

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 January 2006 (19.01.2006)

PCT

(10) International Publication Number
WO 2006/007368 A2

(51) International Patent Classification:
A61L 31/00 (2006.01)

Edward [US/US]; 4 Fallen Oak Court, Durham, NC 27713-9494 (US).

(21) International Application Number:
PCT/US2005/021147

(74) Agents: **THORNE, Leigh, W.** et al.; Alston & Bird LLP, Bank of America Plaza, 101 South Tryon Street, Suite 4000, Charlotte, NC 28280-4000 (US).

(22) International Filing Date: 15 June 2005 (15.06.2005)

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/580,019 16 June 2004 (16.06.2004) US
60/651,338 9 February 2005 (09.02.2005) US
60/651,747 10 February 2005 (10.02.2005) US

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: BIOFUNCTIONAL COATINGS

(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.

WO 2006/007368 A2

BIOFUNCTIONAL COATINGS

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

The research underlying this invention was supported in part with funds from:
NIH grants no. RO1 CA77042 and R21 CA81088; NIH grant no. R01 AI051360-01A1;
and NSF DMR-0239769 Career Award. The United States Government may have an
5 interest in the subject matter of this invention.

FIELD OF THE INVENTION

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

BACKGROUND OF THE INVENTION

The fouling of polymer surfaces by biological materials is a common problem
15 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
20 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%
25 of such cases originate in films of bacteria that adhere to catheter walls (Donlan (2001)
Emerg. Infect. Dis. 7: 277-281).

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 5 antibiotics but also to drugs which are treatments of “last resort.”

Other types of catheters that are frequently used include urinary catheters, which are typically used with incontinent elderly patients and are typically made of silicone 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 10 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).

15 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 20 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.

25 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 30 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, 5 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).

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 10 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 15 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 20 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 25 arthroplasty surgeries each year, infections may affect 4000 to 5000 patients.

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 30 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.

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 5 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.

Biofilm formation is-regulated via the exchange of chemical signals between 10 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 15 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, 20 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 25 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 formation and production of virulence factors (Eberl (1999) *Syst. Appl. Microbiol.* 22(4): 493-506).

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 30 (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.

5 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 10 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 antithrombogenic 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 15 medical implants with an antimicrobial agent") and U.S. Pat. No. 5,709,672 ("Silastic and Polymer-Based Catheters with Improved Antimicrobial/Antifungal Properties").

20

25

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 30 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).

5 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.

Another alternative for preventing biofilm formation is the development of a coating that prevents adherence of bacterial cells to the catheter surface. Such coatings 10 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.* 15 (1999) *Anal. Biochem.* 273(2): 156-62; Ratner (1993) *J. Biomed. Mater. Res.* 27: 837-50).

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 20 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; 25 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 30 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 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.

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

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

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.

5

DETAILED DESCRIPTION OF THE INVENTION

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 inhibit 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 affector 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. Affector modules may have more than one function; thus, for example, a single affector module may have both adhesion-resistance function and behavior modification function. Any affector 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 affector 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.

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.

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.

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.

5 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 No. 10/300,694, filed November 20, 2002 and published on October 2, 2003 as publication number 20030185870. Binding modules can also be identified using the methods described in pending U.S. Patent Application 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.

10 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 15 surface, or a protein typically used for such comparisons such as bovine serum albumin.

20

25

30

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, 5 and antibody fragments that comprise an antigen binding site (*e.g.*, Fab and Fv antibody fragments).

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 10 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 15 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 20 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 25 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, FicollTM, and derivatized celluloses; non-cationic polyacrylates such as poly(acrylic acid); and esters, amides, and hydroxyalkyl amides thereof, and combinations thereof. For example, an IFBM can comprise an effector module that binds human serum albumin, a native 30 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. Patent 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.

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 antimicrobial 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).

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.

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).

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.

- 5 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. Patent Nos. 6,174,708, 10 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 15 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.

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, 20 structure, or conformation. See, e.g., U.S. Patent 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) 25 *Phage Display: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

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 30 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 5 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 10 in the practice of the present invention.

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; 15 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 20 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 25 can be derivatized to form N-im-benzylhistidine.

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 30 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.

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.

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, CA, 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.

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
5 (1993) *Peptides. 1992: Proceedings of the Twenty-Second European Peptide Symposium, September 13-19, 1992, Interlaken, Switzerland*, Escom, Leiden, The Netherlands.

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
10 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 depsi bond (CO-O), a hydroxyethylene bond (CHOH-CH₂), a ketomethylene bond (CO-CH₂), a methylene-oxy bond (CH₂-O), a reduced bond (CH₂-NH), a thiomethylene bond
15 (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.

20 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
25 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
30 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.

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.

5 Representative techniques can be found, for example, in Stewart & Young (1969) *Solid Phase Peptide Synthesis*, (Freeman, San Francisco, California); 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 10 can be found in Andersson *et al.* (2000) *Biopolymers* 55: 227-250, references cited therein, and in U.S. Patent 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, New York). Appropriate protective groups useful for 15 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 20 can be purchased from commercial sources (*e.g.*, Biopeptide Co., LLC of San Diego, California, and PeptidoGenics of Livermore, California).

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 25 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 30 (*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 5 mercapto(amido)carboxylic acid, an acrylamidocarboxylic acid, an acrylamido-amidotriethylene glycolic acid, and derivatives thereof. See, for example, U.S. Patent 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 10 toward themselves, for cross-linking purposes. Fluorescent linkers are also known in the art.

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 15 (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. Patent Nos. 6,280,760 and 6,071,890; and European Patent 20 Nos. 0 439 095 and 0 712 621.

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 25 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 30 used in non-human animals.

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 endotrachial 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

5 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

10 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.

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

15 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

20 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 5 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 E1427-00e1, entitled "Standard Guide for Selecting Test Methods to Determine the Effectiveness of Antimicrobial Agents and Other Chemicals for the Prevention, 10 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.

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 15 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.

20

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 25 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.

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).

THAT WHICH IS CLAIMED:

1. An IFBM comprising at least one surface-binding module and at least one
5 affector module which inhibits biofilm formation, wherein said surface-binding module
comprises a peptide which has the amino acid sequence set forth in any of SEQ ID
NOs: 1-8, 39-43, 95-96, or 97-558.
2. The IFBM of claim 1, wherein said affector module binds to human serum
10 albumin.
3. The IFBM of claim 1, wherein said surface-binding module and said affector
module are joined by a linker which comprises poly(ethylene glycol).
- 15 4. The IFBM of claim 1, wherein said affector module is a biofilm inhibitor
which inhibits biofilm formation by damaging cells.
5. The IFBM of claim 4 , wherein said biofilm inhibitor module is an
anti-microbial peptide.
20
6. The IFBM of claim 5, wherein said affector module comprises magainin.
7. The IFBM of claim 1, wherein said affector module is a biofilm inhibitor
which affects a regulatory mechanism of cells that is involved in their establishment of
25 or participation in a biofilm.
8. The IFBM of claim 7, wherein said affector module is a biofilm inhibitor
which is a quorum-sensing inhibitor.
- 30 9. The IFBM of claim 8, wherein said affector module is RIP.

SEQUENCE LISTING

<110> Affinergy, Inc.
Paul T. Hamilton
Mark W. Grinstaff
Daniel J. Kenan
Dale J. Christensen
Wayne F. Beyer, Jr.
Robin Hyde-DeRuyscher
Ray Edward Benson

<120> Biofunctional Coatings

<130> 47904/293513

<150> 60/580,019
<151> 2004-06-16

<150> 60/651,338
<151> 2005-02-09

<150> 60/651,747
<151> 2005-02-10

<160> 558

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 1
Ser Ser His Lys His Pro Val Thr Pro Arg Phe Phe Val Val Glu Ser
1 5 10 15
Arg

<210> 2
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 2
Ser Ser Cys Asn Cys Tyr Val Thr Pro Asn Leu Leu Lys His Lys Cys
1 5 10 15
Tyr Lys Ile Cys Ser Arg
20

<210> 3
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 3
Ser Ser Cys Ser His Asn His His Lys Leu Thr Ala Lys His Gln Val
1 5 10 15
Ala His Lys Cys Ser Arg
20

<210> 4
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 4
Ser Ser Cys Asp Gln Asn Asp Ile Phe Tyr Thr Ser Lys Lys Ser His
1 5 10 15
Lys Ser His Cys Ser Arg
20

<210> 5
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 5
Ser Ser Ser Ser Asp Val Tyr Leu Val Ser His Lys His His Leu Thr
1 5 10 15
Arg His Asn Ser Ser Arg
20

<210> 6
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 6
Ser Ser Ser Asp Lys Cys His Lys His Trp Tyr Cys Tyr Glu Ser Lys
1 5 10 15
Tyr Gly Gly Ser Ser Arg
20

<210> 7
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 7
His His Lys Leu Lys His Gln Met Leu His Leu Asn Gly Gly
1 5 10

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 8
Gly His His His Lys Lys Asp Gln Leu Pro Gln Leu Gly Gly
1 5 10

<210> 9
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 9
Ser Ser Ser Asp Lys Ser His Lys His Trp Tyr Ser Tyr Glu Ser Lys
1 5 10 15
Tyr Gly Gly Ser Gly Ser Ser Gly Lys
20 25

<210> 10
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 10
Ser Ser Ser Asp Lys Cys His Lys His Trp Tyr Cys Tyr Glu Ser Lys
1 5 10 15
Tyr Gly Gly Ser Gly Ser Ser Gly Lys
20 25

<210> 11
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 11
Ser Ser Asp Trp Gly Val Val Ala Ser Ala Trp Asp Ala Phe Glu Ala
1 5 10 15
Leu Asp Ala Ser Arg
20

<210> 12
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 12
Ser Ser Gly Ala Asp Phe Gly Tyr Gly Ser Trp Val Ser Phe Ser Ala
1 5 10 15
Leu Ser Ala Ser Arg
20

<210> 13
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 13
Ser Arg Gly Glu Ala Ser Gly Trp Glu Ala Phe Ser Ala Leu Glu Ala
1 5 10 15
Ala Val Val Ser Arg
20

<210> 14
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 14
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
20

<210> 15
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 15
Ser Arg Asp Gly Ala Gly Ala Ala Ala Trp Gly Ala Phe Ser Ala Leu
1 5 10 15
Ala Ser Glu Ser Arg
20

<210> 16
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 16
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
20

<210> 17
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 17
Ser Arg Val Ser Gly Val Ala Ala Trp Glu Ala Phe Ala Gly Leu Ser
1 5 10 15
Val Ser Ser Ser Arg
20

<210> 18
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 18
Ser Arg Asp Gly Gly Ser Phe Ser Ala Phe Ser Ser Leu Val Trp Ala
1 5 10 15
Ala Asp Ser Ser Arg
20

<210> 19
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 19
Ser Ser Val Ala Gly Asp Val Gly Ser Ser Trp Ala Ala Phe Ala Ser
1 5 10 15
Leu Ala Ala Ser Arg
20

<210> 20
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 20
Ser Ser Trp Glu Val Phe Ser Ser Leu Glu Ser Gly Ser Val Gly Ala
1 5 10 15
Gly Ala Gly Ser Arg
20

<210> 21
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 21
Ser Ser Ser Ser Gly Ala Val Ser Ser Phe Glu Ser Leu Ser Gly Ser
1 5 10 15
Val Val Ser Ser Arg
20

<210> 22
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 22
Ser Arg Glu Gly Val Ala Trp Glu Ala Phe Gly Ala Leu Ser Ser Phe
1 5 10 15
Ala Ala Asp Ser Arg
20

<210> 23
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 23
Ser Ser Trp Gly Leu Ala Ser Glu Ala Ser Phe Phe Ser Phe Ser Ala
1 5 10 15
Leu Ser Ser Ser Arg
20

<210> 24
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 24
Ser Arg Glu Gly Ala Ala Trp Asp Ser Phe Phe Ala Leu Ser Gly Gly
1 5 10 15
Ser Ala Ala Ser Arg
20

<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 25
Ser Ser Ser Val Asp Leu Tyr Phe Pro Leu Lys Gly Asp Val Val Ser
1 5 10 15
6

Arg

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 26
Ser Ser Phe Glu Pro Leu Arg Phe Pro Leu Lys Gly Val Pro Val Ser
1 5 10 15
Arg

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(1)
<223> Xaa at this position can be Trp, Phe, or Tyr

<221> VARIANT
<222> (2)...(3)
<223> Xaa can be any amino acid

<221> VARIANT
<222> (5)...(5)
<223> Xaa can be any amino acid

<221> VARIANT
<222> (6)...(6)
<223> Xaa at this position can be Ser, Thr, Ala, or Gly

<400> 27
Xaa Xaa Xaa Phe Xaa Xaa Leu
1 5

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(1)
<223> Xaa at this position can be Leu or Val

<221> VARIANT
<222> (2)...(2)
<223> Xaa can be any amino acid

<221> VARIANT
<222> (6)...(6)

<223> Xaa at this position can be Lys or Arg

<400> 28
Xaa Xaa Phe Pro Leu Xaa Gly
1 5

<210> 29
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 29
Ser Ser Phe Glu Pro Leu Arg Phe Pro Leu Lys Gly Val Pro Val Ser
1 5 10 15
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> 30
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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> 31
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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> 32
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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> 33
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 33
Ser Ser Ser Val Asp Leu Tyr Phe Pro Leu Lys Gly Asp Val Val Ser
1 5 10 15
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> 34
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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 Val Asp Leu Tyr Phe Pro Leu
20 25 30
Lys Gly Asp Val Val Ser Arg
35

<210> 35
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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> 36
<211> 43
<212> PRT
<213> Artificial Sequence

<220>

<223> IFBM

<400> 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> 37
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 37
Ser Ser Asp Trp Gly Val Val Ala Ser Ala Trp Asp Ala Phe Glu Ala
1 5 10 15
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> 38
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> IFBM

<400> 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> 39
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 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> 40
<211> 22
<212> PRT
<213> Artificial Sequence

<220>

<223> module peptide

<400> 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> 41
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 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> 42
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 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> 43
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> module peptide

<400> 43
Ser Ser Val Asn Lys Met Asn Arg Leu Trp Glu Pro Leu Ser Arg
1 5 10 15

<210> 44
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 45
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 46
<211> 21
<212> PRT
<213> Artificial Sequence

<400> 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

<210> 47
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 47
Ser Ser Gly Gly Gly Gly Ala Trp Glu Ser Trp Arg Gly Leu Ser Gly
1 5 10 15
Val Glu Leu Ser Arg
20

<210> 48
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 49
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 50
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 51
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 51
Ser Arg Val Glu Gly Gly Ala Trp Gln Ala Leu Ala Gly Leu Thr Val
1 5 10 15
Glu Arg Val Ser Arg
20

<210> 52
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 53
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 54
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 54
Ser Ser Ser Ser Ser Gly^y Thr Trp Gln Ala Phe Thr Gly Leu Ser Gly
1 5 10 15
Glu Arg Val Ser Arg
20

<210> 55
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 56
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 56
Ser Ser Gly Gly Gly Gly Glu Gly Phe Ser Ser Leu Ser Gly
1 5 10 15
Asn Gly Arg Ser Arg
20

<210> 57
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 58
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 59
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 60
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 61
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 62
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 62
Ser Ser Leu Gly Gln Thr Gly Trp Glu Ala Phe Glu Ser Leu Ser Gly
1 5 10 15
15

Thr Arg Gly Ser Arg
20

<210> 63
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 64
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 65
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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

<210> 66
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 67
<211> 21

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 68
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 69
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 70
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 70
Ser Ser Ala Tyr Ser Val Phe Ser Ser Leu Arg Ala Asp Asn Ser Gly
1 5 10 15
Gly Ala Val Ser Arg
20

<210> 71
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 72
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 72
Gly Gly Gly Ala Trp Glu Ala Phe Ser Ser Leu Ser Gly Ser Arg Val
1 5 10 15

<210> 73
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Motif 1a

<221> VARIANT
<222> (0)...(0)
<223> Xaa can be any amino acid

<400> 73
Trp Xaa Xaa Phe Xaa Xaa Leu
1 5

<210> 74
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 74
Ser Ser Gly Ala Trp Glu Ser Phe Ser Ser Leu Ser Gly Ser Ser
1 5 10 15

<210> 75
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> encoding consensus sequence

<400> 75
tcgagtggtg cttgggagtc tttttcgtca ctgagtggat 40

<210> 76
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> partial complement of SEQ ID NO:75

<400> 76
caccacgaac cctcagaaaa agcagtgact cacctagatc 40

<210> 77
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 78
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<221> VARIANT
<222> (18)...(0)
<223> Xaa can be any amino acid

<400> 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> 79
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 80
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 80
Ser Ser Glu Gly Ser Leu Ser Phe Pro Leu Lys Gly Gln Val Tyr Ser
1 5 10 15
Gly Trp Gly Ser Arg
20

<210> 81
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 82
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 83
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 84
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 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> 85
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 86
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 87
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 88
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 89
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 90
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 91
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 92
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 93
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 93

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

Ala

<210> 94

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif 2a

<221> VARIANT

<222> (2)...(0)

<223> Xaa can be any amino acid

<400> 94

Leu Xaa Phe Pro Leu Lys Gly
1 5

<210> 95

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 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> 96

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 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> 97

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 97
Cys Ala Glu Lys Trp Trp Trp Trp Ile Gln Tyr Ala Trp Gly Gly Val
1 5 10 15
Leu Cys

<210> 98
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 98
Cys Asp Asp Ile Asp Tyr Ile Lys Glu Ala Pro Ile Asp Ala Met Met
1 5 10 15
Cys Cys

<210> 99
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 99
Cys Asp Phe Phe Asn Arg His Gly Tyr Asn Ser Gly Cys Glu His Ser
1 5 10 15
Val Cys

<210> 100
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 100
Cys Asp Phe His Ser Asn Lys Tyr Tyr Ile Asn Gln Ile Ala Gly Ser
1 5 10 15
Asp Cys

<210> 101
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 101
Cys Asp Asn Gly Leu Asp Asp Cys Phe Glu Pro Cys Tyr Trp Ile Gln
1 5 10 15
Leu Cys

<210> 102
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 102
Cys Phe Glu Ile Ser Ser Ser Ser Thr Pro Ile Glu Leu Trp Glu Ser
1 5 10 15
Val Cys

<210> 103
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 103
Cys Phe Glu Ser Asp Phe Pro Asn Val Arg His His Val Leu Lys Gln
1 5 10 15
Ser Cys

<210> 104
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 104
Cys Phe Phe Phe Arg Arg Gln Ile Glu Ile Tyr Tyr Ala Arg Phe Gly
1 5 10 15
Phe Cys

<210> 105
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 105
Cys Phe Leu Phe Phe Ser Met Cys Asn Met Ala Cys Thr Lys Ala Lys
1 5 10 15
Glu Cys

<210> 106
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 106
Cys Phe Tyr Gln Asn Val Ile Ser Ser Ser Phe Ala Gly Asn Pro Trp
1 5 10 15
Glu Cys

<210> 107
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 107
Cys Gly Asp His Met Thr Asp Lys Asn Met Pro Asn Ser Gly Ile Ser
1 5 10 15
Gly Cys

<210> 108
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 108
Cys His Arg Tyr Asp Arg Arg Trp Thr Met Tyr Thr Arg Ala Arg Leu
1 5 10 15
Arg Cys

<210> 109
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 109
Cys Ile Met Thr Ser Asp Met Val Asn Ala Ala Ile Trp Asn Glu Val
1 5 10 15
Gln Cys

<210> 110
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 110
Cys Leu Phe Phe Phe Ser Met Ile Met Asn Phe Asp Phe Pro Asn Phe

1 5 10 15
Glu Cys

<210> 111
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 111
Cys Leu Pro Pro Pro Tyr Glu Pro Lys Gln Leu Ala Glu Pro Cys Asp
1 5 10 15
Gly Cys

<210> 112
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 112
Cys Leu Pro Trp Tyr Tyr Tyr Tyr Lys Ala Gln Gln Leu Tyr Asp His
1 5 10 15
Tyr Cys

<210> 113
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 113
Cys Met Arg Arg Trp Asp Arg Trp Val Arg Trp Ala Trp Ser Arg Gln
1 5 10 15
Lys Cys

<210> 114
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 114
Cys Met Trp Trp Trp Gln Trp Gly Ser Tyr Ile Tyr Gly Glu Leu Trp
1 5 10 15
Ile Cys

<210> 115

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 115
Cys Asn Glu Asp Val Asn Asn Phe Pro Pro Arg Met Asn Thr Glu Leu
1 5 10 15
Gly Cys

<210> 116
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 116
Cys Asn Met Leu Leu Asn Ser Leu Pro Leu Pro Ser Glu Asp Trp Ser
1 5 10 15
Ala Cys

<210> 117
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 117
Cys Asn Asn Asn His Arg Asp Val Asn Trp Asn Leu Arg Asp Asn Thr
1 5 10 15
Ala Cys

<210> 118
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 118
Cys Asn Asn Asn Val Asn Trp Tyr His Tyr Met Phe Ile Pro Trp Ala
1 5 10 15
Lys Cys

<210> 119
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 119
Cys Asn Asn Val Asn Ala Cys Gln Asn His Glu Asn Asn Met His Asn
1 5 10 15
Asp Cys

<210> 120
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 120
Cys Asn Pro Gly Tyr Asn Asn Met Met Asn Asp Ser Met Val Met Trp
1 5 10 15
Arg Cys

<210> 121
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 121
Cys Pro Phe Thr His Ser Leu Ala Leu Asn Thr Asp Arg Ala Ser Pro
1 5 10 15
Gly Cys

<210> 122
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 122
Cys Pro His Trp Pro Pro Pro Trp Cys Glu Trp Tyr Pro Glu Asn Trp
1 5 10 15
Cys Cys

<210> 123
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 123
Cys Pro Asn Pro Phe Pro Glu Pro Leu Asn His Asp Ala Ile Asp Trp
1 5 10 15
Cys Cys

<210> 124
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 124
Cys Pro Asn Val Pro Arg Pro Ala Gln Leu Ser Ile Cys Gly Asn Leu
1 5 10 15
Pro Cys

<210> 125
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 125
Cys Pro Pro Met Tyr Pro Gln Trp Glu Gly Asp Pro Asn Gln Arg Tyr
1 5 10 15
Asp Cys

<210> 126
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 126
Cys Pro Pro Pro Gly Gln Val Pro Pro Trp Pro Pro Ser Pro Pro Pro
1 5 10 15
Pro Cys

<210> 127
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 127
Cys Pro Arg Arg His Lys Arg Tyr Asn Trp Phe Ala His Asn Ala Arg
1 5 10 15
Met Cys

<210> 128
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 128
Cys Arg Gln Tyr Arg Phe Arg Pro Ile Val Arg Ala Arg Arg Leu Asn
1 5 10 15
Lys Cys

<210> 129
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 129
Cys Arg Arg Phe Arg Ser Arg Cys Pro Gly Glu Trp Arg Ser Trp Thr
1 5 10 15
Thr Cys

<210> 130
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 130
Cys Arg Val Gly Val Arg Arg Lys Glu Gly Gly Phe Arg Pro Trp Tyr
1 5 10 15
Lys Cys

<210> 131
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 131
Cys Arg Val Arg Arg Glu Pro Arg Met Arg Lys Ile Lys Lys Met Ala
1 5 10 15
Leu Cys

<210> 132
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 132
Cys Arg Tyr Ser Thr Ser Ser Trp Ser Asp Met Thr Cys Gly Cys Gly

1
Gln Cys

5

10

15

<210> 133
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 133
Cys Ser Gly Trp Lys Trp Trp Val Phe His Val Cys Trp Lys Gln Val
1 5 10 15
His Cys

<210> 134
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 134
Cys Ser Asn Ser Ser Cys Thr Ser His Thr Leu Tyr Ser Ser Val Met
1 5 10 15
Gly Cys

<210> 135
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 135
Cys Ser Ser Phe Met Ser Met His His Trp His Val Val Val Asp Ser
1 5 10 15
Cys Cys

<210> 136
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 136
Cys Ser Ser Ile Asn Ser Ser Tyr Val His Cys Leu Gly Cys Thr Glu
1 5 10 15
Ser Cys

<210> 137

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 137
Cys Ser Ser Arg Tyr Ser Thr Ala Tyr His Met Ala Ser Asn Ser Ile
1 5 10 15
Phe Cys

<210> 138
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 138
Cys Thr Glu Arg Arg Arg Phe Asn Arg Asn Arg Pro Ala Lys Met
1 5 10 15
Arg Cys

<210> 139
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 139
Cys Thr Pro Arg Pro Pro Val Pro Val Tyr Ile Pro Tyr Ser Ser Ser
1 5 10 15
Pro Cys

<210> 140
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 140
Cys Val Asp Phe Lys Ser Lys Glu Lys Thr Glu Ile Met Leu Arg His
1 5 10 15
Ala Cys

<210> 141
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 141
Cys Val Phe Asp Ser Lys His Phe Ser Pro Thr His Ser Pro His Asp
1 5 10 15
Val Cys

<210> 142
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 142
Cys Val Tyr Lys Ile Tyr Tyr Leu Tyr Cys His Pro Tyr Leu Thr Phe
1 5 10 15
Pro Cys

<210> 143
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 143
Cys Trp Lys Ser Ser Ser Met Met Thr Ile Val Trp Trp Asn Lys
1 5 10 15
Met Cys

<210> 144
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 144
Cys Trp Met Trp Trp Pro Glu Trp Trp Trp Gln Cys Ala Val Gln Cys
1 5 10 15
Asn Cys

<210> 145
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 145
Cys Trp Tyr Thr Trp Trp Cys Gln Ala Ser Thr Met Gly Gln Ile Tyr
1 5 10 15
Glu Cys

<210> 146
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 146
Cys Tyr Tyr Asp Ser Tyr Pro Ser Val Pro Tyr Tyr Tyr Gln Asn Pro
1 5 10 15
Ser Cys

<210> 147
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 147
Cys Tyr Tyr Phe Tyr Gln Ala Leu Gln Gly Leu Ile Lys Asn His Trp
1 5 10 15
Ala Cys

<210> 148
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 148
Cys Tyr Tyr Lys Pro Tyr Tyr Pro Cys Ser Ala Tyr Met Asn Phe Pro
1 5 10 15
Leu Cys

<210> 149
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 149
Cys Tyr Tyr Asn Gly Leu Val Val His His Ser Asn Ser Gly His Lys
1 5 10 15
Asp Cys

<210> 150
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 150
Cys Ala Asn Phe Leu Ser Phe Val Asn Asn Ser Tyr Cys Ile Asp Ser
1 5 10 15
Asn

<210> 151
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 151
Cys Ala Arg Arg Arg His His His His Pro Pro Met Pro His Phe Arg
1 5 10 15
Arg

<210> 152
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 152
Cys Cys Asp Gly Leu Ile Thr Ser Ser Trp Leu Asn Trp Phe Ala Arg
1 5 10 15
Gly

<210> 153
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 153
Cys Cys Glu Trp Trp Trp Cys Trp Lys Trp Trp Gln Cys Leu Trp Trp
1 5 10 15
Cys

<210> 154
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 154
Cys Cys Phe Asn Phe Phe Thr Ser Phe Asn Gln Gly Lys Asp Asn Phe

1
Val

5

10

15

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 155
Cys Cys Ser Ser Cys Glu Ser His Trp Lys Lys Phe Glu His Asn Arg
1 5 10 15
Gln

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 156
Cys Asp Asp Phe Val Leu Asp Tyr Asp Asp Glu Tyr Met Val Met Asn
1 5 10 15
His

<210> 157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 157
Cys Asp Asp Met Gly Asp Asp Val Lys Asp Pro Glu Asp Tyr Ile Asp
1 5 10 15
Gln

<210> 158
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 158
Cys Asp Phe Cys Phe Thr Asn Val Leu Phe Asp Ala Phe Gly Ser His
1 5 10 15
Val

<210> 159

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 159
Cys Asp Tyr Phe Ser Phe Leu Glu Cys Phe Ser Asn Gly Trp Ser Gly
1 5 10 15
Ala

<210> 160
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 160
Cys Phe Phe Phe Gly Gln Gly Asp Phe Met Cys Trp Ile Cys Leu Thr
1 5 10 15
Val

<210> 161
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 161
Cys Phe Phe Asn Ser Phe Asn Cys Thr Pro Asn Glu Met Trp Tyr Trp
1 5 10 15
Phe

<210> 162
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 162
Cys Phe Phe Ser Tyr Cys Phe Ser His Asp Val Ser Thr Tyr Asn Thr
1 5 10 15
Ala

<210> 163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 163
Cys Phe Phe Ser Tyr Trp Asn Cys Leu Thr Asn Asn Ala Phe Val Lys
1 5 10 15
Pro

<210> 164
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 164
Cys Phe Gly Phe Ser Asp Cys Leu Ser Trp Phe Val Gln Pro Ser Thr
1 5 10 15
Ala

<210> 165
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 165
Cys Phe Gly Asn Phe Leu Ser Phe Gly Phe Asn Cys Glu Ser Ala Leu
1 5 10 15
Gly

<210> 166
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 166
Cys Phe Gly Asn Leu Gly Asn Leu Ile Tyr Thr Cys Asp Arg Leu Met
1 5 10 15
Pro

<210> 167
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 167
Cys Phe Gly Asn Val Phe Cys Val Tyr Asn Gln Phe Ala Ala Gly Leu
1 5 10 15
Phe

<210> 168
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 168
Cys Phe Thr Cys Phe Ser Phe Ala Phe Asn Phe Cys Phe Met Cys Trp
1 5 10 15
Met

<210> 169
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 169
Cys Phe Thr Phe Phe Lys Ala Ser Trp Ser Trp Trp His His Ala Met
1 5 10 15
Met

<210> 170
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 170
Cys Phe Val His Asn Phe Phe Trp Phe Leu Gly Lys Asn Ser Asn Cys
1 5 10 15
Arg

<210> 171
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 171
Cys Phe Trp Tyr Ser Trp Leu Cys Ser Ala Ser Ser Ser Asp Ala Leu
1 5 10 15
Ile

<210> 172
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 172
Cys Gly Tyr Phe Cys Ser Phe Tyr Asn Tyr Leu Asp Ile Gly Thr Ala
1 5 10 15
Ser

<210> 173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 173
Cys His Arg Cys Lys Arg Arg His Leu Leu Arg Arg Lys Gln Ala Asn
1 5 10 15
Arg

<210> 174
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 174
Cys Ile Phe Asn Ser Tyr Phe Cys Ser Phe Gln Leu Thr Ser Tyr Gly
1 5 10 15
Ser

<210> 175
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 175
Cys Lys Ala Phe Phe Phe Asn Phe Gln Cys Phe Val Phe Val Phe His
1 5 10 15
Phe

<210> 176
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 176
Cys Lys Phe Ser Phe Asp Phe Phe Ala Arg Phe Asn Arg His Phe Tyr

1
His

5

10

15

<210> 177
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 177
Cys Lys Ser Lys Lys Ser Ser His Ser Glu Ser Glu His Lys Lys Ser
1 5 10 15
Ser

<210> 178
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 178
Cys Leu Phe Asn Cys Ser Gly Glu Ser Trp Pro Met Ser Ile Val Pro
1 5 10 15
Ser

<210> 179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 179
Cys Leu Lys Asp Tyr Tyr Ser Pro Cys Ser Tyr Ser Cys Asp Gln
1 5 10 15
His

<210> 180
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 180
Cys Leu Leu Lys Tyr Cys Tyr Ser Asp Leu Ala Ser Ser Ser Leu Ser
1 5 10 15
Ile

<210> 181

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 181
Cys Leu Val Phe Met Arg Pro Tyr Phe Leu Leu Val Phe Leu Met Cys
1 5 10 15
Trp

<210> 182
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 182
Cys Leu Tyr Cys His Leu Asn Asn Gln Phe Leu Ser Trp Val Ser Gly
1 5 10 15
Asn

<210> 183
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 183
Cys Leu Tyr Cys Leu Asn Tyr Ala Asn Phe Ser Asp Pro Met Thr Met
1 5 10 15
Phe

<210> 184
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 184
Cys Asn His Leu Gly Phe Phe Ser Ser Phe Cys Asp Arg Leu Val Glu
1 5 10 15
Asn

<210> 185
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 185
Cys Asn Ser Phe Met Phe Ile Asn Gly Ser Phe Lys Glu Thr Gly Gly
1 5 10 15
Cys

<210> 186
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 187
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 188
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 189
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 190
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 191
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 191
Cys Arg Arg Arg Ser Gln Arg Arg Asn Arg Arg Gly Asn Asp Asp Ser
1 5 10 15
Ala

<210> 192
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 192
Cys Ser Phe Phe Met Pro Trp Cys Asn Phe Leu Asn Gly Glu Met Ala
1 5 10 15
Val

<210> 193
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 193
Cys Ser Phe Ser Val Ser Lys Ser Ser Gln Ile Phe Ala Val Ser Tyr
1 5 10 15
Ser

<210> 194
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 194
Cys Ser Leu Thr Gly Cys Leu Tyr Asp Tyr Val Ser Phe Gly Trp Gly
1 5 10 15
Ala

<210> 195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 195
Cys Ser Ser Ser Met Thr Tyr Arg Thr Ser Ser Ser Trp His Leu Lys
1 5 10 15
Ile

<210> 196
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 196
Cys Ser Thr Ser Tyr Ser Trp Asn Lys Trp Gln Ile Ser Ile Ser Ser
1 5 10 15
Tyr

<210> 197
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 197
Cys Thr Cys Phe Asn Leu Phe Asp Met Lys Thr Cys Pro Ser Phe Cys
1 5 10 15
Thr

<210> 198
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 198
Cys Thr Phe Gly Phe Pro Cys Val Met Ser Leu Val Asn His Val Pro

1 5 10 15
Ser

<210> 199
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 199
Cys Thr Asn Ser Asn Leu Asn Ser Ser Trp His Thr Met Val Asp
1 5 10 15
Arg

<210> 200
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 200
Cys Thr Trp Trp Trp Trp Val Val Asn Arg Glu Pro Tyr Val Ala
1 5 10 15
Cys

<210> 201
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 201
Cys Trp Asp Trp Met Thr Trp Gly Asn Asp Val Leu Val Asn Thr Asp
1 5 10 15
Trp

<210> 202
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 202
Cys Trp Leu Asp Asp Asp Ser Asp Asp Tyr Asp Asp Asp Asp Met Met
1 5 10 15
Ala

<210> 203

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 203
Cys Trp Met Gly Leu Phe Glu Cys Pro Asp Ala Trp Leu His Asp Trp
1 5 10 15
Asp

<210> 204
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 204
Cys Trp Asn Ile Ser Cys Met Phe Gly Phe Gly Trp Gly Gly Gly
1 5 10 15
Leu

<210> 205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 205
Cys Tyr Ala Tyr Tyr Phe Phe Phe Tyr Ser Ser Gly Arg Gly Tyr His
1 5 10 15
Gln

<210> 206
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 206
Cys Tyr Phe Pro Phe Tyr Cys Tyr Asn Thr Ser Ser Leu Ser Leu Asp
1 5 10 15
Phe

<210> 207
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 207
Ala Asp Arg Val Trp Pro Arg His Thr Ser Ser Pro Tyr His Arg His
1 5 10 15

<210> 208
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 208
Ala Phe Ile Ser Asn Leu His Ala Ala Cys Ser Val Gly Ser Cys Lys
1 5 10 15

<210> 209
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 209
Cys His Thr Pro Trp Pro Pro Met Asn Arg Tyr Ala Ser Val Leu Ile
1 5 10 15

<210> 210
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 210
Cys Thr Arg Arg Arg Arg Phe Cys Val Ile Ile Phe Arg Arg Glu Met
1 5 10 15

<210> 211
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 211
Cys Thr Ser Ser Ser Gln Lys His Cys Tyr His Gly His Ser Ser Asp
1 5 10 15

<210> 212
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 212
Asp Cys Cys Cys Met Trp Asp Asp Gly Val Gly Asp Asp Val Asp Met
1 5 10 15

<210> 213
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 213
Asp Phe Cys Phe Met Met Asn Cys Thr Met Asn Ala His Tyr Phe
1 5 10 15

<210> 214
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 214
Asp Val Asn Ser Ile Trp Met Ser Arg Val Ile Glu Trp Thr Tyr Asp
1 5 10 15

<210> 215
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 215
Asp Trp Cys Asn Asn Ala Trp Asp Thr Tyr Ala Ile His Asn Asp Cys
1 5 10 15

<210> 216
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 216
Phe Leu Phe Phe Thr Asn Met Val Trp Tyr Phe Phe Ile Met Gly Ala
1 5 10 15

<210> 217
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 217

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

<210> 218
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 218
Gly Ala Gly Gly Phe Phe Leu Pro Cys Leu Trp Asn Pro Asp Arg Thr
1 5 10 15

<210> 219
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 219
Gly Lys Cys Val Phe Arg Arg Glu Asp Cys Phe Trp Tyr Tyr Met His
1 5 10 15

<210> 220
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 220
Gly Ser Ser Ser Cys Gln Gly Val Ser Gly Ser Asp Tyr Val Met Lys
1 5 10 15

<210> 221
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 221
His Ala Ser Ile His His Cys Ser Tyr Gln Gly Tyr Gly Gln Ser Gly
1 5 10 15

<210> 222
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 222
His Cys Asn Asn Glu Asn Arg Trp His His Asn Gly Ala Ile Gly Val

1 5 10 15

<210> 223
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 223
His Ile Ser Ser Cys Gln Met Val Gln Ser Trp Ser Arg Pro Ala His
1 5 10 15

<210> 224
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 224
Ile Trp Glu Trp Phe Glu Leu Glu Met Leu Tyr Val Asn Arg Tyr Cys
1 5 10 15

<210> 225
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 225
Leu Ile His Arg Tyr Cys Arg Arg Val Pro Cys Arg Arg Glu Leu Lys
1 5 10 15

<210> 226
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 226
Met Ser Asn Phe Leu Ile Glu Phe Thr Tyr Asp Asn Val Gly Val Arg
1 5 10 15

<210> 227
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 227
Asn Phe Phe Val Glu Trp Ala Phe Asp Thr Gln Asp Arg Glu Glu Leu
1 5 10 15

<210> 228
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 228
Asn Gly Asn Glu Asn Asp Thr Ile Asn Asp Asn Asp Ile Asn Ala Ser
1 5 10 15

<210> 229
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 229
Asn Ile Asn Ile Val Glu Glu Arg Phe Met Val Glu Trp Asp Val Gln
1 5 10 15

<210> 230
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 230
Asn Pro Trp Ala Ser Ser Leu Val Ala Ala Cys Tyr Leu Asp Glu Ser
1 5 10 15

<210> 231
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 231
Asn Trp Trp Met Val Asn Leu Ile Pro Asp Glu Trp Cys Trp Asn Ser
1 5 10 15

<210> 232
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 232
Pro Phe Leu Phe Glu Ala Ser Asp Arg His Pro Ala Phe Asn His Met
1 5 10 15

<210> 233
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 233
Pro Gly Ser Ser Thr Phe Tyr Ser Ile Thr Met Thr Trp Asp Leu Pro
1 5 10 15

<210> 234
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 234
Pro Pro Ser Ser Asn Ser Asn Phe Met Leu Glu Phe Ser Trp Asp Ser
1 5 10 15

<210> 235
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 235
Pro Gln Ser Glu His Ser Lys Ser Tyr Met Ser Trp Ala Arg Ser Ser
1 5 10 15

<210> 236
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 236
Pro Ser Ala Cys Ser Arg Arg Ile Ile Gln Asp Thr Phe Phe Phe Met
1 5 10 15

<210> 237
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 237
Gln Glu Leu Arg Val Arg Lys Arg Arg Pro Lys Asp His Glu Arg
1 5 10 15

<210> 238
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 238
Gln Glu Met Leu Asn Phe Phe Phe His Asn Gly Asn Phe Phe Phe Val
1 5 10 15

<210> 239
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 239
Gln His Arg Gln His His Asn Val Ile Tyr Ser Ala Val Cys Val Ala
1 5 10 15

<210> 240
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 240
Gln Met Asp Thr Ile Asp Asp Met Thr Trp Thr Gly Asp Asp Asp Cys
1 5 10 15

<210> 241
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 241
Arg Gly Pro Tyr Ile Trp Trp Leu Glu Glu Gln Ser Arg Thr Trp Glu
1 5 10 15

<210> 242
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 242
Arg Arg Arg Asn Lys Leu Ala Arg Thr Leu Val Tyr Arg Arg Arg Val
1 5 10 15

<210> 243

<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 243
Arg Arg Arg Pro Lys Pro Gly Pro His Ile Ile Phe Thr Ala Ile Asn
1 5 10 15

<210> 244
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 244
Arg Arg Tyr Ala Thr Trp Ser Val Ala Ser Ile Gln Glu Cys Pro Arg
1 5 10 15

<210> 245
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 245
Arg Tyr Pro Tyr Asp Met Asp Trp Asp Trp His His Gln Glu Arg Asp
1 5 10 15

<210> 246
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 246
Ser Phe Phe Phe Trp Asp Thr Phe Gly Glu Ser Asn Lys Phe Phe Met
1 5 10 15

<210> 247
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 247
Ser Phe Met Phe Asn Asp Ser Ile Asp Asp Asp Asp Asp Val Ser Glu
1 5 10 15

<210> 248
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 248
Ser Pro Gln Ala Arg Ser His Glu Asp Gln Val Met Gln Trp Trp Ile
1 5 10 15

<210> 249
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 249
Thr Phe Asp Asp Ala Met Leu Glu Trp Ser Leu Val Glu Trp Asp Ile
1 5 10 15

<210> 250
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 250
Thr Gly Gln Ser Ser Met Val Asn His Met Val Ser Glu Asn Gly Gly
1 5 10 15

<210> 251
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 251
Thr Met Gln Asp Phe Ser Ser Asp Glu Phe Tyr Thr Trp Thr Trp Asp
1 5 10 15

<210> 252
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 252
Val Phe Gly Phe Ser Cys Phe Glu Lys Asp Lys Arg Phe Asp Glu Leu
1 5 10 15

<210> 253
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 253

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

<210> 254

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 254

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

<210> 255

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 255

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

<210> 256

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 256

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

<210> 257

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 257

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

<210> 258

<211> 16

<212> PRT

<213> Artificial Sequence

<220>
<223> binding module

<400> 258
Trp Trp Phe Arg Phe Lys Arg Arg Arg Arg Trp Met Lys Ser Val Arg
1 5 10 15

<210> 259
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 259
Tyr Asp Met Met Met Asp Met Leu Lys Asn Asp Asp Lys Gly Phe Phe
1 5 10 15

<210> 260
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 260
Tyr Arg Met Ala Asp Arg Asp Val His Arg Trp Asp Lys Glu Tyr Glu
1 5 10 15

<210> 261
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 261
Tyr Arg Asn Met Glu Arg Ser Asn Met Ala Glu Thr Asn Ile Leu Ala
1 5 10 15

<210> 262
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 262
Tyr Tyr Phe Thr Glu Trp Ser Glu Asp Thr Ser Gly Gly Ser Ser Gly
1 5 10 15

<210> 263
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 263
Ala Lys Ile Leu Tyr Tyr Tyr Asp Met Gln Trp His Ile
1 5 10

<210> 264
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 264
Ala Pro Phe Leu Val Trp Tyr Ala Ser Thr Ser Asp Thr
1 5 10

<210> 265
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 265
Ala Val Ser Thr Ala Leu Tyr Asn Thr Trp Gln Val Leu
1 5 10

<210> 266
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 266
Cys Ala His Pro Pro Pro Tyr Lys Glu Asn Tyr Leu Tyr
1 5 10

<210> 267
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 267
Cys Cys Trp Thr Glu Ala Tyr Asp Ala His Pro Trp Arg
1 5 10

<210> 268
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 268
Cys Lys Phe Phe His Tyr His Ile Gly Phe Ala Thr
1 5 10

<210> 269
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 269
Cys Val Trp Cys Ser Glu Tyr Phe Arg Glu Asp Pro Pro
1 5 10

<210> 270
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 270
Cys Tyr Thr Ser Lys Tyr Tyr Arg Glu Lys Tyr Glu Leu
1 5 10

<210> 271
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 271
Asp Thr Ile Trp Trp Trp Tyr Met Trp Cys Trp His Tyr
1 5 10

<210> 272
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 272
Glu His Gly Pro Phe Val Asp Ser Glu Tyr Pro Gln Pro
1 5 10

<210> 273
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 273
Phe Ala Asp Asn Leu Gly Tyr Val Gly Ser Asp Val Ile
1 5 10

<210> 274
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 274
Phe Ala Pro Met Lys Ser Tyr Gly Val Ser Leu Pro Pro
1 5 10

<210> 275
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 275
Phe Glu Leu Ala Thr Gly Tyr Val Pro Ala Leu Leu Lys
1 5 10

<210> 276
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 276
Phe Phe Phe Ser Met Ser Tyr Phe Phe Phe Arg Ala Ala
1 5 10

<210> 277
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 277
Phe Phe Gly Phe Asp Val Tyr Asp Met Ser Asn Ala Leu
1 5 10

<210> 278
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 278
Phe Phe His Phe Cys Phe Tyr Thr Cys Met Phe His Leu
1 5 10

<210> 279
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 279
Phe Phe Leu Ser Pro Phe Tyr Phe Phe Asn Glu Phe Phe
1 5 10

<210> 280
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 280
Phe Phe Met Ala Ser Ser Tyr Ser Tyr Pro Val Ala Gly
1 5 10

<210> 281
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 281
Phe Phe Pro Ser Ser Trp Tyr Ser His Leu Gly Val Leu
1 5 10

<210> 282
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 282
Phe Phe Val Leu Phe Leu Tyr Leu Trp Leu Gly Val Ser
1 5 10

<210> 283
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 283

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

<210> 284
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 284
Phe Gly Ser Asp Val Phe Tyr Leu Arg Ser Ala Pro His
1 5 10

<210> 285
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 285
Phe His Glu Ala Pro Val Tyr Glu Thr Ser Glu Pro Pro
1 5 10

<210> 286
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 286
Phe Leu Gly Phe Gln Asp Tyr Lys Ser Ala Ala Met Met
1 5 10

<210> 287
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 287
Phe Leu Leu Thr Gly Glu Tyr Val Asp Val Val Ala Ala
1 5 10

<210> 288
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 288
Phe Leu Ser Phe Ala Asn Tyr Glu Asp Glu Leu Leu Arg

1 5 10

<210> 289
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 289
Phe Met Phe Ile Phe Phe Tyr Pro Val Phe Cys Phe Gln
1 5 10

<210> 290
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 290
Phe Arg Phe Phe Asn His Tyr Arg Tyr Pro Ser Gly Gln
1 5 10

<210> 291
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 291
Phe Arg Met Asp Phe Asp Tyr Leu Tyr Pro Ser Leu Pro
1 5 10

<210> 292
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 292
Phe Arg Tyr Phe Tyr Phe Tyr Ser His Gly Phe Lys Phe
1 5 10

<210> 293
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 293
Phe Ser Ala Leu Pro Thr Tyr Glu Val Asn Ser Tyr Lys
1 5 10

<210> 294
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 294
Phe Ser Asp Ser Ser Phe Tyr Ser Asp Leu Ser Val Val
1 5 10

<210> 295
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 295
Phe Ser Ser Val Asp Ser Tyr Ser Gly Pro Arg Pro Asp
1 5 10

<210> 296
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 296
Phe Ser Tyr Ser Val Ser Tyr Ala His Pro Glu Gly Leu
1 5 10

<210> 297
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 297
Phe Val Gly Phe Phe Leu Tyr Leu Thr Leu Leu Leu Pro
1 5 10

<210> 298
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 298
Gly Glu Asn Phe Cys Pro Tyr Ser Phe Phe Gly Cys Gly
1 5 10

<210> 299
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 299
Gly Phe Ala Trp Ser Ser Tyr Leu Gly Thr Thr Val His
1 5 10

<210> 300
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 300
Gly Phe Pro Phe Ile Phe Tyr Val Val Asp Trp Met Arg
1 5 10

<210> 301
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 301
Gly Phe Ser Glu Phe Leu Tyr Asp Leu Glu Val Gly Ile
1 5 10

<210> 302
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 302
Gly Phe Val Ala Tyr Asn Tyr Asp Lys Tyr Ser Gly Ala
1 5 10

<210> 303
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 303
Gly Val Ser Gln Phe Leu Tyr Asp Trp Val Lys Gly Gly
1 5 10

<210> 304
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 304
Gly Tyr Asn Ile Tyr Trp Tyr Ile Asn Asn Val Glu Tyr
1 5 10

<210> 305
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 305
His Tyr Lys Tyr Asn Val Tyr Cys Lys Tyr Asn Gly Tyr
1 5 10

<210> 306
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 306
Ile Phe Leu Pro Trp His Tyr Asp Gly Tyr Thr Phe Ala
1 5 10

<210> 307
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 307
Ile Phe Ser Phe Leu Ser Tyr Val Pro Val Asp Lys Val
1 5 10

<210> 308
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 308
Ile Tyr Ala Ala Leu Tyr Tyr Arg Phe Pro Thr Met Asp
1 5 10

<210> 309

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 309
Lys Phe Phe Phe Trp Phe Tyr Ile Asn Phe Val Met Met
1 5 10

<210> 310
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 310
Leu Asp Pro Leu Val Pro Tyr Leu Tyr Glu Asn Leu Phe
1 5 10

<210> 311
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 311
Leu Phe Asp Ala Tyr Trp Tyr Ser Asp Thr Ala Met Ser
1 5 10

<210> 312
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 312
Leu Leu Phe Phe Asp Asp Tyr Phe Lys Ser Ala Gly Arg
1 5 10

<210> 313
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 313
Leu Asn Phe Met Ile Phe Tyr Leu Ser Leu Asn Pro Trp
1 5 10

<210> 314
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 314
Leu Pro His Leu Ile Gln Tyr Arg Val Leu Leu Val Ser
1 5 10

<210> 315
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 315
Leu Pro Ser Gln Phe Gly Tyr Gly Ser Val Pro Thr Asp
1 5 10

<210> 316
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 316
Leu Pro Ser Gln Phe Gly Tyr Gly Ser Val Pro Thr Asp
1 5 10

<210> 317
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 317
Leu Ser Phe Ser Asp Phe Tyr Phe Ser Glu Gly Ser Glu
1 5 10

<210> 318
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 318
Leu Thr Asn Ser Gly Val Tyr Asp Gly Thr Pro Leu Pro
1 5 10

<210> 319
<211> 13
<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 319

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

<210> 320

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 320

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

<210> 321

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 321

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

<210> 322

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 322

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

<210> 323

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 323

Asn Trp Tyr Ala Glu Tyr Tyr Val Tyr Asp Lys Gly
1 5 10

<210> 324

<211> 13

<212> PRT

<213> Artificial Sequence

<220>
<223> binding module

<400> 324
Asn Tyr Phe Ser Ala Met Tyr Tyr Asp Gly Trp Met Ser
1 5 10

<210> 325
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 325
Pro Ala Ser Leu Glu Leu Tyr Glu Asn Leu Val Ala Gly
1 5 10

<210> 326
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 326
Pro Cys Trp Tyr Arg Tyr Tyr His Glu Phe Trp Ile Trp
1 5 10

<210> 327
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 327
Pro Leu Tyr Tyr Glu Ser Tyr Arg Met Arg Thr Tyr Gln
1 5 10

<210> 328
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 328
Gln Tyr Ala Ser Tyr Met Tyr Tyr Cys Phe Pro Lys Tyr
1 5 10

<210> 329
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 329
Arg Ala Trp Trp Trp Trp Tyr Leu Asp Met Tyr Trp Thr
1 5 10

<210> 330
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 330
Arg Ala Tyr Asn Tyr Tyr Tyr Tyr Val Met Tyr Ala Cys
1 5 10

<210> 331
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 331
Arg Trp Ile Trp Trp Pro Tyr Val Asn Met Ile Trp Thr
1 5 10

<210> 332
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 332
Ser Asp Phe Leu Ser Pro Tyr Leu Ala Tyr Glu Arg Ser
1 5 10

<210> 333
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 333
Ser Phe Asp Val Arg Ser Tyr Val Leu Ala Gly Thr Glu
1 5 10

<210> 334
<211> 13
<212> PRT
<213> Artificial Sequence

<223> binding module

<400> 334
Ser Leu Phe Leu Asp Asp Tyr Ala Leu Gly Pro Arg Val
1 5 10

<210> 335
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 335
Ser Ser Val Leu Gly Phe Tyr Asp Pro Val Glu Val Ser
1 5 10

<210> 336
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 336
Ser Val Ala Phe Tyr Asp Tyr Leu Pro Thr Asp Leu Pro
1 5 10

<210> 337
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 337
Ser Val Leu Asp Phe Asn Tyr Gly His Asp Val Asn Val
1 5 10

<210> 338
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 338
Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> 339
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 339
Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> 340
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 340
Ser Val Ser Asp Phe Leu Tyr Arg Ser Ile Tyr Ser Leu
1 5 10

<210> 341
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 341
Ser Trp Ser Trp Trp Arg Tyr Gly Pro Gln Asn Thr Val
1 5 10

<210> 342
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 342
Ser Tyr Gly Phe Pro Ile Tyr Asp Ala Leu Leu Glu Gln
1 5 10

<210> 343
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 343
Val Phe Asp Val Gly Leu Tyr Trp His Ala Ala Pro Pro
1 5 10

<210> 344
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 344
Val Gly Phe Trp Val Asp Tyr Asp Asn Ser Ser Val Met
1 5 10

<210> 345
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 345
Val Leu Asp Leu Pro Tyr Tyr Trp Pro Val Lys Tyr Thr
1 5 10

<210> 346
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 346
Val Leu Leu Ala Asp Ser Tyr Gln Arg Asp Glu His Met
1 5 10

<210> 347
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 347
Val Leu Leu Phe Asp Asp Tyr Gly Tyr Ala Glu Ser Ala
1 5 10

<210> 348
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 348
Val Ser Ala Ser Gly Met Tyr Asp Gly Val Asp Leu Met
1 5 10

<210> 349
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 349

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

<210> 350
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 350
Val Ser Ser Glu Trp Thr Tyr Gly Ala Val Ala Asp Leu
1 5 10

<210> 351
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 351
Val Ser Val Leu Ser Asp Tyr Ser Ile Lys Ala Leu Leu
1 5 10

<210> 352
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 352
Trp Ala Asp Met Tyr Tyr Tyr Tyr Asp Trp Tyr Thr Met
1 5 10

<210> 353
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 353
Trp Asp Trp Trp Gln Phe Tyr Glu Lys Met Trp Leu Phe
1 5 10

<210> 354
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 354
Trp Asn Trp Trp Gly Val Tyr Leu Gly Ile Cys Trp Leu

1 5 10

<210> 355
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 355
Trp Trp Gln Thr Trp Trp Tyr Arg Thr Tyr Trp Glu Ile
1 5 10

<210> 356
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 356
Tyr Ala Gly Val Tyr Ser Tyr Phe Thr Gly Ser Thr Leu
1 5 10

<210> 357
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 357
Tyr Cys Gln Tyr Arg Glu Tyr Tyr Thr Met Tyr Val Cys
1 5 10

<210> 358
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 358
Tyr Phe Val Glu Thr Tyr Tyr Asn Arg Tyr His Val Ser
1 5 10

<210> 359
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 359
Tyr Leu Ser Leu His Ala Tyr Glu Ser Phe Gly Gly Ser
1 5 10

<210> 360
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 360
Tyr Arg Tyr Gln Met Ser Tyr Tyr Ala Tyr Gln Tyr His
1 5 10

<210> 361
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 361
Tyr Ser Met Tyr Pro Ile Tyr Asn Lys Cys Ser Gln His
1 5 10

<210> 362
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 362
Tyr Trp Ile Tyr Asn Asn Tyr Thr Tyr Tyr Cys Gly
1 5 10

<210> 363
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 363
Tyr Trp Trp Glu Gln Trp Tyr Ser Trp Trp Ile Glu His
1 5 10

<210> 364
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 364
Tyr Tyr Arg Asp Ala Ser Tyr Thr Tyr Pro Tyr Met Tyr
1 5 10

<210> 365
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 365
Tyr Tyr Tyr Ile Pro Val Tyr Ser Ala Gln Cys Tyr Thr
1 5 10

<210> 366
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 366
Ala Cys Pro Trp Pro Ile Pro Pro Trp Pro Leu Arg Val
1 5 10

<210> 367
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 367
Ala Arg Arg Trp Pro Leu Pro Arg Arg Asp Gln Phe Ser
1 5 10

<210> 368
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 368
Cys Arg Arg Ile Gln Gln Pro Cys Val Phe Arg Arg His
1 5 10

<210> 369
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 369
Asp Glu Pro Pro Cys Ala Pro Glu Cys Asn Gly Asp Gly
1 5 10

<210> 370
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 370
Asp Phe Gln Phe Pro Lys Pro Ala Phe Cys Ser Thr Cys
1 5 10

<210> 371
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 371
Glu Leu Tyr Phe Phe Pro Cys Gly Ser Phe Cys Gln
1 5 10

<210> 372
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 372
Phe Phe Gly Phe Asn His Pro Phe Leu Phe Ser Cys Trp
1 5 10

<210> 373
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 373
Phe Phe Gln Ser Ile Gln Pro Ile Phe Ala Arg Ser Met
1 5 10

<210> 374
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 374
Phe Phe Trp Val Lys Asp Pro Ser Pro Cys Phe Asp His
1 5 10

<210> 375

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 375
Phe Gly Lys Phe Phe Asp Pro Leu Arg Arg Ala Lys Asp
1 5 10

<210> 376
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 376
Phe Lys Gly Glu Phe Trp Pro Ala Phe Gly Val Gln Val
1 5 10

<210> 377
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 377
Phe Lys Leu His Trp Phe Pro Thr Cys Pro Phe Ile Gln
1 5 10

<210> 378
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 378
Phe Leu Ser Phe Val Phe Pro Ala Ser Ala Trp Gly Gly
1 5 10

<210> 379
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 379
Phe Met Asp Ile Trp Ser Pro Trp His Leu Leu Gly Thr
1 5 10

<210> 380
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 380
Phe Asn Pro Pro Glu Pro Pro Cys Pro Glu Phe Ser Lys
1 5 10

<210> 381
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 381
Phe Gln Phe Phe Asp Pro Pro Ser Phe Phe Gly Phe Lys
1 5 10

<210> 382
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 382
Phe Gln Phe Ser Phe Gln Pro Asp Gly Val Glu Arg Arg
1 5 10

<210> 383
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 383
Phe Gln Asn Cys Phe Trp Pro Ile Phe Glu Ala Met Glu
1 5 10

<210> 384
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 384
Phe Ser Phe Phe Ala Asp Pro Ile Glu Leu Glu Trp Asp
1 5 10

<210> 385
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> binding module

<400> 385
Phe Ser Ser Leu Phe Phe Pro His Trp Ala Gln Leu
1 5 10

<210> 386
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 386
Phe Tyr Met Pro Phe Gly Pro Thr Trp Trp Gln His Val
1 5 10

<210> 387
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 387
Phe Tyr Tyr Phe Gly Phe Pro Gln Cys Leu Ile Leu Phe
1 5 10

<210> 388
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 388
Gly Phe Glu Glu Phe Gln Pro Val Asp Phe Ile Ile Arg
1 5 10

<210> 389
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 389
Gly Leu Thr Arg Phe Phe Pro Val Ser Phe Ser Phe Phe
1 5 10

<210> 390
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 390
His Ala Arg Pro Pro Cys Pro Phe Val Asn Glu Lys Pro
1 5 10

<210> 391
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 391
His Glu Phe Met Trp Phe Pro Val His Trp Glu Phe His
1 5 10

<210> 392
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 392
His Arg Asn Pro Arg Arg Pro Gln Ile Glu Gly Val Arg
1 5 10

<210> 393
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 393
Ile Ser Gly His Cys Phe Pro Cys Ile Glu Val Ser Asp
1 5 10

<210> 394
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 394
Lys Phe Gln Asp Phe Met Pro Gln Met Phe His Gly Ile
1 5 10

<210> 395
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 395
Leu Phe Phe Met Pro Phe Pro Phe Phe Phe Phe Pro Tyr
1 5 10

<210> 396
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 396
Leu Phe Ser Trp Phe Leu Pro Thr Asp Asn Tyr Pro Val
1 5 10

<210> 397
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 397
Leu Val Cys Ile Arg Arg Pro Arg Arg Arg Cys Phe Cys
1 5 10

<210> 398
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 398
Met Pro Arg Arg Glu Arg Pro Leu Trp Met Leu Thr Arg
1 5 10

<210> 399
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 399
Met Arg Arg His Arg Ala Pro Arg Ser Gln Cys Met Glu
1 5 10

<210> 400
<211> 13
<212> PRT
<213> Artificial Sequence

<223> binding module

<400> 400
Asn Phe Phe Gly Pro Ile Pro Met Asn Phe Ala Phe Thr
1 5 10

<210> 401
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 401
Asn Phe Phe Ser Ile Asp Pro Phe Cys Gln Ala Ile Tyr
1 5 10

<210> 402
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 403
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 404
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

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

<210> 405
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 405
Pro Phe Gly Leu Phe Pro Pro Gln Val Tyr Tyr Phe Leu
1 5 10

<210> 406
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 406
Pro Gly Ala Ala Pro Pro Pro Cys Asn Asn Ser Asp Asn
1 5 10

<210> 407
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 407
Pro Pro Cys Pro Trp Arg Pro Ser Ala Thr His Leu Pro
1 5 10

<210> 408
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 408
Pro Pro Lys Phe Leu Ala Pro His Thr Ser Ala Met Leu
1 5 10

<210> 409
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 409
Pro Pro Arg Val Ala Phe Pro Ile Arg Gln Arg Arg Val
1 5 10

<210> 410
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 410
Pro Thr Arg Pro Asn Gly Pro Glu Ser Glu Asp Leu Phe
1 5 10

<210> 411
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 411
Gln Cys Pro Asp Pro Ser Pro Ser Lys Cys Pro Phe Gly
1 5 10

<210> 412
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 412
Gln Arg Arg Ala Pro Arg Pro Ser Glu His Arg Arg Glu
1 5 10

<210> 413
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 413
Arg Ala Arg Arg Ala Gly Pro Leu Gly Asp Arg Lys Leu
1 5 10

<210> 414
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 414
Arg Glu Gly Arg Thr Arg Pro Arg Tyr Pro Arg Trp Phe
1 5 10

<210> 415
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 415

Arg Glu Pro Asn Pro Pro Pro Leu Gln Ser Pro Met Ser
1 5 10

<210> 416
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 416
Arg Gly Phe Gln Phe Gly Pro Ser Thr Phe Glu Tyr Phe
1 5 10

<210> 417
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 417
Arg Gly Pro Arg Arg Thr Pro Thr Ile His Arg Pro Trp
1 5 10

<210> 418
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 418
Arg His Phe His Val Arg Pro Val Asn Trp Trp Ser Lys
1 5 10

<210> 419
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 419
Arg Ile Asn Arg Ser Arg Pro Ile Met Trp Gln Arg Thr
1 5 10

<210> 420
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 420
Arg Asn Asp Arg Val Arg Pro Trp Lys Val Lys His Gln

1 5 10

<210> 421
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 421
Arg Asn Met Arg Tyr Arg Pro Gln Tyr Ala Asp Leu Cys
1 5 10

<210> 422
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 422
Arg Asn Asn Arg Pro Lys Pro Thr Gln Ser His Arg Val
1 5 10

<210> 423
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 423
Arg Arg His Arg Trp Trp Pro Gln Glu Phe Ser Arg His
1 5 10

<210> 424
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 424
Arg Arg Arg Leu Phe Thr Pro Asn Ser Arg Ala Arg His
1 5 10

<210> 425
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 425
Arg Arg Ser Arg Phe Val Pro Glu Tyr Leu Phe Arg Pro
1 5 10

<210> 426
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 426
Arg Trp His Pro Arg Tyr Pro Val Met Lys Lys Asn Ser
1 5 10

<210> 427
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 427
Arg Trp Ile Pro Arg Pro Pro Arg Arg Ala Cys Arg Arg
1 5 10

<210> 428
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 428
Ser Phe Trp Pro Phe Cys Pro Thr Thr Trp Ala Asn Tyr
1 5 10

<210> 429
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 429
Ser Ile Phe Gln Phe Asn Pro Phe Pro Glu Gly Phe Phe
1 5 10

<210> 430
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 430
Ser Leu Phe Phe Met Pro Pro Glu Arg Leu Asp His Arg
1 5 10

<210> 431
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 431
Ser Asn Arg His Arg Arg Pro Arg Arg Arg Trp Arg Met
1 5 10

<210> 432
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 432
Thr Phe Phe Thr Asn Lys Pro Phe Ser Tyr His Phe Glu
1 5 10

<210> 433
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 433
Thr Thr Pro Val Gln Pro Pro Gly Glu Val Ser Gln Val
1 5 10

<210> 434
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 434
Thr Tyr Asn Ser Phe Phe Pro Phe Arg His Phe Ala Glu
1 5 10

<210> 435
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 435
Val Lys Ile Arg Arg Arg Pro Arg Arg Met Arg Leu Met
1 5 10

<210> 436
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 436
Trp Lys His Pro Pro Arg Pro Tyr Cys Trp Lys Pro Leu
1 5 10

<210> 437
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 437
Tyr Ile Tyr Thr Val Tyr Pro Arg Asn Ser Ser Trp Phe
1 5 10

<210> 438
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 438
Tyr Gln Pro Trp Gly Pro Pro Pro Pro Pro Leu Val Leu
1 5 10

<210> 439
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 439
Ala Arg Asp Tyr Asp Asn Asn Met Lys Tyr Tyr Leu Asp
1 5 10

<210> 440
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 440
Ala Arg Ile Asn Asn Lys Asn Val Ile Thr Phe Gln Pro
1 5 10

<210> 441

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 441
Ala Ser Arg Ser Ser Asp Asn Ile Ser Tyr Ser Ser Thr
1 5 10

<210> 442
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 442
Ala Ser Ser Asp Ala Gly Asn Tyr Glu Ile Ala Gly Pro
1 5 10

<210> 443
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 443
Ala Thr Asp Asp Glu Asn Asn Glu Met Asn Val Gly Met
1 5 10

<210> 444
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 444
Cys Ser Ser Phe Ser Leu Asn Trp Ser Leu Ser Lys Ser
1 5 10

<210> 445
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 445
Asp Cys Asp His Leu Phe Asn Met Glu Gln Thr Leu Arg
1 5 10

<210> 446
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 446
Asp Cys Val Ser Ser Asn Asn His Asp Ile Thr Arg Gly
1 5 10

<210> 447
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 447
Asp Asp Glu Arg Val Ile Asn Ser Asp Tyr Ser Glu Tyr
'1 5 10

<210> 448
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 448
Asp Asp Lys Asn Glu Asp Asn Asp Ile Pro Lys Thr Pro
1 5 10

<210> 449
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 449
Asp Asp Thr Asn Asp Met Asn Asn Ser Glu Glu Lys Phe
1 5 10

<210> 450
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 450
Asp Asp Val Gln Asp Asp Asn Asp Gln Pro Tyr Asn Thr
1 5 10

<210> 451
<211> 13
<212> PRT

<213> Artificial Sequence
<220>
<223> binding module

<400> 451
Asp Lys Gly Asn Asp Gln Asn Asn Ser Pro Leu Trp Ala
1 5 10

<210> 452
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 452
Asp Leu Val Cys Asn Asn Asn Cys Arg Asn Leu Phe Asn
1 5 10

<210> 453
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 453
Asp Asn His Asp Lys Phe Asn Gln Ala Ile Gln Asp Trp
1 5 10

<210> 454
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 454
Asp Arg Cys Asn Gly Asp Asn Trp Cys Asn Gln Gly Asp
1 5 10

<210> 455
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 455
Asp Ser Glu Tyr Leu Ser Asn Lys Ser Val Asn Asp Phe
1 5 10

<210> 456
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 456
Asp Thr Met Thr Asp Asn Asn Gln Gly Asp Asp Gln Trp
1 5 10

<210> 457
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 457
Glu Lys Asn Trp Asn Tyr Asn Pro Val Met Leu Ala Asn
1 5 10

<210> 458
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 458
Phe Phe Ser Phe Leu Pro Asn Ser Asp Arg Phe Gln Trp
1 5 10

<210> 459
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 459
Phe Phe Ser Tyr Trp Ser Asn Phe Asp Ala Ser Trp His
1 5 10

<210> 460
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 460
Phe His Ile Asp Asp Asp Asn Asp Phe Asp Thr Thr Ser
1 5 10

<210> 461
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 461
Phe Asn Asn Phe Asn Asp Asn Glu His Asn Val Asn Lys
1 5 10

<210> 462
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 462
Phe Tyr Asn Ile Val Asn Asn Ile Phe Ile Cys Cys Ile
1 5 10

<210> 463
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 463
Phe Tyr Trp Asp Arg Leu Asn Val Gly Trp Gly Leu Leu
1 5 10

<210> 464
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 464
Gly Asp Asn His Asn His Asn Thr Asn Thr Ile Glu Pro
1 5 10

<210> 465
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 465
His Ala Asp Gln Asp Asp Asn Cys Arg Gly Lys Asp Asp
1 5 10

<210> 466
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 466
His Asp Trp Asp Asp Trp Asn Ile Glu Ala Glu Asp Gly
1 5 10

<210> 467
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 467
His Gly Ser Ser Asp Thr Asn Gly Gln Ile Leu Phe Glu
1 5 10

<210> 468
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 468
His Asn Trp Asn His Asn Asn Asn Leu Ile Asp Arg Phe
1 5 10

<210> 469
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 469
Ile Cys Asp Asp Asp Asn Asn Met His Leu Tyr Glu Pro
1 5 10

<210> 470
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 470
Ile Asp Asp Ser His Leu Asn Asp Gln Cys Arg Asp Asp
1 5 10

<210> 471
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 471
Ile Asn Cys Asn Asn Asn Ser Leu Asn Asn Asn Asn
1 5 10

<210> 472
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 472
Ile Asn Asn Val Val Tyr Asn Leu His Asp Arg Asn Asn
1 5 10

<210> 473
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 473
Ile Ser Asn Cys Asn Ile Asn Asn Gly Asn Asn Asp Ser
1 5 10

<210> 474
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 474
Ile Ser Asn Arg Gln Ser Asn Thr Ser Asn Gly Met Ser
1 5 10

<210> 475
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 475
Lys Phe Ser Ser Leu His Asn Ile Ser Gly Pro Lys Ser
1 5 10

<210> 476
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 476
Lys Asn Leu Asn Gln Asn Asn Asn His Phe Asn Asn
1 5 10

<210> 477
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 477
Lys Asn Arg Val Asn Lys Asn Thr Asn Val His Cys Phe
1 5 10

<210> 478
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 478
Leu Ser Asn Leu Asn Tyr Asn Pro Asn His His Asp Met
1 5 10

<210> 479
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 479
Met Arg Ser Ser Ser Phe Asn Phe Gly Ser Phe Asp Gln
1 5 10

<210> 480
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 480
Met Ser Asn Ser Ser Ser Asn Ser Ser Ser Ser Gly
1 5 10

<210> 481
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 481

Met Tyr Ser Asn Tyr Tyr Asn Phe Leu Gln Lys Ser Trp
1 5 10

<210> 482
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 482
Asn Asp Arg Asn Asp His Asn Gln His Arg Tyr Asp His
1 5 10

<210> 483
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 483
Asn Glu Met Trp Asn Asn Asn Asn Val Met Asn His His
1 5 10

<210> 484
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 484
Asn Glu Asn Glu Asn Asp Asn Asn Met Asn Met Glu Ile
1 5 10

<210> 485
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 485
Asn Asn Asn Ser Asn His Asn Asp Pro Thr Asn Ala Glu
1 5 10

<210> 486
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 486
Asn Asn Val Leu Asn His Asn Cys Asn Met Phe Leu Asn
103

1 5 10

<210> 487
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 487
Asn Pro Thr Lys Asn Arg Asn Thr His Leu Gly Gly Arg
1 5 10

<210> 488
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 488
Asn Arg Glu Val Lys Asn Asn Arg Gln Lys Val Phe Lys
1 5 10

<210> 489
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 489
Asn Arg Asn Asn His Phe Asn Asn Glu Tyr Glu Trp Asn
1 5 10

<210> 490
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 490
Asn Thr Asp Leu Asn Asn Asn Gln Thr Val Ser Asn Arg
1 5 10

<210> 491
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 491
Pro Asp Asp Ala Pro His Asn Tyr Cys Thr Asp Pro Leu
1 5 10

<210> 492
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 492
Pro Lys Asp Asp Arg Asn Asn Thr Val Ala Ser Cys Glu
1 5 10

<210> 493
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 493
Pro Val Asn Tyr Ala Asn Asn Pro Glu Arg Val Gly His
1 5 10

<210> 494
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 494
Pro Tyr Asn Gly Ser Asn Asn Asn Ala Thr Val Pro
1 5 10

<210> 495
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 495
Gln Asn Ser Gln His Asn Asn His His Cys Val Leu Gly
1 5 10

<210> 496
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 496
Arg Ser Ser Ser Ser Gly Asn Ser Ser His His His Met
1 5 10

<210> 497
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 497
Ser Glu Ser Asn Ser Asn Asn Pro Gly His Asn Leu Pro
1 5 10

<210> 498
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 498
Ser Phe Leu Asn Asn Cys Asn His Asn Lys Leu Met Ser
1 5 10

<210> 499
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 499
Ser Ile Phe Asn Ser Ser Asn His Thr His Gln Ser Met
1 5 10

<210> 500
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 500
Ser Asn Met Asp Ser Ser Asn Ala Pro Gln Ser Trp Val
1 5 10

<210> 501
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 501
Ser Asn Ser Trp Asn Asn Asn Glu Asp Lys His Ile Leu
1 5 10

<210> 502
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 502
Ser Arg Ser Gly Trp Ser Asn Tyr Phe Cys Ser Arg Gln
1 5 10

<210> 503
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 503
Ser Ser Met Leu His Asn Asn Pro Trp Ser Lys Trp Ser
1 5 10

<210> 504
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 504
Ser Ser Asn Gln Val Ile Asn Thr Phe Glu Asp Leu Gln
1 5 10

<210> 505
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 505
Ser Ser Gln Ser Met Pro Asn Gly Ser Gly Lys Glu Thr
1 5 10

<210> 506
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 506
Ser Val Ser Cys Ser Cys Asn Thr Ser Arg Gly Cys Ser
1 5 10

<210> 507

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 507
Ser Val Ser Ser Lys Ser Asn Glu Ile Ser Phe Cys Thr
1 5 10

<210> 508
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 508
Thr Asp Ser Gly Ser Ser Asn Ser Ala Lys Ala Ile Cys
1 5 10

<210> 509
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 509
Thr Asn Trp Cys Ser Ser Asn Val Gly Ser Asn Thr Ser
1 5 10

<210> 510
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 510
Thr Ser Ser Trp Ser Phe Asn Gly Thr Asn Gly Ser Ala
1 5 10

<210> 511
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 511
Val Ala Asp Ser Phe Asp Asn Ala Asn Tyr Thr Leu Asp
1 5 10

<210> 512
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 512
Val Asp Asp Gln Tyr Asp Asn Trp Asp Ile Arg Asp Cys
1 5 10

<210> 513
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 513
Tyr Asn Gly Asn Tyr His Asn His Gly Leu Asn Ile Arg
1 5 10

<210> 514
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 514
Cys Phe Val Leu Asn Cys His Leu Val Leu Asp Arg Pro
1 5 10

<210> 515
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 515
Cys Arg Arg Pro Phe Glu His Ala Leu Phe Tyr Ala Ser
1 5 10

<210> 516
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 516
Asp Ser Trp Leu Leu Ser His Ser Arg Ser Lys Ser Met
1 5 10

<210> 517
<211> 13
<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 517
Asp Ser Trp Trp Thr Gln His Ser Gln Ala His Ser Asp
1 5 10

<210> 518
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 518
Asp Thr Asn Met Leu Asn His Gly Met Tyr Gly His Cys
1 5 10

<210> 519
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 519
Glu Asn Ile Asn Ala Ser His Cys Leu Ser Thr Val Asp
1 5 10

<210> 520
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 520
Phe Phe Ser Tyr Ser Gly His Leu Val Gln Lys Val Trp
1 5 10

<210> 521
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 521
Phe Met Phe Ala Val Trp His Asp Gly His Ile Lys Asn
1 5 10

<210> 522
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 522
Phe Met Ser Gln His Phe His Asn Pro Met Met Ile Arg
1 5 10

<210> 523
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 523
Phe Val Phe Tyr Ile Met His Tyr Cys Gly His Phe Met
1 5 10

<210> 524
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 524
His Phe Lys Asp Asp Asp His Met Met Leu Tyr Gly Pro
1 5 10

<210> 525
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 525
His Thr Gln His Arg Leu His Val Gly Gln Ser Ser Ser
1 5 10

<210> 526
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 526
Ile Ser Asn Ser Trp Tyr His Trp Ser Trp Glu Met Trp
1 5 10

<210> 527
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 527
Leu Cys Phe Tyr Glu Tyr His Phe Met Gln Cys Ala Met
1 5 10

<210> 528
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 528
Leu Gly Leu Ser Asp Ser His Tyr Glu Cys Ser Phe Arg
1 5 10

<210> 529
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 529
Leu Arg Ser Thr Ser Phe His Phe Arg Cys Ala Lys Cys
1 5 10

<210> 530
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 530
Leu Ser Val Phe Ser His His Lys Trp Val Tyr Thr Ser
1 5 10

<210> 531
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 531
Met Ala Met His His Met His His Met Ala Asn Asn Leu
1 5 10

<210> 532
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> binding module

<400> 532

Met Ser Ser Phe Asp Val His Arg Ser His Thr Asn Ser
1 5 10

<210> 533

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 533

Pro Gly Ser Leu Ser Glu His Ile Tyr Gln Ala Trp Ser
1 5 10

<210> 534

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 534

Pro Ser Ser Ala Ser Met His Ile Ala Ser Ser Cys Ile
1 5 10

<210> 535

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 535

Gln Tyr Trp Trp Ile Trp His Lys Ser Asp Ser Gly Ser
1 5 10

<210> 536

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 536

Ser Gly Gln Ser Asn Ser His His Asp Lys Thr Ile Cys
1 5 10

<210> 537

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 537
Ser Gly Gln Ser Val Phe His His Phe Phe Pro Asn Asp
1 5 10

<210> 538
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 538
Ser His Val Ser Leu Tyr His Ala Ser Thr Asp Ser Asp
1 5 10

<210> 539
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 539
Ser Met Ser Ser Ser Lys His Met Asp Met Asp Cys Phe
1 5 10

<210> 540
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 540
Ser Ser Cys Leu Pro Ser His Val Arg Ser Asp Thr Lys
1 5 10

<210> 541
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 541
Ser Ser Gly Met Ser Glu His Thr Pro Leu Cys Ser Glu
1 5 10

<210> 542
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 542
Ser Ser Pro Ser Phe Pro His Met Trp Ser Glu Asp Glu
1 5 10

<210> 543
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 543
Val His Ser Glu Ser Trp His Ser Tyr Ser Ile His Ala
1 5 10

<210> 544
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 544
Val Asn Asn Ala Met Gly His Met Gly Met Met Trp Cys
1 5 10

<210> 545
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 545
Val Ser Cys Ser Ser Arg His Tyr Ser Ile Ser Trp Ser
1 5 10

<210> 546
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 546
Trp Thr Trp Lys Arg Gln His His Arg Ser Ser Leu Tyr
1 5 10

<210> 547
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 547

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

<210> 548
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 549
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 550
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 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> 551
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 551
Gly Phe Ala Trp Ser Ser Tyr Leu Gly Thr Thr Val His
1 5 10

<210> 552
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 552
Leu Phe Gly Pro Ile Glu Tyr Thr Gln Phe Leu Ala Asn
1 5 10

<210> 553
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 553
Phe Phe Ser Phe Phe Pro Ala Ser Ala Trp Gly Ser
1 5 10

<210> 554
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 554
Phe Phe Ser Phe Phe Pro Ala Ser Ala Trp Gly Ser Ser Gly Ser
1 5 10 15
Ser Arg Gly Asp
20

<210> 555
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 555
Leu Leu Ser Ile Leu Leu Pro Gly Ser Ser Gly Lys
1 5 10

<210> 556
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> binding module

<400> 556
Ile Ile Ser Ile Ile Ile Pro Gly Ser Ser Gly Lys
1 5 10

<210> 557
<211> 12
<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 557

Phe Trp Ser Phe Trp Phe Pro Gly Ser Ser Gly Lys
1 5 10

<210> 558

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> binding module

<400> 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