

(19) **DANMARK**



Patent- og
Varemærkestyrelsen

(10) **DK/EP 2705144 T4**

(12) Oversættelse af ændret
europæisk patentskrift

-
- (51) Int.Cl.: **C 12 N 9/36 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2019-10-21**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om opretholdelse af patentet i ændret form: **2019-08-28**
- (86) Europæisk ansøgning nr.: **11720345.5**
- (86) Europæisk indleveringsdag: **2011-05-04**
- (87) Den europæiske ansøgnings publiceringsdag: **2014-03-12**
- (86) International ansøgning nr.: **NL2011050307**
- (87) Internationalt publikationsnr.: **WO2012150858**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
- (73) Patenthaver: **Micreos Human Health B.V., Bankplein 2, 2585 EV Den Haag, Holland**
- (72) Opfinder: **LOESSNER, Martin Johannes, Stuhlenstrasse 39, CH-8123 Ebmatingen, Schweiz**
EICHENSEHER, Fritz, Schwamendingenstrasse 30, CH-8050 Zürich, Schweiz
- (74) Fuldmægtig i Danmark: **Zacco Denmark A/S, Arne Jacobsens Allé 15, 2300 København S, Danmark**
- (54) Benævnelse: **POLYPEPTID**
- (56) Fremdragne publikationer:
Becker S et al: "Differentially conserved staphylococcal SH3b_5 cell wall binding domains confer increased staphylolytic and streptolytic activity to a streptococcal prophage endolysin domain", GENE, vol. 443, no. 1-2, August 2009 (2009-08), pages 32-41, XP002582773, WO-A1-2012/146738
WO-A2-2009/024327
SASS PETER ET AL: "Lytic activity of recombinant bacteriophage phi11 and phi12 endolysins on whole cells and biofilms of Staphylococcus aureus", APPLIED AND ENVIRONMENTAL MICROBIOLOGY, AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 73, no. 1, 1 January 2007 (2007-01-01), pages 347-352, XP002499603, ISSN: 0099-2240, DOI: 10.1128/AEM.01616-06
LOESSNER MARTIN J ET AL: "C-terminal domains of Listeria monocytogenes bacteriophage murein hydrolases determine specific recognition and high-affinity binding to bacterial cell wall carbohydrates", MOLECULAR MICROBIOLOGY, WILEY-BLACKWELL PUBLISHING LTD, GB, vol. 44, no. 2, 1 April 2002 (2002-04-01), pages 335-349, XP002291418, ISSN: 0950-382X, DOI: 10.1046/J.1365-2958.2002.02889.X

DESCRIPTION

Field of the invention

[0001] The invention relates to a polypeptide, a corresponding nucleic acid molecule, a construct and/or a vector and/or a cell comprising such nucleic acid molecule and/or a composition comprising said polypeptide, nucleic acid molecule, construct, vector and/or cell. The invention further relates to such polypeptide, corresponding nucleic acid molecule, construct and/or vector and/or cell comprising such nucleic acid molecule and/or composition for medical use, preferably for use in treating an infectious disease. Furthermore, the invention relates to the use of said polypeptide, nucleic acid molecule, construct, vector, cell and/or composition as an antimicrobial, preferably as a food additive or disinfectant, or for detecting bacteria, preferably in a diagnostic application.

[0002] *Staphylococcus aureus* is a major human pathogen frequently implicated in several serious infectious diseases and food poisoning. Its treatment becomes more and more difficult because of emerging antibiotic resistant strains. Endolysins from phages infecting *Staphylococcus aureus* have been shown to potentially control these pathogens and can be used for their specific detection. In most cases, major obstacles in the application of endolysins targeting *Staphylococcus* species are low enzyme activity, difficult production in large quantities and/or protein stability. Becker et al (Gene 443 (2009), 32-41) relates to replacement of streptococcal prophage endolysin wherein the cell wall binding domain is replaced by the cell wall binding domain of lysostaphin of LysK.

Background of the invention

[0003] There is always a need for new antimicrobials with improved characteristics on for example antimicrobial activity and/or stability.

Description of the invention

[0004] Reported here is the newly characterised Ply2638, the endolysin of *S. aureus* bacteriophage Φ 2638a. The enzyme and several engineered derivatives were expressed in a soluble way in *E. Coli* and showed surprising stability after lyophilisation as proven by their lytic activity after reconstitution. In addition to a cell wall-binding domain which binds the cell wall of *Staphylococcus* genera, we showed that two functional domains, i.e. an M23 endopeptidase domain and an amidase domain, are crucial for optimal lytic activity.

[0005] We showed that retrofitting of the enzyme with catalytic domains and/or duplication of the cell wall-binding domain originating from *S. aureus* Φ 11 endolysin, Φ Twort endolysin, and

Lysostaphin resulted in a heterologous polypeptide fusion product with an enhanced lytic activity and/or a shifted pH optimum and/or an increased stability after lyophilisation and reconstitution.

[0006] The embodiments of the invention are presented in the claims herein.

Nucleic acid molecule

[0007] In a first aspect, there is provided a nucleic acid molecule comprising a first nucleotide sequence, wherein said nucleotide sequence has at least 85% sequence identity with SEQ ID NO: 12, wherein said first nucleotide sequence encodes a cell wall-binding domain binding the peptidoglycan cell wall of *Staphylococcus* genera, and wherein said nucleic acid molecule further comprises a heterologous nucleotide sequence encoding a lytic domain exhibiting peptidoglycan hydrolase activity wherein said lytic domain is a second and third nucleotide sequences, wherein said second nucleotide sequence encodes a M23 peptidase domain and said third nucleotide sequence encodes an amidase domain, and wherein said second nucleotide sequence has at least 80% sequence identity with SEQ ID NO: 15.

[0008] Disclosed is a nucleic acid molecule comprising or consisting of a first nucleotide sequence, said nucleotide sequence having 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 12 (referred is to Table 1 for an overview of all SEQ ID NOs used herein). Preferably, said first nucleotide sequence has a length of at least 282, 285, 290, 300, 310, 320, 330, 340, 350, 360 or 370 nucleotides, more preferably, at least 381 nucleotides and/or a length of at most 510, 480, 450, 420 or 390 nucleotides. Preferably, said nucleic acid molecule has a length of at least 282, 285, 290, 300, 310, 320, 330, 340, 350, 360, 370 nucleotides, more preferably at least 381 nucleotides and/or a length of at most 4500, 4200, 3900 and/or 3600 nucleotides. Preferably, said nucleic acid molecule has a length of at least 1200, 1230, 1260, 1290, 1320, 1350, 1380, 1410, 1440, 1470, 1500, 1530 or 1560 nucleotides and/or a length of at most 4500, 4200, 3900 and/or 3600 nucleotides. Also preferred is a nucleic acid molecule according to the invention with a length of at least 1890, 1920, 1950, 1980, 2010, 2040, 2070, 2100, 2130 or 2160 nucleotides and/or a length of at most 4500, 4200, 3900 and/or 3600 nucleotides. Said first nucleotide sequence encodes a cell wall-binding domain which binds the peptidoglycan cell wall of *Staphylococcus* genera. Preferably, said first nucleotide sequence originates from *S. aureus* bacteriophage Φ 2638a endolysin.

[0009] As estimated from alignments with the crystal structure of the C-terminal 92 residues of ALE-1 (Lu et al., J. Biol. Chem., 2006, 281(1):549-58), it was estimated that a minimum of 94 amino acids from the cell wall-binding domain originating from *S. aureus* bacteriophage Φ 2638a endolysin may be sufficient to direct the enzyme to the cell wall of *Staphylococcus* genera.

[0010] Binding of a domain to the peptidoglycan cell wall of *Staphylococcus* genera may be

assessed using assays well known to the artisan. In a preferred embodiment, an immunohistochemical technique and/or a gene fusion technique resulting in labelled constructs are used for assessing specific binding of peptides, polypeptides or proteins to the peptidoglycan cell wall of *Staphylococcus* genera. Quantification methods of signals used in the above mentioned immunohistochemical or fusion techniques are well known in the art.

[0011] In one embodiment, *Staphylococcus* peptidoglycan cell wall-binding can be quantified using a fluorescent fusion construct comprising a polypeptide comprising a domain encoded by a first nucleotide sequence. Such a cell wall-binding assay is described in detail by Loessner et al (Molecular Microbiology 2002, 44(2): 335-349) and in Example 1. In this assay a solution comprising said fluorescent fusion construct or a negative control, preferably Green Fluorescent Protein (GFP), is subjected to *Staphylococcus* cells, preferably *S. aureus* cells, more preferably *S. aureus* BB255 for an indicated time period where after the cells are sedimented by centrifugation together with the bound fluorescent fusion constructs. The fluorescent signal of the *Staphylococcus* cells exposed to a fluorescent fusion construct subtracted by the fluorescence signal of the *Staphylococcus* cells exposed to a negative control, preferably GFP, is a measure for cell binding as meant in this disclosure.

[0012] Preferably, within the context of the invention a nucleic acid molecule will be said to encode a polypeptide domain that binds the peptidoglycan cell wall of *Staphylococcus* genera when using this assay an increase in fluorescent signal of the sedimented cells above the negative control as defined herein is detected. The binding is preferably said to be specific. Preferably, the invention relates to a nucleic acid molecule encoding a polypeptide or a domain which exhibits binding as defined herein of at least 50, 60, 70, 80, 90 or 100, 150 or 200% of peptidoglycan cell wall binding of *S. aureus* bacteriophage Φ 2638a endolysin (Ply2638) encoded by SEQ ID NO: 1.

[0013] Disclosed is a nucleic acid molecule that has at least 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 1 encoding for *S. aureus* bacteriophage Φ 2638 endolysin.

[0014] The nucleic acid molecule comprises in addition to said first nucleotide sequence, a heterologous nucleotide sequence encoding a lytic domain that exhibits peptidoglycan hydrolase activity as defined later herein. Said nucleic acid molecule comprising heterologous nucleotide sequences being defined herein as a "retrofitted construct".

[0015] As used herein the term "heterologous sequence" or "heterologous nucleic acid" is one that is not naturally found operably linked as neighbouring sequence of said first nucleotide sequence. As used herein, the term "heterologous" may mean "recombinant". "Recombinant" refers to a genetic entity distinct from that generally found in nature. As applied to a nucleotide sequence or nucleic acid molecule, this means that said nucleotide sequence or nucleic acid molecule is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in the production of a construct that is distinct from a sequence or molecule found in nature.

[0016] A "peptidoglycan hydrolase activity" herein also defined as a "lytic activity" can be assessed by methods well known to the artisan. In an embodiment, lytic activity can be assessed spectrophotometrically by measuring the drop in turbidity of substrate cell suspensions. Preferably, lytic activity can be assessed spectrophotometrically measuring the drop in turbidity of a *S. aureus* suspension, wherein turbidity is quantified by measuring OD₅₉₅ spectrophotometrically (Libra S22, Biochrom). More preferably, 200 nM of a polypeptide encoded by a nucleic acid molecule as identified herein is incubated together with an *S. aureus* suspension having an initial OD₆₀₀ of 1 ± 0.05 , as assessed spectrophotometrically (Libra S22, Biochrom), in PBS buffer pH 7.4, 120 mM sodium chloride for 30 min at 37°C. The drop in turbidity is calculated by subtracting the OD₅₉₅ after 30 min of incubation from the OD₅₉₅ before 30 min of incubation. Within the context of the invention a nucleic acid molecule will be said to comprise a nucleic acid sequence encoding a lytic domain when using this assay a drop in turbidity of at least 10, 20, 30, 40, 50 or 60% is detected. Preferably, a drop of at least 70% is detected. Preferably, the invention relates to a nucleic acid molecule encoding a polypeptide which exhibits a lytic activity of at least 50, 60, 70, 80, 90, 100, 150 or 200% or more of a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin (Ply2638) encoded by SEQ ID NO: 1.

[0017] A nucleic acid molecule of the invention does not consist of SEQ ID NO:1. SEQ ID NO: 1 encodes for *S. aureus* bacteriophage Φ 2638 endolysin.

[0018] The nucleic acid molecule comprising said first nucleotide sequence as identified herein further comprises as a lytic domain a second and third nucleotide sequences, wherein said second sequence encodes an endopeptidase domain and third nucleotide sequence encodes an amidase domain. Disclosed is a nucleic acid molecule comprising said first nucleotide sequence, wherein said nucleic acid molecule has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 1, or wherein said nucleic acid molecule further comprises a heterologous nucleotide sequence encoding a lytic domain.

[0019] An endopeptidase domain as used herein preferably cleaves the pentaglycine cross-bridges (Trayer, H. R. and Buckley, C. E. (1970) Molecular properties of lysostaphin, a bacteriolytic agent specific for *Staphylococcus aureus*. J. Biol. Chem. 245, 4842-4846) that are found in the cell wall of *Staphylococcus* genera, preferably in the cell wall of *S. aureus*, *S. simulans* and *S. carnosus*. An amidase domain as used herein preferably hydrolyzes gamma-glutamyl-containing substrates. The functionality and activity of these domains in a polypeptide can be confirmed by characterizing the cleavage products upon incubation of said polypeptides containing any of these domains with purified peptidoglycan. Disclosed is that each of the nucleotide sequences encoding the second or third domain is of bacterial or bacteriophage origin. Disclosed is that said second and third nucleotide sequences originate from a gene encoding for an enzyme selected from the group consisting of *S. aureus* bacteriophage Φ 2638a endolysin, *S. aureus* bacteriophage Φ 11 endolysin, *S. aureus* bacteriophage Φ Twort endolysin and *S. Simulans* lysostaphin. Disclosed is that said second nucleotide sequence has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence

identity with SEQ ID NO: 14 or 15 and said third nucleotide sequence has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 16 or 17.

[0020] The invention encompasses all constructs as defined herein containing the functional domains as meant in the invention at any possible location within the construct. In a preferred embodiment, a nucleic acid molecule as defined herein encodes for a polypeptide with a C-terminal domain encoded by a first nucleic acid sequence as identified herein, which is shown herein to encode for functional polypeptides able to target for *Staphylococcus* genera. Even more preferred is a nucleic acid molecule as defined herein comprising a nucleic acid molecule that has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 9. SEQ ID NO: 9 comprises a first nucleotide sequence encoding a C-terminal SH3b homologue cell wall-binding domain (both domains from Ply2638 encoded by SEQ ID NO: 1: Leu138 - Lys486), a second nucleotide sequence encoding a polypeptide comprising an N-terminal M23 glycyl-glycine endopeptidase homologue domain (mature Lysostaphin encoded by SEQ ID NO: 33: Ala1 - Gly154) and a third nucleotide sequence encoding a central amidase-2 homologue domain. It has a theoretical size of 58.266 kDa. A polypeptide encoded by SEQ ID NO: 9 differs from *S. aureus* bacteriophage Φ2638a endolysin in that the N-terminal M23 endopeptidase domain is substituted by an M23 endopeptidase domain from *S. Simulans* lysostaphin. We showed here that a polypeptide encoded by SEQ ID NO: 9 demonstrated at least 20% increased lytic activity as compared to *S. aureus* bacteriophage Φ2638a endolysin while the lytic activity is maintained after lyophilisation and reconstitution. In a preferred embodiment, a nucleic acid molecule comprising said first, second and third nucleotide sequences encodes for a polypeptide exhibiting a lytic activity of at least 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 fold as compared to a lytic activity of *S. aureus* bacteriophage Φ2638a endolysin encoded by SEQ ID NO:1. In a preferred embodiment, a nucleic acid molecule comprising said first, second and third nucleotide sequences encodes for a polypeptide exhibiting a decrease in lytic activity of at most 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10% after lyophilisation and reconstitution as defined herein as compared to freshly prepared polypeptide, wherein "freshly prepared" is preferably defined herein as at most 2 days storage at 1.63 mg/mL in lyophilisation buffer (50mM Tris, 500mM sucrose, 200mM mannitol, 0.05% polysorbate 20 + 50% glycerol) at -20 °C and thawed immediately before assessing lytic activity in an assay as identified herein.

[0021] Lyophilisation and reconstitution is defined herein as dehydration by freeze-drying and subsequent reconstitution of the sample by adding water. In an embodiment, lyophilisation and reconstitution may be done by dialyzing against 3 changes of 300 ml lyophilization buffer (50 mM phosphate or Tris, 500 mM sucrose, 200 mM mannitol, pH 7.4) aliquot and freezing in the gaseous phase of liquid nitrogen. The freeze-drying can be done under standard conditions, preferably at -40°C and vacuum at 75 mTorr for 60 minutes, followed by increasing temperature during 5 hours to -10°C and another 60 minutes at -10°C at the same vacuum levels. As final step, temperature is preferably increased to 25°C during 10 hours. Samples are reconstituted by the addition of water.

[0022] In another preferred embodiment, a nucleic acid molecule as defined herein comprises in addition to the above identified first, second and third nucleotide sequences at least one duplicate identical or heterologous first, second and/or third nucleotide sequence. Preferably, a nucleic acid molecule as defined herein comprises in addition to said first, second and third nucleotide sequences, a duplicate identical first nucleotide sequence. We showed here that duplication of the first nucleotide sequence as defined herein encoding a cell wall-binding domain results in a polypeptide preferably as encoded by SEQ ID NO: 20 which exposes at least 5, 10, 20, 30, 20 or 40% increased lytic activity as compared to a lytic activity of a reference polypeptide encoded by a nucleic acid molecule lacking such duplicate first domain or as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO:1 as assessed in an assay as identified herein, more specifically using equimolar amount of a polypeptide and a modified PBS buffer containing 200, 300, 400, or 1000nM NaCl. Disclosed is a heterologous nucleic acid molecule in which said first, second and third nucleotide sequences originate from the same source being *S. aureus* bacteriophage Φ 2638a, said nucleic acid molecule comprising a sequence that has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO:1 and an additional duplicate identical or heterologous first, second and/or third nucleotide sequence. Also preferred is a nucleic acid molecule as defined herein comprising a nucleotide sequence that has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 6 and 20.

[0023] In another preferred embodiment, a nucleic acid molecule as defined herein comprises a fourth nucleotide sequence encoding a CHAP (cysteine, histidine-dependent amidohydrolases/peptidases) domain. More preferably, said fourth nucleotide sequences originates from *S. aureus* bacteriophage Φ 11 or *S. aureus* bacteriophage Φ Twort endolysin. Even more preferably, said fourth nucleotide sequence has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 18 or SEQ ID NO: 19. Preferably, a nucleic acid molecule as defined herein comprises a nucleotide sequence that has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 5 or 7. We showed here that a molecule comprising said first, second, third and fourth nucleotide sequences as defined by SEQ ID NO: 5 encodes for a polypeptide exhibiting an increased lytic activity and/or a shifted, preferably decreased pH optimum as compared to a polypeptide encoded by a construct lacking said fourth domain and/or compared to *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO: 1. Lytic activity was assessed spectrophotometrically and under the conditions as earlier defined herein. Preferably, said polypeptide exhibits an increase in a lytic activity of at least 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, or 2 fold as compared to a lytic activity of a polypeptide encoded by a reference polypeptide differing from said polypeptide only in lacking said fourth domain or as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO: 1. Even more preferably, said polypeptide exhibits an increase in a lytic activity of at least 2.5 fold as compared to the defined reference polypeptide or a polypeptide encoded by SEQ ID NO: 1.

[0024] A shifted or decreased pH optimum is defined herein as a shift or decrease in optimal

lytic activity to a lower pH value, where ionic strength is kept constant. Lytic activity is preferably assessed spectrophotometrically as defined herein. Preferably, the pH optimum of a lytic activity is decreased 0.5 - 1 pH unit as compared to a lytic activity of a polypeptide encoded by a reference polypeptide differing from said polypeptide only in lacking said fourth domain or as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO:1.

[0025] The invention preferably relates to a nucleic acid molecule comprising a first, second, third and optionally fourth nucleotide sequences as identified herein encoding a polypeptide which has the same lytic activity and/or the same pH optimum or which has an increased lytic activity and/or a decreased pH optimum as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO: 1. The same being identified herein as no detectable difference when using the assay as identified herein or a method well known by the artisan. The current invention also relates to a nucleic acid molecule comprising a first, second, and fourth nucleotide sequence as identified herein encoding a polypeptide which has the same lytic activity and/or the same pH optimum or which has an increased lytic activity and/or a decreased pH optimum as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO: 1. The current invention also relates to a nucleic acid molecule comprising a first, third, and fourth nucleotide sequence as identified herein encoding a polypeptide which has the same lytic activity and/or the same pH optimum or which has an increased lytic activity and/or a decreased pH optimum as compared to a lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO: 1. Each of the nucleotide sequences identified herein, i.e. first, second, third, fourth nucleotide sequences, encoding the individual domain of a polypeptide defined herein can be assembled by any usual method known for constructing and assembling nucleic acid fragments which are well known to those skilled in the art and widely described in the literature (Sambrook, Maniatis et al. (1989) and illustrated experimental part of the disclosure. In a preferred embodiment, a first, second, third and/or fourth nucleotide sequences are operably linked together.

[0026] Accordingly, a nucleic acid molecule of the invention encodes a polypeptide, preferably a polypeptide as identified herein which is able to bind *Staphylococcus* genera via the cell wall-binding domain encoded by a first nucleotide sequence as defined herein and/or lyse said bacteria via an endopeptidase and/or amidase domain and optionally a CHAP domain encoded by a second, third and fourth nucleotide sequence, respectively, as defined herein.

[0027] In a preferred embodiment, a nucleic acid molecule of the invention as defined herein optionally comprises a sequence encoding a tag for ease of purification. Preferably, said tag is selected from, but is not limited to, the group consisting of a FLAG-tag, poly(His)-tag, HA-tag and Myc-tag. More preferably said tag is a 6xHis-tag. Even more preferably, said tag is an N-terminal 6xHis-tag identical to SEQ ID NO: 43.

Polypeptide

[0028] In a further aspect, there is provided a polypeptide encoded by a nucleic acid molecule according to the invention. This polypeptide comprises a cell wall-binding domain and an endopeptidase domain and/or an amidase domain as defined in the previous section.

[0029] A polypeptide domain encompassed by the current disclosure preferably has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 35, 36, 37, 38, 39, 40, 41 and/or 42. Preferably, a polypeptide domain encompassed by the current disclosure preferably comprises one or more putative linkers and has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 51, 52, 53, 54, 55, 56, 57 and/or 58.

[0030] A polypeptide encompassed by the current disclosure preferably has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 21, 25, 26, 27, 29 and/or 32. More preferably, a polypeptide encompassed by the current disclosure preferably has 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 25, 26, 27, 29 and/or 32 with SEQ ID NO: 25, 26, 27, 29 and/or 32.

[0031] In an embodiment of the current disclosure, a polypeptide preferably has at least 80% sequence identity with SEQ ID NO: 21, 25, 26, 27, 29, 32, 35, 36, 37, 38, 39, 40, 41, and/or 42 encoded by a nucleic acid construct with at least 80% identity with SEQ ID NO: 1, 5, 6, 7, 9, 20, 12, 13, 14, 15, 16, 17, 18 and/or 19, respectively. More preferably, a polypeptide of the current disclosure has at least 80% sequence identity with SEQ ID NO: 25, 26, 27, 29, 32, 35, 36, 37, 38, 39, 40, 41, and/or 42 encoded by a nucleic acid construct with at least 80% identity with SEQ ID NO: 5, 6, 7, 9, 20, 12, 13, 14, 15, 16, 17, 18 and/or 19, respectively.

[0032] A polypeptide according to the invention may have a length of at least 94, 95, 96, 100, 110 or 120 amino acids, preferably 127 amino acids and/or at most 1500, 1400, 1300 or 1200 amino acids. Preferably, said polypeptide has a length of at least 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510 or 520 amino acids and/or at most 1500, 1400, 1300 or 1200 amino acids. Also preferred is a polypeptide according to the invention with a length of at least 630, 640, 650, 660, 670, 680, 690, 700, 710 or 720 amino acids and/or at most 1500, 1400, 1300 or 1200 amino acids.

[0033] An amino acid or nucleotide sequence, encompassed by the present disclosure, may be derived from one of the sequences as identified herein by substituting, inserting, deleting, or adding one, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20 or more nucleotides or amino acids, respectively. An amino acid sequence, encompassed by the present invention, may be derived from one of the sequences as identified herein by adding an additional N- or C- terminal amino acids or chemical moieties to increase stability, solubility and activity.

[0034] Disclosed is a variant polypeptide. A variant polypeptide may be a non-naturally occurring form of the polypeptide. A polypeptide variant may differ in some engineered way from the polypeptide isolated from its native source. A variant may be made by site-directed

mutagenesis starting from the nucleotide sequence of SEQ ID NO: 1, 5, 6, 7, 9, 12, 13, 14, 15, 16, 17, 18, 19 and/or 20. Preferably, a polypeptide variant contains mutations that do not alter the biological function of the encoded polypeptide. According to a preferred embodiment, a polypeptide variant exhibits *Staphylococcus* peptidoglycan cell wall-binding and/or a lytic activity which is the same or enhanced as compared to the *Staphylococcus* peptidoglycan cell-wall binding and/or lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO:1. A polypeptide variant of the invention preferably is a variant of SEQ ID NO: 21, 25, 26, 27, 29, 32, 35, 36, 37, 38, 39, 40, 41 and/or 42. A polypeptide variant with the same or an enhanced *Staphylococcus* peptidoglycan cell-wall binding and/or lytic activity is a polypeptide exhibiting a *Staphylococcus aureus* peptidoglycan cell-wall binding and/or lytic activity, which is the same or increased compared to the *Staphylococcus* peptidoglycan cell-wall binding and/or lytic activity of *S. aureus* bacteriophage Φ 2638a endolysin encoded by SEQ ID NO:1 measured in an assay as earlier identified herein.

[0035] A nucleotide sequence of the disclosed is a variant of the nucleotide sequences of SEQ ID NO: 1, 5, 6, 7, 9, 12, 13, 14, 15, 16, 17, 18, 19 and/or 20. Nucleotide sequence variants may be used for preparing a polypeptide variant as defined earlier. A nucleic acid variant may be a fragment of any of the nucleotide sequences as defined above. A nucleic acid variant may also be a nucleotide sequence that differs from SEQ ID NO: 1, 5, 6, 7, 9, 12, 13, 14, 15, 16, 17, 18, 19 and/or 20 by virtue of the degeneracy of the genetic code. A nucleic acid variant may also be an allelic variant of SEQ ID NO: 1, 5, 6, 7, 9, 12, 13, 14, 15, 16, 17, 18, 19 and/or 20. An allelic variant denotes any of two or more alternative forms of a gene occupying the same chromosome locus. A preferred nucleic acid variant is a nucleotide sequence, which contains silent mutation(s). Alternatively or in combination, a nucleic acid variant may also be obtained by introduction of nucleotide substitutions, which do not give rise to another amino acid sequence of the polypeptide encoded by the nucleotide sequence, but which corresponds to the codon usage of the host organism intended for production of the polypeptide of the invention. According to the disclosure, a nucleic acid variant encodes a polypeptide still exhibiting its biological function. More preferably, a nucleotide sequence variant encodes a polypeptide exhibiting *Staphylococcus* peptidoglycan cell wall-binding and/or a lytic activity. Even more preferably, a nucleic acid variant encodes a polypeptide with enhanced *Staphylococcus* peptidoglycan cell wall-binding and/or lytic activity as defined earlier. Nucleic acids encoding a polypeptide exhibiting *Staphylococcus* peptidoglycan cell wall-binding and/or lytic activity may be isolated from any microorganism.

[0036] All these variants can be obtained using techniques known to the skilled person, such as screening of library by hybridisation (southern blotting procedures) under low to medium to high hybridisation conditions with for the nucleotide sequence SEQ ID NO: 1, 5, 6, 7, 9, 12, 13, 14, 15, 16, 17, 18, 19 and/or 20 or a variant thereof which can be used to design a probe. Low to medium to high stringency conditions means prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200pg/ml sheared and denatured salmon sperm DNA, and either 25% 35% or 50% formamide for low to medium to high stringencies respectively. Subsequently, the hybridization reaction is washed three times for 30 minutes each using 2XSSC, 0.2%SDS and either 55°C, 65 °C, or 75°C for low to medium to high stringencies.

[0037] The sequence information as provided herein should not be so narrowly construed as to require inclusion of erroneously identified bases. The skilled person is capable of identifying such erroneously identified bases and knows how to correct for such errors.

Nucleic acid construct

[0038] In a further aspect, there is provided a nucleic acid construct comprising a nucleic acid molecule according to the invention. This nucleic acid construct comprises a first nucleic acid sequence encoding a polypeptide comprising a cell wall-binding domain and further comprises a second or third and optionally fourth nucleic acid sequence as defined in the previous section.

[0039] The invention also relates to an expression vector comprising a nucleic acid construct of the invention. Preferably, an expression vector comprises a nucleotide sequence of the invention, which is operably linked to one or more control sequences, which direct the production or expression of the encoded polypeptide in a cell, a subject, or a cell-free expression system.

[0040] An expression vector may be seen as a recombinant expression vector. This vector can be constituted by a plasmid, a cosmid, a bacteriophage or a virus which is transformed by introducing a nucleic acid molecule according to the invention. Such transformation vectors according to the host organism to be transformed are well known to those skilled in the art and widely described in the literature.

[0041] A further subject of the invention is a process for the transformation of host organisms, by integrating a least one nucleic acid molecule of the invention, which transformation may be carried out by any suitable known means which have been widely described in the specialist literature and in particular in the references cited in the present application, more particularly by the vector according to the invention.

Cell

[0042] In a further aspect, the present invention relates to a cell, which comprises a nucleic acid construct or an expression vector of the invention as defined herein. A cell may be any microbial, prokaryotic or eukaryotic cell, which is suitable for expression of the polypeptide of the invention. In a preferred embodiment, said cell is an *E. Coli*. in an even more preferred embodiment, said cell is *E. coli* CL1blue MRF.

Method

[0043] In a further aspect, there is provided a method for producing, optionally purifying and optionally freeze-drying a polypeptide according to the invention. Said method comprising the steps of:

1. i) producing said polypeptide in a cell according to the invention comprising a nucleic acid construct as defined in the previous section, optionally
2. ii) purifying said polypeptide, and optionally
3. iii) freeze-drying said purified polypeptide.

[0044] In a preferred embodiment, an *E. Coli* is used in step i) for producing a polypeptide using recombinant technologies. More preferably an *E. coli* XLlblueMRF is used in step i) for producing a polypeptide using recombinant technologies. Preferably, in step ii), IMAC and Econo-Pac Chromatography columns (Biorad) packed with 5mL low density Nickel chelating agarose beads (ABT beads) in combination with gravity flow is used to purify said (6xHis-tagged recombinant) polypeptides. The eluted polypeptide can be dialyzed for 2, 4, and 12 hours against 3x11 lyophilization buffer, said buffer preferably comprising 50 mM phosphate, 500mM sucrose, 200mM mannitol, 0.005% polysorbate20, pH 7.4.

Method

[0045] In a further aspect, the invention also relates to a method for producing a polypeptide with an enhanced lytic activity by treating a polypeptide according to the invention or as obtainable by the method described above. Said treatment comprises substituting a divalent metal ion for increasing a lytic activity as compared to an untreated polypeptide, preferably said method comprising the steps of:

1. i) dialyzing said polypeptide against a buffer comprising a chelating compound;
2. ii) dialyzing said polypeptide against a divalent metal ion-containing buffer, preferably said divalent metal ion being selected from the group consisting of Mn^{2+} , Co^{2+} , Cu^{2+} , and Zn^{2+} .

[0046] A "chelating compound" being defined herein as a compound that binds a metal ion. Well known chelating compounds are ethylene diammine tetraacetic acid (EDTA) and ethylene glycol tetraacetic acid (EGTA). Preferably EDTA is used in step i) of the method of the invention.

[0047] Preferably, the divalent metal ion of step ii) is selected from the group consisting Mn^{2+} , Co^{2+} , Cu^{2+} , more preferably, said divalent metal ion is selected from the group consisting of Mn^{2+} and Co^{2+} , even more preferably said divalent metal ion is Mn^{2+} .

[0048] We showed that substituting a divalent metal ion by any of the above defined resulted in an increase of a lytic activity of Ply2638 of 2 - 2.5 fold. Lytic activity was assessed spectrophotometrically as defined herein. Preferably, said method leads to an increase in a lytic activity of at least 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 fold as compared to an untreated polypeptide. Even more preferably, the method leads to an increase in a lytic activity of at least 2.5 fold. Preferably, the treated polypeptide exhibits a 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 to 2 fold increase in lytic activity as compared to the untreated polypeptide encoded by SEQ ID NO: 1.

Composition

[0049] In a further aspect, there is provided a composition comprising a nucleic acid molecule or a nucleic acid construct or a polypeptide or a vector or a cell according to the invention. Preferably, the composition exhibits a lytic activity as defined herein. More preferably, said composition is for use as a medicament. This medicament is preferably for treating, preventing and/or delaying an infectious disease. The invention also relates to a pharmaceutical or medical composition. Even more preferably, the invention relates to a pharmaceutical or medical composition for the treatment of an infectious disease. Preferably, the invention relates to a pharmaceutical or medical composition for the treatment of an infectious disease caused by a bacterium, preferably a bacterium of the genus *Staphylococcus*, more preferably a bacterium of the species *S. aureus*. Preferably, said infectious disease is a skin infection, mastitis, pneumonia, meningitis, endocarditis, Toxic Shock Syndrome (TSS), sepsis, septicemia, bacteremia, or osteomyelitis. Preferably, said skin infection is selected from the group of pimples, impetigo, boils, furuncles, cellulitis folliculitis, carbuncles, scaled skin syndrome and abscesses.

[0050] A composition according to the invention may comprise a mixture of different nucleic acid molecules, and/or nucleic acid constructs and/or polypeptides and/or vectors and/or cells according to the invention.

[0051] A composition according to the invention may comprise one or more additional active ingredients. Active preferably being defined herein as showing a lytic activity as defined herein. Preferably, said one or more additional active ingredients are selected from the group consisting of a bacteriophage or phage and antibiotic. A phage encompassed herein can be any phage known in literature. Preferably, a phage encompassed by the present invention belongs, but is not limited, to a family of the list consisting of *Myoviridae*, *Siphoviridae* and *Podoviridae*. A phage encompassed by the present invention may also belong to a family of the list consisting of *Tectiviridae*, *Corticoviridae*, *Lipothirixviridae*, *Plasmaviridae*, *Rudiviridae*, *Fuselloviridae*, *Inoviridae*, *Microviridae*, *Leviviridae* and *Cystoviridae*. More preferably, said one or more active ingredients comprise and/or consist of lysostaphin, preferably *S. Simulans* lysostaphin having 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% sequence identity with SEQ ID NO: 34, more preferably *S. Simulans* lysostaphin of

SEQ ID NO: 34.). Even more preferably, said one or more active ingredients comprise and/or consist of both one or more different bacteriophages and lysostaphin, preferably, one or more different phages and *S. Simulans* lysostaphin (SEQ ID NO: 34). Within the context of this invention, a combination of active ingredients as defined herein can be administered sequentially and/or simultaneously.

[0052] A composition as defined herein may further comprise a pharmaceutically acceptable carrier. Such composition is preferably for use as a medicine or as a medicament. Preferably the medicament is used in the treatment of infectious diseases. A composition may be in the liquid, solid or semi-liquid or semi-solid form.

[0053] A composition of the invention can be used to treat animals, including humans, infected with *S. aureus*. Any suitable route of administration can be used to administer said composition including but not limited to: oral, aerosol or other device for delivery to the lungs, nasal spray, intravenous, intramuscular, intraperitoneal, intrathecal, vaginal, rectal, topical, lumbar puncture, intrathecal, and direct application to the brain and/or meninges.

[0054] A composition comprising a nucleic acid molecule or a nucleic acid construct or a polypeptide or a vector or a cell according to the invention is preferably said to be active, functional or therapeutically active or able to treat, prevent and/or delay an infectious disease when it decreases the amount of a *Staphylococcus* genera present in a patient or in a cell of said patient or in a cell line or in a cell free in vitro system and preferably means that 99%, 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5% or less of the initial amount of a *Staphylococcus* genera, is still detectable. Preferably no *Staphylococcus* genera is detectable. In this paragraph, the expression "amount of *Staphylococcus* genera" preferably means alive *Staphylococcus* genera. *Staphylococcus* genera may be detected using standard techniques known by the artisan such as immunohistochemical techniques using *Staphylococcus* specific antibodies, tube coagulase tests that detect staphylocoagulase or "free coagulase", detection of surface proteins such as clumping factor (slide coagulase test) and/or protein A (commercial latex tests). Alive *Staphylococcus* genera may be detected using standard techniques known by the artisan such as microbiological bacterial culture techniques and/or real-time quantitative reverse transcription polymerase chain reaction to assay for bacterial mRNA.

Said decrease is preferably assessed in a tissue or in a cell of an individual or a patient by comparison to the amount present in said individual or patient before treatment with said composition or polypeptide of the invention. Alternatively, the comparison can be made with a tissue or cell of said individual or patient which has not yet been treated with said composition or polypeptide in case the treatment is local.

[0055] A composition comprising a nucleic acid molecule or a nucleic acid construct or a polypeptide or a vector or a cell according to the invention may be administered to a patient or of a cell, tissue or organ or said patient at least one week, one month, six month, one year or more.

[0056] In another embodiment, the invention relates to a non-medical composition exhibiting a

binding and/or lytic activity according to the invention. Preferably, such composition relates to an antimicrobial. Preferably, such composition relates to an antimicrobial for lysing a bacterium, preferably a bacterium of the genus *Staphylococcus*, more preferably a bacterium of the species *S. aureus*. Preferably, such composition relates to an antimicrobial as food preservative or disinfectant.

Use

[0057] In a further aspect, the invention relates to the use of a polypeptide according to the invention, a nucleic acid molecule according to the invention, a construct comprising such nucleic acid molecule, a vector comprising such construct, a cell comprising such vector and/or a composition comprising any of the above, preferably as antimicrobial. Preferably, use is as an antimicrobial for lysing a bacterium, preferably a bacterium of the genus *Staphylococcus*, more preferably a bacterium of the species *S. aureus*. Preferably the use relates to an antimicrobial as food preservative or disinfectant. Possibly, such food preservatives or disinfectants are used together with other antimicrobial agents. Preferably, such food preservatives or disinfectants are used in combination with one or more additional active ingredients as defined herein. Preferably, said one or more additional active ingredients are selected from the group consisting of a bacteriophage or phage and antibiotic as defined herein.

[0058] The polypeptide, nucleic acid molecule, construct, vector, cell and/or composition according to the invention can be applied on or into food products, and/or into various physical sites to be disinfected, by a number of means including, but not limited to, admixing said polypeptide and/or cell containing polypeptide of the invention into the food products, spraying said polypeptide and/or cell containing the polypeptide of the invention onto the foodstuffs or physical sites to be disinfected.

[0059] A polypeptide of the invention can be isolated from a cell or a cell containing said polypeptide of the invention can be directly applied or administered without isolation of said polypeptide. For example, a cell which produces a polypeptide of the invention could be administered to a subject (human or animal) or applied to a surface where the polypeptide of the invention would be secreted into food, onto a surface or into the subject's gut. The polypeptide of the invention can then bind and lyse a bacterium of the genus *Staphylococcus*, more preferably a bacterium of the species *S. aureus*, present in this environment.

[0060] Further encompassed is the use of a polypeptide according to the invention, a nucleic acid molecule encoding such polypeptide, a construct comprising such nucleic acid molecule, a vector comprising such construct, a cell comprising such vector and/or a composition comprising any of the above, for detecting bacteria of the genus *Staphylococcus*, more preferably a bacterium of the species *S. aureus*. Preferably, said polypeptide, nucleic acid molecule, construct, vector, cell and/or composition is used in a diagnostic application. Possibly said polypeptide, nucleic acid molecule, a construct, a vector, cell and/or a composition is used together with other detection agents.

Definitions**Sequence identity**

[0061] "Sequence identity" is herein defined as a relationship between two or more amino acid (peptide, polypeptide, or protein) sequences or two or more nucleic acid (nucleotide, polynucleotide) sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between amino acid or nucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Similarity" between two amino acid sequences is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one peptide or polypeptide to the sequence of a second peptide or polypeptide. In a preferred embodiment, identity or similarity is calculated over the whole SEQ ID NO as identified herein. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heine, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48:1073 (1988).

[0062] Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include e.g. the GCG program package (Devereux, J., et al., Nucleic Acids Research 12 (1): 387 (1984)), BestFit, BLASTP, BLASTN, and FASTA (Altschul, S. F. et al., J. Mol. Biol. 215:403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (BLAST Manual, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990)). The well-known Smith Waterman algorithm may also be used to determine identity.

[0063] Preferred parameters for polypeptide sequence comparison include the following: Algorithm: Needleman and Wunsch, J. Mol. Biol. 48:443-453 (1970); Comparison matrix: BLOSSUM62 from Hentikoff and Hentikoff, Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992); Gap Penalty: 12; and Gap Length Penalty: 4. A program useful with these parameters is publicly available as the "Ogap" program from Genetics Computer Group, located in Madison, WI. The aforementioned parameters are the default parameters for amino acid comparisons (along with no penalty for end gaps).

[0064] Preferred parameters for nucleic acid comparison include the following: Algorithm:

Needleman and Wunsch, J. Mol. Biol. 48:443-453 (1970); Comparison matrix: matches=+10, mismatch=0; Gap Penalty: 50; Gap Length Penalty: 3. Available as the Gap program from Genetics Computer Group, located in Madison, Wis. Given above are the default parameters for nucleic acid comparisons.

[0065] Optionally, in determining the degree of amino acid similarity, the skilled person may also take into account so-called "conservative" amino acid substitutions, as will be clear to the skilled person. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulphur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine. Substitutional variants of the amino acid sequence disclosed herein are those in which at least one residue in the disclosed sequences has been removed and a different residue inserted in its place. Preferably, the amino acid change is conservative. Preferred conservative substitutions for each of the naturally occurring amino acids are as follows: Ala to ser; Arg to lys; Asn to gln or his; Asp to glu; Cys to ser or ala; Gln to asn; Glu to asp; Gly to pro; His to asn or gln; Ile to leu or val; Leu to ile or val; Lys to arg; gln or glu; Met to leu or ile; Phe to met, leu or tyr; Ser to thr; Thr to ser; Trp to tyr; Tyr to trp or phe; and, Val to ile or leu.

Nucleic acid construct, transformation, expression vector, operably linked, expression, control sequences, polypeptide Construct

[0066] A nucleic acid molecule is represented by a nucleotide sequence. A polypeptide is represented by an amino acid sequence. A nucleic acid construct is defined as a nucleic acid molecule which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids which are combined or juxtaposed in a manner which would not otherwise exist in nature. A nucleic acid molecule is represented by a nucleotide sequence. Optionally, a nucleotide sequence present in a nucleic acid construct is operably linked to one or more control sequences, which direct the production or expression of said peptide or polypeptide in a cell or in a subject.

[0067] "Operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the nucleotide sequence coding for the polypeptide of the invention such that the control sequence directs the production/expression of the peptide or polypeptide of the invention in a cell and/or in a subject.

[0068] "Operably linked" may also be used for defining a configuration in which a sequence is

appropriately placed at a position relative to another sequence coding for a functional domain such that a chimeric polypeptide is encoded in a cell and/or in a subject.

Expression will be understood to include any step involved in the production of the peptide or polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification and secretion.

[0069] Control sequence is defined herein to include all components which are necessary or advantageous for the expression of a polypeptide. At a minimum, the control sequences include a promoter and transcriptional and translational stop signals. Optionally, a promoter represented by a nucleotide sequence present in a nucleic acid construct is operably linked to another nucleotide sequence encoding a peptide or polypeptide as identified herein.

[0070] The term "transformation" refers to a permanent or transient genetic change induced in a cell following the incorporation of new DNA (i.e. DNA exogenous to the cell). When the cell is a bacterial cell, as is intended in the current invention, the term usually refers to an extrachromosomal, self-replicating vector which harbors a selectable antibiotic resistance.

[0071] An expression vector may be any vector which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of a nucleotide sequence encoding a polypeptide of the invention in a cell and/or in a subject. As used herein, the term "promoter" refers to a nucleic acid fragment that functions to control the transcription of one or more genes or nucleic acids, located upstream with respect to the direction of transcription of the transcription initiation site of the gene. It is related to the binding site identified by the presence of a binding site for DNA-dependent RNA polymerase, transcription initiation sites, and any other DNA sequences, including, but not limited to, transcription factor binding sites, repressor and activator protein binding sites, and any other sequences of nucleotides known to one skilled in the art to act directly or indirectly to regulate the amount of transcription from the promoter. Within the context of the invention, a promoter preferably ends at nucleotide -1 of the transcription start site (TSS).

[0072] "Polypeptide" as used herein refers to any peptide, oligopeptide, polypeptide, gene product, expression product, or protein. A polypeptide is comprised of consecutive amino acids. The term "polypeptide" encompasses naturally occurring or synthetic molecules.

[0073] In this document and in its claims, the verb "to comprise" and its conjugations is used in its non-limiting sense to mean that items following the word are included, but items not specifically mentioned are not excluded. In addition the verb "to consist" may be replaced by "to consist essentially of" meaning that a product or a composition or a nucleic acid molecule or a peptide or polypeptide of a nucleic acid construct or vector or cell as defined herein may comprise additional component(s) than the ones specifically identified; said additional component(s) not altering the unique characteristic of the invention. In addition, reference to an element by the indefinite article "a" or "an" does not exclude the possibility that more than one of the elements is present, unless the context clearly requires that there be one and only one of the elements. The indefinite article "a" or "an" thus usually means "at least one".

[0074] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

Description of the figures

[0075]

Fig. 1. Linear relationship of Ply2638 (SEQ ID NO: 21 encoded by SEQ ID NO: 44) activity against *S. aureus* SA2638/2854 cells in dependency of endolysin concentration. Assays were performed under standard conditions (PBS buffer pH 7.4, 120 mM sodium chloride) in photometric lysis assays. Maximum activity was determined from the first derivative of regression fits from sigmoidal lysis curves, calculated with SigmaPlot software. Error bars represent standard deviation calculated from technical triplicate experiments.

Fig. 2. Influence of divalent cations on lytic activity of Ply2638 (SEQ ID NO: 21, encoded by SEQ ID NO: 44). The enzyme was EDTA treated with subsequent substitution of metal ions by dialysis against MOPS buffer containing MgCl₂, CaCl₂, ZnCl₂, CuCl₂, CoCl₂, or MnSO₄. Ply2638 dialyzed against MOPS buffer omitting EDTA treatment served as reference. Error bars represent standard deviation, calculated from technical triplicate experiments.

Fig. 3. Lytic activity of 50 nM Ply2638 (SEQ ID NO: 21, encoded by SEQ ID NO: 44) on *S. aureus* SA2638/2854 cells after lyophilization and reconstitution. Activity was measured in a turbidity reduction assay under standard conditions. Lyophilization buffer was taken as a control. The triple domain enzyme recovers full lytic activity after freeze-drying.

Fig. 4. Lytic activity of 50 nM M23-LST_Ami2638_CBD2638 (SEQ ID NO: 29, encoded by SEQ ID NO: 48) on *S. aureus* SA2638/2854 cells after lyophilization and reconstitution (indicated as lyophilized) as compared to freshly prepared M23-LST_Ami2638_CBD2638 (SEQ ID NO: 29, encoded by SEQ ID NO: 48) and Ply2638 (SEQ ID NO: 21, encoded by SEQ ID NO: 44). Lyophilization buffer was taken as a control. Activity was measured in a turbidity reduction assay under standard conditions. The triple domain enzyme recovers full lytic activity after freeze-drying.

Fig. 5. Relative activity of Lysostaphin (LST; SEQ ID NO: 34, encoded by SEQ ID NO: 33) and Ply2638 derivatives (SEQ ID NO: 31, 30, 29, 21 and 24, encoded by SEQ ID NO: 11, 10, 48, 44 and 4, respectively) in dependency of the concentration. The activity of LST at 50 nM was set as reference. All assays were done under standard conditions (37°C, pH 7.4 and 120 mM sodium chloride concentration) using *S. aureus* SA2638/2854 substrate cells from frozen stock.

Fig. 6. Relative activities at various pH values (left diagram) and sodium chloride concentrations (right diagram) of truncated and (with PlyTw domains) retrofitted Ply2638 variants determined in turbidity reduction assays. Truncation of the enzyme by one of the two catalytic domains resulted in impaired activities. Duplication of the CBD (M23_Ami_SH3b_SH3b; SEQ ID NO: 32, encoded by SEQ ID NO: 49) accelerates lysis at basic

pH values and elevated salt concentrations. Retrofitting of Ply2638 with CHAP11 domain results in an enzyme which is presumed to attack three different bonds in the peptidoglycan layer of *Staphylococcus*. It shifted pH optima to slight acidic conditions and improved antibacterial activity. However, protein stability of the chimeric enzymes remains a challenge. Maximum lysis velocity of Ply2638 at standard conditions (pH 7.4 and 120 mM sodium chloride concentration) was set as reference. Bars represent mean of triplicate assays, standard deviation is not shown. (CHAP_M23_Ami_SH3b = SEQ ID NO: 25, encoded by SEQ ID NO: 45; Ami_M23_Ami_SH3b = SEQ ID NO: 26, encoded by SEQ ID NO: 46; M23_Ami_SH3b_SH3b = SEQ ID NO: 32, encoded by SEQ ID NO: 49; M23_Ami_SH3b = SEQ ID NO: 21, encoded by SEQ ID NO: 44; Ami_SH3b = SEQ ID NO: 22, encoded by SEQ ID NO: 2; M23_SH3b = SEQ ID NO: 23, encoded by SEQ ID NO: 3).

Fig. 7.: Activity of 50 nM quadruple domain enzymes (SEQ ID NO: 27 and 28, encoded by SEQ ID NO: 47 and 8, respectively), Ply2638 (SEQ ID NO: 21, encoded by SEQ ID NO: 44), and Lyosotaphin (SEQ ID NO: 34, encoded by SEQ ID NO: 33) against using *S. aureus* SA2638/2854 substrate cells under standard conditions. Lyophilization buffer was taken as a control. Quadruple domain enzymes were constructed by combining domains of Ply2638, PlyTw, and Lysostaphin.

Examples

Materials and Methods

Bacterial strains, culture conditions, phages and plasmids

[0076] *E. coli* XL1BlueMRF and *E. coli* Sure was used for the over-expression of 6x-His-tagged (SEQ ID NO: 43) fusion proteins. Both strains were cultured in LB-PE medium at 30°C with 100 µg/ml ampicillin and 30 µg/ml tetracycline for plasmid selection. Phage 2638A lysate were used as template for the amplification of Ply2638A gene or domain coding regions thereof. CHAPT_w domain (SEQ ID NO: 19) was amplified from Phage Twort lysate. Cystein- Histidine dependent amidase/ peptidase (CHAP) domain and amidase domain from phage 11 (SEQ ID NO 18 and 17, respectively; Donovan, et al., 2006 and 2008; Navarre et al., 1999; Sass and Bierbaum 2007) were amplified from a pet21a vector containing phi11 autolysin gene, a kindly gift from Donovan, D.M.. Plasmid LT1215 containing the sequence of mature Lysostaphin (SEQ ID NO: 33) was used as template for domain amplification M23-LST (SEQ ID NO: 15) and CWT-LST (SEQ ID NO: 13).

pQE-30 vector (catalogues number: 32915, Qiagen, Hilden, Germany; SEQ ID NO: 50) was used as cloning and expression vector for the production of 6x-His tagged recombinant fusion proteins in *E. coli* XL1BlueMRF' or *E. coli* Sure respectively.

DNA techniques and cloning procedures

[0077] Standard techniques according to Sambrook, Maniatis et al. (1989) were employed for cloning of single genes and the creation of fusion proteins. High Fidelity PCR Enzyme mix (Fermentas) was used in PCR reactions. DNA concentrations were determined with a spectrophotometer (NanoDrop ND-1000 Spectrophotometer).

pHP12638 is constructed by insertion of Ply2638 (SEQ ID NO: 1) encoding sequence Met1 - Lys486 into pQE30 (SEQ ID NO: 50) sites BamHI - Sall. pHP12638-P12638 construct has the same sequence consecutively inserted into BamHI - SacI - Sall sites. CHAP11 (SEQ ID NO: 18), Ami11 (SEQ ID NO: 17) and CHAP_Ami11 were N-terminal introduced into BamHI digested pHPL2638A. Prior to ligation reaction, the vector was dephosphorylated using shrimp alkaline phosphatase (SAP, Fermentas). pHM23_CBD2638 (SEQ ID NO: 3), and pHM23-2638_Ami2638_CBD2638_CBD2638 (SEQ ID NO: 49) were constructed by a replacement of GFP coding region from pHGFP_CBD2638A-c vector (SEQ ID NO: 59) with the respective inserts using BamHI and SacI restriction sites. pHM23-LST_Ami2638_CBD2638 (SEQ ID NO: 48) has a pQE-30 backbone with mature lysostaphin (SEQ ID NO: 33) coding sequence Ala1 - Gly154 inserted into BamHI and SacI and Ply2638 partial sequence encoding Leu138 - Lys486 in SacI and Sall sites. pHM23-LST_M23-LST_CWT-LST (SEQ ID NO: 11) has mature Lysostaphin (SEQ ID NO: 33) sequences Ala1 - Gly154 inserted into BamHI and SacI and Ala1 - Lys246 into SacI and Sall sites of pQE30. pHLST-LST (SEQ ID NO: 10) is constructed the same way having Ala1 - Lys246 repeatedly in BamHI - SacI and SacI - Sall sites. In plasmids encoding quadruple domain constructs pHCHAPT_{tw}_Ami2638_M23-LST_CBD2638 (SEQ ID NO: 47) and pHCHAPT_{tw}_Ami2638_M23-LST_CWT-LST (SEQ ID NO: 8) the domains are directly fused via splicing overlap extension PCR (SOE) and inserted into pQE30 BamHI and Sall sites. In both constructs, boarder regions of individual domains (CHAPT_{tw}, SEQ ID NO: 19: Met1 - Ile140, Ami2638, SEQ ID NO: 16: Lys141-Gly358 of SEQ ID NO: 1, CBD2638, SEQ ID NO: 12 : Trp393- Lys486 of SEQ ID NO: 1, M23-LST, SEQ ID NO: 15: Ala1 - Gly154 of SEQ ID NO: 33, CWT-LST, SEQ ID NO: 13: Trp155 - Lys246 of SEQ ID NO: 33) were determined with bioinformatics (unpublished data). Plasmids with repetitive sequences were transferred into E. coli Sure strain, all other plasmids into E. coli XL1BlueMRF'.

Expression and purification of recombinant fusion proteins

[0078] Protein overexpression and partial purification was essentially done as previously described by others (Loessner et al., 1996, Schmelcher et al., 2010). In brief, plasmid bearing E. coli were grown in 250 ml modified LB medium (15 g/l tryptose, 8 g/l yeast extract, 5 g/l NaCl, pH 7.8) to an optical density at 600nm (OD_{600nm}) of 0.4 to 0.6 and induced with 1 mM IPTG. Cells were further incubated for 4 hours at 30°C, or 18 hours at 20°C, cooled to 4°C, and harvested by centrifugation. Cell pellets were suspended in 5 ml immobilization buffer (50 mM NaH₂PO₄, 500 mM NaCl, 5 mM imidazole, 0.1 % polysorbate20, pH 7.4). Cytosolic E. coli

contents containing soluble recombinant proteins were liberated by a double passage through a French Pressure Cell Press (1200 psi, SLM Aminco, Urbana, IL, U.S.) operated at 1200 psi. Other downstream processing steps included removal of insoluble cell debris by centrifugation, filter sterilization (0.2 μ m PES membrane, Millipore), and Immobilized Metal Affinity Chromatography (IMAC) purification using Micro-Biospin (Bio-Rad, Hercules, CA, U.S.) columns packet with low density Ni-NTA Superflow resin (Chemie Brunschwig AG, Basel, Switzerland). Ni-NTA immobilized proteins were on-column gravity flow washed with 5-10 column volumes immobilization buffer. Protein fractions were then eluted with elution buffer (50 mM NaH₂PO₄, 500 mM NaCl, 125 mM imidazole, 0.1% polysorbate20, pH 7.4) and dialyzed against two changes of dialysis buffer (50 mM NaH₂PO₄, 100 mM NaCl, 0.1% polysorbate20, pH 7.4). Protein concentrations were defined in a NanoDrop ND-1000 spectrophotometer, corrected for specific absorbance at 280 nm as calculated from the primary amino acid sequence with Vector NTI software (Invitrogen, Carlsbad, CA, U.S.) and estimated for purity by SDS-PAGE. Aliquots were stored at -20°C mixed with 50% glycerol.

Lyophilization of recombinant proteins

[0079] IMAC purified proteins were dialyzed against 3 changes of 300 ml lyophilization buffer (50 mM phosphate or Tris, 500 mM sucrose, 200 mM mannitol, pH 7.4) aliquot and frozen in the gaseous phase of liquid nitrogen. The freeze-drying was done at -40°C and vacuum at 75 mTorr for 60 minutes, followed by increasing temperature during 5 hours to -10°C and another 60 minutes at -10°C at the same vacuum levels. As final step, temperature was increased to 25°C during 10 hours. Samples were reconstituted prior to testing in lysis assays by the addition of water.

Cell wall-binding assay

[0080] As a standard assay to determine the ability of a CBD to direct a GFP fusion to the bacterial surface and mediate tight binding to the cell wall ligand, the following conditions is used: bacteria, preferably *S. aureus* BB255, from late log phase are harvested by centrifugation, resuspended in 1/10th volume of PBS-T (50 mM NaH₂PO₄ 120 mM NaCl [pH 8.0], 0.01% polysorbate 20) and stored on ice. GFP-CBD proteins, preferably SEQ ID NO: 64, encoded by SEQ ID NO: 60, are diluted in the same buffer to a concentration of 400 nM (2x GFP-CBD) and also stored on ice. In a 1.5 ml microcentrifuge cup, 100 μ l cells and 100 μ l of 2x GFP-CBD are mixed and incubated at room temperature for 5 min. Cells are then removed from the supernatant by centrifugation in a microfuge (16000 g, 60 s). The supernatant was discarded and cells were washed twice in 500 μ l of PBS-T buffer. For fluorescence microscopy the pellet was finally resuspended in 50 μ l of buffer. For fluorometer assays, the pellet is finally resuspended in 200 μ l of PBS-T and transferred to a microplate well. Quantitative fluorescence assays can be performed using a multi label counter device (Victor³, Perkin Elmer, Massachusetts, U.S.) with sterile, untreated, black 96-well polystyrene microplates (Nunc,

Roskilde, Denmark). As a negative control GFP can be used.

Quantitative fluorescence assays

[0081] Dependency of pH and salt on CBD2638 to *S. aureus* BB255 cell surface ligand interaction is investigated by incubation of cells from 1 ml volume set to an OD_{600nm} 1 +/- 0.05 (~4 x 10⁹ cells) with 7.5 µg GFP-CBDS2638 fusion protein, SEQ ID NO: 64, encoded by SEQ ID NO: 60. This cell to protein ratio is close to saturation point as determined in previous experiments and enables detection of variations in binding efficiencies. Varying pH is tested using citrate buffers pH 4.5 to 6.5 and phosphate buffers pH 6 to 9. After incubation with GFP-CBD2638 protein in pH buffer, cells are washed with respective pH buffer followed by standard PBS-T (pH 8) washing. Finally, cells are adjusted to an OD_{595nm} = 0.3 to detect fluorescence from 200 µl suspensions thereof with a Victor³ multi label counter. Similar experiments are performed using buffers prepared with increasing sodium chloride concentrations (10 mM NaH₂PO₄, 0 - 1000 mM NaCl, 0.1% polysorbate 20, pH 6).

[0082] Quantification of CBD binding capacity of *Staphylococcus* strains with altered cell surface properties is tested by recording relative fluorescence units (RFU) of washed and heat killed cells previously incubated with excessive GFP-CBD2638 protein. Fluorescence of equal volumes (200 µl) of GFP-CBD2638 labeled cells, adjusted to an OD_{595nm} = 0.3, are measured using appropriate filter sets in a multi label counter device. Comparison and quantification of absorption levels of GFP-CBD2638 (SEQ ID NO: 64, encoded by SEQ ID NO: 60), GFP-CBD2638-CBD2638 (SEQ ID NO 65 and/or 66, encoded by SEQ ID NO: 61 and 62, respectively), and GFP-CBD2638-CBD2638-CBD2638 (SEQ ID NO: 67, encoded SEQ ID NO: 63) on *S. aureus* BB255 cells and SDS treated cells is done the same way.

Lysis assays

[0083] Substrate cell for lytic activity assays were grown to an optical density at 600nm (OD₆₀₀) of 0.4, washed twice with PBST pH 7.4 and re- suspended in 15% glycerol containing PBS buffer pH 7.4 concentrating it at the same time 100 fold. The cells were stored at -20°C. For further use in binding or lytic activity assays the cells were thaw, washed with PBS pH 7.4 and diluted to an OD₆₀₀ of 1 ± 0.05. In standard lytic activity assays protein samples were diluted to equimolar amounts and distributed in transparent 96-well tissue culture test plates (SPL life sciences, Pocheon, Korea). Substrate cells were added to a final volume and drop in optical density at 595nm (OD_{595nm}) were recorded for about 1 hour at 37°C.

[0084] Lytic activity of retrofitted and deletion constructs of Ply2638 were tested against Phage 2638A propagation strain *S. aureus* SA2638/2854 from frozen stock in lysis assays. We tested the activity at various buffer conditions. pH values from 4.6 to 9 in 0.4 increments were tested

using Citrate/ Phosphate buffers (25 mM Citrate, 25 mM Phosphate, 120 mM NaCl, pH 4.6 - 6.6) and Tris/ Phosphate buffers (25 mM Tris, 25 mM Phosphate, 120 mM NaCl). The activity of Ply2638A derivatives at salt concentrations ranging from 0 to 1000 mM Sodium chloride (in 10 mM phosphate buffer pH 7.4) was tested. The Ply2638A derivatives were diluted to 10 μ M final concentration with MQ prior to its application in lysis assays. Here, 4 μ l of 10 μ M Ply2638A derivatives were applied to 196 μ l substrate cell suspensions using a multichannel pipette, resulting in an assay concentration of 200 nM protein. The substrate cell suspensions were prepared from frozen stocks, diluting it with pH or salt buffers and standardizing it spectrophotometrically (Libra S22, Biochrom) to an initial OD₆₀₀ of 1 ± 0.05 . Decrease in optical density at 595 nm (OD₅₉₅) was measured using a Victor3 1420 Multilabel Counter instrument (Perkin Elmer) during 1 hour. Plates were shaken vigorously for 1 second (double orbit, 0.1mm diameter) after every single read out. As positive control served N-terminal 6xHis tagged Lysostaphin (HLST), commercially available Lysostaphin (recombinant, E. coli originated, Sigma). As negative control we applied MilliQ water.

Influence of divalent metal ions on the activity of Ply2638

[0085] Partially purified Ply2638 (SEQ ID NO: 21) was dialyzed for 2 hours against EDTA containing buffer (50 mM MOPS, 100 mM sodium chloride, 0.005% polysorbate20, 10 mM EDTA) followed by dialysis against buffer containing the respective divalent metal ions (50 mM MOPS, 100 mM sodium chloride, 0.005% polysorbate20, and 10 mM CaCl₂, 10 mM MgCl₂, 1 mM CoCl₂, 1 mM CuCl₂, 1 mM MnSO₄ or 1 mM ZnCl₂ respectively). Cells used as substrate were SDS treated and EDTA washed prior to its application in standard lysis assays.

Tabel 1. SEQ ID NO identification

enzyme/domain/construct/vector	nucleic acid sequence	amino acid sequence	amino acid sequence of domain with putative linker	nucleic acid sequence of His-tagged construct
Mature enzyme				
Ply2638	SEQ ID NO: 1	SEQ ID NO: 21		SEQ ID NO: 44
LST	SEQ ID NO: 33	SEQ ID NO: 34		
Domain				
CBD-2638	SEQ ID NO: 12	SEQ ID NO: 35	SEQ ID NO: 51	
CWT-LST	SEQ ID NO: 13	SEQ ID NO: 36	SEQ ID NO: 52	

enzyme/domain/construct/vector	nucleic acid sequence	amino acid sequence	amino acid sequence of domain with putative linker	nucleic acid sequence of His-tagged construct
M23-2638	SEQ ID NO: 14	SEQ ID NO: 37	SEQ ID NO: 53	
M23-LST	SEQ ID NO: 15	SEQ ID NO: 38	SEQ ID NO: 54	
Ami-2638	SEQ ID NO: 16	SEQ ID NO: 39	SEQ ID NO: 55	
Ami- Φ 11	SEQ ID NO: 17	SEQ ID NO: 40	SEQ ID NO: 56	
CHAP- Φ 11	SEQ ID NO: 18	SEQ ID NO: 41	SEQ ID NO: 57	
CHAP- Φ Twort	SEQ ID NO: 19	SEQ ID NO: 42	SEQ ID NO: 58	
Retrofitted construct				
CHAP11_M23-2638_Ami2638_CBD2638	SEQ ID NO: 5	SEQ ID NO: 25		SEQ ID NO: 45
Ami11_M23-2638_Ami2638_CBD2638	SEQ ID NO: 6	SEQ ID NO: 26		SEQ ID NO: 46
CHAPT _w _Ami2638_M23-LST_CBD2638	SEQ ID NO: 7	SEQ ID NO: 27		SEQ ID NO: 47
M23-LST_Ami2638_CBD2638	SEQ ID NO: 9	SEQ ID NO: 29		SEQ ID NO: 48
M23-2638_Ami2638_CBD2638_CBD2638	SEQ ID NO: 20	SEQ ID NO: 32		SEQ ID NO: 49
Ami2638-CBD2638		SEQ ID NO: 22		SEQ ID NO: 2
M23-2638-CBD2638		SEQ ID NO: 23		SEQ ID NO: 3
Ply2638-Ply2638		SEQ ID NO: 24		SEQ ID NO: 4
CHAPT _w _Ami2638_M23-LST_CWT-LST		SEQ ID NO: 28		SEQ ID NO: 8
LST_LST		SEQ ID NO: 30		SEQ ID NO: 10
M23-LST_M23-LST_CWT-LST		SEQ ID NO: 31		SEQ ID NO: 11

enzyme/domain/construct/vector	nucleic acid sequence	amino acid sequence	amino acid sequence of domain with putative linker	nucleic acid sequence of His-tagged construct
GFP_CBD2638		SEQ ID NO: 64		SEQ ID NO: 60
GFP_CBD2638_CBD2638 var.1		SEQ ID NO: 65		SEQ ID NO: 61
GFP_CBD2638_CBD2638 var. 2		SEQ ID NO: 66		SEQ ID NO: 62
GFP_CBD2638_CBD2638 CBD2638		SEQ ID NO: 67		SEQ ID NO: 63
Tag				
6xHis-tag		SEQ ID NO: 43		
Vector				
pQE-30 vector	SEQ ID NO: 50			
pHGFP_CBD2638_c vector	SEQ ID NO: 59			

SEQ ID NO: 1 (Ply2638)**[0086]**

ATGCTAACTGCTATTGACTATCTTACGAAAAAAGGTTGGAAAATATCATCT
 GACCCTCGCACTTACGATGGTTACCCTAAAAACTACGGCTACAGAAATTAC
 CATGAAAACGGCATTAAATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTT
 TTGATGTTTACAGTAACGAACTAACGACGTGCCTGCTGTTACTAGCGGAA
 CAGTTATTGAAGCAAACGATTACGGTAATTTTGGTGGTACATTCGTTATTAG
 AGACGCTAACGATAACGATTGGATATATGGGCATCTACAACGTGGCTCAAT
 GCGATTTGTTGTAGGCGACAAAGTCAATCAAGGTGACATTATTGGTTTACA
 AGGTAATAGCAACTATTACGACAATCCTATGAGTGTACATTTACATTTACA
 ATTACGCCCTAAAGACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTG
 GTTTGGCTATGGAAAAATATGACATTACAAATTTAAATGCTAAACAAGATA
 AATCAAAGAATGGGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCAT
 ATTAAAGGTAACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTC
 ATCCACAATGATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTAT

ATGCACGTGAGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTTTATG
CAAATAGAAACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGC
ATTGTGGTAATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTG
AGTCGTATCCTGGTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAG
CGACATTGAAAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTA
ATCGCAACACTGTACGTCTGCATAACGAATTCTTCGGAACCTTCTTGTCACA
TCGTTTCGTGGGACTTGTCATGTTGGCAAAGGTGAGCCTTACACAACACTAA
TATTAATAAAAATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGA
CGGTGGAAAGCTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACG
TTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACA
GATTGGAAACAGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCG
TTCACAGTGACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGG
ACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATAT
GATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTT
GAGGGCGAAACTGTATACATGCCGGTACGCACATGGGACGCTAAAACTGG
TAAAGTTGGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 2 (Ami2638 CBD2638 + 6xHis and cloning sites)

[0087]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTTACGCCCTAAAGAC
GCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAAA
ATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGGA
GCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAGGTAACAAGA
TTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTATG
GTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAATA
ACGGTACACACGTTAACGGTTGGGCTAGTGTTTATGCAAATAGAAACGAAG
TGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAAT
GGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGTA
GAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTAG
CTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTAC
GTCTGCATAACGAATTCTTCGGAACCTTCTTGTCACATCGTTTCGTGGGACTT
GCATGTTGGCAAAGGTGAGCCTTACACAACACTACTAATATTAATAAAATGAA
AGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAGA
AGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTA
AAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAAT
AAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCA
CCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAA
GCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAA
TTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTA

TACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGTTG
TGGGGCGAAATTAAATAA

SEQ ID NO: 3 (M23-2638 CBD2638 + 6xHis and cloning sites)

[0088]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGCTAACTGCTATT
GACTATCTTACGAAAAAAGGTTGGAAAATATCATCTGACCCTCGCACTTAC
GATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGAAAACGGCATT
AATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTA
ACGAAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAA
ACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGACGCTAACGATA
ACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAG
GCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGTAATAGCAACT

ATTACGACAATCCTATGAGTGTACATTTACATTTACAATTACGCCCTAAAGA
CGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAA
AATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGG
AGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACAAG
ATTACAGCACCAAAACCTAGTATTCAAGGTGAGCTCGGTGGAAAGCTAGAA
GTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAA
AAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATA
AAGATGGCATTGTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCAC
CAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAG
CTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAAT
TTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTAT
ACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGTTGT
GGGGCGAAATTAAATAA

SEQ ID NO: 4 (Ply2638-Ply2638 + 6x His and cloning sites))

[0089]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGCTAACTGCTATT
GACTATCTTACGAAAAAAGGTTGGAAAATATCATCTGACCCTCGCACTTAC
GATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGAAAACGGCATT
AATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTA
ACGAAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAA
ACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGACGCTAACGATA
ACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAG

GCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGTAATAGCAACT
ATTACGACAATCCTATGAGTGTACATTTACATTTACAATTACGCCCTAAAGA
CGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAA
AATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGG
AGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACAAG
ATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTAT
GGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAAT
AACGGTACACACGTTAACGGTTGGGCTAGTGTATTATGCAAATAGAAACGAA
GTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAA
TGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGT
AGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTA

GCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTA
CGTCTGCATAACGAATTCCTCGGAACTTCTTGTCCACATCGTTCGTGGGACT
TGCATGTTGGCAAAGGTGAGCCTTACACAACACTACTAATATTAATAAAATGA
AAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAG
AAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTT
AAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGA
ATAAAGATGGCATTGTTGTTATAAAGCTGAACATGCTTCGTTACAGTGACAG
CACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCAC
AAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAA
AATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTG
TATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGT
TGTGGGGCGAAATTAAGAGGCTCATGCTAACTGCTATTGACTATCTTACGA
AAAAAGGTTGGAAAATATCATCTGACCCCTCGCACTTACGATGGTTACCCTA
AAAACACTACGGCTACAGAAATTACCATGAAAACGGCATTAAATTATGATGAGT
TTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTAACGAAACTAACGA
CGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAAACGATTACGGTAA
TTTTGGTGGTACATTCGTTATTAGAGACGCTAACGATAACGATTGGATATAT
GGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAGGCGACAAAGTCAAT
CAAGGTGACATTATTGGTTTACAAGGTAATAGCAACTATTACGACAATCCT
ATGAGTGTACATTTACATTTACAATTACGCCCTAAAGACGCAAAGAAAGAT
GAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAAAATATGACATTACA
AATTTAAATGCTAAACAAGATAAATCAAAGAATGGGAGCGTGAAAGAGTT
GAAACATATCTATTCAAACCATATTAAAGGTAACAAGATTACAGCACCAAA
ACCTAGTATTCAAGGTGTGGTCATCCACAATGATTATGGTAGTATGACACC
TAGTCAATACTTACCATGGTTATATGCACGTGAGAATAACGGTACACACGT
TAACGGTTGGGCTAGTGTATTATGCAAATAGAAACGAAGTGCTTTGGTATCA
TCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAATGGGCAAATGCTAA
CTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGTAGAATCTCGGACAA
ATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTAGCTGCGGATGTGAT
GAAGTCGTACGGATTACCAGTTAATCGCAACACTGTACGTCCTGCATAACGA

ATTCTTCGGAACCTTCTTGCCACATCGTTCTGTTGGGACTTGCATGTTGGCAA
 GGTGAGCCTTACACAACCTACTAATATTAATAAAATGAAAGACTACTTCATC
 AAACGCATCAAACATTATTATGACGGTGGAAAGCTAGAAGTAAGCAAAGC
 AGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAG
 CAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATT
 TGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAATT
 ATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTA
 CAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCAT
 GTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTA
 CGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAAATT
 AAATAA

SEQ ID NO: 5 (CHAP11 M23-2638 Ami2638 CBD2638)

[0090]

ATGCAAGCAAAATTAACATAAAATGAGTTTATAGAGTGGTTGAAAACCTCT
 GAGGGAAAACAATTCAATGTGGACTTATGGTATGGATTTCAATGCTTTGAT
 TATGCCAATGCTGGTTGGAAAGTTTTGTTTGGATTACTTCTAAAAGGTTTAG
 GTGCAAAAGATATTCGTTTCGCTAACAACTTCGACGGATTAGCTACTGTAT
 ACCAAAATACACCGGACTTCTTAGCACAACCTGGCGACATGGTGGTATTCG
 GTAGCAACTACGGTGCTGGATATGGTCACGTTGCATGGGTAATTGAAGCAA
 CTTTAGATTACATCATTGTATATGAGCAGAATTGGCTAGGCGGTGGCTGGA
 CTGACGGAATCGAACAACCCGGCTGGGGTTGGGAAAAAGTTACAAGACGA
 CAACATGCTTATGATTTCCCTATGTGGTTTATCCGTCGGAATTTTAAAAGTG
 AGACAGCGCCACGATCAGTTCAATCTCTACACAAGCACCTAAAAAGAA
 ACAGCTGGATCCATGCTAACTGCTATTGACTATCTTACGAAAAAAGGTTGG
 AAAATATCATCTGACCCTCGCACTTACGATGGTTACCCTAAAAACTACGGC
 TACAGAAATTACCATGAAAACGGCATTAAATTATGATGAGTTTTGTGGTGGT
 TATCATAGAGCITTTGATGTTTACAGTAACGAAACTAACGACGTGCCTGCT
 GTTACTAGCGGAACAGTTATTGAAGCAAACGATTACGGTAATTTTGGTGGT
 ACATTCGTTATTAGAGACGCTAACGATAACGATTGGATATATGGGCATCTA
 CAACGTGGCTCAATGCGATTTGTTGTAGGCGACAAAGTCAATCAAGGTGAC
 ATTATTGGTTTACAAGGTAATAGCAACTATTACGACAATCCTATGAGTGTA
 CATTTACATTTACAATTACGCCCTAAAGACGCAAAGAAAGATGAAAAATCA
 CAAGTATGTAGTGGTTTGGCTATGGAAAAATATGACATTACAAATTTAAAT
 GCTAAACAAGATAAATCAAAGAATGGGAGCGTGAAAGAGTTGAAACATAT
 CTATTCAAACCATATTAAGGTAACAAGATTACAGCACCAAAACCTAGTAT
 TCAAGGTGTGGTCATCCACAATGATTATGGTAGTATGACACCTAGTCAATA

CTTACCATGGTTATATGCACGTGAGAATAACGGTACACACGTTAACGGTTG
GGCTAGTGTATTATGCAAATAGAAACGAAGTGCTTTGGTATCATCCGACAGA
CTACGTAGAGTGGCATTGTGGTAATCAATGGGCAAATGCTAACTTAATCGG
ATTTGAAGTGTGTGAGTCGTATCCTGGTAGAATCTCGGACAAATTATTCTTA
GAAAATGAAGAAGCGACATTGAAAGTAGCTGCGGATGTGATGAAGTCGTA
CGGATTACCAGTTAATCGCAACACTGTACGTCTGCATAACGAATTCTTCGG
AACTTCTTGTCCACATCGTTCGTGGGACTTGCATGTTGGCAAAGGTGAGCCT
TACACAACCTACTAATATTAATAAAAATGAAAGACTACTTCATCAAACGCATC
AAACATTATTATGACGGTGGAAGCTAGAAGTAAGCAAAGCAGCAACTAT
CAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAA
TTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATTGTGGTATAAA
GCTGAACATGCTTCGTTCACAGTGACAGCACCAGAGGGAATTATCACAAAGA
TACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGT
CAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTA
TCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTACGCACATGG
GACGCTAAAACCTGGTAAAGTTGGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 6 (Ami11 M23-2638 Ami2638 CBD2638)

[0091]

AAGCCACAACCTAAAGCAGTAGAACTTAAATCATCAAAGATGTGGTTAA
AGGTTATGACCTACCTAAGCGTGGTAGTAACCCTAAAGGTATAGTTATACA
CAACGACGCAGGGAGCAAAGGGGCGACTGCTGAAGCATATCGTAACGGAT
TAGTAAATGCACCTTTATCAAGATTAGAAGCGGGCATTGCGCATAGTTACG
TATCAGGCAACACAGTTTGGCAAGCCTTAGATGAATCACAAGTAGGTTGGC
ATACCGCTAATCAAATAGGTAATAAATATTATTACGGTATTGAAGTATGTC
AATCAATGGGCGCAGATAACGCGACATTCTTAAAAAATGAACAGGCAACTT
TCCAAGAATGCGCTAGATTGTTGAAAAAATGGGGATTACCAGCAAACAGA
AATACAATCAGATTGCACAATGAATTTACTTCAACATCATGCCCTCATAGA
AGTTCGGTTTTACACACTGGTTTTGACCCAGTAACTCGCGGTCTATTGCCAG
AAGACAAGCGGTTGCAACTTAAAGACTACTTTATCAAGCAGATTAGGGCGT
ACATGGATGGTAAAATACCGGTTGCCACTGTCTCTAATGAGTCAAGCGCTT
CAAGTAATACAGTTAAACCAGTTGCAAGTGCAGGATCCATGCTAACTGCTA
TTGACTATCTTACGAAAAAAGGTTGGAAAAATATCATCTGACCCTCGCACTT
ACGATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGAAAACGGCA

TTAATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAG
TAACGAAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGC
AAACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGACGCTAACGA
TAACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGATTTGTTGT
AGGCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGTAATAGCAA

CTATTACGACAATCCTATGAGTGTACATTTACATTTACAATTACGCCCTAAA
GACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGA
AAAATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATG
GGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACA
AGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATT
ATGGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGA
ATAACGGTACACACGTTAACGGTTGGGCTAGTGTATGCAAATAGAAACG
AAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATC
AATGGGCAAATGCTAACTTAATCGGATTGAAAGTGTGTGAGTCGTATCCTG
GTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAG
TAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTG
TACGTCTGCATAACGAATTCTTCGGAACCTCTTGTCCACATCGTTTCGTGGGA
CTTGCAATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAATAAAAT
GAAAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCT
AGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAG
TTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAG
AATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACA
GCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCA
CAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAA
AAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACT
GTATACATGCCGGTACGCACATGGGACGCTAAAACCTGGTAAAGTTGGTAAG
TTGTGGGGCGAAATTAAATAA

SEQ ID NO: 7 (CHAPTw_Ami2638_M23-LST_CBD2638)

[0092]

ATGAAAACCCTGAAACAAGCAGAGTCCTACATTAAGAGTAAAGTAAATAC
AGGAACTGATTTTGATGGTTTATATGGGTATCAGTGTATGGACTTAGCAGT
AGATTATATTTACCATGTAACAGATGGTAAATAAGAATGTGGGGTAATGC
TAAGGATGCGATAAATAACTCTTTTGGTGGTACTGCTACGGTATATAAAAA

CTACCCTGCTTTTAGACCTAAGTACGGTGATGTAGTCGTATGGACTACTGGT
AATTTTGCAACTTATGGTCATATCGCAATAGTTACTAACCCTGACCCTTATG
GAGACCTTCAATATGTTACAGTTCTTGAACAAAACCTGGAACGGTAACGGGA
TTTATAAAACCGAGTTAGCTACAATCAGAACACACGATTACACAGGAATTA
CACATTTTATTAAAGACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTG
GTTTGGCTATGGAAAAATATGACATTACAAATTTAAATGCTAAACAAGATA
AATCAAAGAATGGGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCAT
ATTAAAGGTAACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTC
ATCCACAATGATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTAT

ATGCACGTGAGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTATTATG
CAAATAGAAACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGC
ATTGTGGTAATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTG
AGTCGTATCCTGGTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAG
CGACATTGAAAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTA
ATCGCAACACTGTACGTCTGCATAACGAATTCTTCGGAACCTTCTTGTCCACA
TCGTTCTGTTGGGACTTGCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAA
TATTAATAAAAATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGA
CGGTGGAAAGCTAGAAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACG
TTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACA
GATGCTGCAACACATGAACATTCAGCACAAATGGTTGAATAATTACAAAAA
GGATATGGTTACGGTCCTTATCCATTAGGTATAAATGGCGGTATGCACTAC
GGAGTTGATTTTTTTATGAATATTGGAACACCAGTAAAAGCTATTTCAAGC
GGAAAAATAGTTGAAGCTGGTTGGAGTAATTACGGAGGAGGTAATCAAAT
AGGTCTTATTGAAAATGATGGAGTGCATAGACAATGGTATATGCATCTAAG
TAAATATAATGTTAAAGTAGGAGATTATGTCAAAGCTGGTCAAATAATCGG
TTGGTCTGGAAGCACTGGTTATTCTACAGCACCACATTTACACTTCCAAAGA
ATGGTTAATTCATTTTCAAATTCAACTGCCCAAGATCCAATGCCTTTCTTAA
AGAGCGCAGGATATGGAAAAGCAGGTGGTACAGTAACTCCAACGCCGAAT
ACAGGTTGGAAACAGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCT
TCGTTACAGTGACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCT
TGGACTGGTCACCCACAAGCTGGTGTATTACAAAAGGTCAAACGATTAAA
TATGATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACG

TTTGAGGGCGAAACTGTATACATGCCGGTACGCACATGGGACGCTAAAACCT
GGTAAAGTTGGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 8 (CHAPTw Ami2638 M23-LST CWT-LST +6xHis and cloning site)

[0093]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAAAACCCCTGAAA
CAAGCAGAGTCCTACATTAAGAGTAAAGTAAATACAGGAACTGATTTTGAT
GGTTTATATGGGTATCAGTGTATGGACTTAGCAGTAGATTATATTTACCATG
TAACAGATGGTAAAATAAGAATGTGGGGTAATGCTAAGGATGCGATAAAT
AACTCTTTTGGTGGTACTGCTACGGTATATAAAAACTACCCTGCTTTTAGAC
CTAAGTACGGTGATGTAGTCGTATGGACTACTGGTAATTTTGCAACTTATGG
TCATATCGCAATAGTTACTAACCCTGACCCTTATGGAGACCTTCAATATGTT
ACAGTTCTTGAAACAAAACCTGGAACGGTAACGGGATTTATAAAACCGAGTTA
GCTACAATCAGAACACACGATTACACAGGAATTACACATTTTATTAAAGAC

GCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAAA
ATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGGA
GCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAGGTAACAAGA
TTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTATG
GTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAATA
ACGGTACACACGTTAACGGTTGGGCTAGTGTTTATGCAAATAGAAACGAAG
TGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAAT
GGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGTA
GAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTAG
CTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTAC
GTCTGCATAACGAATTCTTCGGAACCTTCTTGTCCACATCGTTCGTGGGACTT
GCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAATAAAATGAA
AGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAGA
AGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTA
AAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATGCTGCAACACAT
GAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGGATATGGTTACGGT
CCTTATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTTTTTA
TGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTTGAAG
CTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAAAATG
ATGGAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTTAAAG

TAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGCACTG
GTTATTCTACAGCACCACATTTACACTTCCAAAGAATGGTTAATTCATTTTC
AAATTCAACTGCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGATATGG
AAAAGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTTGGAAAACAA
ACAAATATGGCACACTATATAAATCAGAGTCAGCTAGCTTCACACCTAATA
CAGATATAATAACAAGAACGACTGGTCCATTTAGAAGCATGCCGCAGTCAG
GAGTCTTAAAAGCAGGTCAAACAATTCATTATGATGAAGTGATGAAACAAG
ACGGTCATGTTTGGGTAGGTTATACAGGTAACAGTGGCCAACGTATTTACT
TGCCTGTAAGAACATGGAATAAATCTACTAATACTTTAGGTGTTCTTTGGGG
AACTATAAAGTAA

SEQ ID NO: 9 (M23-LST_Ami2638_CBD2638)

[0094]

GCTGCAACACATGAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGG
ATATGGTTACGGTCCTTATCCATTAGGTATAAATGGCGGTATGCACTACGG
AGTTGATTTTTTTATGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGG
AAAAATAGTTGAAGCTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAG
GTCTTATTGAAAATGATGGAGTGCATAGACAATGGTATATGCATCTAAGTA

AATATAATGTTAAAGTAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTT
GGTCTGGAAGCACTGGTTATTCTACAGCACCACATTTACACTTCCAAAGAA
TGGTTAATTCATTTTCAAATTCAACTGCCCAAGATCCAATGCCTTTCTTAA
GAGCGCAGGATATGGAAAAGCAGGTGGTACAGTAACTCCAACGCCGAATA
CAGGTGAGCTCTTACGCCCTAAAGACGCAAAGAAAGATGAAAAATCACAA
GTATGTAGTGGTTTGGCTATGGAAAAATATGACATTACAAATTTAAATGCT
AAACAAGATAAATCAAAGAATGGGAGCGTGAAAGAGTTGAAACATATCTA
TTCAAACCATATTAAAGGTAACAAGATTACAGCACCAAAACCTAGTATTCA
AGGTGTGGTCATCCACAATGATTATGGTAGTATGACACCTAGTCAATACTT
ACCATGGTTATATGCACGTGAGAATAACGGTACACACGTTAACGGTTGGGC
TAGTGTTTATGCAAATAGAAACGAAGTGCTTTGGTATCATCCGACAGACTA
CGTAGAGTGGCATTGTGGTAATCAATGGGCAAATGCTAACTTAATCGGATT
TGAAGTGTGTGAGTCGTATCCTGGTAGAATCTCGGACAAATTATTCTTAGA
AAATGAAGAAGCGACATTGAAAGTAGCTGCGGATGTGATGAAGTCGTACG
GATTACCAGTTAATCGCAACACTGTACGTCTGCATAACGAATTCTTCGGAA
CTTCTTGTCCACATCGTTTCGTGGGACTTGCATGTTGGCAAAGGTGAGCCTTA

CACAACTACTAATATTAATAAAATGAAAGACTACTTCATCAAACGCATCAA
ACATTATTATGACGGTGGAAAGCTAGAAGTAAGCAAAGCAGCAACTATCA
AACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATT
GTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATTGTTGGTATAAAGC
TGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAATTATCACAAGATA
CAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCA
AACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATC
GTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTACGCACATGGG
ACGCTAAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 10 (LST LST + 6xHis and cloning sites)

[0095]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCTGCAACACATGAA
CATTACGCACAATGGTTGAATAATTACAAAAAAGGATATGGTTACGGTCCT
TATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTTTTTATGA
ATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTTGAAGCTG
GTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAAAATGATG
GAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTTAAAGTAG
GAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGCACTGGTT
ATTCTACAGCACCATTTACACTTCCAAAGAATGGTTAATTCATTTTCAA
TTCAACTGCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGATATGGAAA
AGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTTGGAAAACAAACA

AATATGGCACACTATATAAATCAGAGTCAGCTAGCTTCACACCTAATACAG
ATATAATAACAAGAACGACTGGTCCATTTAGAAGCATGCCGCAGTCAGGAG
TCTTAAAAGCAGGTCAAACAATTCATTATGATGAAGTGATGAAACAAGACG
GTCATGTTTGGGTAGGTTATACAGGTAACAGTGGCCAACGTATTTACTTGCC
TGTAAGAACATGGAATAAATCTACTAATACTTTAGGTGTTCTTTGGGGAAC
TATAAAGGAGCTCGCTGCAACACATGAACATTCAGCACAAATGGTTGAATAA
TTACAAAAAAGGATATGGTTACGGTCCTTATCCATTAGGTATAAATGGCGG
TATGCACTACGGAGTTGATTTTTTTTATGAATATTGGAACACCAGTAAAAGCT
ATTTCAAGCGGAAAAATAGTTGAAGCTGGTTGGAGTAATTACGGAGGAGGT
AATCAAATAGGTCTTATTGAAAATGATGGAGTGCATAGACAATGGTATATG
CATCTAAGTAAATATAATGTTAAAGTAGGAGATTATGTCAAAGCTGGTCAA
ATAATCGGTTGGTCTGGAAGCACTGGTTATTCTACAGCACCACATTTACACT

TCCAAAGAATGGTTAATTCATTTTCAAATTCAACTGCCCAAGATCCAATGCC
TTTCTTAAAGAGCGCAGGATATGGAAAAGCAGGTGGTACAGTAACTCCAAC
GCCGAATACAGGTTGGAAAACAAACAAATATGGCACACTATATAAATCAG
AGTCAGCTAGCTTCACACCTAATACAGATATAATAACAAGAACGACTGGTC
CATTTAGAAGCATGCCGCAGTCAGGAGTCTTAAAAGCAGGTCAAACAATTC
ATTATGATGAAGTGATGAAACAAGACGGTCATGTTTGGGTAGGTTATACAG
GTAACAGTGGCCAACGTATTTACTTGCCTGTAAGAACATGGAATAAATCTA
CTAATACTTTAGGTGTTCTTTGGGGAACATAAAAGTGA

SEQ ID NO: 11 (M23-LST M23-LST CWT-LST +6xHis and cloning sites)

[0096]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCTGCAACACATGAA
CATTACGCACAATGGTTGAATAATTACAAAAAAGGATATGGTTACGGTCCT
TATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTTTTTATGA
ATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTTGAAGCTG
GTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAAAATGATG
GAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTTAAAGTAG
GAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGCACTGGTT
ATTCTACAGCACCACATTTACACTTCCAAAGAATGGTTAATTCATTTTCAAA
TTCAACTGCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGATATGGAAA
AGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTGAGCTCGCTGCAAC
ACATGAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGGATATGGTTA
CGGTCCTTATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTT
TTTATGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTT
GAAGCTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAA
AATGATGGAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTT

AAAGTAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGC
ACTGGTTATTCTACAGCACCATTTACACTTCCAAAGAATGGTTAATTCAT
TTTCAAATTCAACTGCCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGAT
ATGGAAAAGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTGGA
ACAAACAAATATGGCACACTATATAAATCAGAGTCAGCTAGCTTCACACCT
AATACAGATATAATAACAAGAACGACTGGTCCATTTAGAAGCATGCCGCAG
TCAGGAGTCTTAAAAGCAGGTCAAACAATTCATTATGATGAAGTGATGAAA
CAAGACGGTCATGTTTGGGTAGGTTATACAGGTAACAGTGGCCAACGTATT
TACTTGCCTGTAAGAACATGGAATAAATCTACTAATACTTTAGGTGTTCTTT
GGGGAACATAAAGTGA

SEQ ID NO: 12 (CBD-2638)

[0097]

TGGAAACAGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTT
ACAGTGACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGAC
TGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGA
TGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGA
GGGCGAAACTGTATACATGCCGGTACGCACATGGGACGCTAAAACCTGGTA
AAGTTGGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 13 (CWT-LST)

[0098]

TGGAACAAACAAATATGGCACACTATATAAATCAGAGTCAGCTAGCTTC
ACACCTAATACAGATATAATAACAAGAACGACTGGTCCATTTAGAAGCATG
CCGCAGTCAGGAGTCTTAAAAGCAGGTCAAACAATTCATTATGATGAAGTG
ATGAAACAAGACGGTCATGTTTGGGTAGGTTATACAGGTAACAGTGGCCAA
CGTATTTACTTGCCTGTAAGAACATGGAATAAATCTACTAATACTTTAGGTG
TTCTTTGGGGAACATAAAGTGA

SEQ ID NO: 14 (M23-2638)

[0099]

ATGCTAACTGCTATTGACTATCTTACGAAAAAAGGTTGGAAAATATCATCT
GACCTCGCACTTACGATGGTTACCCTAAAAACTACGGCTACAGAAATTAC
CATGAAAACGGCATTAAATTATGATGAGTTTGTGGTGGTTATCATAGAGCTT

TTGATGTTTACAGTAACGAACTAACGACGTGCCTGCTGTTACTAGCGGAA
CAGTTATTGAAGCAAACGATTACGGTAATTTTGGTGGTACATTTCGTTATTAG
AGACGCTAACGATAACGATTGGATATATGGGCATCTACAACGTGGCTCAAT
GCGATTTGTTGTAGGCGACAAAGTCAATCAAGGTGACATTATTGGTTTACA
AGGTAATAGCAACTATTACGACAATCCTATGAGTGTACATTTACATTTACA
ATTACGCCCTAAAGACGCAAAGAAAGAT

SEQ ID NO: 15 (M23-LST)

[0100]

GCTGCAACACATGAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGG
ATATGGTTACGGTCCTTATCCATTAGGTATAAATGGCGGTATGCACTACGG

AGTTGATTTTTTTATGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGG
AAAAATAGTTGAAGCTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAG
GTCTTATTGAAAATGATGGAGTGCATAGACAATGGTATATGCATCTAAGTA
AATATAATGTTAAAGTAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTT
GGTCTGGAAGCACTGGTTATTCTACAGCACCACATTTACACTTCCAAAGAA
TGGTTAATTCATTTTCAAATTCAACTGCCCAAGATCCAATGCCTTTCTTAAA
GAGCGCAGGATAT

SEQ ID NO: 16 (Ami-2638)

[0101]

GGTAACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCAC
AATGATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCAC
GTGAGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTTTATGCAAATA
GAAACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTG
GTAATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGT
ATCCTGGTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACAT
TGAAAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCA
ACACTGTACGTCTGCATAACGAATTCTTCGGAACCTTCTTGCCACATCGTTC
GTGGGACTTGTCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAA
TAAATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGACGGT

SEQ ID NO: 17 (Ami-Φ11)

[0102]

AAGCCACAACCTAAAGCAGTAGAACTTAAAATCATCAAAGATGTGGTTAA
AGGTTATGACCTACCTAAGCGTGGTAGTAACCCTAAAGGTATAGTTATACA
CAACGACGCAGGGAGCAAAGGGGCGACTGCTGAAGCATATCGTAACGGAT
TAGTAAATGCACCTTTATCAAGATTAGAAGCGGGCATTGCGCATAGTTACG
TATCAGGCAACACAGTTTGGCAAGCCTTAGATGAATCACAAGTAGGTTGGC
ATACCGCTAATCAAATAGGTAATAAATATTATTACGGTATTGAAGTATGTC
AATCAATGGGCGCAGATAACGCGACATTCTTAAAAAATGAACAGGCAACTT
TCCAAGAATGCGCTAGATTGTTGAAAAAATGGGGATTACCAGCAAACAGA
AATACAATCAGATTGCACAATGAATTTACTTCAACATCATGCCCTCATAGA
AGTTCCGGTTTACACACTGGTTTTGACCCAGTAACTCGCGGTCTATTGCCAG
AAGACAAGCGGTGCAACTTAAAGACTACTTTATCAAGCAGATTAGGGCGT
ACATGGATGGTAAAATACCGGTTGCCACTGTCTCTAATGAGTCAAGCGCTT

CAAGTAATACAGTTAAACCAGTTGCAAGTGCA

SEQ ID NO:18 (CHAP-Φ11)**[0103]**

ATGCAAGCAAAATTAACATAAAATGAGTTTATAGAGTGGTTGAAAACCTCT
GAGGGAAAACAATTCAATGTGGACTTATGGTATGGATTTCAATGCTTTGAT
TATGCCAATGCTGGTTGGAAAGTTTTGTTTGGATTACTTCTAAAAGGTTTAG
GTGCAAAAGATATTCGTTTCGCTAACAACTTCGACGGATTAGCTACTGTAT
ACCAAAATACACCGGACTTCTTAGCACAACTGGCGACATGGTGGTATTCG
GTAGCAACTACGGTGCTGGATATGGTCACGTTGCATGGGTAATTGAAGCAA
CTTTAGATTACATCATTGTATATGAGCAGAATTGGCTAGGCGGTGGCTGGA
CTGACGGAATCGAACAAACCGGCTGGGGTTGGGAAAAAGTTACAAGACGA
CAACATGCTTATGATTTCCCTATGTGGTTTATCCGTCCGAATTTTAAAAGTG
AGACAGCGCCACGATCAGTTCAATCTCCTACACAAGCACCTAAAAAAGAA
ACAGCT

SEQ ID NO:19 (CHAP-ΦTwort)**[0104]**

ATGAAACCCTGAAACAAGCAGAGTCCTACATTAAGAGTAAAGTAAATAC
AGGAACTGATTTTGATGGTTTATATGGGTATCAGTGTATGGACTTAGCAGT
AGATTATATTTACCATGTAACAGATGGTAAAATAAGAATGTGGGGTAATGC
TAAGGATGCGATAAATAACTCTTTTGGTGGTACTGCTACGGTATATAAAAA

CTACCCTGCTTTTAGACCTAAGTACGGTGATGTAGTCGTATGGACTACTGGT
AATTTTGCAACTTATGGTCATATCGCAATAGTTACTAACCCTGACCCTTATG
GAGACCTTCAATATGTTACAGTTCTTGAACAAAACCTGGAACGGTAACGGGA
TTTATAAAACCGAGTTAGCTACAATCAGAACACACGATTACACAGGAATTA
CACATTTTATT

SEQ ID NO:20 (M23-2638 Ami2638 CBD2638 CBD2638)

[0105]

ATGCTAACTGCTATTGACTATCTTACGAAAAAAGGTTGGAAAATATCATCT
GACCCTCGCACTTACGATGGTTACCCTAAAAACTACGGCTACAGAAATTAC
CATGAAAACGGCATTAAATTATGATGAGTTTGTGGTGGTTATCATAGAGCTT
TTGATGTTTACAGTAACGAACTAACGACGTGCCTGCTGTTACTAGCGGAA
CAGTTATTGAAGCAAACGATTACGGTAATTTTGGTGGTACATTCGTTATTAG
AGACGCTAACGATAACGATTGGATATATGGGCATCTACAACGTGGCTCAAT

GCGATTTGTTGTAGGCGACAAAGTCAATCAAGGTGACATTATTGGTTTACA
AGGTAATAGCAACTATTACGACAATCCTATGAGTGTACATTTACATTTACA
ATTACGCCCTAAAGACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTG
GTTTGGCTATGGAAAAATATGACATTACAAATTTAAATGCTAAACAAGATA
AATCAAAGAATGGGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCAT
ATTAAAGGTAACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTC
ATCCACAATGATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTAT
ATGCACGTGAGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTTTATG
CAAATAGAAACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGC
ATTGTGGTAATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTG
AGTCGTATCCTGGTAGAATCTCGGACAAATTATTCTTAGAAAAATGAAGAAG
CGACATTGAAAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTA
ATCGCAACACTGTACGTCTGCATAACGAATTCTTCGGAACCTTCTGTCCACA
TCGTTTCGTGGGACTTGCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAA
TATTAATAAAATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGA
CGGTGGAAAGCTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACG
TTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACA
GATTGGAAACAGAATAAAGATGGCATTGTTGTTGTTGTTGTTGTTGTTGTTG
TTCACAGTGACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGG
ACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATAT
GATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTT
GAGGGCGAAACTGTATACATGCCGGTACGCACATGGGACGCTAAAACCTGG
TAAAGTTGGTAAGTTGTGGGGCGAAATTAAAGAGCTCGGTGGAAAGCTAG
AAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTT

 AAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGA
 ATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAG
 CACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCAC
 AAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAA
 AATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTG
 TATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAAGT
 TGTGGGGCGAAATTAAATAA

SEQ ID NO: 21 (Ply2638)

[0106]

MRGSHHHHHHGSMLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYHENGI
 NYDEFCCGYHRAFDVYSNETNDVPAVTS GTVIEANDYGNFGGTFVIRDANDN
 DWIYGHLQRGSMRFVVGDKVNQGDIIQLQGNSNYIDNPMSVHLHLQLRPKD
 AKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITA
 PKPSIQGVVIHNDYGSMTSPSYLPWLYARENNGTHVNGWASVYANRNEVLW
 YHPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEATLKVAADV
 MKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKDYFI
 KRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDWKQNKDGIW
 YKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVW
 VSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 22 (Ami2638 CBD2638)

[0107]

MRGSHHHHHHGSRLPKDAKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNG
 SVKELKHIYSNHIKGNKITAPKPSIQGVVIHNDYGSMTSPSYLPWLYARENNGT
 HVNGWASVYANRNEVLWYHPTDYVEWHCGNQWANANLIGFEVCESYPGRIS
 DKLFLNEEATLKVAADVMKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVG
 KGEPYTTTNINKMKDYFIKRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQ
 QIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKG
 QTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 23 (M23-2638 CBD2638)

[0108]

MRGSHHHHHHGSMLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYHENGI
 NYDEFCGGYHRAFDVYSNETNDVPAVTS GTVIEANDYGNFGGTFVIRDANDN
 DWIYGHLQRGSMRFVVGDKVNQGDII GLQGNSNY YDNPM SVHLHLQLRPKD
 AKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITA
 PKPSIQGELGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDWKQNKDGIW
 YKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVW
 VSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 24 (Ply2638-Ply2638)

[0109]

MRGSHHHHHHGSMLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYHENGI
 NYDEFCGGYHRAFDVYSNETNDVPAVTS GTVIEANDYGNFGGTFVIRDANDN
 DWIYGHLQRGSMRFVVGDKVNQGDII GLQGNSNY YDNPM SVHLHLQLRPKD
 AKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITA
 PKPSIQGVVIHNDYGSMTPSQYLPWLYARENNGTHVNGWASVYANRNEVLW
 YHPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLENEEATLKVAADV
 MKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVKGGEPTYTTNINKMKDYFI
 KRIKHYDGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDWKQNKDGIW
 YKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVW
 VSWETFEGETVYMPVRTWDAKTGKVGKLWGEIKELMLTAIDYLTKKGWKISS
 DPRTYDGYPKNYGYRNYHENGINYDEFCGGYHRAFDVYSNETNDVPAVTS GT
 VIEANDYGNFGGTFVIRDANDNDWIYGHLQRGSMRFVVGDKVNQGDII GLQG
 NSNY YDNPM SVHLHLQLRPKDAKKDEKSQVCSGLAMEKYDITNLNAKQDKS
 KNGSVKELKHIYSNHIKGNKITAPKPSIQGVVIHNDYGSMTPSQYLPWLYAREN
 NGTHVNGWASVYANRNEVLWYHPTDYVEWHCGNQWANANLIGFEVCESYP
 GRISDKLFLENEEATLKVAADV MKSYGLPVNRNTVRLHNEFFGTSCPHRSWDL
 HVKGGEPTYTTNINKMKDYFIKRIKHYDGGKLEVSKAATIKQSDVKQEVKK
 QEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGV
 LQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWG
 EIK

SEQ ID NO: 25 (CHAP11_M23-2638 Ami2638 CBD2638)

[0110]

MRGSHHHHHHGSMAKLTKNFIEWLKTSEGKQFNVDLWYGFQCFDYANA
 GWKVLFGLLKGLGAKDIPFANNFDGLATVYQNTPDFLAQPGDMVVFGSNYG
 AGYGHVAWVIEATLDYIIVYEQNWLGGGWTGIEQPGWGWEKVTRRQHAYD

FPMWFIRPNFKSETAPRSVQSPTQAPKKETAGSMLTAIDYLTKKGWKISSDPRT
 YDGYPKNYGYRNYHENGINYDEFCCGGYHRAFDVYSNETNDVPAVTSGTVIEA
 NDYGNFGGTFVIRDANDNDWIYGHQLQRGSMRFVVGDKVNQGDIIQLQGNSNY
 YDNPMSVHLHLQLRPKDAKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGS
 VKELKHIYSNHIKGNKITAPKPSIQGVVIHNDYGSMTPSQYLPWLYARENNGTH
 VNGWASVYANRNEVLWYHPTDYVEWHCGNQWANANLIGFEVCESYPGRISD
 KLFLNEEEATLKVAADVMSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGK
 GEPYTTTNINKMKDYFIKRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQK
 IVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQ
 TIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 26 (Ami11_M23-2638_Ami2638_CBD2638)

[0111]

MRGSHHHHHHGSKPQKAVELKIIKDVVKGYDLPKRGSNPKGIVIHNDAGSK
 GATAEAYRNLVNAPLSRLEAGIAHSYVSGNTVWQALDESQVGWHTANQIGN
 KYYYGIEVCQSMGADNATFLKNEQATFQECARLLKKWGLPANRNTIRLHNEF
 TSTSCPHRSSVLHTGFDPVTRGLLPEDKRLQLKDYFIKQIRAYMDGKIPVATVS
 NESSASSNTVKPVASAGSMLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYH
 ENGINYDEFCCGGYHRAFDVYSNETNDVPAVTSGTVIEANDYGNFGGTFVIRDA
 NDNDWIYGHQLQRGSMRFVVGDKVNQGDIIQLQGNSNYDNPMSVHLHLQLR
 PKDAKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGN
 KITAPKPSIQGVVIHNDYGSMTPSQYLPWLYARENNGTHVNGWASVYANRNE
 VLWYHPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEEATLKVA
 ADVMSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKD
 YFIKRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQKIVKATDWKQNKDG
 IWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHV
 WVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 27 (CHAPTW_Ami2638_M23-LST_CBD2638)

[0112]

MRGSHHHHHHGSMTLTKQAESYIKSKVNTGTDFDGLYGYQCMDLAVDIY
 HVTDGKIRMWGNKADAINNSFGGTATVYKNYPAFRPKYGDVVVWTTGNFAT
 YGHIAIVTNPDYPYGDLYVTVLEQNWNGNGIYKTELATIRTHDYTGITHFIKDA
 KKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITAP
 KPSIQGVVIHNDYGSMTPSQYLPWLYARENNGTHVNGWASVYANRNEVLWY
 HPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEEATLKVAADVMSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKD

KSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKDYFIKR
 IKHYDGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDAATHEHSAQWLN
 NYKKGYGYGPYPLGINGGMHYGVDFMNIIGTPVKAISSGKIVEAGWSNYGGG
 NQIGLIENDGVHRQWYMHLSKYNVKVGDYVKAGQIIGWSGSTGYSTAPHLHF
 QRMVNSFSNSTAQDPMFLKSAGYGKAGGTVTPTNTGWKQNKDGIWYKAE
 HASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWE
 TFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 28 (CHAPT_w_Ami2638_M23-LST_CWT-LST)

[0113]

MRGSHHHHHHGSMTLKQAESYIKSKVNTGTDFDGLYGYQCMDLAVDYIY

HVTDGKIRMWGNADAINNSFGGTATVYKNYPFRPKYGDVVVWTTGNFAT
 YGHIAIVTNPDPYGDLYVTVLEQNWNGNGIYKTELATIRTHDYTGITHFIKDA
 KKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITAP
 KPSIQGVVIHNDYGSMTSPSYLPWLYARENNGTHVNGWASVYANRNEVLWY
 HPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEATLKVAADVM
 KSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKDYFIKR
 IKHYDGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDAATHEHSAQWLN
 NYKKGYGYGPYPLGINGGMHYGVDFMNIIGTPVKAISSGKIVEAGWSNYGGG
 NQIGLIENDGVHRQWYMHLSKYNVKVGDYVKAGQIIGWSGSTGYSTAPHLHF
 QRMVNSFSNSTAQDPMFLKSAGYGKAGGTVTPTNTGWKTNKYGTLYKSES
 ASFTPNTDIITRTTGPFPSMPQSGVLKAGQTIHYDEVMKQDGHVWVGYTGNSG
 QRIYLPVRTWNKSTNTLGVLWGNIK

SEQ ID NO: 29 (M23-LST_Ami2638_CBD2638)

[0114]

MRGSHHHHHHGSAATHEHSAQWLN NYKKGYGYGPYPLGINGGMHYGVDF
 MNIGTPVKAISSGKIVEAGWSNYGGGNQIGLIENDGVHRQWYMHLSKYNVKV
 GDYVKAGQIIGWSGSTGYSTAPHLHFQRMVNSFSNSTAQDPMFLKSAGYGK
 AGGTVTPTNTGELLRPKDAKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNG
 SVKELKHIYSNHIKGNKITAPKPSIQGVVIHNDYGSMTSPSYLPWLYARENNGT
 HVNGWASVYANRNEVLWYHPTDYVEWHCGNQWANANLIGFEVCESYPGRIS
 DKLFLNEEATLKVAADVMKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVG
 KGEPYTTTNINKMKDYFIKRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQ
 IIVKATDVKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKG

QTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 30 (LST LST)

[0115]

MRGSHHHHHHGSAATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGVDF
 MNIGTPVKAISSGKIVEAGWSNYGGGNQIGLIENDGVHRQWYMHLKYNV
 KVG
 GDYVKAGQIIGWSGSTGYSTAPHLHFQRMVNSFSNSTAQDMPFLKSAGY
 GK
 AGGTVTPTPNTGWKTNKYGTLYKSESASFTPNTDII TRTTGPFRSMPQSG
 VLKA
 GQTIHYDEVMKQDGHVWVG YTGNSGQRIYLPVRTWNKSTNTLGVLWG
 TIKE
 LAATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGVDFFMNIGTPVKA
 ISSG
 KIVEAGWSNYGGGNQIGLIENDGVHRQWYMHLKYNV KVG
 GDYVKAGQIIGW
 SGSTGYSTAPHLHFQRMVNSFSNSTAQDMPFLKSAGY GKAGGTVTPT
 PNTG
 WKTNKYGTLYKSESASFTPNTDII TRTTGPFRSMPQSGVLKAGQTIHY
 DEVMK
 QDGHVWVG YTGNSGQRIYLPVRTWNKSTNTLGVLWG
 TIK

SEQ ID NO: 31 (M23-LST_M23-LST_CWT-LST)

[0116]

MRGSHHHHHHGSAATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGVDF
 MNIGTPVKAISSGKIVEAGWSNYGGGNQIGLIENDGVHRQWYMHLKYNV
 KVG
 GDYVKAGQIIGWSGSTGYSTAPHLHFQRMVNSFSNSTAQDMPFLKSAGY
 GK
 AGGTVTPTPNTGELAATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGV
 DF
 FMNIGTPVKAISSGKIVEAGWSNYGGGNQIGLIENDGVHRQWYMHLKYN
 VK
 VGDYVKAGQIIGWSGSTGYSTAPHLHFQRMVNSFSNSTAQDMPFLKSAGY
 G
 KAGGTVTPTPNTGWKTNKYGTLYKSESASFTPNTDII TRTTGPFRSMPQ
 SGVLK
 AGQTIHYDEVMKQDGHVWVG YTGNSGQRIYLPVRTWNKSTNTLGVLWG
 TIK

SEQ ID NO: 32 (M23-2638 Ami2638 CBD2638 CBD2638)

[0117]

MRGSHHHHHHGSMLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYHEN
 GI
 NYDEFCGGYHRAFDVYSNETNDVPAVTS GTVIEANDYGNFGGTFVIR
 DANDN
 DWIYGHLQRGSMRFVVGDKVNQGDII GLQGNSNYDNPMSVHLHLQLRP
 KD
 AKKDEKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGN
 KITA
 PKPSIQGVVIHNDYGSMTPSQYLPWLYARENNGTHVNGWASVYANRNEV
 LW

YHPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLENEEATLKVAADV
MKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVGKGEPYTTTNINKMKDYFI
KRIKHYYDGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDWKQNKDGIW
YKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVW
VSWETFEGETVYMPVRTWDAKTGKVGLWGEIKELGGKLEVSKAATIKQSDV
KQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTG
HPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWDAKTGK
VGKLWGEIK

SEQ ID NO: 33 (LST)

[0118]

GCTGCAACACATGAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGG
ATATGGTTACGGTCCTTATCCATTAGGTATAAATGGCGGTATGCACTACGG
AGTTGATTTTTTTATGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGG
AAAAATAGTTGAAGCTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAG
GTCTTATTGAAAATGATGGAGTGCATAGACAATGGTATATGCATCTAAGTA
AATATAATGTTAAAGTAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTT
GGTCTGGAAGCACTGGTTATTCTACAGCACCACATTTACACTTCCAAAGAA
TGGTTAATTCATTTTCAAATTCAACTGCCCAAGATCCAATGCCTTTCTTAAA
GAGCGCAGGATATGGAAAAGCAGGTGGTACAGTAACTCCAACGCCGAATA
CAGGTTGGAAAACAAACAAATATGGCACACTATATAAATCAGAGTCAGCT
AGCTTCACACCTAATACAGATATAATAACAAGAACGACTGGTCCATTTAGA
AGCATGCCGCAGTCAGGAGTCTTAAAAGCAGGTCAAACAATTCATTATGAT
GAAGTGATGAAACAAGACGGTCATGTTTGGGTAGGTTATACAGGTAACAGT
GGCCAACGTATTTACTTGCCTGTAAGAACATGGAATAAATCTACTAATACT
TTAGGTGTTCTTTGGGGAACATAAAGTGA

SEQ ID NO: 34 (LST aa)

[0119]

AATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGVDFFMNIGTPVKAISSGK
IVEAGWSNYGGGNQIGLIENDGVHRQWYMHLSKYNVKVGDYVKAGQIIGWS
GSTGYSTAPHLHFQRMVNSFSNSTAQDPMPLKSAGYGKAGGTVTPNTGW
KTNKYGTLYKSESASFPTNTDIITRTTGPFPSMPQSGVLKAGQTIHYDEVKQD
GHVWVGYYTGNQRIYLPVRTWNKSTNTLGVLWGVIK

SEQ ID NO: 35 (CBD-2638)**[0120]**

WKQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDE
VQKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 36 (CWT-LST)**[0121]**

WKTNKYGTLYKSESASFTPNTDIITRTTGPFERSMPQSGVLKAGQTIHYDEV
QDGHVWVGYTGNQSGQRIYLPVRTWNKSTNTLGVLWGTIK

SEQ ID NO: 37 (M23-2638)**[0122]**

MLTAIDYLTCKGWKISSDPRTYDGYPKNYGYRNYHENGINYDEFCCGGYHRAF
DVYSNETNDVPAVTSGTVIEANDYGNFGGTFVIRDANDNDWIYGHQGRGSMR
FVVGDKVNQGDIIQLQGNNSYYDNPMVHHLQLRPKDAKKD

SEQ ID NO: 38 (M23-LST)**[0123]**

AATHEHSAQWLNNYKKGYYGYGPYPLGNGGMHYGVDFFMNIGTPVKAISSGK
IVEAGWSNYGGGNQIGLIENDGVHRQWYMHLSKYNVKVGDYVKAGQIIGWS
GSTGYSTAPHLHFQRMVNSFSNSTAQDPMPLKSAGY

SEQ ID NO: 39 (Ami-2638)**[0124]**

NKITAPKPSIQGVVIHNDYGSMTSPQYLPWLYARENNGTHVNGWASVYANRN
EVLWYHPTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEATLKV
AADVMKSYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVKGGEPTTTNINKMK
DYFIKRIKHYYDG

SEQ ID NO: 40 (Ami-Φ11)

[0125]

NPKGIVIHNDAGSKGATAEAYRNGLVNAPLSRLEAGIAHSYVSGNTVWQALD
ESQVGWHTANQIGNKYYYGIEVCQSMGADNATFLKNEQATFQECARLLKKW
GLPANRNTIRLHNEFTSTSCPHRSSVLHTGFDPVTRGLLPEDKRLQLKDYFIKQI
RAYMD

SEQ ID NO: 41 (CHAP-Φ11)

[0126]

MSHMEVATMQAKLTKNEFIEWLKTSEGKQFNVDLWYGFQCFDYANAGWKV
LFGLLLKGLGAKDIPFANNFDGLATVYQNTPDFLAQPGDMVVFGSNYGAGYG
HVAWVIEATLDYIIVYEQNWLGCGWTDGIEQPGWGWEKVTRRQHAYDFPMW
FIRP

SEQ ID NO: 42(CHAP-ΦTwort)

[0127]

MKTLKQAESYIKSKVNTGTDFDGLYGYQCMDLAVDYIYHVTGKIRMWGNA
KDAINNSFGGTATVYKNYPAPFRPKYGDVVVWTTGNFATYGHIAIVTNPDYGY
DLQYVTVLEQNWNGNGIYKTELATIRTHDYTGITHFI

SEQ ID NO 43 (6xHis tag N terminal)

[0128] MRGSHHHHHHGS

SEQ ID NO: 44 (Ply2638 + 6xHis and cloning sites)

[0129]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGCTAACTGCTATT
GACTATCTTACGAAAAAAGGTTGGAAAAATATCATCTGACCCTCGCACTTAC
GATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGAAAACGGCATT

AATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTA
ACGAAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAA
ACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGACGCTAACGATA
ACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAG
GCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGTAATAGCAACT
ATTACGACAATCCTATGAGTGTACATTTACATTTACAATTACGCCCTAAAGA
CGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAA
AATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGG
AGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACAAG
ATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTAT
GGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAAT
AACGGTACACACGTTAACGGTTGGGCTAGTGTATGCAAATAGAAACGAA
GTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAA
TGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGT
AGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTA
GCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTA
CGTCTGCATAACGAATTCTTCGGAACCTTCTTGTCACATCGTTCGTGGGACT
TGCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAATAAAATGA
AAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAG
AAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTT
AAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGA
ATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTCACAGTGACAG
CACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCAC
AAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAA
AATTGACGGTCATGTTTGGGTATCGTGCGGAAACGTTTGAGGGCGAAACTG
TATACATGCCGGTACGCACATGGGACGCTAAACTGGTAAAGTTGGTAAGT
TGTGGGGCGAAATTAAATAA

SEQ ID NO: 45 (CHAP 11 M23-2638 Ami2638 CBD2638+6xHis and cloning sites)

[0130]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGCAAGCAAAATTA
ACTAAAAATGAGTTTATAGAGTGGTTGAAAACCTTCTGAGGGAAAACAATTC

AATGTGGACTTATGGTATGGATTTCATGCTTTGATTATGCCAATGCTGGTT
GGAAAGTTTTGTTTGGATTACTTCTAAAAGGTTTAGGTGCAAAAGATATTCC
GTTTCGTAACAACCTCGACGGATTAGCTACTGTATACCAAAATACACCGGA
CTTCTTAGCACAACCTGGCGACATGGTGGTATTCGGTAGCAACTACGGTGC
TGGATATGGTCACGTTGCATGGGTAATTGAAGCAACTTTAGATTACATCATT
GTATATGAGCAGAATTGGCTAGGCGGTGGCTGGACTGACGGAATCGAACA
ACCCGGCTGGGGTTGGCAAAAAGTTACAAGACGACAAACATGCTTATGATT

CCCTATGTGGTTTATCCGTCCGAATTTTAAAAGTGAGACAGCGCCACGATC
 AGTTCAATCTCCTACACAAGCACCTAAAAAAGAAACAGCTGGATCCATGCT
 AACTGCTATTGACTATCTTACGAAAAAAGGTTGGAAAATATCATCTGACCC
 TCGCACTTACGATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGA
 AAACGGCATTAAATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGAT
 GTTTACAGTAACGAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTT
 ATTGAAGCAAACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGAC
 GCTAACGATAACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGA
 TTTGTTGTAGGCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGT
 AATAGCAACTATTACGACAATCCTATGAGTGTACATTTACATTTACAATTAC
 GCCCTAAAGACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTG
 GCTATGGAAAAATATGACATTACAAATTTAAATGCTAAACAAGATAAATCA
 AAGAATGGGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAA
 GGTAACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCAC
 AATGATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCAC
 GTGAGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTATTATGCAAATA
 GAAACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTG
 GTAATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGT
 ATCCTGGTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACAT
 TGAAAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCA
 AACTGTACGTCTGCATAACGAATTCCTTCGGAACCTTCTGTCCACATCGTTC
 GTGGGACTTGCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAA
 TAAAATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGG
 AAAGCTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTAAAGC
 AAGAAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGG
 AAACAGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTTACA

GTGACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGT
 CACCCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAG
 GTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGC
 GAAACTGTATACATGCCGGTACGCACATGGGACGCTAAACTGGTAAAGTT
 GGTAAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 46 (Ami11 M23-2638 Ami2638 CBD2638+6xHis and cloning sites)

[0131]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCAAGCCACAACCTAAA
 GCAGTAGAACTTAAATCATCAAAGATGTGGTTAAAGGTTATGACCTACCT
 AAGCGTGGTAGTAACCCTAAAGGTATAGTTATACACAACGACGCAGGGAG
 CAAAGGGGGCGACTGCTGAAGCATATCGTAACGGATTAGTAAATGCACCTTT

ATCAAGATTAGAAGCGGGCATTGCGCATAGTTACGTATCAGGCAACACAGT
TTGGCAAGCCTTAGATGAATCACAAGTAGGTTGGCATACCGCTAATCAAAT
AGGTAATAAATATTATTACGGTATTGAAGTATGTCAATCAATGGGCGCAGA
TAACGCGACATTCTTAAAAAATGAACAGGCAACTTTCCAAGAATGCGCTAG
ATTGTTGAAAAAATGGGGATTACCAGCAAACAGAAATACAATCAGATTGC
ACAATGAATTTACTTCAACATCATGCCCTCATAGAAGTTCGGTTTTACACAC
TGGTTTTGACCCAGTAACTCGCGGTCTATTGCCAGAAGACAAGCGGTTGCA
ACTTAAAGACTACTTTATCAAGCAGATTAGGGCGTACATGGATGGTAAAAT
ACCGGTTGCCACTGTCCTAATGAGTCAAGCGCTTCAAGTAATACAGTTAA
ACCAGTTGCAAGTGCAGGATCCATGCTAACTGCTATTGACTATCTTACGAA
AAAAGGTTGGAAAAATATCATCTGACCCTCGCACTTACGATGGTTACCCTAA
AAACTACGGCTACAGAAATTACCATGAAAACGGCATTAAATTATGATGAGTT
TTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTAACGAAACTAACGAC
GTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAAACGATTACGGTAAT
TTTGGTGGTACATTCGTTATTAGAGACGCTAACGATAACGATTGGATATAT
GGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAGGCGACAAAGTCAAT
CAAGGTGACATTATTGGTTTACAAGGTAATAGCAACTATTACGACAATCCT
ATGAGTGTACATTTACATTTACAATTACGCCCTAAAGACGCAAAGAAAGAT
GAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAAAATATGACATTACA
AATTTAAATGCTAAACAAGATAAATCAAAGAATGGGAGCGTGAAAGAGTT
GAAACATATCTATTCAAACCATATTAAGGTAACAAGATTACAGCACCAAA
ACCTAGTATTCAAGGTGTGGTCATCCACAATGATTATGGTAGTATGACACC

TAGTCAATACTTACCATGGTTATATGCACGTGAGAATAACGGTACACACGT
TAACGGTTGGGCTAGTGTATTATGCAAATAGAAACGAAGTGCTTTGGTATCA
TCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAATGGGCAAATGCTAA
CTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGTAGAATCTCGGACAA
ATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTAGCTGCGGATGTGAT
GAAGTCGTACGGATTACCAGTTAATCGCAACACTGTACGTCTGCATAACGA
ATTCTTCGGAACCTTCTTGCCACATCGTTCGTGGGACTTGCATGTTGGCAAA
GGTGAGCCTTACACAACCTACTAATATTAATAAAATGAAAGACTACTTCATC
AAACGCATCAAACATTATTATGACGGTGGAAGCTAGAAGTAAGCAAAGC
AGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAG
CAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATT
TGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAATT
ATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTA
CAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCAT
GTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTA
CGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAAATT
AAATAA

SEQ ID NO: 47 (CHAPTw_Ami2638 M23-LST CBD2638 +6xHis and cloning sites)

[0132]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAAAACCCTGAAA
CAAGCAGAGTCCTACATTAAGAGTAAAGTAAATACAGGAACTGATTTTGAT
GGTTTATATGGGTATCAGTGTATGGACTTAGCAGTAGATTATATTTACCATG
TAACAGATGGTAAAATAAGAATGTGGGGTAATGCTAAGGATGCGATAAAT
AACTCTTTTGGTGGTACTGCTACGGTATATAAAAACTACCCTGCTTTTAGAC
CTAAGTACGGTGATGTAGTCGTATGGACTACTGGTAATTTTGCAACTTATGG
TCATATCGCAATAGTTACTAACCCTGACCCTTATGGAGACCTTCAATATGTT
ACAGTTCTTGAACAAAACCTGGAACGGTAACGGGATTTATAAAACCGAGTTA
GCTACAATCAGAACACACGATTACACAGGAATTACACATTTTATTAAAGAC
GCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAAA
ATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGGA
GCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACAAGA
TTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTATG
GTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAATA

ACGGTACACACGTTAACGGTTGGGCTAGTGTTTATGCAAATAGAAACGAAG
TGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAAT
GGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGTA
GAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTAG
CTGCCGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTAC
GTCTGCATAACGAATTCCTCGGAACCTCTTGTCCACATCGTTCGTGGGACTT
GCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAATAAAATGAA
AGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAGA
AGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTA
AAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATGCTGCAACACAT
GAACATTCAGCACAAATGGTTGAATAATTACAAAAAAGGATATGGTTACGGT
CCTTATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTTTTTA
TGAATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTTGAAG
CTGGTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAAAATG
ATGGAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTTAAAG
TAGGAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGCACTG
GTTATTCTACAGCACCATTTACACTTCCAAAGAATGGTTAATTCATTTTC
AAATTCAACTGCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGATATGG
AAAAGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTTGGAAACAGA
ATAAAGATGGCATTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAG
CACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCAC
AAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAA

AATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTG
TATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGT
TGTGGGGCGAAATTAAATAA

SEQ ID NO: 48 (M23-LST_Ami2638 CBD2638 + 6xHis and cloning sites)

[0133]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCTGCAACACATGAA
CATTACAGCACAATGGTTGAATAATTACAAAAAAGGATATGGTTACGGTCCT
TATCCATTAGGTATAAATGGCGGTATGCACTACGGAGTTGATTTTTTTTATGA
ATATTGGAACACCAGTAAAAGCTATTTCAAGCGGAAAAATAGTTGAAGCTG
GTTGGAGTAATTACGGAGGAGGTAATCAAATAGGTCTTATTGAAAATGATG
GAGTGCATAGACAATGGTATATGCATCTAAGTAAATATAATGTAAAGTAG

GAGATTATGTCAAAGCTGGTCAAATAATCGGTTGGTCTGGAAGCACTGGTT
ATTCTACAGCACCACATTTACACTTCCAAAGAATGGTTAATTCATTTTCAA
TTCAACTGCCCAAGATCCAATGCCTTTCTTAAAGAGCGCAGGATATGGAAA
AGCAGGTGGTACAGTAACTCCAACGCCGAATACAGGTGAGCTCTTACGCCC
TAAAGACGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTA
TGAAAAAATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAG
AATGGGAGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGT
AACAAGATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAAT
GATTATGGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTG
AGAATAACGGTACACACGTTAACGGTTGGGCTAGTGTTTATGCAAATAGAA
ACGAAGTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTA
ATCAATGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATC
CTGGTAGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGA
AAGTAGCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACA
CTGTACGTCTGCATAACGAATTCTTCGGAACTTCTTGTCCACATCGTTCGTG
GGACTTGCATGTTGGCAAAGGTGAGCCTTACACAACCTACTAATATTAATAA
AATGAAAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGAAAA
GCTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAG
AAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGAAAA
CAGAATAAAGATGGCATTGTTGATAAAGCTGAACATGCTTCGTTACAGTG
ACAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCAC
CCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTT
CAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAA
ACTGTATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGT
AAGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 49 (M23-2638 Ami2638 CBD2638 CBD2638 + 6xHis and cloning sites)

[0134]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGCTAACTGCTATT
GACTATCTTACGAAAAAAGGTTGGAAAATATCATCTGACCCTCGCACTTAC
GATGGTTACCCTAAAAACTACGGCTACAGAAATTACCATGAAAACGGCATT
AATTATGATGAGTTTTGTGGTGGTTATCATAGAGCTTTTGATGTTTACAGTA
ACGAAACTAACGACGTGCCTGCTGTTACTAGCGGAACAGTTATTGAAGCAA

ACGATTACGGTAATTTTGGTGGTACATTCGTTATTAGAGACGCTAACGATA
ACGATTGGATATATGGGCATCTACAACGTGGCTCAATGCGATTTGTTGTAG
GCGACAAAGTCAATCAAGGTGACATTATTGGTTTACAAGGTAATAGCAACT
ATTACGACAATCCTATGAGTGTACATTTACATTTACAATTACGCCCTAAAGA
CGCAAAGAAAGATGAAAAATCACAAGTATGTAGTGGTTTGGCTATGGAAA
AATATGACATTACAAATTTAAATGCTAAACAAGATAAATCAAAGAATGGG
AGCGTGAAAGAGTTGAAACATATCTATTCAAACCATATTAAAGGTAACAAG
ATTACAGCACCAAAACCTAGTATTCAAGGTGTGGTCATCCACAATGATTAT
GGTAGTATGACACCTAGTCAATACTTACCATGGTTATATGCACGTGAGAAT
AACGGTACACACGTTAACGGTTGGGCTAGTGTATGCAAATAGAAACGAA
GTGCTTTGGTATCATCCGACAGACTACGTAGAGTGGCATTGTGGTAATCAA
TGGGCAAATGCTAACTTAATCGGATTTGAAGTGTGTGAGTCGTATCCTGGT
AGAATCTCGGACAAATTATTCTTAGAAAATGAAGAAGCGACATTGAAAGTA
GCTGCGGATGTGATGAAGTCGTACGGATTACCAGTTAATCGCAACACTGTA
CGTCTGCATAACGAATTCTTCGGAACCTTCTTGTCACATCGTTCGTGGGACT
TGCATGTTGGCAAAGGTGAGCCTTACACAATACTAATATTAATAAAATGA
AAGACTACTTCATCAAACGCATCAAACATTATTATGACGGTGGAAAGCTAG
AAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTT
AAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGA
ATAAAGATGGCATTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAG
CACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCAC
AAGCTCGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAA
AATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTG
TATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGT
TGTGGGGCGAAATTAAAGAGCTCGGTGGAAAGCTAGAAGTAAGCAAAGCA
GCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAGC
AAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATT
GGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAATTA
TCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTAC
AAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCATG
TTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTAC
GCACATCGGACCGCTAA A A CTGCTA A AGTTGCTA AGTTCTGGGGCGA A ATTA

[0135]

CTCGAGAAATCATAAAAAATTTATTGGCTTTGTGAGCGGATAACAATTATA
ATAGATTCAATTGTGAGCGGATAACAATTTACACAGAATTCATTAAAGAG
GAGAAATTAACATATGAGAGGATCGCATCACCATCACCATCACGGATCCGCA
TGCGAGCTCGGTACCCCGGGTCGACCTGCAGCCAAGCTTAATTAGCTGAGC
TTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTT
GTTCAGAACGCTCGGTGCGCGCGGGCGTTTTTTATTGGTGAGAATCCAAG
CTAGCTTGCGGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA
ATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACAT
TTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAGC
TGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTT
ATCCGGCCTTTATTACATTTCTTGCCCGCCTGATGAATGCTCATCCGGAATT
TCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTACCCC
TTGTTACACCGTTTTTCCATGAGCAAACCTGAAACGTTTTTCATCGCTCTGGAGT
GAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTG
GCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAAT
ATGTTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAA
ACGTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTTTCACCATGGGCAAAT
ATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATC
ATGCCGTTTGTGATGGCTTCCATGTGCGGCAGAATGCTTAATGAATTACAAC
AGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATT
GGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAGCTTGAGGCATCAAATA
AAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGT
CGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCCTCTAGAGCTGCCTCGC
GCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGAC
GGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAAG
GCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCAC
GTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGAT
TGTA CTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAG
GAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTG
CGCTCGGTTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTA
ATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGC
AAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT

TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAA
 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC
 CTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTGCCGCTTACCGGATA
 CCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC
 TGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGC
 ACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCT
 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG
 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAA
 GTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGC
 TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGG
 CAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGAT
 TACGCGCAGAAAAAAGGATCTCAAGAAGATCCITTGATCTTTTCTACGGG
 GTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAG
 ATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTT
 AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGC
 TTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAG
 TTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCAT
 CTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAG
 ATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGT
 CCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTA
 GAGTAAGTAGTTCGCCAGTTAATAGTTTGCACAACGTTGTTGCCATTGCTAC
 AGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGT
 TCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCG
 GTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGT
 TATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATC
 CGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGA
 ATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAA
 TACCGCGCCACATAGCAGAACTTTAAAGTGCTCATTCATTGGAAAACGTTT
 TTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCGAT
 GTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTACCAGC
 GTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAAT
 AAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTCAATATTAT

TGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
 TTTAGAAAAATAAACAAATAGGGGTTCGCGCACATTTCCCCGAAAAAGTGC
 CACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATA
 GGGGTATCACGAGGCCCTTTCGTCTTAC

SEQ ID NO: 51 (CBD-2638 with putative linker indicated in bold)

[0136]

GKLEVSKAATIKQSDVKQEVKKQEAKQIVKATDWKQNKDGIWYKAEHASF
 TVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEG
 ETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 52 (CWT-LST with putative linker indicated in bold)

[0137]

GKAGGTVTPNTGWKTNKYGTLYKSESASFTPNTDIITRTTGPFERSMPQSGV
 LKAGQTIHYDEVMKQDGHVWVGTYGNSGQRIYLPVRTWNKSTNTLGVLWGT
 IK

SEQ ID NO: 53 (M23-2638 with putative linker indicated in bold)

[0138]

MLTAIDYLTKKGWKISSDPRTYDGYPKNYGYRNYHENGINYDEFCCGGYHRAF
 DVYSNETNDVPAVTS GTVIEANDYGNFGGTFVIRDANDNDWIYGHLQRGSMR
 FVVGDKVNQGDII GLQGNSNYDNPM SVHLHLQLRPKDAKKDEKSQVCSGL
 AMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKG

SEQ ID NO: 54 (M23-LST with putative linker indicated in bold)

[0139]

AATHEHSAQWLNNYKKGYGYGPYPLGINGGMHYGVDFFMNIGTPVKAISSGK
 IVEAGWSNYGGGNQIGLIENDGVHRQWYMHLSKYNVKVGDYVKAGQIIGWS
 GSTGYSTAPHLHFQRMVNSFSNSTAQDPMPFLKSAGYGKAGGTVTPNTG

SEQ ID NO: 55 (Ami-2638 with putative linker indicated in bold)

[0140]

EKSQVCSGLAMEKYDITNLNAKQDKSKNGSVKELKHIYSNHIKGNKITAPK
 PSIQGVVIHNDYGSMTPSQYLPWLYARENNGTHVNGWASVYANRNEVLWYH
 PTDYVEWHCGNQWANANLIGFEVCESYPGRISDKLFLNEEATLKVAADVMK
 SYGLPVNRNTVRLHNEFFGTSCPHRSWDLHVKGGEPYTTTNINKMKDYFIKRI
 KHYYDGGKLEVSKAATIKQSDVKQEVKKQEAKQIVKATD

SEQ ID NO: 56 (Ami-Φ11 with putative linker indicated in bold)**[0141]**

PKKETAKPQPKAVELK**IIKDVVKG**YDL**PK**RGSNPKGIVIHNDAGSKGATAE
 AYRNLVNAPLSRLEAGIAHSYVSGNTVWQALDESQVGWHTANQIGNKYYY
 GIEVCQSMGADNATFLKNEQATFQECARLLKKWGLPANRNTIRLHNEFTSTSC
 PHRSSVLHTGFDPVTRGLLPEDKRLQLKDYFIKQIRAYMDGKIPVATVSNESSA
 SSNTVKPVASA

SEQ ID NO: 57 (CHAP-Φ11 with putative linker indicated in bold)**[0142]**

MSIIMEVATMQAKLTKNEFIEWLKTSEKQFNVDLWYGFQCFDYANAGWKV
 LFGLLLKGLGAKDIPFANNFDGLATVYQNTPDFLAQPGDMVVFGSNYGAGYG
 HVAWVIEATLDYIIVYEQNWLGGGWTDGIEQPGWGWEKVTRRQHAYDFPMW
 FIRPNFKSETAPRSVQSPTQAP**KKETAKPQPKAVELKIIKDVVKG**YDL**PK**RG

SEQ ID NO: 58 (CHAP-ΦTwort with putative linker indicated in bold)**[0143]**

MKTLKQAESYIKSKVNTGTDFDGLYGYQCMDLAVDYIYHVTGKIRMWGNA
 KDAINNSFGGTATVYKNYPAFRPKYGDVVVWTTGNFATYGHIAIVTNPDY
 DLQYVTVLEQNWNGNGIYKTELATIRTHDYTGITHFIRPNFATESSV**KKK**DTK
 KKP**KPSNRD**GINKDKIVYDRTNINYNMV**KRG**

SEQ ID NO: 59 (pHGFP_CBD2638_c_vector)**[0144]**

CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATA
 ATAGATTCAATTGTGAGCGGATAACAATTTACACAGAATTCATTAAAGAG
 GAGAAATTAACATGAGAGGATCGCATCACCATCACCATCACGGATCCATG
 AGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAATTCTTGTTGAATTA
 GATGGTGATGTTAATGGGCACAAATTTTCTGTCACTGGAGAGGGTGAAGGT
 GATGCAACATACGGAAAACCTTACCCTTAAATTTATTTGCACTACTGGAAAA

CTACCTGTTCCATGGCCAACACTTGTCACTACTTTTCGCGTATGGTCTTCAAT
GCTTTGCGAGATACCCAGATCATATGAAACGGCATGACTTTTTCAAGAGTG
CCATGCCCGAAGGTTATGTACAGGAAAGAACTATATTTTTCAAAGATGACG
GGAACAACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTA
ATAGAATCGAGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTG
GACACAAATTGGAATACAATACTACACAATGTATACATCATGGCAG
ACAAACAAAAGAATGGAATCAAAGTTAACTTCAAAATTAGACACAACATT

GAAGATGGAAGCGTTCAACTAGCAGACCATTATCAACAAAATACTCCAATT
GGCGATGGCCCTGTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTG
CCCTTTGAAAGATCCCAACGAAAAGAGAGACCACATGGTCTTCTTGAGT
TTGTAACAGCTGCTGGGATTACACATGGCATGGATGAACTATACAAAGAGC
TCGGTGGAAAGCTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGAC
GTTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAAC
AGATTGGAACAGAATAAAGATGGCATTGTGTATAAAGCTGAACATGCTTC
GTTACAGTGACAGCACCAGAGGGAATTATCACAAAGATACAAAGGTCCTTG
GACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATA
TGATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTT
TGAGGGCGAACTGTATACATGCCGCTACGCACATGGGACGCTAAAACTG
GTAAAGTTGGTAAGTTGTGGGGCGAAATTAAATAAGTCGACCTGCAGCCAA
GCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAG
AACTCCATCTGGATTTGTTTCAAGACGCTCGGTTGCCGCCGGGCGTTTTTAT
TGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTA
AAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGC
ATCGTAAAGAACATTTTGAGGCATTTTCAAGTCAGTTGCTCAATGTACCTATAA
CCAGACCGTTCAAGCTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAA
TAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAAT
GCTCATCCGGAATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGG
GATAGTGTTACCCCTTGTTACACCGTTTTCCATGAGCAAACCTGAAACGTTTT
CATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATAT
ATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAG
GGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTAC
CAGTTTTGATTTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTTT
ACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCG
ATTCAGGTTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCAGAATGCTTA
ATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTT
AAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAGCTTG
AGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTT
ATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCCTCTA
GAGCTGCCTCGCGCGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCA
GCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA
AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCAT

GACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCA
TCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCAC
AGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTCCGCTTCCTCGCTC
ACTGACTCGCTGCGCTCGGTTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCAC
TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA
GAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCG
CGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAA
ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGC
CGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTC
TCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAG
CTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCC
GGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG
GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGC
TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGT
ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG
TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT
TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTT
GATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGG
GATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAAT
TAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACTTGCTCT
GACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTAT
TTCGTTTCATCCATAGTTGCTGACTCCCCGTCGTGTAGATAACTACGATACG
GGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACG
CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGA
GCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGT
TGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTT
GTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTT
CATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTT
GTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
GTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTT
ACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCA

AGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGT
CAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCA
TTGGAACCGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGA
GATCCAGTTCGATGTAACCCACTCGTGACCCAACTGATCTTCAGCATCTTT
TACTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGC
AAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATAC
ATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTT
CCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTA
ACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAC

SEQ ID NO: 60 (GFP_CBD2638)

[0145]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAGTAAAGGAGA
AGAACTTTTCACTGGAGTTGTCCCAATTCTTGTGAATTAGATGGTGATGTT
AATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATAC
GGAAAACCTTACCCTTAAATTTATTTGCACTACTGGAAAACCTGTTCCAT
GGCCAACACTTGTCACTACTTTTCGCGTATGGTCTTCAATGCTTTGCGAGATA
CCCAGATCATATGAAACGGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGG
TTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACACAAAGAC
ACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTT
AAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGA
ATACAACCTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGA
ATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGC
GTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCT
GTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAG
ATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTG
CTGGGATTACACATGGCATGGATGAACTATACAAAGAGCTCGGTGGAAG
CTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGA
AGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAAC
AGAATAAAGATGGCATTGTGTATAAAGCTGAACATGCTTCGTTACAGTGA
CAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACC
CACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTC
AAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAA

CTGTATACATGCCGGTACGCACATGGGACGCTAAAACCTGGTAAAGTTGGTA
AGTTGTGGGGCGAAATTAAATAA

SEQ ID NO: 61 (GFP_CBD2638 CBD2638 Variant 1. Restriction sites used for construction: BamHI - SacI - SacI- SalI. TAA Stop codon derived from 2nd CBD2638)

[0146]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAGTAAAGGAGA
AGAACTTTTCACTGGAGTTGTCCCAATTCTTGTGAATTAGATGGTGATGTT
AATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATAC
GGAAAACCTTACCCTTAAATTTATTTGCACTACTGGAAAACCTGTTCCAT
GGCCAACACTTGTCACTACTTTTCGCGTATGGTCTTCAATGCTTTGCGAGATA
CCCAGATCATATGAAACGGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGG

TTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGAC
 ACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTT
 AAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGA
 ATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGA
 ATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGC
 GTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCT
 GTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAG
 ATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTG
 CTGGGATTACACATGGCATGGATGAACTATACAAAGAGCTCGGTGGAAG
 CTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGA
 AGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAC
 AGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTACAGTGA
 CAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACC
 CACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTT
 AAAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAA
 CTGTATACATGCCGGTACGCACATGGGACGCTAAAACTGGTAAAGTTGGTA
 AGTTGTGGGGCGAAATTAAGAGCTCGGTGGAAGCTAGAAGTAAGCAAA
 GCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGA
 AGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCA
 TTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAA
 TTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTAT
 TACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTC
 ATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGG
 TACGCACATGGGACGCTAAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAA
 ATTAAATAAGTCGAC

SEQ ID NO: 62 (GFP CBD2638 CBD2638 Variant 2. Restriction sites used for construction: BamHI - SacI - KpnI - Sall. Stop codon is encoded by vector)

[0147]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAGTAAAGGAGA
 AGAACTTTTCACTGGAGTTGTCCCAATTCTTGTTGAATTAGATGGTGTATGTT
 AATGGGCACAAATTTTCTGTCACTGGAGAGGGTGAAGGTGATGCAACATAC
 GGAAAACTTACCCTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCAT
 GGCCAACACTTGTCACTACTTTCGCGTATGGTCTTCAATGCTTTGCGAGATA
 CCCAGATCATATGAAACAGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGG
 TTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGAC
 ACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTT
 AAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGA

ATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGA
 ATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGC
 GTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCT
 GTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTTCGAAAG
 ATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTG
 CTGGGATTACACATGGCATGGATGAACTATACAAAGAGCTCGGTGGAAAG
 CTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGA
 AGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAGCAACAGATTGGAAAC
 AGAATAAAGATGGCATTGTTGGTATAAAGCTGAACATGCTTCGTTACAGTGA
 CAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACC
 CACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTT
 AAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAA
 CTGTATACATGCCGGTACGCACATGGGACGCTAAACTGGTAAAGTTGGTA
 AGTTGTGGGGCGAAATTAAAGGTACCGGTGGAAAGCTAGAAGTAAGCAAA
 GCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGA
 AGCAAAACAAATTGTGAAAGCAACAGATTGGAAACAGAATAAAGATGGCA
 TTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAA
 TTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTAT

TACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTC
 ATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGG
 TACGCACATGGGACGCTAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAA
 ATTAAAGTCGACCTGCAGCCAAGCTTAATTAGCTGA

SEQ ID NO: 63 (GFP_CBD2638_CBD2638_CBD2638. Restriction sites used for construction: BamHI - SacI - KpnI-Sall - PstI. Stop codon is encoded by vector)

[0148]

ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGAGTAAAGGAGA
 AGAACTTTTACTGGAGTTGTCCCAATTCTTGTGAATTAGATGGTGATGTT
 AATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATAC
 GGAAAACCTTACCCTTAAATTTATTTGCACTACTGGAAAACCTACCTGTTCCAT
 GGCCAACACTTGTCACTACTTTTCGCGTATGGTCTTCAATGCTTTGCGAGATA
 CCCAGATCATATGAAACAGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGG
 TTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGAC
 ACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTT
 AAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGA
 ATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGA
 ATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGC
 GTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCT
 GTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTTCGAAAG

ATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTG
CTGGGATTACACATGGCATGGATGAACTATACAAAGAGCTCGGTGGAAAG
CTAGAAGTAAGCAAAGCAGCAACTATCAAACAATCTGACGTTAAGCAAGA
AGTTAAAAAGCAAGAAGCAAAACAAATTGTGAAAAGCAACAGATTGGAAAC
AGAATAAAGATGGCATTGTGTATAAAGCTGAACATGCTTCGTTACAGTGA
CAGCACCAGAGGGAATTATCACAAGATACAAAGGTCCTTGGACTGGTCACC
CACAAGCTGGTGTATTACAAAAAGGTCAAACGATTAAATATGATGAGGTTT
AAAAATTTGACGGTCATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAA
CTGTATACATGCCGGTACGCACATGGGACGCTAAACTGGTAAAGTTGGTA
AGTTGTGGGGCGAAATTAAAGGTACCGGTGGAAAGCTAGAAGTAAGCAAA
GCAGCAACTATCAAACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGA
AGCAAAACAAATTGTGAAAAGCAACAGATTGGAAACAGAATAAAGATGGCA
TTTGGTATAAAGCTGAACATGCTTCGTTACAGTGACAGCACCAGAGGGAA
TTATCACAAGATACAAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTAT
TACAAAAAGGTCAAACGATTAAATATGATGAGGTTCAAAAATTTGACGGTC
ATGTTTGGGTATCGTGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGG
TACGCACATGGGACGCTAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAA
ATTAAAGTCGACGGTGGAAAGCTAGAAGTAAGCAAAGCAGCAACTATCAA
ACAATCTGACGTTAAGCAAGAAGTTAAAAAGCAAGAAGCAAAACAAATTG
TGAAAGCAACAGATTGGAAACAGAATAAAGATGGCATTGTGTATAAAGCT
GAACATGCTTCGTTACAGTGACAGCACCAGAGGGAATTATCACAAGATAC
AAAGGTCCTTGGACTGGTCACCCACAAGCTGGTGTATTACAAAAAGGTCAA
ACGATTAAATATGATGAGGTTCAAAAATTTGACGGTCATGTTTGGGTATCG
TGGGAAACGTTTGAGGGCGAAACTGTATACATGCCGGTACGCACATGGGAC
GCTAAACTGGTAAAGTTGGTAAGTTGTGGGGCGAAATTAAACTGCAGCCA
AGCTTAATTAGCTGA

SEQ ID NO: 64 (GFP_CBD2638 aa)

[0149]

MRGSHHHHHHGSMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGDATY
GKLTLKFICTTGKLPVPWPTLVTTFAAYGLQCFARYPDHMKRHDFFKSAMPEGY
VQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYN
SHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNH
YLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYKELGGKLEVSKAATI
KQSDVKQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYK
GPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWD
AKTGKVGKLWGEIK

SEQ ID NO: 65 (GFP_CBD2638_CBD2638 Variant 1 aa)

[0150]

MRGSHHHHHHGSMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATY
GKLTCLKFICTTGKLPVPWPTLVTTTFAYGLQCFARYPDHMKRHDFFKSAMPEGY
VQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNIN
SHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNH
YLSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYKELGGKLEVSKAATI
KQSDVKQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYK
GPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWD
AKTGKVGKLWGEIKELGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDW

KQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEV
QKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIK

SEQ ID NO: 66 (GFP_CBD2638_CBD2638 Variant 2 aa)

[0151]

MRGSHHHHHHGSMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATY
GKLTCLKFICTTGKLPVPWPTLVTTTFAYGLQCFARYPDHMKQHDFFKSAMPEGY
VQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNIN
SHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNH
YLSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYKELGGKLEVSKAATI
KQSDVKQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIITRYK
GPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWD
AKTGKVGKLWGEIKGTGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDW
KQNKDGIWYKAEHASFTVTAPEGIITRYKGPWTGHPQAGVLQKGQTIKYDEV
QKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIKVDLQPSLIS

SEQ ID NO: 67 (GFP_CBD2638_CBD2638_CBD2638 aa)

[0152]

MRGSHHHHHHGSMSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATY
GKLTCLKFICTTGKLPVPWPTLVTTTFAYGLQCFARYPDHMKQHDFFKSAMPEGY
VQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNIN
SHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNH
YLSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYKELGGKLEVSKAATI

KQSDVKQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGIIITRYK
 GPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPVRTWD
 AKTGKVGKLWGEIKGTGGKLEVSKAATIKQSDVKQEVKKQEAQIVKATDW
 KQNKDGIWYKAEHASFTVTAPEGIIITRYKGPWTGHPQAGVLQKGQTIKYDEV
 QKFDGHVWVSWETFEGETVYMPVRTWDAKTGKVGKLWGEIKVDGGKLEVS
 KAATIKQSDVKQEVKKQEAQIVKATDWKQNKDGIWYKAEHASFTVTAPEGI
 ITRYKGPWTGHPQAGVLQKGQTIKYDEVQKFDGHVWVSWETFEGETVYMPV
 RTWDAKTGKVGKLWGEIKLQPSLIS

SEQUENCE LISTING

[0153]

<110> EBI Food Safety B.V.

<120> A polypeptide

<130> P6035159PCT

<160> 67

<170> PatentIn version 3.3

<210> 1

<211> 1461

<212> DNA

<213> Staphylococcus aureus bacteriophage 2638a

<400> 1

atgctaactg ctattgacta tcttacgaaa aaaggttgga aaatatcatc tgaccctcgc	60
acttacgatg gttaccctaa aaactacggc tacagaaatt accatgaaaa cggcattaat	120
tatgatgagt tttgtggtgg ttatcataga gcttttgatg tttacagtaa cgaaactaac	180
gacgtgcctg ctgttactag cggaacagtt attgaagcaa acgattacgg taattttggt	240
ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt	300
ggctcaatgc gatttggtgt aggcgacaaa gtcaatcaag gtgacattat tggtttacia	360
ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgccct	420
aaagacgcaa agaaagatga aaaatcacaa gtatgtagtg gtttggtctat ggaaaaatat	480
gacattacaa atttaaattgc taaacaagat aaatcaaaga atgggagcgt gaaagagttg	540
aaacatatct attcaaacca tattaaaggt aacaagatta cagcaccaaa acctagtatt	600
caaggtgtgg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg	660
ttatatgcac gtgagaataa cgttacacac gttaacgggtt gggctagtgt ttatgcaaat	720
agaaacgaag tgcttttgta tcatccgaca gactacgtag agtggcattg tggtaatcaa	780
tgggcaaatg ctaacttaat cggatttgaa gtgtgtgagt cgtatcctgg tagaatctcg	840

```

gacaaattat tcttagaaaa tgaagaagcg acattgaaag tagctgcgga tgtgatgaag 900
tcgtacggat taccagttaa tcgcaacact gtacgtctgc ataacgaatt cttcggaact 960
tcttgtccac atcgttcgtg ggacttgcac gttggcaaag gtgagcctta cacaactact 1020
aatattaata aatgaaaga ctacttcac aaacgcacaa aacattatta tgacggtgga 1080
aagctagaag taagcaaagc agcaactatc aaacaatctg acgttaagca agaagttaa 1140
aagcaagaag caaaacaaat tgtgaaagca acagattgga aacagaataa agatggcatt 1200
tggatataag ctgaacatgc ttcgttcaca gtgacagcac cagaggggaat taccacaaga 1260
tacaaggtc cttggactgg tcacccacaa gctggtgtat taaaaaagg tcaaacgatt 1320
aaatatgatg aggttcaaaa atttgacggt catgtttggg tatcgtggga aacgtttgag 1380

ggcgaaactg tatacatgcc ggtacgcaca tgggacgcta aaactggtaa agttggtaag 1440
ttgtggggcg aaattaaata a 1461

```

<210> 2

<211> 1086

<212> DNA

<213> artificial

<220>

<223> His-tagged Ami2638_CBD2368

<400> 2

```

atgagaggat cgcacaccca tcaccatcac ggatccttac gccctaaaga cgcaaagaaa 60
gatgaaaaat cacaagtatg tagtggtttg gctatggaaa aatatgacat tacaatttta 120
aatgctaaac aagataaatc aaagaatggg agcgtgaaag agttgaaaca tatctattca 180
aaccatatta aaggtaacaa gattacagca ccaaaccta gtattcaagg tgtggtcatc 240
cacaatgatt atggtagtat gacacctagt caatacttac catggttata tgcacgtgag 300
aataacggta cacacgttaa cggttgggct agtgtttatg caaatagaaa cgaagtgcct 360
tggtatcatc cgacagacta cgtagagtgg cattgtggtg atcaatgggc aaatgctaac 420
ttaatcggat ttgaagtgtg tgagtcgtat cctggtagaa tctcggacaa attattctta 480
gaaaatgaag aagcgacatt gaaagtagct gcggatgtga tgaagtcgta cggattacca 540
gttaatcgca acactgtacg tctgcataac gaattcttcg gaacttcttg tccacatcgt 600
tcgtgggact tgcattgttg caaaggtagg ccttacacaa ctactaatat taataaaatg 660
aaagactact tcatcaaacg catcaaacat tattatgacg gtggaaagct agaagtaagc 720
aaagcagcaa ctatcaaca atctgacgtt aagcaagaag ttaaaaagca agaagcaaaa 780
caaatgtga aagcaacaga ttggaaacag aataaagatg gcatttggtg taaagctgaa 840
catgcttcgt tcacagtgc agcaccagag ggaattatca caagatacaa aggtccttgg 900
actggtcacc cacaagctgg tgtattacaa aaagggtcaa cgattaaata tgatgaggtt 960
caaaaatttg acggtcatgt ttgggtatcg tgggaaacgt ttgagggcga aactgtatac 1020
atgccggtac gcacatggga cgctaaaact ggtaaagttg gtaagttgtg gggcgaaatt 1080
aaataa 1086

```

<210> 3

<211> 1035

<212> DNA

<213> artificial

<220>

<223> His-tagged M23-2638_CBD2638

<400> 3

atgagaggat cgcacaccca tcacccatcac ggatccatgc taactgctat tgactatctt	60
acgaaaaaag gttggaaaat atcatctgac cctcgcaactt acgatgggta ccctaaaaac	120
tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tgggtgggtat	180
catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga	240
acagttattg aagcaaacga ttacggtaat tttgggtgta cattcggttat tagagacgct	300
aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc	360
gacaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat	420
cctatgagtg tacatttaca ttacaatta cgcacctaaag acgcaaagaa agatgaaaaa	480
tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa	540
caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt	600
aaaggtaaac agattacagc accaaaaact agtattcaag gtgagctcgg tggaaagcta	660
gaagtaagca aagcagcaac tatcaaaca tctgacgtta agcaagaagt taaaaagcaa	720
gaagcaaac aaattgtgaa agcaacagat tggaaacaga ataaagatgg catttggtat	780
aaagctgaac atgcttcgtt cacagtgaca gcaccagagg gaattatcac aagatacaaa	840
ggtccttgga ctggctaccc acaagctggt gtattacaaa aagggtcaaac gattaaatat	900
gatgaggttc aaaaatttga cggctcatgt tgggtatcgt gggaaacgtt tgaggggcga	960
actgtataca tgccggtacg cacatgggac gctaaaactg gtaaagttgg taagttgtgg	1020
ggcgaaatta aataa	1035

<210> 4

<211> 2961

<212> DNA

<213> artificial

<220>

<223> His-tagged Ply2638_Ply2638

<400> 4

atgagaggat cgcacaccca tcacccatcac ggatccatgc taactgctat tgactatctt	60
acgaaaaaag gttggaaaat atcatctgac cctcgcaactt acgatgggta ccctaaaaac	120
tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tgggtgggtat	180
catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga	240
acagttattg aagcaaacga ttacggtaat tttgggtgta cattcggttat tagagacgct	300
aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc	360

gacaaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat	420
cctatgagtg tacatttaca tttaacaatta cgccttaaag acgcaaagaa agatgaaaaa	480
tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa	540
caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt	600
aaaggtaaca agattacagc accaaaaact agtattcaag gtgtggtoat ccacaatgat	660
tatggtagta tgacacctag tcaataactta ccatggttat atgcacgtga gaataacggt	720
acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgtc ttggtatcat	780
ccgacagact acgtagagtg gcatttggtt aatcaatggg caaatgctaa cttaatcgga	840
tttgaagtg gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa	900
gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc	960
aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac	1020
ttgcatgttg gcaaaggtag gccttacaca actactaata ttaataaaat gaaagactac	1080
ttcatcaaac gcatacaaca ttattatgac ggtggaaaagc tagaagtaag caaagcagca	1140
actatcaaac aatctgacgt taagcaagaa gttaaaaaagc aagaagcaaa acaaatgtg	1200
aaagcaacag attggaacaa gaataaagat ggcatttggt ataaagctga acatgcttcg	1260
ttcacagtga cagcaccaga gggaattatc acaagataca aaggctcctg gactggtcac	1320
ccacaagctg gtgtattaca aaaagggtcaa acgattaaat atgatgaggt tcaaaaattt	1380
gacggtoatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgccggt	1440
cgcacatggg acgctaaaac tggtaaagtt ggtaagttgt ggggcgaaat taaagagctc	1500
atgctaactg ctattgacta tcttacgaaa aaagggttga aaatatcatc tgaccctcgc	1560
acttacgatg gttaccctaa aaactacggc tacagaaatt accatgaaaa cggcattaat	1620
tatgatgagt tttgtggtgg ttatcataga gcttttgatg tttacagtaa cgaaactaac	1680
gacgtgcctg ctgttactag cggaacagtt attgaagcaa acgattacgg taattttggt	1740
ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt	1800
ggctcaatgc gatttggtgt aggcgacaaa gtcaatcaag gtgacattat tggtttacia	1860
ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgcct	1920
aaagacgcaa agaaagatga aaaatcacaa gtatgtagtg gtttggtat ggaaaaatat	1980
gacattacaa atttaaatgc taaacaagat aaatcaaaga atgggagcgt gaaagagttg	2040
aaacatatct attcaaacca tattaaggtt aacaagatta cagcaccaaa acctagtatt	2100
caaggtgtgg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg	2160
ttatatgcac gtgagaataa cggtagacac gttaacggtt gggctagtgt ttatgcaaat	2220
agaaacgaag tgcttttggt tcatccgaca gactacgtag agtggcattg tggtaatcaa	2280
tgggcaaatg ctaacttaat cggatttgaa gtgtgtgagt cgtatcctgg tagaatctcg	2340
gacaaattat tottagaaaa tgaagaagcg acattgaaag tagctgcgga tgtgatgaag	2400
togtacggat taccagttaa tcgcaacact gtacgtctgc ataacgaatt cttcggaact	2460
tcttgccac atcgttcgtg ggacttgcat gttggcaaag gtgagcctta cacaactact	2520
aatattaata aaatgaaaga ctacttcac aaacgcacat aacattatta tgacgggtgga	2580
aagctagaag taagcaaacg agcaactatc aaacaatctg acgttaagca agaagttaaa	2640
aagcaagaag caaaacaaat tgtgaaagca acagattgga aacagaataa agatgacatt	2700

```

tggtataaag ctgaacatgc ttctgttcaca gtgacagcac cagaggggaat tatcacaaga 2760
tacaaagggtc cttggactgg tcacccacaa gctgggtgtat tacaaaaagg tcaaacgatt 2820
aaatatgatg aggttcacaaa atttgacggt catgtttggg tatcgtggga aacgtttgag 2880
ggcgaaactg tatacatgcc ggtacgcaca tgggacgcta aaactggtaa agttggtaag 2940
ttgtggggcg aaattaaata a 2961

```

<210> 5

<211> 1983

<212> DNA

<213> artificial

<220>

<223> CHAP11_M23-2638_Ami2638_CBD2638

<400> 5

```

atgcaagcaa aattaactaa aaatgagttt atagagtggg tgaaaacttc tgagggaaaa 60
caattcaatg tggacttatg gtatggattt caatgctttg attatgccaa tgctggttgg 120
aaagttttgt ttggattact tctaaaagggt ttaggtgcaa aagatattcc gtctgctaac 180
aacttcgacg gattagctac tgtataccaa aatacaccgg acttcttagc acaacctggc 240
gacatgggtg tattcggtag caactacggt gctggatatg gtcaogttgc atgggtaatt 300
gaagcaactt tagattacat cattgtatat gacgagaatt ggctaggcgg tggctggact 360
gacggaatcg aacaaccogg ctgggggttg gaaaaagtta caagacgaca acatgcttat 420
gatttcoccta tgtggtttat ccgtccgaat tttaaaagtg agacagcgcc acgatcagtt 480
caatctccta cacaagcacc taaaaaagaa acagctggat ccatgctaac tgctattgac 540
tatcttacga aaaaagggtg gaaaatatca tctgacctc gcacttacga tggttaccct 600
aaaaactacg gctacagaaa ttaccatgaa aacggcatta attatgatga gttttgtggg 660
ggttatcata gagcttttga tgtttacagt aacgaaacta acgacgtgcc tgctgttact 720
agcggaaacag ttattgaagc aaacgattac ggtaattttg gtggtacatt cgttattaga 780
gacgctaacg ataacgattg gatatatggg catctacaac gtggctcaat gogatttgtt 840
gtaggcgaca aagtcaatca aggtgacatt attggtttac aaggtaatag caactattac 900
gacaatccta tgagtgtaca ttacattta caattacgcc ctaaagacgc aaagaaagat 960
gaaaaatcac aagtatgtag tggtttgggt atggaaaaat atgacattac aaatttaaat 1020

gctaaacaag ataaatcaaa gaatgggagc gtgaaagagt tgaaacatat ctattcaaac 1080
catattaaag gtaacaagat tacagcacca aaacctagta ttcaagggtg ggtcatccac 1140
aatgattatg gtagtatgac acctagtcac tacttaccat gggtatatgc acgtgagaat 1200
aacggtacac acgttaacgg ttgggctagt gtttatgcaa atagaaacga agtgctttgg 1260
tatcatccga cagactacgt agagtggcat tgtggtaatc aatgggcaaa tgctaactta 1320
atcggttttg aagtgtgtga gtcgtatcct ggtagaatct cggacaaatt attcttagaa 1380
aatgaagaag cgacattgaa agtagctgcg gatgtgatga agtcgtacgg attaccagtt 1440
aatcgcaaca ctgtacgtct gcataacgaa ttcttcggaa cttcttgtcc acatcgttcg 1500

```

```

tggtgacttgc atgttgccaa aggtgagcct tacacaacta ctaatattaa taaaatgaaa 1560
gactacttca tcaaacgcat caaacattat tatgacgggtg gaaagctaga agtaagcaaa 1620
gcagcaacta tcaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 1680
attgtgaaag caacagattg gaaacagaat aaagatggca tttgggtataa agctgaacat 1740
gcttcgttca cagtgcacgc accagaggga attatcacaa gatacaaagg tccttggact 1800
ggtcacccac aagctgggtg attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa 1860
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1920
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 1980
taa 1983

```

<210> 6

<211> 2109

<212> DNA

<213> artificial

<220>

<223> Ami11_M23-2638_Ami2638_CBD2638

<400> 6

```

aagccacaac ctaaagcagt agaacttaaa atcatcaaag atgtgggttaa aggttatgac 60
ctacctaagc gtggtagtaa ccctaaaggt atagttatac acaacgacgc agggagcaaa 120
ggggcgactg ctgaagcata tcgtaacgga ttagtaaatg cacctttatc aagattagaa 180
gcgggcattg cgcatagtta cgtatcaggc aacacagttt ggcaagcctt agatgaatca 240
caagtaggtt ggcatacgcg taatcaaata ggtaataaat attattacgg tattgaagta 300
tgtcaatcaa tgggcgcaga taacgcgaca ttcttaaaaa atgaacaggc aactttccaa 360
gaatgcgcta gattgttgaa aaaatgggga ttaccagcaa acagaaatac aatcagattg 420
cacaatgaat ttacttcaac atcatgcctt catagaagtt cggttttaca cactggtttt 480
gaccocagta ctcgcggtct attgccagaa gacaagcggg tgcaacttaa agactacttt 540

atcaagcaga ttagggcgta catggatggt aaaataccgg ttgccactgt ctctaattgag 600
tcaagcgctt caagtaatac agttaaacca gttgcaagtg caggatccat gctaactgct 660
attgactatc ttacgaaaaa aggttggaat atatcatctg accctcgac ttacgatggt 720
taccctaaaa actacggcta cagaaattac catgaaaacg gcattaatta tgatgagttt 780
tgtgtgtggt atcatagagc ttttgatggt tacagtaacg aaactaacga cgtgcctgct 840
gttactagcg gaacagttat tgaagcaaac gattacggta attttggtgg tacattcgtt 900
attagagacg ctaacgataa cgattggata tatgggcacg tacaacgtgg ctcaatgcga 960
tttgtgttag gcgacaaagt caatcaaggt gacattattg gtttacaagg taatagcaac 1020
tattacgaca atcctatgag tgtacattta catttacaat tacgccctaa agacgcaaag 1080
aaagatgaaa aatcacaagt atgtagtggg ttggctatgg aaaaatatga cattacaaat 1140
ttaaattgcta aacaagataa atcaaagaat gggagcgtga aagagttgaa acatatctat 1200
tcaaaccata ttaaaggtaa caagattaca gcacaaaaac ctagtattca aggtgtggtc 1260
atccacaatg attatggtag tatgacacct agtcaatact taccatggtt atatgcacgt 1320
aagaataacg ctacacacgt taacggttgc ctaagtgttt atgcaaatag aaacgaagtc 1380

```

```

ctttggtatc atccgacaga ctacgtagag tggcattgtg gtaatcaatg ggcaaatgct 1440
aacttaatcg gatttgaagt gtgtgagtcg tatcctggta gaatctcgga caaattatto 1500
ttagaaaatg aagaagcgac attgaaagta gctgcggtatg tgatgaagtc gtacggatta 1560
ccagttaatc gcaacactgt acgtctgcat aacgaattct tcggaaacttc ttgtccacat 1620
cgttcgtggg acttgcattgt tggcaaaggt gagccttaca caactactaa tattaataaa 1680
atgaaagact acttcatcaa acgcatcaaa cattattatg acggtggaaa gctagaagta 1740
agcaaagcag caactatcaa acaatctgac gttaagcaag aagttaaaaa gcaagaagca 1800
aaacaaattg tgaaagcaac agattggaaa cagaataaag atggcatttg gtataaagct 1860
gaacatgctt cgttcacagt gacagcacca gaggggaatta tcacaagata caaaggctct 1920
tggactggtc acccacaagc tgggtgatta caaaaaggtc aaacgattaa atatgatgag 1980
gttcaaaaat ttgacggtca tgtttgggta tcgtgggaaa cgtttgaggg cgaaactgta 2040
tacatgccgg tacgcacatg ggacgctaaa actggtaaag ttggtaagtt gtggggcgaa 2100
attaaataa 2109

```

<210> 7

<211> 1923

<212> DNA

<213> artificial

<220>

<223> CHAPTw_Ami2638_M23-LST_CBD2638

<400> 7

```

atgaaaaccc tgaacaagc agagtcctac attaagagta aagtaaatac aggaactgat 60
tttgatgggt tatatgggta tcagtgtatg gacttagcag tagattatat ttaccatgta 120
acagatggta aaataagaat gtggggtaat gctaaggatg cgataaataa ctcttttggt 180
ggtactgcta cggatatata aaactaccct gcttttagac ctaagtacgg tgatgtagtc 240
gtatggacta ctggtaatth tgcaacttat ggtcatatcg caatagttac taacctgac 300
ccttatggag acctcaata tgttacagtt cttgaacaaa actggaacgg taacgggatt 360
tataaaaccg agttagctac aatcagaaca cagcattaca caggaattac acattttatt 420
aaagacgcaa agaaagatga aaaatcacia gtatgtagtg gtttggctat ggaaaaatat 480
gacattacaa atttaaatgc taaacaagat aaatcaaaga atgggagcgt gaaagagttg 540
aaacatatct attcaaacca tattaaaggt aacaagatta cagcaccaaa acctagtatt 600
caagggtgtg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg 660
ttatatgcac gtgagaataa cggtaacacac gttaacgggt gggctagtgt ttatgcaaat 720
agaaaacgaag tgctttggta tcatccgaca gactacgtag agtggcattg tggtaatcaa 780
tgggcaaatg ctaacttaat cggatttgaa gtgtgtgagt cgtatcctgg tagaatctcg 840
gacaaattat tcttagaaaa tgaagaagcg acattgaaag tagctgcgga tgtgatgaag 900
tcgtacggat taccagttaa tcgcaacact gtacgtctgc ataacgaatt ctccggaact 960
tcttgtccac atcgttcgtg ggacttgcac gttggcaaaag gtgagcctta cacaactact 1020
aatattaata aaatgaaaga ctacttcac aaacgcatca aacattatta tgacggtgga 1080
aagctagaag taagcaaacg agcaactatc aaacaatctg acgttaagca agaagttaaa 1140

```

```

aagcaagaag caaaacaaat tgtgaaagca acagatgctg caacacatga acattcagca 1200
caatgggtga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 1260
ggcggtatgc actacggagt tgattttttt atgaatattg gaacaccagt aaaagctatt 1320
tcaagcggaa aaatagttga agctgggttg agtaattacg gaggaggtaa tcaaataggt 1380
cttattgaaa atgatggagt gcatagacaa tggatatatgc atctaagtaa atataatggt 1440
aaagtaggag attatgtcaa agctgggtcaa ataatcggtt ggtctggaag cactgggtat 1500
tctacagcac cacatttaca cttccaaaga atggttaatt catthttcaa ttcaactgcc 1560
caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 1620
ccaacgccga atacaggttg gaaacagaat aaagatggca tttggtataa agctgaacat 1680
gcttcgttca cagtgcagc accagaggga attatcacaa gatacaaagg tccttgact 1740
ggtcaccac aagctgggtg attacaaaaa ggtcaaacga ttaaataatga tgagggtcaa 1800
aaatttgacg gtcatgtttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1860

ccggtacgca catgggacgc taaaactggt aaagttggtg agttgtgggg cgaaattaaa 1920
taa 1923

```

<210> 8

<211> 1953

<212> DNA

<213> artificial

<220>

<223> His-tagged CHAPTw_Ami2638_M23-LST_CWT-LST

<400> 8

```

atgagaggat cgcacaccca tcaccatcac ggatccatga aaacctgaa acaagcagag 60
tctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 120
tgtatggact tagcagtaga ttatatattac catgtaacag atggtaaaat aagaatgtgg 180
ggtaatgcta aggatgcgat aaataactct tttggtggtg ctgctacggg atataaaaac 240
taccctgctt ttagacctaa gtacgggtgat gtagtcgtat ggactactgg taattttgca 300
acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatggt 360
acagttcctg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 420
agaacacacg attacacagg aattacacat tttattaaag acgcaaagaa agatgaaaaa 480
tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540
caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600
aaaggtaaca agattacagc accaaaacct agtattcaag gtgtgggtcat ccacaatgat 660
tatggtagta tgacacctag tcaatactta ccattggttat atgcacgtga gaataacggg 720
acacacgtta acggttgggc tagtggtttat gcaaatagaa acgaagtgtt ttggtatcat 780
ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcgga 840
tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900
gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960
aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttctggtggac 1020
ttgcatgttg gcaaaggtga gccttacaca actactaata ttaataaaat gaaagactac 1080

```

```

ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140
actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200
aaagcaacag atgctgcaac acatgaacat tcagcacaat ggttgaataa ttacaaaaaa 1260
ggatatgggt acggtcctta tccattaggt ataaatggcg gtatgcacta cggagttgat 1320
ttttttatga atattggaac accagtaaaa gctatttcaa gcggaaaaat agttgaagct 1380
ggttggagta attacggagg aggtaatcaa ataggtctta ttgaaaatga tggagtgcac 1440
agacaatggt atatgcatct aagtaaatat aatgttaaag taggagatta tgtcaaagct 1500

ggtc aaataa tgggttggtc tggaagcact ggttattota cagcaccaca tttacacttc 1560
caaagaatgg ttaattcatt ttcaaattca actgcccagg atccaatgcc tttcttaaag 1620
agcgcaggat atggaaaagc aggtgggtaca gtaactccaa cgccgaatac aggttggaaa 1680
acaaacaaat atggcacact atataaatca gagtcagcta gcttcacacc taatacagat 1740
ataataacaa gaacgactgg tccatttaga agcatgccgc agtcaggagt cttaaaagca 1800
ggtcaaacaa ttcatatga tgaagtgatg aaacaagacg gtcagtgttg ggtaggttat 1860
acaggtaaca gtggccaacg tatttacttg cctgtaagaa catggaataa atctactaat 1920
actttaggtg ttctttgggg aactataaag taa 1953

```

<210> 9

<211> 1518

<212> DNA

<213> artificial

<220>

<223> M23-LST_Ami2638_CBD2638

<400> 9

```

gctgcaacac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac 60
ggtccttata cattaggtat aaatggcggg atgcactacg gagttgattt ttttatgaat 120
attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180
tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatac acaatggtat 240
atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc 300
ggttgggtotg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360
aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420
ggaaaagcag gtggtacagt aactccaacg ccgaatacag gtgagctctt acgccctaaa 480
gacgcaaaga aagatgaaaa atcacaagta tgtagtggtt tggctatgga aaaatatgac 540
attacaaatt taaatgctaa acaagataaa tcaaagaatg ggagcgtgaa agagttgaaa 600
catatctatt caaacatat taaaggtaac aagattacag caccaaaacc tagtattcaa 660
ggtgtggtca tccacaatga ttatggtagt atgacaccta gtcaatactt accatggtta 720
tatgcacgtg agaataacgg tacacacgtt aacggttggg ctagtgttta tgcaaataga 780
aacgaagtgc tttggtatca tccgacagac tacgtagagt ggcattgtgg taatcaatgg 840
gcaaatgcta acttaatcgg atttgaagtg tgtgagtcgt atcctggtag aatctcggac 900
aaattattct tagaaaatga agaagcgaca ttgaaagtag ctgcggatgt gatgaagtcg 960

```

```

tacggattac cagttaatcg caacactgta cgtctgcata acgaattctt cggaacttct 1020
tgtccacatc gttcgtggga cttgcatggt ggcaaagggt agccttacac aactactaat 1080

attaataaaa tgaaagacta cttoatcaaa cgcacaaac attattatga cgggtggaaag 1140
ctagaagtaa gcaaagcagc aactatcaaa caatctgacg ttaagcaaga agttaaaaag 1200
caagaagcaa aacaaattgt gaaagcaaca gattggaaac agaataaaga tggcatttgg 1260
tataaagctg aacatgcttc gttcacagtg acagcaccag agggaattat cacaagatac 1320
aaaggtcctt ggactgggtc cccacaagct ggtgtattac aaaaagggtc aacgattaaa 1380
tatgatgagg ttcaaaaatt tgacgggtcat gtttgggtat cgtgggaaac gtttgagggc 1440
gaaactgtat acatgcgggt acgcacatgg gacgctaaaa ctggtaaagt tggtaagttg 1500
tggggcgaaa ttaataaa 1518

```

<210> 10

<211> 1521

<212> DNA

<213> artificial

<220>

<223> His-tagged LST_LST

<400> 10

```

atgagaggat cgcacacca tcaccatcac ggatccgctg caacacatga acattcagca 60
caatgggtga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 120
ggcgggtatgc actacggagt tgattttttt atgaatattg gaacaccagt aaaagctatt 180
tcaagcggaa aaatagttga agctgggttg agtaattacg gaggaggtaa tcaaataggt 240
cttattgaaa atgatggagt gcatagacaa tggatatgac atctaagtaa atataatggt 300
aaagtaggag attatgtcaa agctgggtcaa ataategggt ggtctggaag cactgggtat 360
tctacagcac cacatttaca cttccaaaga atggttaatt ctttttcaa ttcaactgoc 420
caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 480
ccaacgccga atacaggttg gaaaacaaac aaatatggca cactatataa atcagagtca 540
gctagcttca cacctaatac agatataata acaagaacga ctggtccatt tagaagcatg 600
ccgcagtcag gagtcttaa agcaggtcaa acaattcatt atgatgaagt gatgaaacaa 660
gacgggtcatg tttgggtagg ttatacaggt aacagtggcc aacgtattta ctgacctgta 720
agaacatgga ataaatctac taatacttta ggtgttctt gggaactat aaaggagctc 780
gctgcaacac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac 840
ggtccttata cattaggtat aaatggcgggt atgcaactac gagttgattt ttttatgaat 900
attggaacac cagtaaaagc tttttcaagc ggaaaaatag ttgaagctgg ttggagtaat 960
tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatggtat 1020
atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaataatc 1080
ggttgggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 1140

aattcatttt caaattcaac tgcccaagat ccaatgcctt tottaaagag cgcaggatat 1200
gaaaaacag atggtacant aactccaag ccgaatcacg attggaaaac aaacaaatat 1260

```

```

ggcagactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 1320
acgactgggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 1380
cattatgatg aagtgatgaa acaagacggg catgtttggg taggttatac aggtaacagt 1440
ggccaacgta tttacttgcc tgtaagaaca tggaataaat ctactaatac tttaggtgtt 1500
ctttggggaa ctataaagtg a 1521

```

<210> 11

<211> 1245

<212> DNA

<213> artificial

<220>

<223> His-tagged M23-LST_M23_LST-CWT-LST

<400> 11

```

atgagaggat cgcacaccca tcaccatcac ggatccgctg caacacatga acattcagca 60
caatgggtga ataattacaa aaaaggatat ggttacgggc cttatccatt aggtataaat 120
ggcgggtatgc actacggagt tgattttttt atgaatattg gaacaccagt aaaagctatt 180
tcaagcggaa aaatagttga agctgggttg agtaattacg gaggaggtaa tcaaataagg 240
cttattgaaa atgatggagt gcatagacaa tggatatatgc atctaagtaa atataatgtt 300
aaagtaggag attatgtcaa agctgggtcaa ataatcgggt ggtctggaag cactgggtat 360
tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 420
caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 480
ccaacgccga atacaggtga gctcgctgca acacatgaac attcagcaca atgggtgaat 540
aattacaaaa aaggatatgg ttacgggtcct tatccattag gtataaatgg cggtatgcac 600
tacggagttg atttttttat gaatattgga acaccagtaa aagctatttc aagcggaaaa 660
atagttgaag ctgggttgag taattacgga ggaggtaatc aaataggtct tattgaaaat 720
gatggagtgc atagacaatg gtatatgcat ctaagtaaat ataatgttaa agtaggagat 780
tatgtcaaag ctgggtcaa atcgggttg tctggaagca ctggtatttc tacagcacca 840
catttacact tccaaagaat ggttaattca ttttcaaatt caactgocca agatccaatg 900
cctttcttaa agagcgcgagg atatggaaaa gcaggtggta cagtaactcc aacgccgaat 960
acaggttgga aaacaaacaa atatggcaca ctatataaat cagagtcagc tagcttcaca 1020
cctaatacag atataataac aagaacgact ggtccattta gaagcatgcc gcagtcagga 1080
gtctttaaag caggtcaaac aattcattat gatgaagtga tgaaacaaga cggtcatgtt 1140

tgggtaggtt atacaggtaa cagtggccaa cgtatttact tgctgttaag aacatggaat 1200
aaatctacta atactttagg tgttctttgg ggaactataa agtga 1245

```

<210> 12

<211> 285

<212> DNA

<213> Staphylococcus aureus bacteriophage 2638a

<400> 12

tggaacaga ataaagatgg catttggat aaagctgaac atgcttcgtt cacagtgaca	60
gcaccagagg gaattatcac aagatacaaa ggtccttggc ctggtcaccc acaagctggt	120
gtattacaaa aaggtcaaac gattaaatat gatgaggttc aaaaatttga cggtcagtgt	180
tgggtatcgt gggaaacggt tgagggcgaa actgtatata tgccggtacg cacatgggac	240
gctaaaactg gtaaagtggg taagttgtgg ggcgaaatta aataa	285

<210> 13

<211> 279

<212> DNA

<213> Staphylococcus simulans

<400> 13

tggaacaaa acaaatatgg cacactatat aaatcagagt cagctagctt cacaccta	60
acagatataa taacaagaac gactggtcca tttagaagca tgccgcagtc aggagtctta	120
aaagcaggtc aaacaattca ttatgatgaa gtgatgaaac aagacgggtca tgtttgggta	180
ggttatatac gtaacagtgg ccaacgtatt tacttgcctg taagaacatg gaataaatct	240
actaatactt taggtgttct ttggggaact ataaagtga	279

<210> 14

<211> 438

<212> DNA

<213> Staphylococcus aureus bacteriophage 2638a

<400> 14

atgctaactg ctattgacta tcttacgaaa aaagggttgg aaatatcatc tgaccctcgc	60
acttacgatg gttaccctaa aaactacggc tacagaaatt accatgaaaa cggcattaat	120
tatgatgagt tttgtggtgg ttatcataga gcttttgatg tttacagtaa cgaaactaac	180
gacgtgcctg ctgttactag cggaacagtt attgaagcaa acgattacgg taattttggt	240
ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt	300
ggctcaatgc gatttgttgt aggcgacaaa gtcaatcaag gtgacattat tggtttaca	360
ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgcct	420
aaagacgcaa agaaagat	438

<210> 15

<211> 420

<212> DNA

<213> Staphylococcus simulans

<400> 15

gtgcaacac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac	60
ggtccttata cattaggtat aaatggcggg atgcactacg gagttgattt ttttatgaat	120
attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat	180
tacggaggag gtaatcaaat aggtottatt gaaaatgatg gagtgcatac acaatggtat	240
atgcactata gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc	300

ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360
aattcattttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420

<210> 16

<211> 510

<212> DNA

<213> Staphylococcus aureus bacteriophage 2638a

<400> 16

ggtaacaaga ttacagcacc aaaacctagt attcaaggtg tggatcatcca caatgattat 60
ggtagtatga cacctagtca atacttacca tggttatatg cacgtgagaa taacggtaca 120
cacgttaacg gttgggctag tgtttatgca aatagaaacg aagtgccttg gtatcatccg 180
acagactacg tagagtggca ttgtggtaat caatgggcaa atgctaactt aatcggattt 240
gaagtgtgtg agtcgtatcc tggtagaata tcggacaaat tattcttaga aaatgaagaa 300
gcgacattga aagtagctgc ggatgtgatg aagtcgtacg gattaccagt taatcgcaac 360
actgtacgtc tgcataacga attcttcgga acttcttgtc cacatogttc gtgggacttg 420
catgttgcca aaggtgagcc ttacacaact actaatatta ataaaatgaa agactacttc 480
atcaaacgca tcaaacatta ttatgacggt 510

<210> 17

<211> 642

<212> DNA

<213> Staphylococcus aureus phage phi 11

<400> 17

aagccacaac ctaaagcagt agaacttaaa atcatcaaag atgtgggttaa aggttatgac 60
ctacctaagc gtggtagtaa ccctaaaggt atagttatac acaacgacgc agggagcaaa 120
ggggcgactg ctgaagcata tcgtaacgga ttagttaaag caccctttatc aagattagaa 180
gcgggcattg cgcatagtta cgtatcaggc aacacagttt ggcaagcctt agatgaatca 240
caagtaggtt ggcataccgc taatcaaata ggttaataat attattacgg tattgaagta 300
tgtcaatcaa tgggcgcaga taacgcgaca ttcttaaaaa atgaacaggc aactttccaa 360
gaatgcgcta gattgttgaa aaaatgggga ttaccagcaa acagaaatac aatcagattg 420
cacaatgaat ttacttcaac atcatgcct catagaagt cggttttaca cactggtttt 480
gaccagtaa ctgcggtct attgccagaa gacaagcggg tgcaacttaa agactacttt 540
atcaagcaga ttagggcgta catggatggg aaaataccgg ttgccactgt ctctaagag 600
tcaagcgctt caagtaatac agttaaacca gttgcaagtg ca 642

<210> 18

<211> 516

<212> DNA

<213> Staphylococcus aureus phage phi 11

<400> 18

```

atgcaagcaa aattaactaa aaatgagttt atagagtggg tgaaaaactt tgagggaaaa    60
caattcaatg tggacttatg gtatggattt caatgctttg attatgccaa tgctgggttg    120
aaagttttgt ttggattact tctaaaagggt ttaggtgcaa aagatattcc gttcgctaac    180
aacttcgacg gattagctac tgtataccaa aatacaccgg acttccttagc acaacctggc    240
gacatgggtg tattcggtag caactacggg gctggatatg gtcacgttgc atgggtaatt    300
gaagcaactt tagattacat cattgtatat gagcagaatt ggctaggcgg tggctggact    360
gacggaatcg aacaacccgg ctgggggttg gaaaaagtta caagacgaca acatgcttat    420
gatttcocct tgtggtttat ccgtccgaat tttaaaagtg agacagcgcc acgatcagtt    480
caatctccta cacaagcacc taaaaaagaa acagct                                516

```

<210> 19

<211> 420

<212> DNA

<213> Staphylococcus phage Twort

<400> 19

```

atgaaaaccc tgaaacaagc agagtcctac attaagagta aagtaaatac aggaactgat    60
tttgatgggt tatatgggta tcagtgtatg gacttagcag tagattatat ttaccatgta    120
acagatggta aaataagaat gtggggtaat gctaaggatg cgataaataa ctcttttggt    180
ggtagtgcta cggatatata aaactaccct gcttttagac ctaagtacgg tgatgtagtc    240
gtatggacta ctggtaattt tgcaacttat ggtcatatcg caatagttac taacctgac    300
ccttatggag accttcaata tgttacagtt cttgaacaaa actggaacgg taacgggatt    360
tataaaaccg agtttagctac aatcagaaca cagattaca caggaattac acattttatt    420

```

<210> 20

<211> 1851

<212> DNA

<213> artificial

<220>

<223> M23-2638_Ami2638_CBD2638_CBD2638

<400> 20

```

atgctaactg ctattgacta tottacgaaa aaagggtgga aaatatcatc tgaccctcgc    60
acttacgatg gttaccctaa aaactacggc tacagaaatt accatgaaaa cggcattaat    120
tatgatgagt tttgtgggtg ttatcataga gcttttgatg tttacagtaa cgaaactaac    180
gacgtgcctg ctgttactag cgggaacagtt attgaagcaa acgattacgg taattttggt    240
ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt    300
ggctcaatgc gatttggtgt aggcgacaaa gtcaatcaag gtgacattat tggtttacia    360
ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgcctc    420
aaagacgcaa agaaagatga aaaatcacaa gtatgtagtg gtttggctat ggaaaaatat    480
gacattacaa atttaaatgc taaacaagat aaatcaaaga atgggagcgt gaaagagttg    540
aaacatatct attcaaacca tattaagggt aacaagatta cagcaccaaa acctagtatt    600

```

```

caaggtgtgg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg 660
ttatatgcac gtgagaataa cggtagacac gttaacgggt gggctagtgt ttatgcaa 720
agaaacgaag tgctttggta tcatccgaca gactacgtag agtggcattg tggtaatcaa 780
tgggcaaata ctaacttaat cggatttgaa gtgtgtgagt cgtatcctgg tagaatctcg 840
gacaaattat tcttagaaaa tgaagaagcg acattgaaag tagctgcgga tgtgatgaag 900
tcgtacggat taccagttaa tcgcaacact gtacgtctgc ataacgaatt ctcgggaact 960
tcttgtccac atcgttcgtg ggacttgcac gttggcaaag gtgagcctta cacaactact 1020
aatattaata aaatgaaaga ctacttcac aaacgcacaa aacattatta tgacggtgga 1080
aagctagaag taagcaaagc agcaactatc aaacaatctg acgttaagca agaagttaaa 1140
aagcaagaag caaaacaaat tgtgaaagca acagattgga aacagaataa agatggcatt 1200
tgggtataaag ctgaacatgc ttcgttcaca gtgacagcac cagaggggaat tatcacaaga 1260
tacaagggtc cttggactgg tcaccacaaa gctggtgtat tacaaaaagg tcaaacgatt 1320
aaatatgatg aggttcacaaa atttgacggt catgtttggg tatcgtggga aacgtttgag 1380
ggcgaaactg tatacatgcc ggtacgcaca tgggacgcta aaactggtaa agttggtaag 1440
tttgtgggcg aaattaaaga gtcggtgga aagctagaag taagcaaagc agcaactatc 1500
aaacaatctg acgttaagca agaagttaaa aagcaagaag caaaacaaat tgtgaaagca 1560
acagattgga aacagaataa agatggcatt tgggtataaag ctgaacatgc ttcgttcaca 1620
gtgacagcac cagaggggaat tatcacaaga tacaagggtc cttggactgg tcaccacaaa 1680
gctggtgtat tacaaaaagg tcaaacgatt aaatatgatg aggttcacaaa atttgacggt 1740
catgtttggg tatcgtggga aacgtttgag ggcgaaactg tatacatgcc ggtacgcaca 1800

```

```

tgggacgcta aaactggtaa agttggtaag ttgtgggcg aaattaaata a 1851

```

<210> 21

<211> 498

<212> PRT

<213> artificial

<220>

<223> His-tagged Ply2638

<400> 21

```

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1           5           10           15

```

```

Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
20           25           30

```

```

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35           40           45

```

```

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50           55           60

```

```

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65           70           75           80

```

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
 85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
 100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
 115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
 130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
 145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
 165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
 180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
 195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
 210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
 225 230 235 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
 245 250 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
 260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
 275 280 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
 290 295 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
 305 310 315 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
 325 330 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
 340 345 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
 355 360 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400

Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala
 405 410 415

Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg
 420 425 430

Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
 435 440 445

Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val

450 455 460

Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
 465 470 475 480

Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
 485 490 495

Ile Lys

<210> 22

<211> 361

<212> PRT

<213> artificial

<220>

<223> His-tagged Ami2638_CBD2638

<400> 22

Met Arg Gly Ser His His His His His Gly Ser Leu Arg Pro Lys
 1 5 10 15

Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met
 20 25 30

Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys
 35 40 45

Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys
 50 55 60

Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile
 65 70 75 80

His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu
 85 90 95

Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val
 100 105 110

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

Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe
 130 135 140

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

<210> 23

<211> 344

<212> PRT

<213> artificial

<220>

<223> His-tagged M23-2638_CBD2638

<400> 23

Met Arg Gly Ser His His His His His Gly Ser Met Leu Thr Ala
 1 5 10 15

Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
 20 25 30

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
 35 40 45
 Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
 50 55 60
 Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
 65 70 75 80
 Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
 85 90 95
 Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
 100 105 110
 Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
 115 120 125
 Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
 130 135 140
 His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
 145 150 155 160
 Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
 165 170 175
 Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
 180 185 190
 Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
 195 200 205
 Lys Pro Ser Ile Gln Gly Glu Leu Gly Gly Lys Leu Glu Val Ser Lys
 210 215 220
 Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
 225 230 235 240
 Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp
 245 250 255
 Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro
 260 265 270
 Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
 275 280 285
 Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln
 290 295 300
 Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu
 305 310 315 320
 Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
 325 330 335
 Gly Lys Leu Trp Gly Glu Ile Lys
 340

<210> 24

<211> 986

<212> PRT

<213> artificial

<220>

<223> His-tagged Ply2638_Ply2638

<400> 24

```

Met Arg Gly Ser His His His His His Gly Ser Met Leu Thr Ala
1           5           10           15

Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
20           25           30

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35           40           45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50           55           60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65           70           75           80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85           90           95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100          105          110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115          120          125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130          135          140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145          150          155          160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165          170          175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180          185          190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195          200          205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210          215          220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225          230          235          240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
245          250          255

```

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
 260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
 275 280 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
 290 295 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
 305 310 315 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
 325 330 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
 340 345 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
 355 360 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400

Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala
 405 410 415

Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg
 420 425 430

Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
 435 440 445

Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val
 450 455 460

Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
 465 470 475 480

Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
 485 490 495

Ile Lys Glu Leu Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
 500 505 510

Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
 515 520 525

Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
 530 535 540

Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
 545 550 555 560

Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
 565 570 575

Gly Asn Phe Gly Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp
 580 585 590

Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
 595 600 605

Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn
 610 615 620

Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
 625 630 635 640

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
 645 650 655

Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser
 660 665 670

Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile
 675 680 685

Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val
 690 695 700

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
 705 710 715 720

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
 725 730 735

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
 740 745 750

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
 755 760 765

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
 770 775 780

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
 785 790 795 800

Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu
 805 810 815

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
 820 825 830

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
 835 840 845

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
 850 855 860

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
 865 870 875 880

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
 885 890 895

885 890 895
 Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
 900 905 910
 Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
 915 920 925
 Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu
 930 935 940
 Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
 945 950 955 960
 Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
 965 970 975
 Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
 980 985

<210> 25

<211> 672

<212> PRT

<213> artificial

<220>

<223> His-tagged CHAP11_M23-2638_Ami2638_CBD2638

<400> 25

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

Val Thr Arg Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg
 145 150 155 160

Pro Asn Phe Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr
 165 170 175

Gln Ala Pro Lys Lys Glu Thr Ala Gly Ser Met Leu Thr Ala Ile Asp
 180 185 190

Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr
 195 200 205

Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly
 210 215 220

Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe Asp Val
 225 230 235 240

Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly Thr Val
 245 250 255

Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val Ile Arg
 260 265 270

Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg Gly Ser
 275 280 285

Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile Ile Gly
 290 295 300

Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val His Leu
 305 310 315 320

His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln
 325 330 335

Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn
 340 345 350

Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His
 355 360 365

Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro
 370 375 380

Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro
 385 390 395 400

Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His
 405 410 415

Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp
 420 425 430

Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala
 435 440 445

Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg
 450 455 460

Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val
 465 470 475 480
 Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr
 485 490 495
 Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser
 500 505 510
 Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile
 515 520 525
 Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp
 530 535 540
 Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp
 545 550 555 560
 Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala
 565 570 575
 Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His
 580 585 590
 Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys
 595 600 605
 Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln
 610 615 620
 Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val
 625 630 635 640
 Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr
 645 650 655
 Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
 660 665 670
 <210> 26
 <211> 714
 <212> PRT
 <213> artificial
 <220>
 <223> His-tagged Ami11_M23-2638_Ami2638_CBD2638
 <400> 26
 Met Arg Gly Ser His His His His His His Gly Ser Lys Pro Gln Pro
 1 5 10 15
 Lys Ala Val Glu Leu Lys Ile Ile Lys Asp Val Val Lys Gly Tyr Asp
 20 25 30
 Leu Pro Lys Arg Gly Ser Asn Pro Lys Gly Ile Val Ile His Asn Asp
 35 40 45
 Ala Gly Ser Lys Gly Ala Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val

```

50          55          60

Asn Ala Pro Leu Ser Arg Leu Glu Ala Gly Ile Ala His Ser Tyr Val
65          70          75          80

Ser Gly Asn Thr Val Trp Gln Ala Leu Asp Glu Ser Gln Val Gly Trp
85          90          95

His Thr Ala Asn Gln Ile Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val
100         105         110

Cys Gln Ser Met Gly Ala Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln
115         120         125

Ala Thr Phe Gln Glu Cys Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro
130         135         140

Ala Asn Arg Asn Thr Ile Arg Leu His Asn Glu Phe Thr Ser Thr Ser
145         150         155         160

Cys Pro His Arg Ser Ser Val Leu His Thr Gly Phe Asp Pro Val Thr
165         170         175

Arg Gly Leu Leu Pro Glu Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe
180         185         190

Ile Lys Gln Ile Arg Ala Tyr Met Asp Gly Lys Ile Pro Val Ala Thr
195         200         205

Val Ser Asn Glu Ser Ser Ala Ser Ser Asn Thr Val Lys Pro Val Ala
210         215         220

Ser Ala Gly Ser Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
225         230         235         240

Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
245         250         255

Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
260         265         270

Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
275         280         285

Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
290         295         300

Gly Asn Phe Gly Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp
305         310         315         320

Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
325         330         335

Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn
340         345         350

Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
355         360         365

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
370         375         380

```

370

375

380

Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser
385 390 395 400

Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile
405 410 415

Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val
420 425 430

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
435 440 445

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
450 455 460

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
465 470 475 480

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
485 490 495

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
500 505 510

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
515 520 525

Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu
530 535 540

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
545 550 555 560

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
565 570 575

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
580 585 590

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
595 600 605

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
610 615 620

Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
625 630 635 640

Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
645 650 655

Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu
660 665 670

Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
675 680 685

Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
690 695 700

Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
705 710

<210> 27

<211> 652

<212> PRT

<213> artificial

<220>

<223> His-tagged CHAPTw_Ami2638_M23-LST_CBD2638

<400> 27

Met Arg Gly Ser His His His His His His Gly Ser Met Lys Thr Leu
1 5 10 15

Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr Asp
20 25 30

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys Asn
65 70 75 80

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
115 120 125

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

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
 225 230 235 240
 Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
 245 250 255
 Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
 260 265 270
 Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
 275 280 285
 Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
 290 295 300
 Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
 305 310 315 320
 Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
 325 330 335
 Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
 340 345 350
 Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
 355 360 365
 Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380
 Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400
 Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
 405 410 415
 Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
 420 425 430
 Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
 435 440 445
 Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
 450 455 460
 Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
 465 470 475 480
 Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
 485 490 495
 Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
 500 505 510
 Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
 515 520 525
 Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
 530 535 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545 550 555 560

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
565 570 575

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
580 585 590

Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
595 600 605

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
610 615 620

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys

625 630 635 640

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
645 650

<210> 28

<211> 650

<212> PRT

<213> artificial

<220>

<223> His-tagged CHAPTw_Ami2638_M23-LST_CWT-LST

<400> 28

Met Arg Gly Ser His His His His His His Gly Ser Met Lys Thr Leu
1 5 10 15

Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr Asp
20 25 30

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys Asn
65 70 75 80

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
115 120 125

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

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225 230 235 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
245 250 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
275 280 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
290 295 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305 310 315 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
325 330 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
340 345 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
355 360 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
370 375 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385 390 395 400

Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
405 410 415

Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
420 425 430

Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro

435

440

445

Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
450 455 460

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
465 470 475 480

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
485 490 495

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
500 505 510

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
515 520 525

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
530 535 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545 550 555 560

Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr
565 570 575

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
580 585 590

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
595 600 605

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
610 615 620

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
625 630 635 640

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
645 650

<210> 29

<211> 517

<212> PRT

<213> artificial

<220>

<223> His-tagged M23-LST_Ami2638_CBD2638

<400> 29

Met Arg Gly Ser His His His His His His Gly Ser Ala Ala Thr His
1 5 10 15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
 50 55 60
 Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
 65 70 75 80
 Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
 85 90 95
 Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
 100 105 110
 Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
 115 120 125
 Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
 130 135 140
 Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
 145 150 155 160
 Pro Thr Pro Asn Thr Gly Glu Leu Leu Arg Pro Lys Asp Ala Lys Lys
 165 170 175
 Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp
 180 185 190
 Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val
 195 200 205
 Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile
 210 215 220
 Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr
 225 230 235 240
 Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu
 245 250 255
 Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg
 260 265 270
 Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys
 275 280 285
 Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu
 290 295 300
 Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu
 305 310 315 320
 Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro
 325 330 335
 Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser
 340 345 350
 Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr
 355 360 365

Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile
370 375 380

Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr
385 390 395 400

Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys
405 410 415

Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp
420 425 430

Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile
435 440 445

Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val
450 455 460

Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp
465 470 475 480

Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr
485 490 495

Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu
500 505 510

Trp Gly Glu Ile Lys
515

<210> 30

<211> 506

<212> PRT

<213> artificial

<220>

<223> His-tagged LST_LST

<400> 30

Met Arg Gly Ser His His His His His His Gly Ser Ala Ala Thr His
1 5 10 15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
65 70 75 80

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

385 390 395 400

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
405 410 415

Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr
420 425 430

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
435 440 445

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
450 455 460

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
465 470 475 480

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
485 490 495

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
500 505

<210> 31

<211> 414

<212> PRT

<213> artificial

<220>

<223> His-tagged M23-LST_M23-LST_CWT-LST

<400> 31

Met Arg Gly Ser His His His His His His Gly Ser Ala Ala Thr His
1 5 10 15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
65 70 75 80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
85 90 95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
100 105 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
115 120 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met

130 135 140
 Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
 145 150 155 160
 Pro Thr Pro Asn Thr Gly Glu Leu Ala Ala Thr His Glu His Ser Ala
 165 170 175
 Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro
 180 185 190
 Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn
 195 200 205
 Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala
 210 215 220
 Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn
 225 230 235 240
 Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val
 245 250 255
 Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly
 260 265 270
 Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val
 275 280 285
 Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys
 290 295 300
 Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn
 305 310 315 320
 Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser
 325 330 335
 Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro
 340 345 350
 Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile
 355 360 365
 His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr
 370 375 380
 Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn
 385 390 395 400
 Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
 405 410

<210> 32

<211> 628

<212> PRT

<213> artificial

<220>

<223> His-tagged M23-2638_Ami2638_CBD2638_CBD2638

<400> 32

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1 5 10 15

Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
20 25 30

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu

180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225 230 235 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
245 250 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
 275 280 285
 Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
 290 295 300
 Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
 305 310 315 320
 Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
 325 330 335
 Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
 340 345 350
 Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
 355 360 365
 Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380
 Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400
 Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala
 405 410 415
 Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg
 420 425 430
 Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
 435 440 445
 Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val
 450 455 460
 Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
 465 470 475 480
 Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
 485 490 495
 Ile Lys Glu Leu Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile
 500 505 510
 Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln
 515 520 525
 Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr
 530 535 540
 Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile
 545 550 555 560
 Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu
 565 570 575

Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly
580 585 590

His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met
595 600 605

Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
610 615 620

Gly Glu Ile Lys
625

<210> 33

<211> 741

<212> DNA

<213> Staphylococcus simulans

<400> 33

```

gctgcaaac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac      60
ggtccttata cattaggtat aaatggcggg atgcactacg gagttgattt ttttatgaat      120
attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat      180
tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatgggat      240
atgcatctaa gtaaatataa tgtaaagta ggagattatg tcaaagctgg tcaaataatc      300
ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt      360
aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat      420
ggaaaagcag gtggtacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat      480
ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga      540
acgactgggc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt      600
cattatgatg aagtgatgaa acaagacggg catgtttggg taggttatac aggtaacagt      660
ggccaacgta ttacttgcc tgtaagaaca tggataaat ctactaatac tttaggtgtt      720
ctttggggaa ctataaagtg a                                     741

```

<210> 34

<211> 246

<212> PRT

<213> Staphylococcus simulans

<400> 34

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
1 5 10 15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
35 40 45

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
130 135 140

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr
145 150 155 160

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
165 170 175

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
180 185 190

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
195 200 205

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
210 215 220

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
225 230 235 240

Leu Trp Gly Thr Ile Lys
245

<210> 35

<211> 94

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 35

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
1 5 10 15

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
20 25 30

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
35 40 45

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
50 55 60

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
65 70 75 80

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
85 90

<210> 36

<211> 92

<212> PRT

<213> Staphylococcus simulans

<400> 36

Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser
1 5 10 15

Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg
20 25 30

Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr
35 40 45

Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly
50 55 60

Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser
65 70 75 80

Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
85 90

<210> 37

<211> 146

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 37

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

Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg
20 25 30

Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr
35 40 45

His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala
50 55 60

Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly
65 70 75 80

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
85 90 95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
100 105 110

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
115 120 125

Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
 130 135 140

Lys Asp
 145

<210> 38

<211> 140

<212> PRT

<213> Staphylococcus simulans

<400> 38

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
 1 5 10 15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
 20 25 30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
 35 40 45

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
 50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
 65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
 85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
 100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
 115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
 130 135 140

<210> 39

<211> 169

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 39

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
 1 5 10 15

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
 20 25 30

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
 35 40 45

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
 50 55 60

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
65 70 75 80

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
85 90 95

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
100 105 110

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
115 120 125

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
130 135 140

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
145 150 155 160

Lys Arg Ile Lys His Tyr Tyr Asp Gly
165

<210> 40

<211> 163

<212> PRT

<213> Staphylococcus aureus phage phi 11

<400> 40

Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
1 5 10 15

Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg
20 25 30

Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp
35 40 45

Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile
50 55 60

Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
65 70 75 80

Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
85 90 95

Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
100 105 110

Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
115 120 125

Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
130 135 140

Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
145 150 155 160

Tyr Met Asp

<210> 41

<211> 158

<212> PRT

<213> Staphylococcus aureus phage phi 11

<400> 41

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro
145 150 155

<210> 42

<211> 140

<212> PRT

<213> Staphylococcus phage Twort

<400> 42

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn
1 5 10 15

Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
20 25 30

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
35 40 45

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
50 55 60

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val

65	70								75								80			
Val	Trp	Thr	Thr	Gly	Asn	Phe	Ala	Thr	Tyr	Gly	His	Ile	Ala	Ile	Val					
				85					90					95						
Thr	Asn	Pro	Asp	Pro	Tyr	Gly	Asp	Leu	Gln	Tyr	Val	Thr	Val	Leu	Glu					
			100					105					110							
Gln	Asn	Trp	Asn	Gly	Asn	Gly	Ile	Tyr	Lys	Thr	Glu	Leu	Ala	Thr	Ile					
		115					120					125								
Arg	Thr	His	Asp	Tyr	Thr	Gly	Ile	Thr	His	Phe	Ile									
130						135					140									

<210> 43
<211> 12
<212> PRT
<213> artificial

<220>
<223> His-tag

```
<400> 43
Met Arg Gly Ser His His His His His His Gly Ser
1             5             10
```

<210> 44
<211> 1497
<212> DNA
<213> artificial

<220>
<223> His-tagged Ply2638

<400> 44	
atgagaggat cgcacacacca tcaccatcac ggatccatgc taactgctat tgactatcct	60
acgaaaaaag gttggaaaat atcatctgac cctcgcaactt acgatgggta ccctaaaaac	120
tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tggtgggtat	180
catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga	240
acagttattg aagcaaacga ttacggtaat tttggtggtta cattcggtat tagagacgct	300
aacgataacg attggatata tgggcaccta caacgtggct caatgcgatt tgttgtaggc	360
gacaaagtca atcaaggtga cattattgggt ttacaaggta atagcaacta ttacgacaat	420
cctatgagtg tacatttaca tttaacaatta cgccctaaag acgcaaagaa agatgaaaaa	480
tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa	540
caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt	600
aaaggtaca agattacagc accaaaacct agtattcaag gtgtgggtcat ccacaatgat	660
tatggtagta tgacacctag tcaatactta ccatgggttat atgcacgtga gaataacggt	720
acacacgtta acggttgggc tagtggttat gcaaatagaa acgaagtgct ttggtatcat	780
ccgacagact acgtagagtg gcatttgtgt aatcaatggg caaatgctaa cttaatcgga	840

```

tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900
gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960
aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac 1020
ttgcatgttg gcaaaggtga gccttacaca actactaata ttaataaaat gaaagactac 1080
ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140
actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200
aaagcaacag attggaaaca gaataaagat ggcatttggt ataaagctga acatgcttcg 1260
ttcacagtga cagcaccaga ggaattatc acaagataca aaggtccttg gactggtcac 1320

ccacaagctg gtgtattaca aaaaggtcaa acgattaaat atgatgaggt tcaaaaattt 1380
gacggtcatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgcggta 1440
cgcacatggg acgctaaaac tggtaaagtt ggtaagttgt ggggcgaaat taaataa 1497

```

<210> 45

<211> 2019

<212> DNA

<213> artificial

<220>

<223> His-tagged CHAP11-M23-2638_Ami2638_CBD2638

<400> 45

```

atgagaggat cgcataacca tcaccatcac ggatccatgc aagcaaaatt aactaaaaat 60
gagtttatag agtggttgaa aacttctgag ggaaaacaat tcaatgtgga cttatgggat 120
ggatttcaat gctttgatta tgccaatgct ggttggaag ttttgttgg attacttcta 180
aaaggtttag gtgcaaaaga tattccgttc gctaacaact tcgacggatt agctactgta 240
taccaaaata caccggactt cttagcaca cctggcgaca tggtggtatt cggtagcaac 300
tacggtgctg gatatggtca cgttgcatgg gtaattgaag caactttaga ttacatcatt 360
gtatatgagc agaattggct aggcggtggc tggactgacg gaatogaaca acccggtg 420
ggttgggaaa aagttacaag acgacaacat gcttatgatt tccctatgtg gtttatccgt 480
ccgaatttta aaagtgagac agcgccacga tcagttcaat ctctacaca agcacctaaa 540
aaagaaacag ctggatccat gctaactgct attgactatc ttacgaaaaa aggttgga 600
atatcatctg accctgcac ttacgatggt taccctaaa actacggcta cagaaattac 660
catgaaaacg gcattaatta tgatgagttt tgtggtggt atcatagagc ttttgatggt 720
tacagtaacg aaactaacga cgtgcctgct gttactagcg gaacagttat tgaagcaaac 780
gattacggta attttgggtg tacattcgtt attagagacg ctaacgataa cgattggata 840
tatgggcctc tacaacgtgg ctcaatgcga tttgtttag gcgacaaagt caatcaaggt 900
gacattattg gtttacaagg taatagcaac tattacgaca atcctatgag tgtacattta 960
catttacaat tacgccttaa agacgcaaag aaagatgaaa aatcacaagt atgtagtgg 1020
ttggctatgg aaaaatatga cattacaaat ttaaagcta aacaagataa atcaaagaat 1080
gggagcgtga aagagttgaa acatatctat tcaaaccata ttaaaggtaa caagattaca 1140
gcacccaaac ctagtattca aggtgtggtc atccacaatg attatgtag tatgacacct 1200

```

agtcaatact taccatggtt atatgcacgt gagaataacg gtacacacgt taacggttgg 1260
 gctagtgttt atgcaaatag aaacgaagtg ctttggatc atccgacaga ctacgtagag 1320
 tggcattgtg gtaatcaatg ggcaaatgct aacttaatcg gatttgaagt gtgtgagtcg 1380
 tatcctggta gaatctcgga caaattattc ttagaaaatg aagaagcgac attgaaagta 1440

gctgcggatg tgatgaagtc gtacggatta ccagttaatc gcaacactgt acgtctgcat 1500
 aacgaattct tcggaacttc ttgtccacat cgttcgtggg acttgcatgt tggcaaaggt 1560
 gagccttaca caactactaa tattaataaa atgaaagact acttcatcaa acgcatcaaa 1620
 cattattatg acggtggaaa gctagaagta agcaaagcag caactatcaa acaatctgac 1680
 gttaagcaag aagttaaaaa gcaagaagca aaacaaattg tgaaagcaac agattggaaa 1740
 cagaataaag atggcatttg gtataaagct gaacatgctt cgttcacagt gacagcacca 1800
 gagggaaatta tcacaagata caaaggtcct tggactggtc acccacaagc tgggtgatta 1860
 caaaaaggtc aaacgattaa atatgatgag gttcaaaaat ttgacgggtca tgtttgggta 1920
 tcgtgggaaa cgtttgaggg cgaaactgta tacatgccgg tacgcacatg ggacgctaaa 1980
 actggtaaag ttggtaagtt gtggggcgaa attaaataa 2019

<210> 46

<211> 2145

<212> DNA

<213> artificial

<220>

<223> His-tagged Ami11_M23-2638_Ami2638_CBD2638

<400> 46

atgagaggat cgcacaccca tcaccatcac ggatccaagc cacaacctaa agcagtagaa 60
 cttaaaaatca tcaaatatgt gggttaaaggt tatgacctac ctaagcgtgg tagtaacctt 120
 aaaggtatag ttatacacia cgacgcaggg agcaaagggg cgactgctga agcatatcgt 180
 aacggattag taaatgcacc tttatcaaga ttagaagcgg gcattgcgca tagttacgta 240
 tcaggcaaca cagtttggca agccttagat gaatcacaag taggttggca taccgctaatt 300
 caaataggta ataatatta ttacggtatt gaagtatgtc aatcaatggg cgcagataac 360
 gcgacattct taaaaaatga acaggcaact ttccaagaat gcgctagatt gttgaaaaaa 420
 tggggattac cagcaaacag aaatacaatc agattgcaca atgaatttac ttcaacatca 480
 tgccctcata gaagttcggg ttacacact ggttttgacc cagtaactcg cggctctattg 540
 ccagaagaca agcggttgca acttaagac tactttatca agcagattag ggcgtacatg 600
 gatggtaaaa taccggttgc cactgtctct aatgagtcaa gcgcttcaag taatacagtt 660
 aaaccagttg caagtgcagg atccatgcta actgctattg actatcttac gaaaaaaggt 720
 tggaaaatat catctgacct tcgcacttac gatggttacc ctaaaaacta cggctacaga 780
 aattaccatg aaaacggcat taattatgat gagttttgtg gtggttatca tagagctttt 840
 gatgtttaca gtaacgaaac taacgacgtg cctgctgtta ctacgggaac agttattgaa 900
 gcaaacgatt acggtaatth ttggtgtaca ttcgttatta gagacgctaa cgataacgat 960

```

tggatatatg ggcattctaca acgtggctca atgcgatttg ttgtaggcga caaagtcaat 1020
caaggtgaca ttattggttt acaaggtaat agcaactatt acgacaatcc tatgagtgtg 1080
catttacatt tacaattacg cccataagac gcaaagaaaag atgaaaaatc acaagtatgt 1140
agtggtttgg ctatggaaaa atatgacatt acaaatttaa atgctaaaca agataaatca 1200
aagaatggga gcgtagaaga gttgaaacat atctattcaa accatattaa aggtacaag 1260
attacagcac caaacctag tattcaaggt gtggcatcc acaatgatta tggtagtatg 1320
acacctagtc aatacttacc atggttatat gcacgtgaga ataacggtac acacgttaac 1380
ggttgggcta gtgtttatgc aaatagaaac gaagtgcctt ggtatcatcc gacagactac 1440
gtagagtggc attgtggtaa tcaatgggca aatgctaact taatcggatt tgaagtgtgt 1500
gagtcgtatc ctggtagaat ctccgacaaa ttattcttag aaaatgaaga agcgacattg 1560
aaagtagctg cggatgtgat gaagtcgtac ggattaccag ttaatcgaa cactgtacgt 1620
ctgcataacg aattcttcgg aacttcttgt ccacatcgtt cgtgggactt gcatgttggc 1680
aaaggtgagc cttacacaac tactaatatt aataaaatga aagactactt catcaaacgc 1740
atcaaacatt attatgacgg tggaaagcta gaagtaagca aagcagcaac tatcaaaaaa 1800
tctgacgtta agcaagaagt taaaaagcaa gaagcaaaac aaattgtgaa agcaacagat 1860
tggaaacaga ataaagatgg catttggtat aaagctgaac atgcttcgtt cacagtgaca 1920
gcaccagagg gaattatcac aagatacaaa ggtccttggg ctggtcaccc acaagctggg 1980
gtattacaaa aaggtcaaac gattaaatat gatgagggtc aaaaatttga cggtcattgtt 2040
tgggtatcgt gggaaaacgtt tgagggcgaa actgtataca tgccggtagc cacatgggac 2100
gctaaaactg gtaaagtggg taagttgtgg ggcgaaatta aataa 2145

```

<210> 47

<211> 1959

<212> DNA

<213> artificial

<220>

<223> His-tagged CHAPTw_Ami2638_M23-LST_CBD2638

<400> 47

```

atgagaggat cgcattacca tcaccatcac ggatccatga aaacctgaa acaagcagag 60
tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 120
tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 180
ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaaa 240
taccctgctt ttagacctaa gtacggtgat gtatcgtat ggactactgg taattttgca 300
acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 360
acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 420

agaacacacg attacacagg aattacacat tttattaaag acgcaaagaa agatgaaaaa 480
tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540
caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaacatatt 600
aaaggtaca agattacagc accaaaacct agtattcaag gtgtggcat ccacaatgat 660

```

tatggtagta tgacacctag tcaatactta ccatggttat atgcacgtga gaataacggt	720
acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgtt ttggtatcat	780
ccgacagact acgtagagtgt gcattgtggt aatcaatggg caaatgctaa cttaatcgga	840
tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa	900
gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc	960
aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac	1020
ttgcatgttg gcaaagggtga gccttacaca actactaata ttaataaaat gaaagactac	1080
ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca	1140
actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg	1200
aaagcaacag atgctgcaac acatgaacat tcagcacaat ggttgaataa ttacaaaaaa	1260
ggatatggtt acggtcctta tccattaggt ataaatggcg gtatgacta cggagttgat	1320
ttttttatga atattggaac accagtaaaa gctatttcaa gcggaaaaat agttgaagct	1380
ggttggagta attacggagg aggtaatcaa ataggtctta ttgaaaatga tggagtgcac	1440
agacaatggt atatgcatct aagtaaatat aatgttaaag taggagatta tgtcaaagct	1500
ggtcaaataa tcggttggtc tggaagcact gggtattcta cagcaccaca ttacacttc	1560
caaagaatgg ttaattcatt ttcaaattca actgcccaag atccaatgcc tttcttaaag	1620
agcgcaggat atggaaaagc aggtggtaca gtaactcaa cgcgcaatac aggttggaaa	1680
cagaataaag atggcatttg gtataaagct gaacatgctt cgttcacagt gacagcacca	1740
gagggaatta tcacaagata caaaggctct tggactggtc acccacaagc tgggtgtatta	1800
caaaaaggct aaacgattaa atatgatgag gttcaaaaat ttgacgggtca tgtttgggta	1860
tcgtgggaaa cgtttgaggg cgaaactgta tacatgccgg tacgcacatg ggacgctaaa	1920
actggtaaag ttggttaagtt gtggggcgaa attaaataa	1959

<210> 48

<211> 1554

<212> DNA

<213> artificial

<220>

<223> His-tagged M23-LST_Ami2638_CBD2638

<400> 48

atgagaggat cgcacacca tcaccatcac ggatccgctg caacacatga acattoagca	60
caatgggtga ataattacaa aaaaggatat ggttacggtc cttatocatt aggtataaat	120
ggcggtatgc actacggagt tgattttttt atgaatattg gaacaccagt aaaagctatt	180
tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt	240
cttattgaaa atgatggagt gcatagacaa tggatatatg atctaagtaa atataatggt	300
aaagtaggag attatgtcaa agctggtcaa ataatcgggt ggtctggaag cactggttat	360
tctacagcac cacatttaca cttccaaaga atgggttaatt cattttcaaa ttcaactgcc	420
caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcagggtg tacagtaact	480
ccaacgccga atacagggtga gctcttacgc cctaaagacg caaagaaaga tgaaaaatca	540
caagtatgta gtggtttggc tatggaaaaa tatgacatta caaatttaaa tgctaataca	600

gataaatcaa agaatgggag cgtgaaagag ttgaaacata tctattcaaa ccatattaaa 660
 ggtaacaaga ttacagcacc aaaacctagt attcaagggtg tggatcatcca caatgattat 720
 ggtagtatga cacctagtca ataottacca tggttatatg cacgtgagaa taacgggtaca 780
 cacgttaacg gttgggctag tgtttatgca aatagaaacg aagtgccttg gtatcatccg 840
 acagactacg tagagtggca ttgtggtaat caatgggcaa atgctaactt aatcggattt 900
 gaagtgtgtg agtcgtatcc tggtagaata tcggacaaat tattcttaga aaatgaagaa 960
 gcgacattga aagtagctgc ggatgtgatg aagtcgtacg gattaccagt taatcgcaac 1020
 actgtacgtc tgcataacga attcttcgga acttcttctc caccatcgttc gtgggacttg 1080
 catgttggca aaggtgagcc ttacacaact actaatatta ataaaatgaa agactacttc 1140
 atcaaacgca tcaaacatta ttatgacggt ggaaagctag aagtaagcaa agcagcaact 1200
 atcaaacaat ctgacgttaa gcaagaagtt aaaaagcaag aagcaaaaca aattgtgaaa 1260
 gcaacagatt ggaaacagaa taaagatggc atttgggtata aagctgaaca tgcttctgtc 1320
 acagtgcacg caaccagagg aattatcaca agatacaaag gtccttggac tggtcaccca 1380
 caagctgggtg tattacaaaa aggtcaaacg attaaatatg atgaggttca aaaatttgac 1440
 ggtcatgttt ggttatcgtg ggaaacgttt gagggcgaaa ctgtatacat gccggtacgc 1500
 acatgggacg ctaaaactgg taaagttggt aagttgtggg gcgaaattaa ataa 1554

<210> 49

<211> 1887

<212> DNA

<213> artificial

<220>

<223> His-tagged M23-2638_Ami2638_CBD2638_CBD2638

<400> 49

atgagaggat cgcataacca tcaccatcac ggatccatgc taactgctat tgactatctt 60

acgaaaaaag gttggaaaat atcatctgac cctcgcactt acgatgggta ccctaaaaac 120
 tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tggtggttat 180
 catagagctt ttgatgttta cagtaacgaa actaacgacg tgcttctgt tactagcgga 240
 acagttattg aagcaaacga ttacggtaat tttgggtgta cattcgttat tagagacgct 300
 aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgtttaggc 360
 gacaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat 420
 cctatgagtg tacatttaca tttaacaatta cgccctaaag acgcaaagaa agatgaaaaa 480
 tcacaagtat gtagtgtttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540
 caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600
 aaaggttaaca agattacagc accaaaacct agtattcaag gtgtgggtcat ccacaatgat 660
 tatggtagta tgacacctag tcaatactta ccatgggttat atgcacgtga gaataacggt 720
 acacacgtta acggttgggc tagtggttat gcaaatagaa acgaagtgtt ttggtatcat 780
 ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcggg 840
 tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900

```

gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc      960
aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac      1020
ttgcatgttg gcaaagggtg gccttacaca actactaata ttaataaaat gaaagactac      1080
ttcatcaaac gcatcaaacg ttattatgac ggtggaaaagc tagaagtaag caaagcagca      1140
actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg      1200
aaagcaacag attggaaaca gaataaagat ggcatttggg ataaagctga acatgcttcg      1260
ttcacagtga cagcaccaga gggaattatc acaagataca aaggtccttg gactggtcac      1320
ccacaagctg gtgtattaca aaaagggtcaa acgattaaat atgatgaggt tcaaaaattt      1380
gacggctcatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgccggta      1440
cgcacatggg acgctaaaac tggtaaaagt ggtaagttgt ggggcgaaat taaagagctc      1500
ggtggaaagc tagaagtaag caaagcagca actatcaaac aatctgacgt taagcaagaa      1560
gttaaaaagc aagaagcaaa acaaattgtg aaagcaacag attggaaaca gaataaagat      1620
ggcatttggg ataaagctga acatgcttcg ttcacagtga cagcaccaga gggaattatc      1680
acaagataca aaggtccttg gactggtcac ccacaagctg gtgtattaca aaaagggtcaa      1740
acgattaaat atgatgaggt tcaaaaattt gacggctcatg tttgggtatc gtgggaaacg      1800
tttgagggcg aaactgtata catgccggta cgcacatggg acgctaaaac tggtaaaagt      1860
gqtaagttgt ggggcgaaat taaataa                                     1887

```

<210> 50

<211> 3461

<212> DNA

<213> artificial

<220>

<223> pQE-30 vector

<400> 50

```

ctcgagaaat cataaaaaat ttatttgctt tgtgagcggg taacaattat aatagattca      60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga      120
ggatcgcatc accatcacca tcacggatcc gcatgcgagc tcggtaaccc gggtcgacct      180
gcagccaagc ttaattagct gagcttgac tcctgttgat agatccagta atgacctcag      240
aactccatct ggatttgctc agaacgctcg gttgccgccg ggcgtttttt attggtgaga      300
atccaagcta gcttggcgag attttcagga gctaaggaag ctaaaatgga gaaaaaaatc      360
actggatata ccacggttga tatacccaa tggcatcgta aagaacattt tgaggcattt      420
cagtcagttg ctcaatgtac ctataaccag accgttcagc tggatattac ggccttttta      480
aagaccgtaa agaaaaataa gcacaagttt tatccggcct ttattcacat tcttgcccgc      540
ctgatgaatg ctcatccgga atttcgtatg gcaatgaaag acggtgagct ggtgatatgg      600
gatagtgttc acccttggtt caccgttttc catgagcaaa ctgaaacggt ttcacgcctc      660
tgagtgtaat accacgacga tttccggcag tttctacaca tatattcgca agatgtggcg      720
tgttacggtg aaaacctggc ctatttcctt aaagggttta ttgagaatat gtttttcgtc      780
tcagccaatc cctgggtgag tttcaccagt tttgatttaa acgtggccaa tatggacaac      840

```

ttcttcgccc ccgttttcac catgggcaaa tattatacgc aaggcgacaa ggtgctgatg	900
ccgctggcga ttcaggttca tcatgccgtt tgtgatggct tccatgtcgg cagaatgctt	960
aatgaattac aacagtactg cgatgagtgg cagggcgggg cgtaattttt ttaaggcagt	1020
tattggtgcc cttaaacgcc tggggtaatg actctctagc ttgaggcatc aaataaaacg	1080
aaaggctcag tcgaaagact gggcctttcg ttttatctgt tgtttgtcgg tgaacgctct	1140
cctgagtagg acaaatccgc cctctagagc tgcctcgcgc gtttcgggtga tgacggtgaa	1200
aacctctgac acatgcagct cccggagacg gtcacagctt gtctgtaagc ggatgccggg	1260
agcagacaag cccgtcaggg cgcgtcagcg ggtgttggcg ggtgtcgggg cgcagccatg	1320
accagtcac gtagcgatag cggagtgtat actggcttaa ctatgcggca tcagagcaga	1380
ttgtactgag agtgcaccat atgcggtgtg aaataccgca cagatgcgta aggagaaaat	1440
accgcacag ggcgtcttcc gcttcctcgc tcaactgactc gctgcgctcg gtcgttcggc	1500
tgcggcgagc ggtatcagct cactcaaagg cggtaatacg gttatccaca gaatcagggg	1560
ataacgcagg aaagaacatg tgagcaaaag gccagcaaaa ggccagggaac cgtaaaaagg	1620
ccgcgttget ggcgtttttc cataggctcc gccccctga cgagcatcac aaaaatcgac	1680
gctcaagtca gaggtggcga aacccgacag gactataaag ataccaggcg tttccccctg	1740
gaagctccct cgtgcgtctc cctgttccga ccctgccgtt taccggatac ctgtccgcct	1800
ttctcccttc gggaagcgtg gcgctttctc atagctcacg ctgtagggtat ctgagttcgg	1860
tgtaggctgt tcgctccaag ctgggctgtg tgcacgaacc cccggttcag cccgaccgct	1920
gcgccttacc cggtaactat cgtcttgagt ccaaccgggt aagacacgac ttatcgccac	1980
tggcagcagc cactggtaac aggattagca gagcgaggta tgtaggcggg gctacagagt	2040
tcttgaagtg gtggcctaac tacggctaca ctagaaggac agtatttggg atctgcgctc	2100
tgctgaagcc agttaccttc ggaaaaagag ttggtagctc ttgatccggc aaacaaacca	2160
ccgctggtag cggtggtttt tttgtttgca agcagcagat tacgcgcaga aaaaaaggat	2220
ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc tcagtggaaac gaaaactcac	2280
gttaagggat tttggtcatg agattatcaa aaaggatctt cacttagatc cttttaaatt	2340
aaaaatgaag ttttaaatca atctaaagta tatatgagta aacttgggtc gacagttacc	2400
aatgcttaat cagtgaggca cctatctcag cgatctgtct atttcgttca tccatagttg	2460
cctgactccc cgtcgtgtag ataactacga tacggggagg cttaccatct ggccccagtg	2520
ctgcaatgat accgcgagac ccacgctcac cggtccaga tttatcagca ataaaccagc	2580
cagccggaag ggcgagcgc agaagtggc ctgcaacttt atccgcctcc atccagtcta	2640
ttaattgttg ccgggaagct agagtaagta gttcgccagt taatagtttg cgcaacgttg	2700
ttgccattgc tacaggcatc gtggtgtcac gctcgtcgtt tggatatggc tcattcagct	2760
ccggttccca acgatcaagg cgagttacat gatcccccat gttgtgcaaa aaagcggtta	2820
gtcccttcgg tcctccgacg gttgtcagaa gtaagttggc cgcagtgtta tcaactcatg	2880
ttatggcagc actgataat tctottactg tcatgccatc cgtaagatgc ttttctgtga	2940
ctggtgagta ctcaaccaag tcattctgag aatagtgtat gcggcgaccg agttgctctt	3000
gccccgcgtc aatacgggat aataccgcgc cacatagcag aactttaaaa gtgctcatca	3060
ttggaaaaacg ttcttcgggg cgaaaactct caaggatctt accgctgttg agatccagtt	3120
cgatgtaacc cactcgtgca cccaactgat cttcagcatc ttttactttc accagcgttt	3180

```

ctgggtgagc aaaaacagga aggcaaaatg ccgcaaaaaa ggaataagc ggcacacgga 3240
aatgttgaat actcatactc ttcttttttc aatattattg aagcatttat cagggttatt 3300
gtctcatgag cggatacata tttgaatgta tttagaaaaa taaacaaata ggggttccgc 3360
gcacatttcc ccgaaaagtg ccacctgacg tctaagaaac cattattatc atgacattaa 3420
cctataaaaa taggcgtatc acgaggccct ttctgtttca c 3461

```

<210> 51

<211> 127

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 51

```

Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val
1           5           10          15

```

```

Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr
20          25          30

```

```

Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala
35          40          45

```

```

Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly
50          55          60

```

```

Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr
65          70          75          80

```

```

Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser
85          90          95

```

```

Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp
100         105         110

```

```

Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
115         120         125

```

<210> 52

<211> 106

<212> PRT

<213> Staphylococcus simulans

<400> 52

```

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
1           5           10          15

```

```

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

```

```

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
35          40          45

```

```

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
50          55          60

```

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
65 70 75 80

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
85 90 95

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
100 105

<210> 53

<211> 190

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 53

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

Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg
20 25 30

Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr
35 40 45

His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala
50 55 60

Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly
65 70 75 80

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
85 90 95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
100 105 110

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
115 120 125

Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
130 135 140

Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr
145 150 155 160

Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser
165 170 175

Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
180 185 190

<210> 54

<211> 154

<212> PRT

<213> Staphylococcus simulans

<400> 54

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
1 5 10 15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
35 40 45

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
130 135 140

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly
145 150

<210> 55

<211> 246

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 55

Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile
1 5 10 15

Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys

20

25

30

Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr
35 40 45

Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly
50 55 60

Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn
65 70 75 80

Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn
85 90 95

Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly

```

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

```

<210> 56

<211> 220

<212> PRT

<213> Staphylococcus aureus phage phi 11

<400> 56

```

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

```

```

110              120              125
Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
130              135              140

Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
145              150              155              160

Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
165              170              175

Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
180              185              190

Tyr Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser
195              200              205

Ala Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala
210              215              220

```

<210> 57

<211> 206

<212> PRT

<213> Staphylococcus aureus phage phi 11

<400> 57

```

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1      5      10      15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20     25     30

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35     40     45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50     55     60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65     70     75     80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85     90     95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100    105    110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115    120    125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130    135    140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145    150    155    160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
165    170    175

```

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly
195 200 205

<210> 58

<211> 187

<212> PRT

<213> Staphylococcus phage Twort

<400> 58

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn

1 5 10 15

Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
20 25 30

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
35 40 45

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
50 55 60

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
65 70 75 80

Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
85 90 95

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
100 105 110

Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile
115 120 125

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe
130 135 140

Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys
145 150 155 160

Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg
165 170 175

Thr Asn Ile Asn Tyr Asn Met Val Lys Arg Gly
180 185

<210> 59

<211> 4546

<212> DNA

<213> artificial

<220>

<223> pHGFP_CBD2638_c vector

<400> 59

```

ctcgcgaaaat cataaaaaat ttatttgctt tgtgagcggg taacaattat aatagattca      60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga      120
ggatcgcatc accatcacca tcacggatcc atgagtaaag gagaagaact ttctactgga      180
gttgtcccaa ttottgttga attagatggt gatgttaatg ggcacaaatt ttctgtcagt      240

ggagaggggtg aaggtgatgc aacatacggg aaacttacct ttaaatttat ttgcactact      300
ggaaaactac ctgttccatg gccaacactt gtcactactt tcgcgtatgg tcttcaatgc      360
tttgcgagat acccagatca tatgaaacgg catgactttt tcaagagtgc catgcccgaa      420
ggttatgtac aggaagaagc tatatttttc aaagatgacg ggaactacaa gacacgtgct      480
gaagtcaagt ttgaaggtga taccottgtt aatagaatcg agttaaaagg tattgatttt      540
aaagaagatg gaacattctt tggacacaaa ttggaataca actataactc acacaatgta      600
tacatcatgg cagacaaaac aaagaatgga atcaaagtta acttcaaat tagacacaaac      660
attgaagatg gaagcgttca actagcagac cattatcaac aaaatactcc aattggcgat      720
ggcctgtcc ttttaccaga caaccattac ctgtccacac aatctgccct ttcgaaagat      780
cccaacgaaa agagagacca catggctcct cttgagtttg taacagctgc tgggattaca      840
catggcatgg atgaactata caaagagctc ggtggaaagc tagaagtaag caaagcagca      900
actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg      960
aaagcaacag attggaaaca gaataaagat ggcatttggg ataaagctga acatgcttcg     1020
ttcacagtga cagcaccaga gggaattatc acaagataca aaggtccttg gactggtcac     1080
ccacaagctg gtgtattaca aaaaggtcaa acgattaaat atgatgaggt tcaaaaattt     1140
gacggctcatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgccggta     1200
cgcacatggg acgctaaaac tggtaaagtt ggtaagttgt ggggcgaaat taaataagtc     1260
gacctgcagc caagcttaat tagctgagct tggactcctg ttgatagatc cagtaatgac     1320
ctcagaactc catctggatt tgttcagaac gctcgggttc cgcggggcgt tttttattgg     1380
tgagaatcca agctagcttg gcgagatttt caggagctaa ggaagctaaa atggagaaaa     1440
aaatcactgg atataccacc gttgatatat cccaatggca tcgtaaagaa cattttgagg     1500
catttcagtc agttgctcaa tgtacctata accagaccgt tcagctggat attacggcct     1560
ttttaagac cgtaaagaaa aataagcaca agttttatcc ggcctttatt cacattcttg     1620
cccgctgat gaatgctcat ccggaatttc gtatggcaat gaaagacggg gagctgggta     1680
tatgggatag tgttcacctt gtttacaccg ttttccatga gcaaaactgaa acgttttcat     1740
cgctctggag tgaataccac gacgatttcc ggcagtttct acacatatat tcgcaagatg     1800
tggcgtgta cggtgaaaac ctggcctatt tccctaaagg gtttattgag aatatgtttt     1860
tcgtctcagc caatccctgg gtgagtttca ccagttttga tttaaactg gccaatatgg     1920
acaacttctt cgcctccgtt ttcacatgg gcaaatatta tacgcaaggc gacaagggtgc     1980
tgatgccgct ggcgattcag gttcatcatg ccgtttgtga tggcttccat gtcggcagaa     2040
tgcttaatga attacaacag tactgcatg agtggcaggg cggggcgtaa tttttttaag     2100

gcagttattg gtgccttaa acgcctgggg taatgactct ctagcttgag gcataaata     2160

```

aaacgaaagg ctacgtcgaa agactgggcc ttctgtttta tctgttgttt gtcggtgaac 2220
 gctctcctga gtaggacaaa tccgccctct agagctgcct cgcgcgtttc ggtgatgacg 2280
 gtgaaaaact ctgacacatg cagctcccg agacggtcac agottgtctg taagcggatg 2340
 cggggagcag acaagcccgt cagggcgct cagcgggtgt tggcgggtgt cggggcgag 2400
 ccatgaccca gtcacgtagc gatagcggag tgtatactgg cttaactatg cggcatcaga 2460
 gcagattgta ctgagagtgc accatatgcg gtgtgaaata ccgcacagat gcgtaaggag 2520
 aaaataccgc atcaggcgcct ctccgccttc ctgcctcact gactcgtctg gctcggctct 2580
 tcggctgcgg cgagcggat cagctcactc aaaggcggta atacggttat ccacagaatc 2640
 aggggataac gcaggaaaga acatgtgagc aaaaggccag caaaaggcca ggaaccgtaa 2700
 aaaggcgcgg ttgtcggcgt tttccatag gctccgcctc cctgacgagc atcacaaaaa 2760
 togacgctca agtcagaggt ggcgaaaccc gacaggacta taaagatacc aggcgtttcc 2820
 ccctggaagc tccctcgtgc gctctcctgt tccgaccctg ccgcttaccg gatacctgtc 2880
 cgcctttctc ccttcgggaa gcgtggcgt ttctcatagc tcacgctgta ggtatctcag 2940
 ttcggtgtag gtcgttcgt ccaagctggg ctgtgtgcac gaacccccc ttcagccga 3000
 ccgctgcgcc ttatccgta actatcgtct tgagtccaac ccgtaagac acgacttctc 3060
 gccactggca gcagccactg gtaacaggat tagcagagcg aggtatgtag gcggtgctac 3120
 agagtctctg aagtgggtgc ctaactacgg ctacactaga aggacagtat ttggtatctg 3180
 cgctctgctg aagccagtta ccttcggaaa aagagttggt agctcttgat ccggcaaaca 3240
 aaccacgcgt ggtagcggtg gtttttttgt ttgcaagcag cagattacgc gcagaaaaaa 3300
 aggatctcaa gaagatcctt tgatcttttc taoggggtct gacgctcagt ggaacgaaaa 3360
 ctacagttaa gggatttttg tcatgagatt atcaaaaagg atcttcacct agatcctttt 3420
 aaattaaaaa tgaagtttta aatcaatcta aagtatatat gagtaaacct ggtctgacag 3480
 ttaccaatgc ttaatcagtg aggcacctat ctacagcagc tgtctatttc gttcatccat 3540
 agttgcctga ctcccgctg tgtagataac tacgatacgg gagggcttac catctggccc 3600
 cagtgtgca atgataccgc gagaccacg ctaccggct ccagatttat cagcaataaa 3660
 ccagccagcc ggaaggccg agcgcagaag tggctctgca actttatccg cctccatcca 3720
 gtctattaat tgttgccggg aagctagagt aagtagttcg ccagttaata gtttgcgcaa 3780
 cgttggtgcc attgctacag gcacgtggt gtcacgctcg tcgtttggtg tggcttcatt 3840
 cagctccggt tccaacgat caaggcagat tacatgatcc cccatgttgt gcaaaaaagc 3900
 ggttagctcc ttcggtctc cgatcgttgt cagaagtaag ttggccgcag tgttatcaet 3960
 catggttatg gcagcactgc ataattctct tactgtcatg ccacccgtaa gatcttttc 4020

tgtgactggt gagtactcaa ccaagtcatt ctgagaatag tgtatgcggc gaccgagttg 4080
 ctcttgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtgtc 4140
 catcattgga aaacgttctt cggggcgaaa actctcaagg atcttaccgc tgttgagatc 4200
 cagttcgatg taacccactc gtgcacccaa ctgatcttca gcactttta ctttcaccag 4260
 cgtttctggg tgagcaaaaa caggaaggca aaatgcgcga aaaaagggaa taaggcgagc 4320
 acggaaatgt tgaatactca tactcttctt ttttcaatat tattgaagca tttatcaggg 4380
 ttattgtctc atgagcggat acatatttga atgtatttag aaaaataaac aaataggggt 4440
 tccgcgcaca tttccccgaa aagtgcaccc tgacgtctaa gaaaccatta ttatcatgac 4500

attaacctat aaaaataggc gtatcacgag gccctttcgt cttcac

4546

<210> 60

<211> 1143

<212> DNA

<213> artificial

<220>

<223> His-tagged GFP_CBD2638

<400> 60

atgagaggat cgcacaccca tcaccatcac ggatccatga gtaaaggaga agaacttttc	60
actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct	120
gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc	180
actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggtctt	240
caatgctttg cgagataccc agatcatatg aaacggcatg actttttcaa gagtgccatg	300
cccgaaggtt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca	360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt	420
gattttaaag aagatggaaa cattcttggg cacaatttgg aatacaacta taactcacac	480
aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga	540
cacaacattg aagatggaa cgttcaacta gcagaccatt atcaacaaaa tactccaatt	600
ggcagatggc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg	660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg	720
attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa	780
gcagcaacta tcaacaatc tgacgttaag caagaagta aaaagcaaga agcaaaacaa	840
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat	900
gcttcgttca cagtgcacgc accagaggga attatcacia gatacaaagg tccttggact	960
ggtcaccac aagctggtgt attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa	1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg	1080
cgggtacgca catgggacgc taaaactggt aaagttggtg agttgtgggg cgaaattaaa	1140
taa	1143

<210> 61

<211> 1539

<212> DNA

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638 var.1

<400> 61

atgagaggat cgcacaccca tcaccatcac ggatccatga gtaaaggaga agaacttttc	60
actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct	120
gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc	180

```

actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggtcct 240
caatgctttg cgagataccc agatcatatg aaacggcatg actttttcaa gagtgccatg 300
cccgaaaggtt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt 420
gattttaaag aagatggaaa cattcttggg cacaatttgg aatacaacta taactcacac 480
aatgtatata tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540
cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600
ggcgtatggc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720
attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa 780
gcagcaacta tcaacaatc tgacgttaag caagaagta aaaagcaaga agcaaaacaa 840
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat 900
gcttcgttca cagtgcagc accagagggg attatcacia gatacaaagg tccttggact 960
ggtcaccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa 1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 1140
gagctcggtg gaaagctaga agtaagcaaa gcagcaacta tcaacaatc tgacgttaag 1200
caagaagta aaaagcaaga agcaaaacaa attgtgaaag caacagattg gaaacagaat 1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcagc accagagggg 1320
attatcacia gatacaaagg tccttggact ggtcaccac aagctggtgt attacaaaaa 1380
ggtcaaacga ttaaataatga tgaggttcaa aaatttgacg gtcattgttg ggtatcgtgg 1440

gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt 1500
aaagttggta agttgtgggg cgaaattaaa taagtcgac 1539

```

<210> 62

<211> 1560

<212> DNA

<213> artificial

<220>

<223> Hist-tagged GFP_CBD2638_CBD2638 var. 2

<400> 62

```

atgagaggat cgcacacca tcaccatcac ggatccatga gtaaaggaga agaacttttc 60
actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct 120
gtcagtgagg aggggtaagg tgatgcaaca tacggaaaac ttaccotaa atttatttgc 180
actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggtcct 240
caatgctttg cgagataccc agatcatatg aaacagcatg actttttcaa gagtgccatg 300
cccgaaaggtt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt 420
gattttaaag aagatgaaa cattcttqga cacaatttqg aatacaacta taactcacac 480

```

```

aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540
cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600
ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720
attacacatg gcatggatga actatacaaa gagctcgggtg gaaagctaga agtaagcaaa 780
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 840
atttgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat 900
gcttcgttca cagtgcacgc accagaggga attatcacia gatacaaagg tccttggtact 960
ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa 1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1080
ccggtacgca catgggacgc taaaactggt aaagttggtg agttgtgggg cgaaattaaa 1140
ggtaccgggtg gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag 1200
caagaagtta aaaagcaaga agcaaaacaa atttgtgaaag caacagattg gaaacagaat 1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcacgc accagaggga 1320
attatcacia gatacaaagg tccttggtact ggtcaccac aagctggtgt attacaaaaa 1380
ggtcaaacga ttaaatatga tgaggttcaa aaatttgacg gtcattgttg ggtatcgtgg 1440

gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt 1500
aaagttggtg agttgtgggg cgaaattaaa gtcgacctgc agccaagctt aattagctga 1560

```

<210> 63

<211> 1944

<212> DNA

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638_CBD2638

<400> 63

```

atgagaggat cgcacaccca tcaccatcac ggatccatga gtaaaggaga agaacttttc 60
actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct 120
gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc 180
actactggaa aactacctgt tccatggcca acacttgta ctactttgcg gtatggtctt 240
caatgctttg cgagataccc agatcatatg aaacagcatg actttttcaa gagtgccatg 300
ccgaagggtt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt 420
gatttttaag aagatggaaa cattcttgga cacaatttgg aatacaacta taactcacac 480
aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540
cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600
ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720
attacacatg gcatggatga actatacaaa gagctcgggtg gaaagctaga agtaagcaaa 780

```

```

gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa      840
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat      900
gcttcgttca cagtgcacgc accagaggga attatcacaa gatacaaagg tccttggact      960
ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa    1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg    1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa    1140
ggtaccggtg gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag    1200
caagaagtta aaaagcaaga agcaaaacaa attgtgaaag caacagattg gaaacagaat    1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcacgc accagaggga    1320
attatcacaa gatacaaagg tccttggact ggtcacccac aagctggtgt attacaaaaa    1380
ggtcaaacga ttaaataatga tgaggttcaa aaatttgacg gtcattgttg ggtatcgtgg    1440
gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt    1500

aaagttggta agttgtgggg cgaaattaaa gtcgacggtg gaaagctaga agtaagcaaa    1560
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa    1620
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat    1680
gcttcgttca cagtgcacgc accagaggga attatcacaa gatacaaagg tccttggact    1740
ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa    1800
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg    1860
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa    1920
ctgcagccaa gcttaattag ctga                                           1944

```

<210> 64

<211> 380

<212> PRT

<213> artificial

<220>

<223> His-tagged GFP_CBD2638

<400> 64

```

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1           5           10          15

```

```

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
20          25          30

```

```

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35          40          45

```

```

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50          55          60

```

```

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65          70          75          80

```

```

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
85          90          95

```

80 90 100
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 100 105 110
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 115 120 125
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 130 135 140
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 145 150 155 160
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 165 170 175
 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 180 185 190
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 195 200 205
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 210 215 220
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 225 230 235 240
 Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
 245 250 255
 Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
 260 265 270
 Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
 275 280 285
 Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
 290 295 300
 Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
 305 310 315 320
 Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
 325 330 335
 Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
 340 345 350
 Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
 355 360 365
 Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
 370 375 380

<210> 65

<211> 510

<212> PRT

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638 var.1

<400> 65

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
20 25 30

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
85 90 95

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
100 105 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
130 135 140

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
145 150 155 160

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
165 170 175

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
180 185 190

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
195 200 205

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
210 215 220

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
225 230 235 240

Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
245 250 255

Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
260 265 270

Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
275 280 285

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
290 295 300

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
305 310 315 320

Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
325 330 335

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
340 345 350

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
355 360 365

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Glu Leu Gly Gly
370 375 380

Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
385 390 395 400

Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
405 410 415

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
420 425 430

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
435 440 445

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
450 455 460

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
465 470 475 480

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
485 490 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
500 505 510

<210> 66

<211> 519

<212> PRT

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638 var. 2

<400> 66

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
20 25 30

20	20	30
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp 35 40 45		
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys 50 55 60		
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu 65 70 75 80		
Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe 85 90 95		
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe 100 105 110		
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly 115 120 125		
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 130 135 140		
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 145 150 155 160		
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 165 170 175		
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 180 185 190		
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 195 200 205		
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 210 215 220		
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 225 230 235 240		
Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu 245 250 255		
Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu 260 265 270		
Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys 275 280 285		
Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr 290 295 300		
Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr 305 310 315 320		
Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr 325 330 335		

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
340 345 350

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
355 360 365

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Gly Thr Gly Gly
370 375 380

Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
385 390 395 400

Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
405 410 415

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
420 425 430

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
435 440 445

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
450 455 460

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
465 470 475 480

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
485 490 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Val Asp
500 505 510

Leu Gln Pro Ser Leu Ile Ser
515

<210> 67

<211> 647

<212> PRT

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638_CBD2638

<400> 67

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
20 25 30

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
 65 70 75 80
 Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
 85 90 95
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 100 105 110
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 115 120 125
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 130 135 140
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 145 150 155 160
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 165 170 175
 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 180 185 190
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 195 200 205
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 210 215 220
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 225 230 235 240
 Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
 245 250 255
 Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
 260 265 270
 Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
 275 280 285
 Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
 290 295 300
 Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
 305 310 315 320
 Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
 325 330 335
 Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
 340 345 350
 Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
 355 360 365
 Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Gly Thr Gly Gly
 370 375 380

Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
 385 390 395 400
 Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
 405 410 415
 Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
 420 425 430
 Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
 435 440 445
 Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
 450 455 460
 Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
 465 470 475 480
 Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
 485 490 495
 Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Val Asp
 500 505 510
 Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp
 515 520 525
 Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala
 530 535 540
 Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His
 545 550 555 560
 Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys
 565 570 575
 Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln
 580 585 590
 Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val
 595 600 605
 Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr
 610 615 620
 Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
 625 630 635 640
 Leu Gln Pro Ser Leu Ile Ser
 645

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Non-patent literature cited in the description

- **BECKER et al.**Gene, 2009, vol. 443, 32-41 [0002]
- **LU et al.**J. Biol. Chem., 2006, vol. 281, 1549-58 [0009]
- **LOESSNER et al.**Molecular Microbiology, 2002, vol. 44, 2335-349 [0011]
- **TRAYER, H. R.BUCKLEY, C. E.**Molecular properties of lysostaphin, a bacteriolytic agent specific for Staphylococcus aureusJ. Biol. Chem., 1970, vol. 245, 4842-4846 [0019]
- Computational Molecular BiologyOxford University Press19880000 [0061]
- Biocomputing: Informatics and Genome ProjectsAcademic Press19930000 [0061]
- Computer Analysis of Sequence DataHumana Press19940000 [0061]
- **VON HEINE, G.**Sequence Analysis in Molecular BiologyAcademic Press19870000 [0061]
- Sequence Analysis PrimerM Stockton Press19910000 [0061]
- **CARILLO, H.LIPMAN, D.SIAM J.**Applied Math., 1988, vol. 48, 1073- [0061]
- **DEVEREUX, J. et al.**Nucleic Acids Research, 1984, vol. 12, 1387- [0062]
- **ALTSCHUL, S. F. et al.**J. Mol. Biol., 1990, vol. 215, 403-410 [0062]
- **ALTSCHUL, S. et al.**BLAST ManualNCBI [0062]
- **ALTSCHUL, S. et al.**J. Mol. Biol., 1990, vol. 215, 403-410 [0062]
- Algorithm: Needleman and WunschJ. Mol. Biol., 1970, vol. 48, 443-453 [0063] [0064]
- **HENTIKOFFHENTIKOFF**Proc. Natl. Acad. Sci. USA., 1992, vol. 89, 10915-10919 [0063]

P a t e n t k r a v

5 1. Nukleinsyremolekyle omfattende en første nukleotidsekvens, hvor nukleotidsekvensen har mindst 85 % sekvensidentitet med SEQ ID NO: 12, hvor den første nukleotidsekvens koder for et cellevægbindingsdomæne, der binder peptidoglycan-cellevæggen af *Staphylococcus*-slægter, hvor nukleinsyremolekylet yderligere omfatter en heterolog nukleotidsekvens, der koder for et lytisk domæne, som udviser peptidoglycan-hydrolase-aktivitet, hvor det lytiske domæne er en anden og tredje nukleotidsekvens, hvor den anden nukleotidsekvens koder for et M23-endopeptidasedomæne, og den tredje nukleotidsekvens koder for et amidasedomæne, og hvor den anden nukleotidsekvens har mindst 80 % sekvensidentitet med SEQ ID NO: 15.

15 2. Nukleinsyremolekyle ifølge krav 1, hvor nukleinsyremolekylet har mindst 80 % sekvensidentitet med SEQ ID NO: 1.

20 3. Nukleinsyremolekyle ifølge krav 2, hvor den tredje nukleotidsekvens har mindst 80 % sekvensidentitet med SEQ ID NO: 16 eller 17, fortrinsvis hvor nukleinsyremolekylet har mindst 80 % sekvensidentitet med SEQ ID NO: 9.

25 4. Nukleinsyremolekyle ifølge krav 2 eller 3, yderligere omfattende en fjerde nukleotidsekvens, der koder for et CHAP (cystein, histidin-afhængige amidohydrolaser/peptidaser)-domæne, fortrinsvis hvor den fjerde nukleotidsekvens stammer fra *S. aureus*-bakteriofag Φ11 eller *S. aureus*-bakteriofag ΦTwort-endolysin, mere fortrinsvis hvor den fjerde nukleotidsekvens har mindst 80 % sekvensidentitet med SEQ ID NO: 18 eller SEQ ID NO: 19.

30 5. Nukleinsyremolekyle ifølge et hvilket som helst af kravene 2-4, som koder for et polypeptid, der har den samme eller en øget lytisk aktivitet og/eller den samme eller et reduceret pH-optimum sammenlignet med *S. aureus*-bakteriofag Φ2638a-endolysin, der kodes af SEQ ID NO: 1.

35 6. Polypeptid, der kodes af et nukleinsyremolekyle ifølge et hvilket som helst af kravene 1 - 5, omfattende:

- et cellevægbindingsdomæne og
- et endopeptidasedomæne og et amidasedomæne.

7. Nukleinsyrekonstrukt omfattende et nukleinsyremolekyle ifølge et hvilket som helst af kravene 1 - 5.

5 **8.** Ekspressionsvektor omfattende et nukleinsyrekonstrukt ifølge krav 7, funktionsmæssigt forbundet med en eller flere kontrolsekvenser, som styrer produktionen eller ekspressionen af det kodede polypeptid i en celle, et individ eller et cellefrit ekspressionssystem.

10 **9.** Celle omfattende nukleinsyrekonstruktet ifølge krav 7 eller ekspressionsvektoren ifølge krav 8, hvilken celle er en mikrobiel, prokaryotisk eller eukaryotisk celle.

15 **10.** Fremgangsmåde til fremstilling, eventuelt oprensning og eventuelt frysetørring af et polypeptid, der kodes af et nukleinsyremolekyle omfattende en første nukleotidsekvens, hvor nukleotidsekvensen har mindst 85 % sekvensidentitet med SEQ ID NO: 12, hvor den første nukleotidsekvens koder for et cellevægbindingsdomæne, der binder peptidoglycan-cellevæggen af *Staphylococcus*-slægter, hvilken fremgangsmåde omfatter trinnene:

20 i) at fremstille polypeptidet i en celle ifølge krav 9, omfattende et nukleinsyrekonstrukt ifølge krav 7, eventuelt
ii) at oprense polypeptidet og eventuelt
iii) at frysetørre det oprensede polypeptid.

25 **11.** Fremgangsmåde til fremstilling af et polypeptid med en forstærket lytisk aktivitet ved behandling af et polypeptid ifølge krav 6, hvor fremgangsmåden omfatter trinnene:

30 i) at dialysere polypeptidet mod en buffer omfattende en chelaterende forbindelse,
ii) at dialysere polypeptidet mod en divalent metalionholdig buffer, idet den divalente metalion fortrinsvis er udvalgt fra gruppen bestående af Co^{2+} , Cu^{2+} , Mn^{2+} og Zn^{2+} .

35 **12.** Sammensætning omfattende et nukleinsyremolekyle ifølge et hvilket som helst af kravene 1 - 5, et polypeptid ifølge krav 6 og/eller et nukleinsyrekonstrukt ifølge krav 7 og/eller en vektor ifølge krav 8 og/eller en celle ifølge krav

9, fortrinsvis yderligere omfattende en eller flere yderligere aktive bestanddele, fortrinsvis udvalgt fra gruppen bestående af en bakteriofag og et antibiotikum.

5 **13.** Sammensætning ifølge krav 12 til anvendelse som et medikament, fortrinsvis til anvendelse som et medikament til behandling af en infektionssygdom.

10 **14.** *In vitro*-anvendelse af et nukleinsyremolekyle ifølge et hvilket som helst af kravene 1 - 5, et polypeptid ifølge krav 6, et nukleinsyrekonstrukt ifølge krav 7, en vektor ifølge krav 8, en celle ifølge krav 9 og/eller en sammensætning ifølge krav 12 som et antimikrobielt middel, fortrinsvis som et fødevaretilsætningsstof eller et desinfektionsmiddel.

15 **15.** *In vitro*-anvendelse af et nukleinsyremolekyle ifølge et hvilket som helst af kravene 1 - 5, et polypeptid ifølge krav 6, et nukleinsyrekonstrukt ifølge krav 7, en vektor ifølge krav 8, en celle ifølge krav 9 og/eller en sammensætning ifølge krav 12 til detektering af en *Staphylococcus*, fortrinsvis i en diagnostisk anvendelse.

DRAWINGS

Fig 1

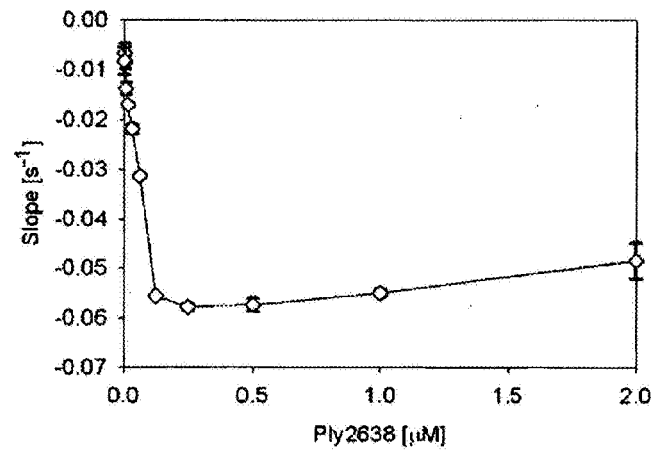


Fig 2

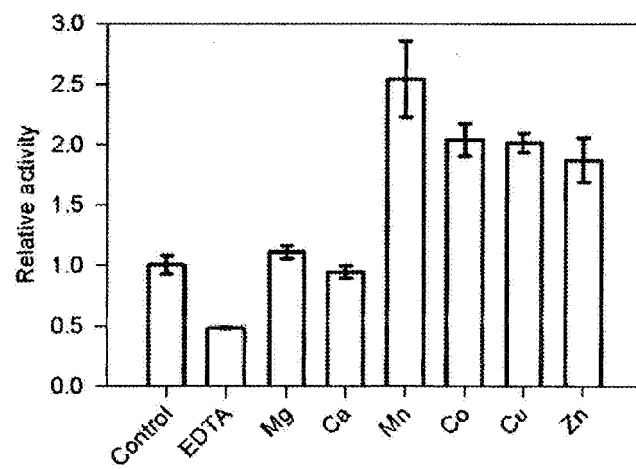


Fig 3

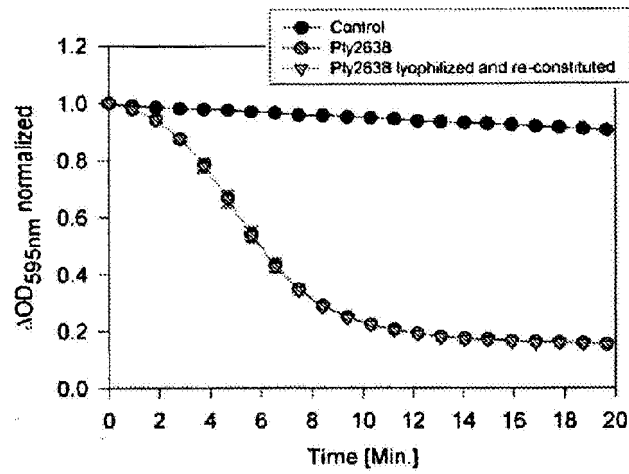


Fig 4

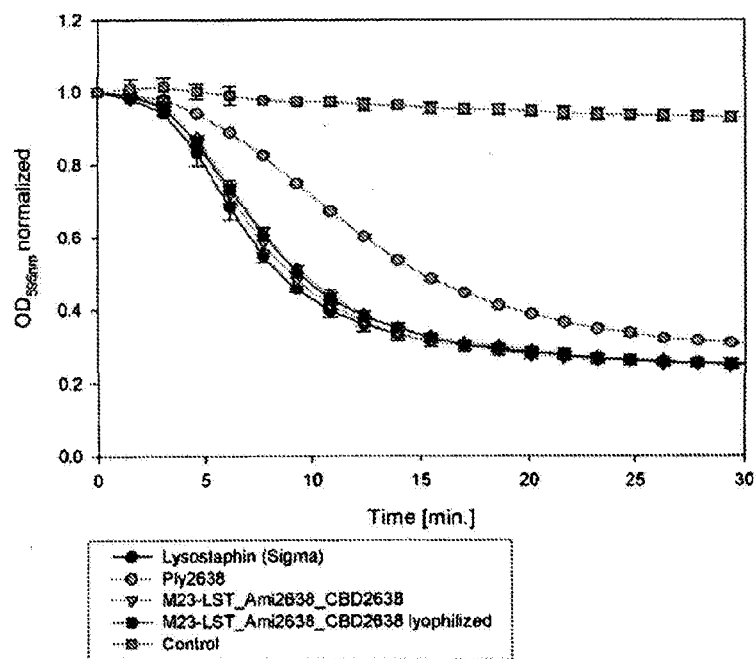


Fig 5

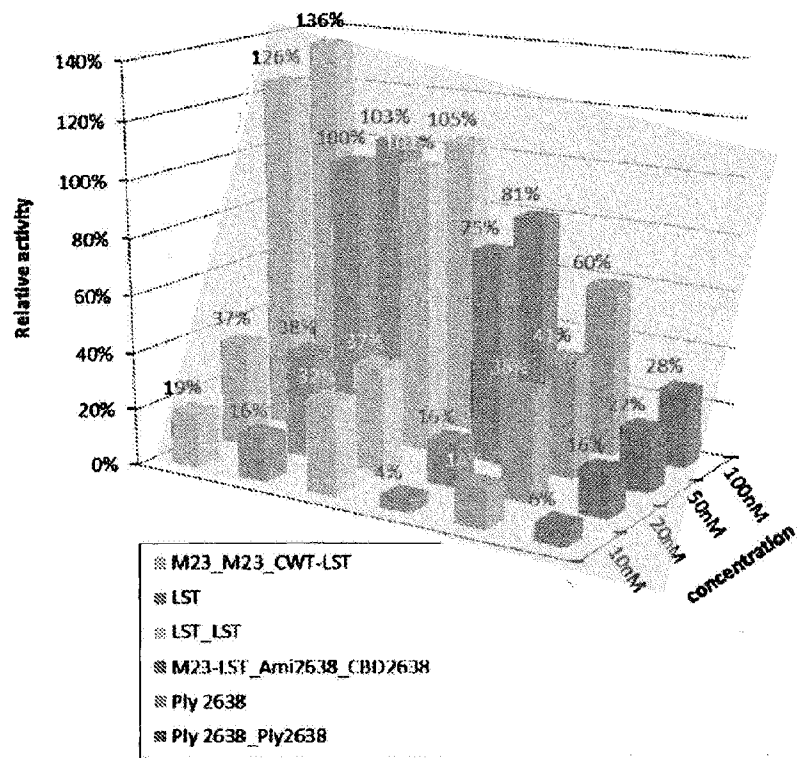


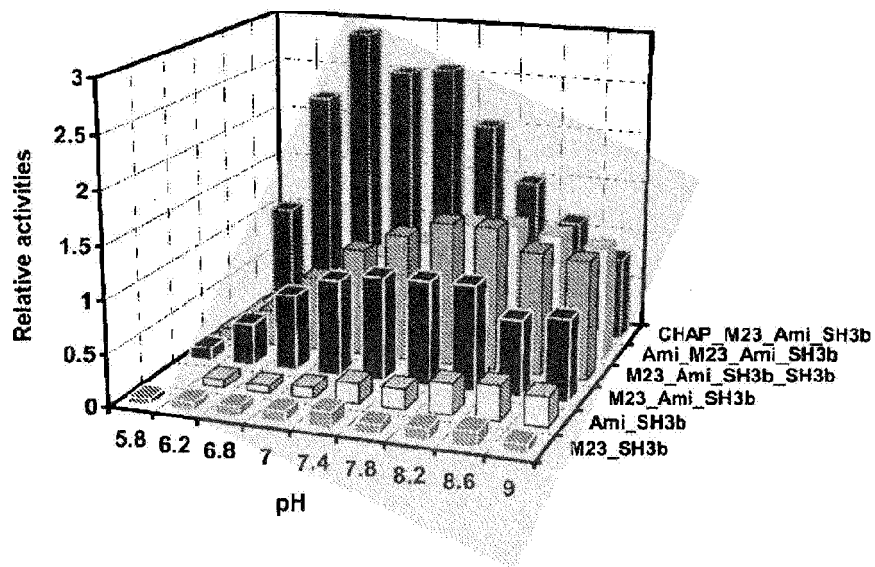
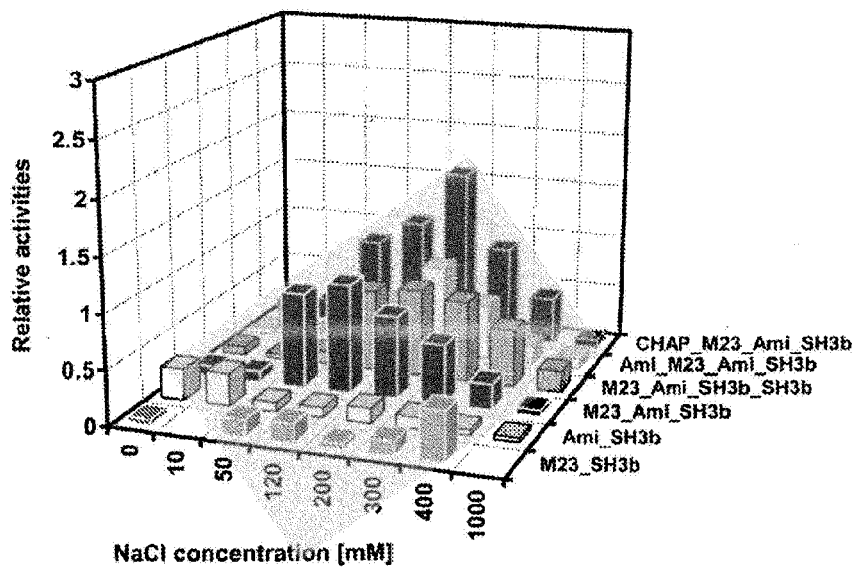
Fig 6a*Fig 6b*

Fig 7