359
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 359

Tyr Leu Ser Leu His Ala Tyr Glu Ser Phe Gly Gly Ser
1 5 10

<210> SEQ ID NO 360
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 360

Tyr Arg Tyr Gln Met Ser Tyr Tyr Ala Tyr Gln Tyr His
1 5 10

<210> SEQ ID NO 361
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 361

Tyr Ser Met Tyr Pro Ile Tyr Asn Lys Cys Ser Gln His
1 5 10

<210> SEQ ID NO 362
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 362

Tyr Trp Ile Tyr Asn Asn Tyr Thr Tyr Tyr Tyr Cys Gly
1 5 10

<210> SEQ ID NO 363
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 363

Tyr Trp Trp Glu Gln Trp Tyr Ser Trp Trp Ile Glu His

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1 5 10

<210> SEQ ID NO 364
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 364

Tyr Tyr Arg Asp Ala Ser Tyr Thr Tyr Pro Tyr Met Tyr
1 5 10

<210> SEQ ID NO 365
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 365

Tyr Tyr Tyr Ile Pro Val Tyr Ser Ala Gln Cys Tyr Thr
1 5 10

<210> SEQ ID NO 366
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 366

Ala Cys Pro Trp Pro Ile Pro Pro Trp Pro Leu Arg Val
1 5 10

<210> SEQ ID NO 367
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 367

Ala Arg Arg Trp Pro Leu Pro Arg Arg Asp Gln Phe Ser
1 5 10

<210> SEQ ID NO 368
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 368

Cys Arg Arg Ile Gln Gln Pro Cys Val Phe Arg Arg His
1 5 10

<210> SEQ ID NO 369
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 369

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Asp Glu Pro Pro Cys Ala Pro Glu Cys Asn Gly Asp Gly
1 5 10

<210> SEQ ID NO 370
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 370

Asp Phe Gln Phe Pro Lys Pro Ala Phe Cys Ser Thr Cys
1 5 10

<210> SEQ ID NO 371
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 371

Glu Leu Tyr Phe Phe Phe Pro Cys Gly Ser Phe Cys Gln
1 5 10

<210> SEQ ID NO 372
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 372

Phe Phe Gly Phe Asn His Pro Phe Leu Phe Ser Cys Trp
1 5 10

<210> SEQ ID NO 373
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 373

Phe Phe Gln Ser Ile Gln Pro Ile Phe Ala Arg Ser Met
1 5 10

<210> SEQ ID NO 374
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 374

Phe Phe Trp Val Lys Asp Pro Ser Pro Cys Phe Asp His
1 5 10

<210> SEQ ID NO 375
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 375

Phe Gly Lys Phe Phe Asp Pro Leu Arg Arg Ala Lys Asp
1 5 10

<210> SEQ ID NO 376
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 376

Phe Lys Gly Glu Phe Trp Pro Ala Phe Gly Val Gln Val
1 5 10

<210> SEQ ID NO 377
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 377

Phe Lys Leu His Trp Phe Pro Thr Cys Pro Phe Ile Gln
1 5 10

<210> SEQ ID NO 378
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 378

Phe Leu Ser Phe Val Phe Pro Ala Ser Ala Trp Gly Gly
1 5 10

<210> SEQ ID NO 379
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 379

Phe Met Asp Ile Trp Ser Pro Trp His Leu Leu Gly Thr
1 5 10

<210> SEQ ID NO 380
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 380

Phe Asn Pro Pro Glu Pro Pro Cys Pro Glu Phe Ser Lys
1 5 10

<210> SEQ ID NO 381
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 381

Phe Gln Phe Phe Asp Pro Pro Ser Phe Phe Gly Phe Lys
1 5 10

<210> SEQ ID NO 382
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 382

Phe Gln Phe Ser Phe Gln Pro Asp Gly Val Glu Arg Arg
1 5 10

<210> SEQ ID NO 383
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 383

Phe Gln Asn Cys Phe Trp Pro Ile Phe Glu Ala Met Glu
1 5 10

<210> SEQ ID NO 384
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 384

Phe Ser Phe Phe Ala Asp Pro Ile Glu Leu Glu Trp Asp
1 5 10

<210> SEQ ID NO 385
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 385

Phe Ser Ser Leu Phe Phe Pro His Trp Ala Gln Leu
1 5 10

<210> SEQ ID NO 386
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 386

Phe Tyr Met Pro Phe Gly Pro Thr Trp Trp Gln His Val
1 5 10

<210> SEQ ID NO 387
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 387

Phe Tyr Tyr Phe Gly Phe Pro Gln Cys Leu Ile Leu Phe
1 5 10

<210> SEQ ID NO 388
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 388

Gly Phe Glu Glu Phe Gln Pro Val Asp Phe Ile Ile Arg
1 5 10

<210> SEQ ID NO 389
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 389

Gly Leu Thr Arg Phe Phe Pro Val Ser Phe Ser Phe Phe
1 5 10

<210> SEQ ID NO 390
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 390

His Ala Arg Pro Pro Cys Pro Phe Val Asn Glu Lys Pro
1 5 10

<210> SEQ ID NO 391
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 391

His Glu Phe Met Trp Phe Pro Val His Trp Glu Phe His
1 5 10

<210> SEQ ID NO 392
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 392

His Arg Asn Pro Arg Arg Pro Gln Ile Glu Gly Val Arg
1 5 10

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<210> SEQ ID NO 393
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 393

Ile Ser Gly His Cys Phe Pro Cys Ile Glu Val Ser Asp
1 5 10

<210> SEQ ID NO 394
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 394

Lys Phe Gln Asp Phe Met Pro Gln Met Phe His Gly Ile
1 5 10

<210> SEQ ID NO 395
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 395

Leu Phe Phe Met Pro Phe Pro Phe Phe Phe Pro Tyr
1 5 10

<210> SEQ ID NO 396
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 396

Leu Phe Ser Trp Phe Leu Pro Thr Asp Asn Tyr Pro Val
1 5 10

<210> SEQ ID NO 397
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 397

Leu Val Cys Ile Arg Arg Pro Arg Arg Cys Phe Cys
1 5 10

<210> SEQ ID NO 398
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 398

Met Pro Arg Arg Glu Arg Pro Leu Trp Met Leu Thr Arg
1 5 10

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<210> SEQ ID NO 399
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 399
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Met Arg Arg His Arg Ala Pro Arg Ser Gln Cys Met Glu
 1           5           10
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<210> SEQ ID NO 400
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 400
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Asn Phe Phe Gly Pro Ile Pro Met Asn Phe Ala Phe Thr
 1           5           10
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<210> SEQ ID NO 401
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 401
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Asn Phe Phe Ser Ile Asp Pro Phe Cys Gln Ala Ile Tyr
 1           5           10
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<210> SEQ ID NO 402
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 402
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Asn Asn Gly Ala Arg Arg Pro Tyr Val Ala Ser Asn Pro
 1           5           10
```

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<210> SEQ ID NO 403
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 403
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Asn Arg Arg Arg Tyr Arg Pro Arg Phe Tyr Arg Arg Cys
 1           5           10
```

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<210> SEQ ID NO 404
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 404
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Pro Phe Phe Trp Met Phe Pro Ile Cys Phe Pro Pro Asn
1 5 10

<210> SEQ ID NO 405
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 405

Pro Phe Gly Leu Phe Pro Pro Gln Val Tyr Tyr Phe Leu
1 5 10

<210> SEQ ID NO 406
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 406

Pro Gly Ala Ala Pro Pro Pro Cys Asn Asn Ser Asp Asn
1 5 10

<210> SEQ ID NO 407
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 407

Pro Pro Cys Pro Trp Arg Pro Ser Ala Thr His Leu Pro
1 5 10

<210> SEQ ID NO 408
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 408

Pro Pro Lys Phe Leu Ala Pro His Thr Ser Ala Met Leu
1 5 10

<210> SEQ ID NO 409
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 409

Pro Pro Arg Val Ala Phe Pro Ile Arg Gln Arg Arg Val
1 5 10

<210> SEQ ID NO 410
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 410

Pro Thr Arg Pro Asn Gly Pro Glu Ser Glu Asp Leu Phe
1 5 10

<210> SEQ ID NO 411
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 411

Gln Cys Pro Asp Pro Ser Pro Ser Lys Cys Pro Phe Gly
1 5 10

<210> SEQ ID NO 412
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 412

Gln Arg Arg Ala Pro Arg Pro Ser Glu His Arg Arg Glu
1 5 10

<210> SEQ ID NO 413
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 413

Arg Ala Arg Arg Ala Gly Pro Leu Gly Asp Arg Lys Leu
1 5 10

<210> SEQ ID NO 414
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 414

Arg Glu Gly Arg Thr Arg Pro Arg Tyr Pro Arg Trp Phe
1 5 10

<210> SEQ ID NO 415
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 415

Arg Glu Pro Asn Pro Pro Pro Leu Gln Ser Pro Met Ser
1 5 10

<210> SEQ ID NO 416
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 416

Arg Gly Phe Gln Phe Gly Pro Ser Thr Phe Glu Tyr Phe
1 5 10

<210> SEQ ID NO 417

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 417

Arg Gly Pro Arg Arg Thr Pro Thr Ile His Arg Pro Trp
1 5 10

<210> SEQ ID NO 418

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 418

Arg His Phe His Val Arg Pro Val Asn Trp Trp Ser Lys
1 5 10

<210> SEQ ID NO 419

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 419

Arg Ile Asn Arg Ser Arg Pro Ile Met Trp Gln Arg Thr
1 5 10

<210> SEQ ID NO 420

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 420

Arg Asn Asp Arg Val Arg Pro Trp Lys Val Lys His Gln
1 5 10

<210> SEQ ID NO 421

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 421

Arg Asn Met Arg Tyr Arg Pro Gln Tyr Ala Asp Leu Cys
1 5 10

<210> SEQ ID NO 422

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 422

Arg Asn Asn Arg Pro Lys Pro Thr Gln Ser His Arg Val
1 5 10

<210> SEQ ID NO 423
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<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 423

Arg Arg His Arg Trp Trp Pro Gln Glu Phe Ser Arg His
1 5 10

<210> SEQ ID NO 424
<211> LENGTH: 13
<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 424

Arg Arg Arg Leu Phe Thr Pro Asn Ser Arg Ala Arg His
1 5 10

<210> SEQ ID NO 425
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 425

Arg Arg Ser Arg Phe Val Pro Glu Tyr Leu Phe Arg Pro
1 5 10

<210> SEQ ID NO 426
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 426

Arg Trp His Pro Arg Tyr Pro Val Met Lys Lys Asn Ser
1 5 10

<210> SEQ ID NO 427
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 427

Arg Trp Ile Pro Arg Pro Pro Arg Arg Ala Cys Arg Arg
1 5 10

<210> SEQ ID NO 428

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 428

Ser Phe Trp Pro Phe Cys Pro Thr Thr Trp Ala Asn Tyr
1 5 10

<210> SEQ ID NO 429
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 429

Ser Ile Phe Gln Phe Asn Pro Phe Pro Glu Gly Phe Phe
1 5 10

<210> SEQ ID NO 430
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 430

Ser Leu Phe Phe Met Pro Pro Glu Arg Leu Asp His Arg
1 5 10

<210> SEQ ID NO 431
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 431

Ser Asn Arg His Arg Arg Pro Arg Arg Arg Trp Arg Met
1 5 10

<210> SEQ ID NO 432
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 432

Thr Phe Phe Thr Asn Lys Pro Phe Ser Tyr His Phe Glu
1 5 10

<210> SEQ ID NO 433
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 433

Thr Thr Pro Val Gln Pro Pro Gly Glu Val Ser Gln Val
1 5 10

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<210> SEQ ID NO 434
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 434

Thr Tyr Asn Ser Phe Phe Pro Phe Arg His Phe Ala Glu
1 5 10

<210> SEQ ID NO 435
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 435

Val Lys Ile Arg Arg Arg Pro Arg Arg Met Arg Leu Met
1 5 10

<210> SEQ ID NO 436
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 436

Trp Lys His Pro Pro Arg Pro Tyr Cys Trp Lys Pro Leu
1 5 10

<210> SEQ ID NO 437
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 437

Tyr Ile Tyr Thr Val Tyr Pro Arg Asn Ser Ser Trp Phe
1 5 10

<210> SEQ ID NO 438
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 438

Tyr Gln Pro Trp Gly Pro Pro Pro Pro Leu Val Leu
1 5 10

<210> SEQ ID NO 439
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 439

Ala Arg Asp Tyr Asp Asn Asn Met Lys Tyr Tyr Leu Asp

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1 5 10

<210> SEQ ID NO 440
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 440

Ala Arg Ile Asn Asn Lys Asn Val Ile Thr Phe Gln Pro
1 5 10

<210> SEQ ID NO 441
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 441

Ala Ser Arg Ser Ser Asp Asn Ile Ser Tyr Ser Ser Thr
1 5 10

<210> SEQ ID NO 442
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 442

Ala Ser Ser Asp Ala Gly Asn Tyr Glu Ile Ala Gly Pro
1 5 10

<210> SEQ ID NO 443
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 443

Ala Thr Asp Asp Glu Asn Asn Glu Met Asn Val Gly Met
1 5 10

<210> SEQ ID NO 444
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 444

Cys Ser Ser Phe Ser Leu Asn Trp Ser Leu Ser Lys Ser
1 5 10

<210> SEQ ID NO 445
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 445

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Asp Cys Asp His Leu Phe Asn Met Glu Gln Thr Leu Arg
1 5 10

<210> SEQ ID NO 446
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 446

Asp Cys Val Ser Ser Asn Asn His Asp Ile Thr Arg Gly
1 5 10

<210> SEQ ID NO 447
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 447

Asp Asp Glu Arg Val Ile Asn Ser Asp Tyr Ser Glu Tyr
1 5 10

<210> SEQ ID NO 448
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 448

Asp Asp Lys Asn Glu Asp Asn Asp Ile Pro Lys Thr Pro
1 5 10

<210> SEQ ID NO 449
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 449

Asp Asp Thr Asn Asp Met Asn Asn Ser Glu Glu Lys Phe
1 5 10

<210> SEQ ID NO 450
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 450

Asp Asp Val Gln Asp Asp Asn Asp Gln Pro Tyr Asn Thr
1 5 10

<210> SEQ ID NO 451
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 451

Asp Lys Gly Asn Asp Gln Asn Asn Ser Pro Leu Trp Ala
1 5 10

<210> SEQ ID NO 452

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 452

Asp Leu Val Cys Asn Asn Cys Arg Asn Leu Phe Asn
1 5 10

<210> SEQ ID NO 453

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 453

Asp Asn His Asp Lys Phe Asn Gln Ala Ile Gln Asp Trp
1 5 10

<210> SEQ ID NO 454

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 454

Asp Arg Cys Asn Gly Asp Asn Trp Cys Asn Gln Gly Asp
1 5 10

<210> SEQ ID NO 455

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 455

Asp Ser Glu Tyr Leu Ser Asn Lys Ser Val Asn Asp Phe
1 5 10

<210> SEQ ID NO 456

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 456

Asp Thr Met Thr Asp Asn Asn Gln Gly Asp Asp Gln Trp
1 5 10

<210> SEQ ID NO 457

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 457

Glu Lys Asn Trp Asn Tyr Asn Pro Val Met Leu Ala Asn
1 5 10

<210> SEQ ID NO 458
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 458

Phe Phe Ser Phe Leu Pro Asn Ser Asp Arg Phe Gln Trp
1 5 10

<210> SEQ ID NO 459
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 459

Phe Phe Ser Tyr Trp Ser Asn Phe Asp Ala Ser Trp His
1 5 10

<210> SEQ ID NO 460
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 460

Phe His Ile Asp Asp Asp Asn Asp Phe Asp Thr Thr Ser
1 5 10

<210> SEQ ID NO 461
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 461

Phe Asn Asn Phe Asn Asp Asn Glu His Asn Val Asn Lys
1 5 10

<210> SEQ ID NO 462
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 462

Phe Tyr Asn Ile Val Asn Asn Ile Phe Ile Cys Cys Ile
1 5 10

<210> SEQ ID NO 463
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 463

Phe Tyr Trp Asp Arg Leu Asn Val Gly Trp Gly Leu Leu
1 5 10

<210> SEQ ID NO 464
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 464

Gly Asp Asn His Asn His Asn Thr Asn Thr Ile Glu Pro
1 5 10

<210> SEQ ID NO 465
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 465

His Ala Asp Gln Asp Asp Asn Cys Arg Gly Lys Asp Asp
1 5 10

<210> SEQ ID NO 466
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 466

His Asp Trp Asp Asp Trp Asn Ile Glu Ala Glu Asp Gly
1 5 10

<210> SEQ ID NO 467
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 467

His Gly Ser Ser Asp Thr Asn Gly Gln Ile Leu Phe Glu
1 5 10

<210> SEQ ID NO 468
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 468

His Asn Trp Asn His Asn Asn Leu Ile Asp Arg Phe
1 5 10

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<210> SEQ ID NO 469
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 469

Ile Cys Asp Asp Asp Asn Asn Met His Leu Tyr Glu Pro
1 5 10

<210> SEQ ID NO 470
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 470

Ile Asp Asp Ser His Leu Asn Asp Gln Cys Arg Asp Asp
1 5 10

<210> SEQ ID NO 471
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 471

Ile Asn Cys Asn Asn Asn Ser Leu Asn Asn Asn Asn
1 5 10

<210> SEQ ID NO 472
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 472

Ile Asn Asn Val Val Tyr Asn Leu His Asp Arg Asn Asn
1 5 10

<210> SEQ ID NO 473
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 473

Ile Ser Asn Cys Asn Ile Asn Asn Gly Asn Asn Asp Ser
1 5 10

<210> SEQ ID NO 474
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 474

Ile Ser Asn Arg Gln Ser Asn Thr Ser Asn Gly Met Ser
1 5 10

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<210> SEQ ID NO 475
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 475
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Lys Phe Ser Ser Leu His Asn Ile Ser Gly Pro Lys Ser
1 5 10

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<210> SEQ ID NO 476
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 476
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Lys Asn Leu Asn Gln Asn Asn Asn His Phe Asn Asn
1 5 10

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<210> SEQ ID NO 477
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 477
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Lys Asn Arg Val Asn Lys Asn Thr Asn Val His Cys Phe
1 5 10

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<210> SEQ ID NO 478
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 478
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Leu Ser Asn Leu Asn Tyr Asn Pro Asn His His Asp Met
1 5 10

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<210> SEQ ID NO 479
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 479
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Met Arg Ser Ser Ser Phe Asn Phe Gly Ser Phe Asp Gln
1 5 10

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<210> SEQ ID NO 480
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 480
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Met Ser Asn Ser Ser Ser Asn Ser Ser Ser Ser Gly
1 5 10

<210> SEQ ID NO 481
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 481

Met Tyr Ser Asn Tyr Tyr Asn Phe Leu Gln Lys Ser Trp
1 5 10

<210> SEQ ID NO 482
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 482

Asn Asp Arg Asn Asp His Asn Gln His Arg Tyr Asp His
1 5 10

<210> SEQ ID NO 483
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 483

Asn Glu Met Trp Asn Asn Asn Asn Val Met Asn His His
1 5 10

<210> SEQ ID NO 484
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 484

Asn Glu Asn Glu Asn Asp Asn Asn Met Asn Met Glu Ile
1 5 10

<210> SEQ ID NO 485
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries
<400> SEQUENCE: 485

Asn Asn Asn Ser Asn His Asn Asp Pro Thr Asn Ala Glu
1 5 10

<210> SEQ ID NO 486
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 486

Asn Asn Val Leu Asn His Asn Cys Asn Met Phe Leu Asn
1 5 10

<210> SEQ ID NO 487
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 487

Asn Pro Thr Lys Asn Arg Asn Thr His Leu Gly Gly Arg
1 5 10

<210> SEQ ID NO 488
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 488

Asn Arg Glu Val Lys Asn Asn Arg Gln Lys Val Phe Lys
1 5 10

<210> SEQ ID NO 489
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 489

Asn Arg Asn Asn His Phe Asn Asn Glu Tyr Glu Trp Asn
1 5 10

<210> SEQ ID NO 490
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 490

Asn Thr Asp Leu Asn Asn Gln Thr Val Ser Asn Arg
1 5 10

<210> SEQ ID NO 491
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 491

Pro Asp Asp Ala Pro His Asn Tyr Cys Thr Asp Pro Leu
1 5 10

<210> SEQ ID NO 492
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 492

Pro Lys Asp Asp Arg Asn Asn Thr Val Ala Ser Cys Glu
1 5 10

<210> SEQ ID NO 493

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 493

Pro Val Asn Tyr Ala Asn Asn Pro Glu Arg Val Gly His
1 5 10

<210> SEQ ID NO 494

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 494

Pro Tyr Asn Gly Ser Asn Asn Asn Ala Thr Val Pro
1 5 10

<210> SEQ ID NO 495

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 495

Gln Asn Ser Gln His Asn Asn His His Cys Val Leu Gly
1 5 10

<210> SEQ ID NO 496

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 496

Arg Ser Ser Ser Ser Gly Asn Ser Ser His His His Met
1 5 10

<210> SEQ ID NO 497

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 497

Ser Glu Ser Asn Ser Asn Asn Pro Gly His Asn Leu Pro
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<210> SEQ ID NO 498

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 498

Ser Phe Leu Asn Asn Cys Asn His Asn Lys Leu Met Ser
1 5 10

<210> SEQ ID NO 499
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 499

Ser Ile Phe Asn Ser Ser Asn His Thr His Gln Ser Met
1 5 10

<210> SEQ ID NO 500
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 500

Ser Asn Met Asp Ser Ser Asn Ala Pro Gln Ser Trp Val
1 5 10

<210> SEQ ID NO 501
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 501

Ser Asn Ser Trp Asn Asn Asn Glu Asp Lys His Ile Leu
1 5 10

<210> SEQ ID NO 502
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 502

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<210> SEQ ID NO 503
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 503

Ser Ser Met Leu His Asn Asn Pro Trp Ser Lys Trp Ser
1 5 10

<210> SEQ ID NO 504

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<211> LENGTH: 13
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 504

Ser Ser Asn Gln Val Ile Asn Thr Phe Glu Asp Leu Gln
1 5 10

<210> SEQ ID NO 505
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 505

Ser Ser Gln Ser Met Pro Asn Gly Ser Gly Lys Glu Thr
1 5 10

<210> SEQ ID NO 506
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 506

Ser Val Ser Cys Ser Cys Asn Thr Ser Arg Gly Cys Ser
1 5 10

<210> SEQ ID NO 507
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 507

Ser Val Ser Ser Lys Ser Asn Glu Ile Ser Phe Cys Thr
1 5 10

<210> SEQ ID NO 508
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 508

Thr Asp Ser Gly Ser Ser Asn Ser Ala Lys Ala Ile Cys
1 5 10

<210> SEQ ID NO 509
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 509

Thr Asn Trp Cys Ser Ser Asn Val Gly Ser Asn Thr Ser
1 5 10

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<210> SEQ_ID NO 510
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 510

Thr Ser Ser Trp Ser Phe Asn Gly Thr Asn Gly Ser Ala
1 5 10

<210> SEQ_ID NO 511
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 511

Val Ala Asp Ser Phe Asp Asn Ala Asn Tyr Thr Leu Asp
1 5 10

<210> SEQ_ID NO 512
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 512

Val Asp Asp Gln Tyr Asp Asn Trp Asp Ile Arg Asp Cys
1 5 10

<210> SEQ_ID NO 513
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 513

Tyr Asn Gly Asn Tyr His Asn His Gly Leu Asn Ile Arg
1 5 10

<210> SEQ_ID NO 514
<211> LENGTH: 13
<212> TYPE: PRT
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 514

Cys Phe Val Leu Asn Cys His Leu Val Leu Asp Arg Pro
1 5 10

<210> SEQ_ID NO 515
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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 515

Cys Arg Arg Pro Phe Glu His Ala Leu Phe Tyr Ala Ser

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1 5 10

<210> SEQ ID NO 516
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 516

Asp Ser Trp Leu Leu Ser His Ser Arg Ser Lys Ser Met
1 5 10

<210> SEQ ID NO 517
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 517

Asp Ser Trp Trp Thr Gln His Ser Gln Ala His Ser Asp
1 5 10

<210> SEQ ID NO 518
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 518

Asp Thr Asn Met Leu Asn His Gly Met Tyr Gly His Cys
1 5 10

<210> SEQ ID NO 519
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 519

Glu Asn Ile Asn Ala Ser His Cys Leu Ser Thr Val Asp
1 5 10

<210> SEQ ID NO 520
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 520

Phe Phe Ser Tyr Ser Gly His Leu Val Gln Lys Val Trp
1 5 10

<210> SEQ ID NO 521
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 521

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Phe Met Phe Ala Val Trp His Asp Gly His Ile Lys Asn
1 5 10

<210> SEQ ID NO 522
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 522

Phe Met Ser Gln His Phe His Asn Pro Met Met Ile Arg
1 5 10

<210> SEQ ID NO 523
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<212> TYPE: PRT
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<220> FEATURE:
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<400> SEQUENCE: 523

Phe Val Phe Tyr Ile Met His Tyr Cys Gly His Phe Met
1 5 10

<210> SEQ ID NO 524
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 524

His Phe Lys Asp Asp Asp His Met Met Leu Tyr Gly Pro
1 5 10

<210> SEQ ID NO 525
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His Thr Gln His Arg Leu His Val Gly Gln Ser Ser Ser
1 5 10

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<400> SEQUENCE: 526

Ile Ser Asn Ser Trp Tyr His Trp Ser Trp Glu Met Trp
1 5 10

<210> SEQ ID NO 527
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<212> TYPE: PRT
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<220> FEATURE:
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<400> SEQUENCE: 527

Leu Cys Phe Tyr Glu Tyr His Phe Met Gln Cys Ala Met
1 5 10

<210> SEQ ID NO 528

<211> LENGTH: 13
<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 528

Leu Gly Leu Ser Asp Ser His Tyr Glu Cys Ser Phe Arg
1 5 10

<210> SEQ ID NO 529

<211> LENGTH: 13
<212> TYPE: PRT
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<220> FEATURE:
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<400> SEQUENCE: 529

Leu Arg Ser Thr Ser Phe His Phe Arg Cys Ala Lys Cys
1 5 10

<210> SEQ ID NO 530

<211> LENGTH: 13
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<400> SEQUENCE: 530

Leu Ser Val Phe Ser His His Lys Trp Val Tyr Thr Ser
1 5 10

<210> SEQ ID NO 531

<211> LENGTH: 13
<212> TYPE: PRT
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<400> SEQUENCE: 531

Met Ala Met His His Met His His Met Ala Asn Asn Leu
1 5 10

<210> SEQ ID NO 532

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 532

Met Ser Ser Phe Asp Val His Arg Ser His Thr Asn Ser
1 5 10

<210> SEQ ID NO 533

<211> LENGTH: 13
<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 533

Pro Gly Ser Leu Ser Glu His Ile Tyr Gln Ala Trp Ser
1 5 10

<210> SEQ ID NO 534
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 534

Pro Ser Ser Ala Ser Met His Ile Ala Ser Ser Cys Ile
1 5 10

<210> SEQ ID NO 535
<211> LENGTH: 13
<212> TYPE: PRT
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<400> SEQUENCE: 535

Gln Tyr Trp Trp Ile Trp His Lys Ser Asp Ser Gly Ser
1 5 10

<210> SEQ ID NO 536
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<212> TYPE: PRT
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<400> SEQUENCE: 536

Ser Gly Gln Ser Asn Ser His His Asp Lys Thr Ile Cys
1 5 10

<210> SEQ ID NO 537
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<400> SEQUENCE: 537

Ser Gly Gln Ser Val Phe His His Phe Phe Pro Asn Asp
1 5 10

<210> SEQ ID NO 538
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<400> SEQUENCE: 538

Ser His Val Ser Leu Tyr His Ala Ser Thr Asp Ser Asp
1 5 10

<210> SEQ ID NO 539
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 539

Ser Met Ser Ser Ser Lys His Met Asp Met Asp Cys Phe
1 5 10

<210> SEQ ID NO 540
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 540

Ser Ser Cys Leu Pro Ser His Val Arg Ser Asp Thr Lys
1 5 10

<210> SEQ ID NO 541
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 541

Ser Ser Gly Met Ser Glu His Thr Pro Leu Cys Ser Glu
1 5 10

<210> SEQ ID NO 542
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 542

Ser Ser Pro Ser Phe Pro His Met Trp Ser Glu Asp Glu
1 5 10

<210> SEQ ID NO 543
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<212> TYPE: PRT
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<400> SEQUENCE: 543

Val His Ser Glu Ser Trp His Ser Tyr Ser Ile His Ala
1 5 10

<210> SEQ ID NO 544
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 544

Val Asn Asn Ala Met Gly His Met Gly Met Met Trp Cys
1 5 10

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<210> SEQ ID NO 545
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 545

Val Ser Cys Ser Ser Arg His Tyr Ser Ile Ser Trp Ser
1 5 10

<210> SEQ ID NO 546
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 546

Trp Thr Trp Lys Arg Gln His His Arg Ser Ser Leu Tyr
1 5 10

<210> SEQ ID NO 547
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 547

Tyr Ile Ser Phe Phe Glu His Gln Ile Val Asp Ser
1 5 10

<210> SEQ ID NO 548
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 548

Ser Cys Leu Val Phe Met Arg Pro Tyr Phe Leu Leu Val Phe Leu Met
1 5 10 15

Cys Trp Ser

<210> SEQ ID NO 549
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 549

Ser Cys Thr Phe Gly Phe Pro Cys Val Met Ser Leu Val Asn His Val
1 5 10 15

Pro Ser Ser

<210> SEQ ID NO 550
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

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<400> SEQUENCE: 550

Ser Cys Leu Tyr Cys Leu Asn Tyr Ala Asn Phe Ser Asp Pro Met Thr
1 5 10 15

Met Phe Ser

<210> SEQ ID NO 551
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 551

Gly Phe Ala Trp Ser Ser Tyr Leu Gly Thr Thr Val His
1 5 10<210> SEQ ID NO 552
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 552

Leu Phe Gly Pro Ile Glu Tyr Thr Gln Phe Leu Ala Asn
1 5 10<210> SEQ ID NO 553
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 553

Phe Phe Ser Phe Phe Phe Pro Ala Ser Ala Trp Gly Ser
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<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 554

Phe Phe Ser Phe Phe Phe Pro Ala Ser Ala Trp Gly Ser Ser Gly Ser
1 5 10 15Ser Arg Gly Asp
20<210> SEQ ID NO 555
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 555

Leu Leu Ser Leu Leu Leu Pro Gly Ser Ser Gly Lys
1 5 10

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<210> SEQ ID NO 556
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 556

Ile Ile Ser Ile Ile Ile Pro Gly Ser Ser Gly Lys
1 5 10

<210> SEQ ID NO 557
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 557

Phe Trp Ser Phe Trp Phe Pro Gly Ser Ser Gly Lys
1 5 10

<210> SEQ ID NO 558
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: isolated from phage display libraries

<400> SEQUENCE: 558

Ser Cys Ser Asp Cys Leu Lys Ser Val Asp Phe Ile Pro Ser Ser Leu
1 5 10 15

Ala Ser Ser Ser Ser Gly Arg Gly Asp Ser Pro Gly Arg Gly Asp Ser
20 25 30

1-9. (canceled)

10. A medical device having an interfacial biomaterial coating on a portion of the surface thereof which inhibits formation of a biofilm thereon wherein the interfacial biomaterial comprises a plurality of moieties each moiety comprising:

a) a binding module comprising a peptide of at least 3 amino acids to about 50 amino acids and having a binding affinity for the surface of the medical device to be coated of $1 \times 10^4 M^{-1}$;

b) an effector module selected from the group consisting of:

1) a peptide of at least 3 amino acids to about 50 amino acids that acts to inhibit formation of the biofilm adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;

2) a peptide of at least 3 amino acids to about 50 amino acids having a binding affinity of $1 \times 10^4 M^{-1}$ for a protein bound thereto that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;

3) a peptide of at least 3 amino acids to about 50 amino acids having a binding affinity of $1 \times 10^4 M^{-1}$ for a

non-protein bound thereto that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;

4) a non-peptide that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;

c) a linker module that links the binding module to the effector module.

11. A device according to claim 10 wherein the medical device is a patient implant.

12. A device according to claim 10 wherein the medical device is a medical conduit.

13. A device according to claim 10 wherein the medical device is a storage device for biological materials.

14. An interfacial biomaterial for coating at least a portion of the surface of a selected medical device which comprises a plurality of moieties each moiety comprising:

a) a binding module comprising a peptide of at least 3 amino acids to about 50 amino acids and having a binding affinity for the surface of the medical device to be coated of $1 \times 10^4 M^{-1}$;

b) an effector module selected from the group consisting of:

- 1) a peptide of at least 3 amino acids to about 50 amino acids that acts to inhibit formation of the biofilm adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;
- 2) a peptide of at least 3 amino acids to about 50 amino acids having a binding affinity of $1\times 10^4 M^{-1}$ for a protein bound thereto that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;
- 3) a peptide of at least 3 amino acids to about 50 amino acids having a binding affinity of $1\times 10^4 M^{-1}$ for a non-protein bound thereto that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;
- 4) a non-peptide that acts to inhibit formation of adhesion to the medical device by at least 5% compared to the surface of the medical device that is coated;
- c) a linker module that links the binding module to the effector module.

15. An interfacial biomaterial according to claim 14 wherein the effector module binds the biofilm inhibitor albumin.

16. An interfacial biomaterial according to claim 14 wherein the effector module inhibits biofilm formation by damaging cells capable of forming a biofilm.

17. An interfacial biomaterial according to claim 16 wherein the effector module is an anti-microbial or where the effector module binds an antimicrobial.

18. An interfacial biomaterial according to claim 14 wherein the effector module affects a regulatory mechanism of cells capable of forming a biofilm where the regulatory mechanism is involved in the cells establishment of or participation in biofilm formation.

19. An interfacial biomaterial according to claim 18 wherein the effector module is a quorum-sensing inhibitor.

20. An interfacial biomaterial according to claim 19 wherein the effector module is RIP.

21. An interfacial biomaterial according to claim 14 wherein the effector module is poly(ethylene glycol).

* * * * *