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(12) **United States Patent**
Karplus et al.(10) **Patent No.:** **US 11,434,263 B2**(45) **Date of Patent:** **Sep. 6, 2022**(54) **STABILIZED POLYPEPTIDES AND USES THEREOF**(71) Applicant: **PRESIDENT AND FELLOWS OF HARVARD COLLEGE**, Cambridge, MA (US)(72) Inventors: **Martin Karplus**, Cambridge, MA (US); **Victor G Ovchinnikov**, Watertown, MA (US)(73) Assignee: **PRESIDENT AND FELLOWS OF HARVARD COLLEGE**, Cambridge, MA (US)

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(51) **Int. Cl.**
A61K 38/10 (2006.01)
C07K 7/08 (2006.01)
C07K 14/195 (2006.01)
A61K 38/00 (2006.01)(52) **U.S. Cl.**
CPC **C07K 14/195** (2013.01); **C07K 7/08** (2013.01); **A61K 38/00** (2013.01); **A61K 38/10** (2013.01)(58) **Field of Classification Search**

CPC A61K 38/10; A61K 38/164; C07K 7/08; C07K 14/195

See application file for complete search history.

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Primary Examiner — Jeffrey E. Russel(74) *Attorney, Agent, or Firm* — Hogan Lovells US LLP(57) **ABSTRACT**The present invention features polypeptides which inhibit dimerization of small multidrug resistance transporters including a stabilized α -helix, and the use of such polypeptides in the treatment of bacterial infections.**20 Claims, 2 Drawing Sheets****Specification includes a Sequence Listing.**

FIG. 1A

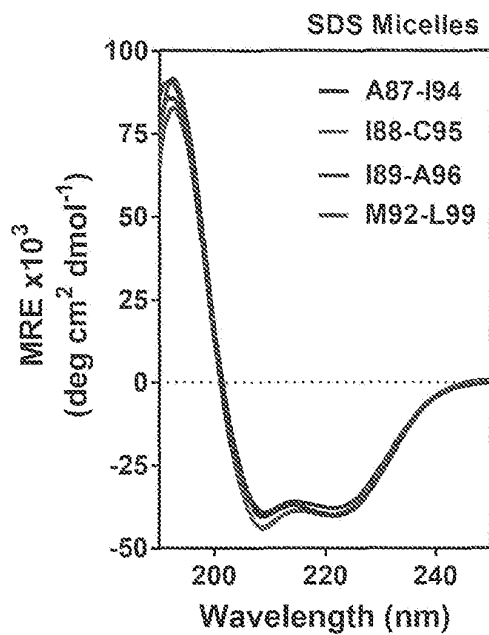


FIG. 1B

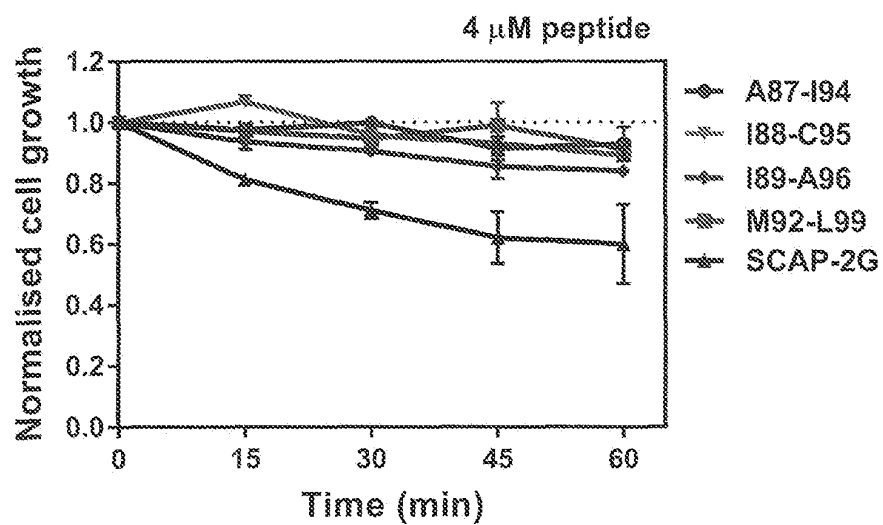
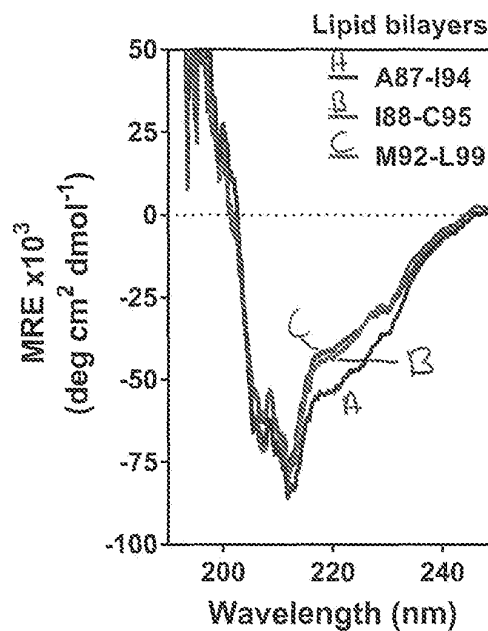


FIG. 2

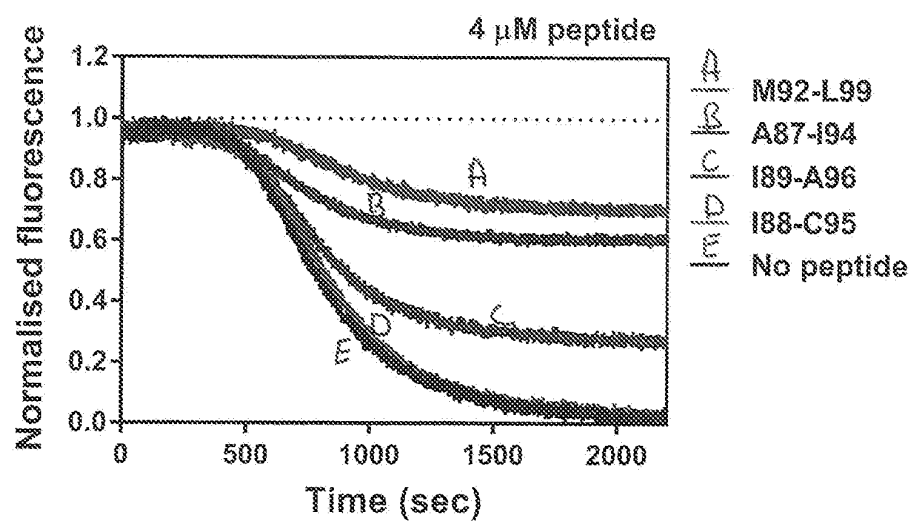


FIG. 3

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STABILIZED POLYPEPTIDES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a U.S. National Stage application under 35 U.S.C. 371 of PCT/US2019/012291, filed on Jan. 4, 2019, which claims the benefit of U.S. Provisional Patent Application No. 62/613,994, filed on Jan. 5, 2018, and also claims the benefit of U.S. Provisional Patent Application No. 62/714,464, filed on Aug. 3, 2018, each of which are incorporated herein by reference in their entireties.

GOVERNMENT INTEREST

This invention was made with government support under grant A1111416 awarded by the National Institutes of Health. The government has certain rights in the invention.

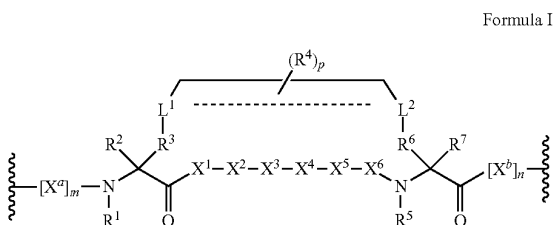
BACKGROUND OF THE INVENTION

Multidrug resistance poses serious challenges for the treatment of many infectious diseases. A common mechanism by which multidrug resistance is conferred to bacteria is based on the active efflux of a wide range of cytotoxic compounds by transmembrane pumps. Some of these systems utilize supplier proteins, such as multidrug transporter EmrE in *E. coli*, which transport compounds into the periplasm from the cytoplasm. The various suppliers have overlapping specificities, and collectively form a multidrug resistance network of proteins that renders bacteria effectively immune to a broad range of compounds. The small multidrug resistance family of membrane bound transporters is ubiquitous in bacteria. Accordingly, compounds capable of inhibiting these transporters could be useful in the treatment of bacterial infections.

SUMMARY OF THE INVENTION

The present invention features polypeptides which inhibit dimerization of small multidrug resistance transporters containing a stabilized α -helix, and the use of such polypeptides in the treatment of bacterial infections.

Accordingly, in an aspect, the invention features a polypeptide, or a pharmaceutically acceptable salt thereof, including a stabilized α -helix, wherein the polypeptide includes the structure of Formula I:



wherein the dotted line represents an optional double bond;

m is 1, 2, 3, 4, 5, or 6;

n is 6-m;

p is 0, 1, or 2;

each of $[X^a]_m$, $[X^b]_n$, and X^1-X^6 consist of consecutive amino acids of an α -helix of a monomer of a small multidrug

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resistance transporter (e.g., an α -helix of any one of SEQ ID NOs: 1-421), or conservative substitutions thereof;

R^1 and R^2 are, independently, hydrogen, optionally substituted acyl, or optionally substituted C_1-C_6 alkyl;

R^2 and R^7 are, independently, optionally substituted C_1-C_6 alkyl, optionally substituted C_1-C_6 alkenyl, optionally substituted C_1-C_6 alkynyl, optionally substituted C_1-C_6 heteroalkyl, optionally substituted C_3-C_6 carbocyclyl, or optionally substituted C_2-C_9 heterocyclyl;

R^3 and R^6 are, independently, optionally substituted C_1-C_6 alkylene, optionally substituted C_1-C_6 heteroalkylene, optionally substituted C_3-C_6 carbocyclyl, or optionally substituted C_2-C_9 heterocyclyl, or R^1 and R^3 or R^5 and R^6 combine with the atoms to which they are attached to form an optionally substituted C_5-C_6 heterocyclyl;

L^1 and L^2 are, independently, absent, optionally substituted C_1-C_6 alkylene, or $-C(=O)OR^{L1}$, wherein each R^{L1} is, independently, an optionally substituted C_1-C_6 alkyl; and

each R^4 is, independently, optionally substituted C_1-C_6 alkyl, optionally substituted C_1-C_6 heteroalkyl, optionally substituted C_5-C_{10} alkyl,

wherein the polypeptide binds to the monomer of a small multidrug resistance transporter.

In some embodiments, the structure of Formula I includes the sequence of an α -helix of a monomer of a small multidrug resistance transporter (e.g., an α -helix of any one of SEQ ID NOs: 1-421) in which two of the amino acids are replaced with a cross-link.

In some embodiments, R^2 is optionally substituted C_1-C_6 alkyl (e.g., methyl). In some embodiments, R^7 is optionally substituted C_1-C_6 alkyl (e.g., methyl). In some embodiments, R^1 is hydrogen. In some embodiments, R^5 is hydrogen. In some embodiments, p is 0. In some embodiments, R^6 is optionally substituted C_1-C_6 alkylene (e.g., methylene). In some embodiments, R^3 is optionally substituted C_1-C_6 alkylene (e.g., methylene). In some embodiments, L^1 is optionally substituted C_1-C_6 alkylene (e.g., pentylene). In some embodiments, L^2 is optionally substituted C_1-C_6 alkylene (e.g., ethylene). In some embodiments, the dotted line represents a double bond.

In some embodiments, X^1 is glycine, alanine, valine, leucine, or isoleucine; X^2 is glycine, alanine, valine, leucine, or isoleucine; X^3 is glycine, alanine, valine, leucine, or isoleucine; X^4 is serine, cysteine, selenocysteine, threonine, or methionine; X^5 is serine, cysteine, selenocysteine, threonine, or methionine; and/or X^6 is histidine, lysine, or arginine.

In some embodiments, X^1 is glycine, alanine, valine, leucine, or isoleucine; X^2 is glycine, alanine, valine, leucine, or isoleucine; X^3 is serine, cysteine, selenocysteine, threonine, or methionine; X^4 is serine, cysteine, selenocysteine, threonine, or methionine; X^5 is histidine, lysine, or arginine, and/or X^6 is glycine, alanine, valine, leucine, or isoleucine.

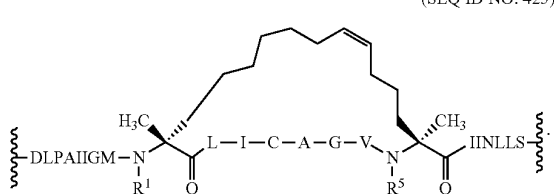
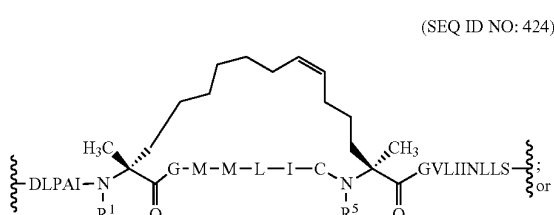
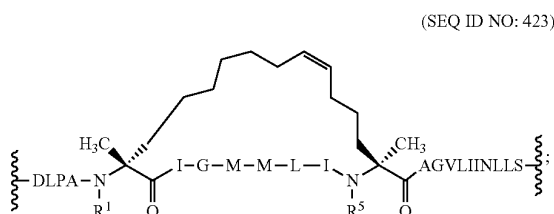
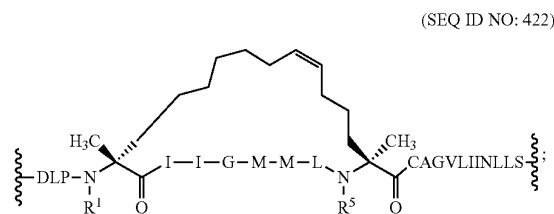
In some embodiments, X^1 is glycine, alanine, valine, leucine, or isoleucine; X^2 is serine, cysteine, selenocysteine, threonine, or methionine; X^3 is serine, cysteine, selenocysteine, threonine, or methionine; X^4 is histidine, lysine, or arginine; X^5 is glycine, alanine, valine, leucine, or isoleucine; and/or X^6 is serine, cysteine, selenocysteine, threonine, or methionine.

In some embodiments, X^1 is histidine, lysine, or arginine; X^2 is glycine, alanine, valine, leucine, or isoleucine; X^3 is serine, cysteine, selenocysteine, threonine, or methionine; X^4 is glycine, alanine, valine, leucine, or isoleucine; X^5 is glycine, alanine, valine, leucine, or isoleucine; and/or X^6 is glycine, alanine, valine, leucine, or isoleucine.

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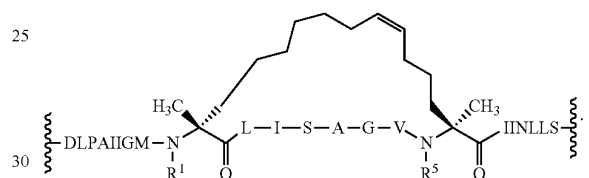
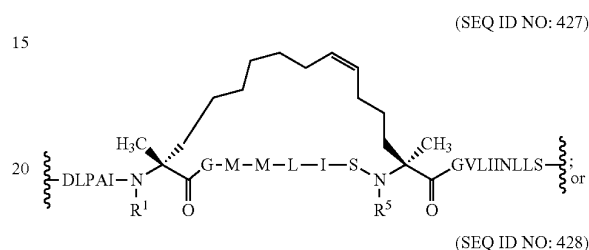
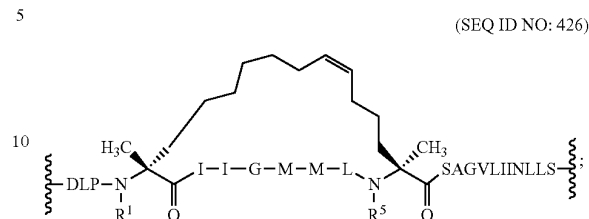
In some embodiments, $[X^b]_n$ includes the sequence lysine-lysine-serine, or conservative substitutions thereof. In some embodiments, $[X^b]_n$ includes the sequence isoleucine-isoleucine-asparagine-lysine-lysine-serine (SEQ ID NO: 436), or conservative substitutions thereof. In some embodiments, X^1 - X^6 or $[X^b]_n$ includes the sequence cysteine-alanine-glycine, or conservative substitutions thereof. In some embodiments, $[X^b]_n$ includes the sequence cysteine-alanine-glycine-valine-leucine-isoleucine-isoleucine-asparagine-lysine-lysine-serine (SEQ ID NO: 437), or conservative substitutions thereof. In some embodiments, $[X^a]_m$ includes the sequence Aspartic acid-leucine-proline, or conservative substitutions thereof. In some embodiments, $[X^a]_m$ includes the sequence Aspartic acid-leucine-proline-alanine-isoleucine-isoleucine-glycine-methionine (SEQ ID NO: 438), or conservative substitutions thereof.

In some embodiments, the polypeptide includes the structure:

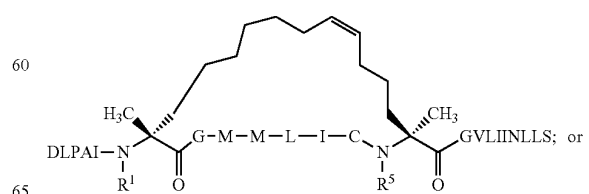
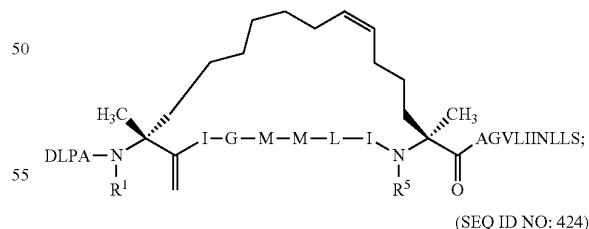
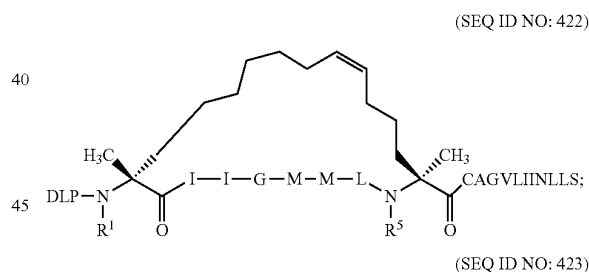


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In some embodiments, the polypeptide includes the structure:



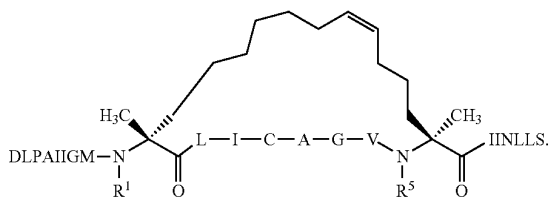
In some embodiments, the polypeptide consists of the structure:



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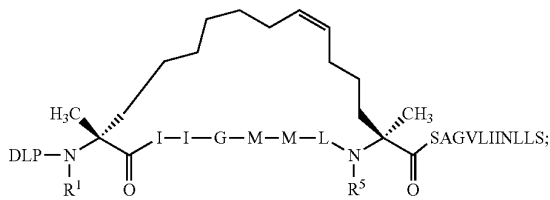
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(SEQ ID NO: 425)

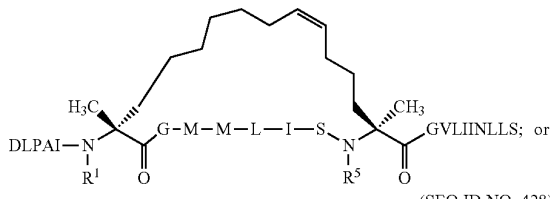


In some embodiments, the polypeptide consists of the structure:

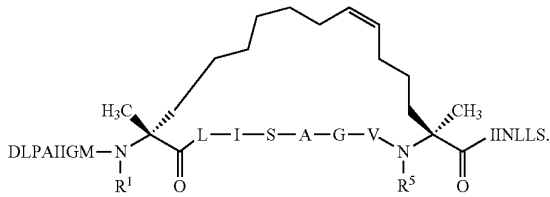
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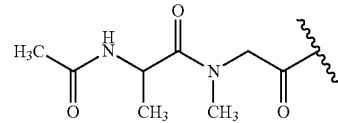
(SEQ ID NO: 427)



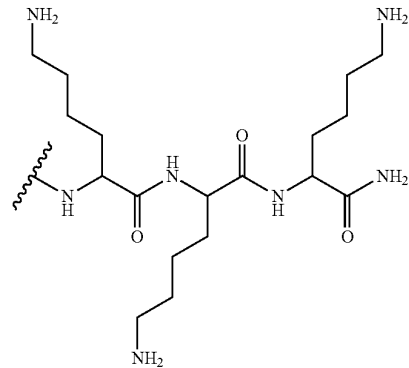
(SEQ ID NO: 428)

**6**

In some embodiments, the polypeptide includes a solubility tag (e.g., one or more lysine residues or a sarcosine-containing tag) at the N- and/or C-terminus. In some embodiments, the polypeptide is acetylated at the N-terminus. In some embodiments, the polypeptide is amidated at the C-terminus. In some embodiments, the polypeptide includes a solubility tag including at least one lysine (e.g., at least two, at least three, at least four, at least five) at the C-terminus. In some embodiments, the polypeptide includes (e.g., at the N-terminus) the structure:

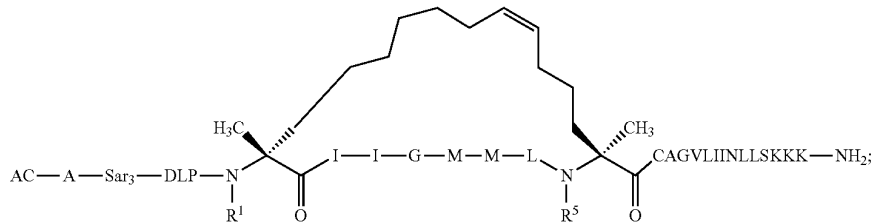


In some embodiments, the polypeptide includes (e.g., at the C-terminus) the structure:

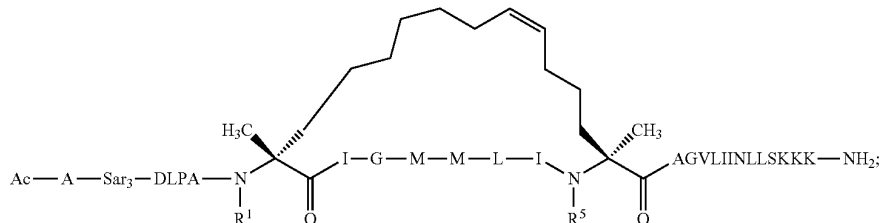


In some embodiments, the polypeptide consists of the structure:

(SEQ ID NO: 429)

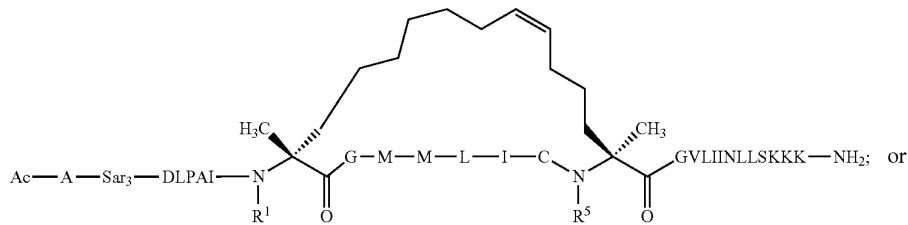


(SEQ ID NO: 430)

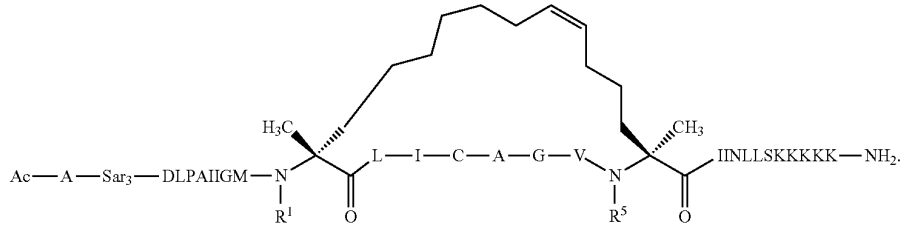


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(SEQ ID NO: 431)



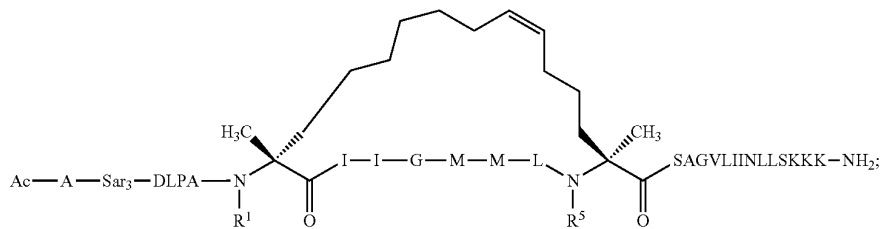
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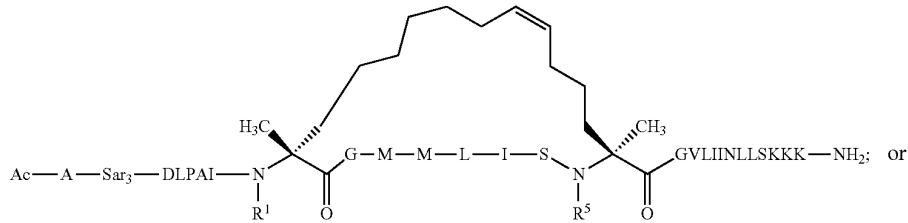
In some embodiments, the polypeptide consists of the structure:

embodiments, the bacterial cell is a gram-positive bacteria (e.g., *S. aureus* or *B. anthracis*).

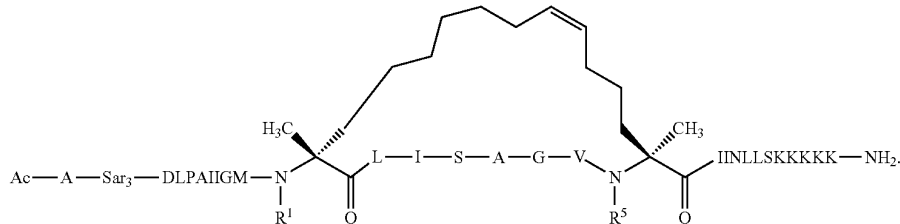
(SEQ ID NO: 433)



(SEQ ID NO: 434)



(SEQ ID NO: 435)



In another aspect, the invention features a pharmaceutical composition including any of the foregoing polypeptides and a pharmaceutically acceptable carrier.

In another aspect, the invention features, a method of reducing efflux in a bacterial cell, the method including contacting the cell with any of the foregoing polypeptides or pharmaceutical compositions. In some embodiments, the bacterial cell is a gram-negative bacteria (e.g., *E. coli*, *P. aeruginosa*, *B. pertussis*, or *N. meningitidis*). In some

In another aspect, the invention features a method of treating a bacterial infection in a subject in need thereof, the method including administering any of the foregoing polypeptides or pharmaceutical compositions. In some embodiments, the bacterial infection includes bacteria which are resistant to one or more antibacterial agents or the bacterial infection has failed to respond to treatment with one or more antibacterial agents. In some embodiments, the bacterial infection includes bacteria which express one or more small

molecule resistance membrane-bound transporters. In some embodiments, the method further includes administering one or more antibacterial agents (e.g., ampicillin, erythromycin, or tetracycline). In some embodiments, the one or more antibacterial agents is a β -lactam antibiotic, a cephalosporin antibiotic, a carbapenem antibiotic, a polymyxin antibiotic, a rifamycin antibiotic, a lipiarycin antibiotic, a quinolone antibiotic, a sulfonamide antibiotic, a macrolide antibiotic, a lincosamide antibiotic, a tetracycline antibiotic, an aminoglycoside antibiotic, a cyclic lipopeptide antibiotic, a glycylicyline antibiotic, an oxazolidinone antibiotic, or a combination thereof. In some embodiments, the one or more antibacterial agent and any of the foregoing polypeptides or pharmaceutical compositions are administered within 28 days of each other (e.g., within 21, 14, 10, 7, 5, 4, 3, 2, or 1 days) or within 24 hours (e.g., 12, 6, 3, 2, or 1 hours; or concomitantly) each in an amount that together are effective to treat the subject.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A and 1B are CD spectra of polypeptides of the invention. FIG. 1A is a CD spectrum of polypeptides of the invention in micelles. FIG. 1B is a CD spectrum of polypeptides of the invention in lipid bilayers.

FIG. 2 is a graph illustrating the toxicity of polypeptides of the invention to *E. coli* cells.

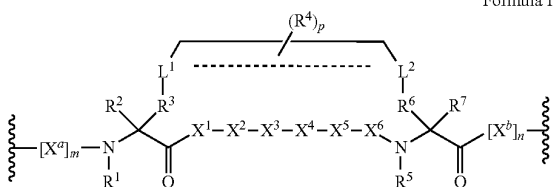
FIG. 3 is a graph illustrating the efflux of ethidium bromide from *E. coli* cells in the presence and absence of polypeptides of the invention.

DETAILED DESCRIPTION

Peptide stapling and stitching is a synthetic strategy known to increase helix stabilization, in which adjacent or subsequent turns of an α -helix are cross-linked by a macrocyclic bridge. See, e.g., Kim et al., *Nat. Protoc.* (2011) 6:761-771. This incorporated staple can enforce the bioactive α -helical conformation of a synthetic peptide and confer on it increased target affinity, robust cell penetration, and/or extended in vivo half-life. The present invention features polypeptides which inhibit dimerization of small multidrug resistance transporters including a stabilized α -helix, and the use of such polypeptides in the treatment of bacterial infections.

Polypeptides

Exemplary polypeptides of the invention comprise the structure of Formula I:



wherein the dotted line represents an optional double bond;

m is 1, 2, 3, 4, 5, or 6;

n is 6-m;

p is 0, 1, or 2;

each of $[X^a]_m$, $[X^b]_n$, and X^1 - X^6 consist of consecutive amino acids of an α -helix of a monomer of a small multidrug resistance transporter, or conservative substitutions thereof;

R^1 and R^5 are, independently, hydrogen, optionally substituted acyl, or optionally substituted C_1 - C_6 alkyl;

R^2 and R^7 are, independently, optionally substituted C_1 - C_6 alkyl, optionally substituted C_1 - C_6 alkenyl, optionally substituted C_1 - C_6 alkynyl, optionally substituted C_1 - C_6 heteroalkyl, optionally substituted C_3 - C_6 carbocyclyl, or optionally substituted C_2 - C_9 heterocyclyl;

R^3 and R^6 are, independently, optionally substituted C_1 - C_6 alkylene, optionally substituted C_1 - C_6 heteroalkylene, optionally substituted C_3 - C_6 carbocyclyl, or optionally substituted C_2 - C_9 heterocyclyl, or R^1 and R^3 or R^5 and R^6 combine with the atoms to which they are attached to form an optionally substituted C_5 - C_6 heterocyclyl;

L^1 and L^2 are, independently, absent, optionally substituted C_1 - C_6 alkylene, or $-(C(=O)OR^{L1})-$, wherein each R^{L1} is, independently, an optionally substituted C_1 - C_6 alkyl; and

each R^4 is, independently, optionally substituted C_1 - C_6 alkyl, optionally substituted C_1 - C_6 heteroalkyl, optionally substituted C_5 - C_{10} alkyl,

wherein the polypeptide binds to the monomer of a small multidrug resistance transporter.

Peptide Staples

Groups R^2 , R^3 , R^6 , R^7 , L^1 , and L^2

As generally defined above, R^2 is substituted or unsubstituted alkyl; substituted or unsubstituted alkenyl; substituted or unsubstituted alkynyl; substituted or unsubstituted heteroalkyl; substituted or unsubstituted carbocyclyl; substituted or unsubstituted heterocyclyl. In certain embodiments, R^2 is substituted or unsubstituted C_{1-10} alkyl. In certain embodiments, R^2 is substituted methyl. In certain embodiments, R^2 is unsubstituted methyl. In certain embodiments, R^2 is substituted ethyl. In certain embodiments, R^2 is unsubstituted ethyl. In certain embodiments, R^2 is substituted n-propyl. In certain embodiments, R^2 is unsubstituted n-propyl. In certain embodiments, R^2 is substituted isopropyl. In certain embodiments, R^2 is unsubstituted isopropyl. In certain embodiments, R^2 is substituted or unsubstituted heteroalkyl. In certain embodiments, R^2 is substituted or unsubstituted heteroalkyl with at least one nitrogen. In certain embodiments, R^2 is unsubstituted heteroalkyl containing at least one nitrogen. In certain embodiments, R^2 is substituted heteroalkyl containing at least one nitrogen.

As generally defined above, R^3 is substituted or unsubstituted alkylene; substituted or unsubstituted heteroalkylene; substituted or unsubstituted carbocyclylene; or substituted or unsubstituted heterocyclylene; or optionally R^2 , R^3 and the carbon to which R^2 and R^3 are attached are joined to form a ring. In certain embodiments, R^3 is substituted or unsubstituted alkylene. In certain embodiments, R^3 is substituted or unsubstituted alkylene. In certain embodiments, R^3 is substituted C_{1-10} alkylene. In certain embodiments, R^3 is unsubstituted C_{1-10} alkylene. In certain embodiments, R^3 is substituted or unsubstituted heteroalkylene. In certain embodiments, R^3 is substituted heteroalkylene. In certain embodiments, R^3 is unsubstituted heteroalkylene. In certain embodiments, R^3 is substituted or unsubstituted heteroalkylene containing at least one nitrogen. In certain embodiments, R^3 is $-(CH_2)_j-Y_1-$, wherein j is an integer between 0 and 10, inclusive; and Y_1 is a bond, $-CR^8R^9-$ or $-NR^{10}-$, wherein each of R^8 and R^9 is independently hydrogen, halogen, or C_{1-6} alkyl; and R^{10} is hydrogen; acyl; optionally substituted C_{1-6} alkyl; or an amino protecting group. In certain embodiments, R^3 is $-(CH_2)_j-$. In certain embodiments, R^3 is $-(CH_2)_j-NR^1-$. In certain embodiments, R^3 is $-(CH_2)_j-NH-$. In certain embodiments, R^3

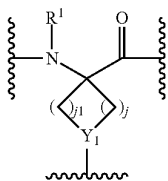
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is $-(CH_2)_j-$. In certain embodiments, j is 0. In certain embodiments, j is 1. In certain embodiments, j is 2. In certain embodiments, j is 3. In certain embodiments, j is 4. In certain embodiments, j is 5. In certain embodiments, j is 6. In certain embodiments, j is 7. In certain embodiments, j is 8. In certain embodiments, j is 9. In certain embodiments, j is 10.

As generally defined above, each instance of R^{10} is, independently, hydrogen; acyl; optionally substituted C_{1-6} alkyl; or an amino protecting group. In certain embodiments, R^{10} is hydrogen. In certain embodiments, R^{10} is acyl; optionally substituted C_{1-6} alkyl; or an amino protecting group. In certain embodiments, R^{10} is acyl or optionally substituted C_{1-6} alkyl. In certain embodiments, R^{10} is substituted or unsubstituted alkyl. In certain embodiments, R^{10} is substituted or unsubstituted C_{1-6} alkyl. In certain embodiments, R^{10} is unsubstituted C_{1-6} alkyl. In certain embodiments, R^{10} is methyl, ethyl, or propyl. In certain embodiments, R^{10} is acyl. In certain embodiments, R^{10} is acetyl ($-C(=O)CH_3$). In certain embodiments, R^{10} is an amino protecting group. In certain embodiments, R^{10} is TBS, TBPS, Bn, BOC, Cbz, Fmoc, trifluoroacetyl, triphenylmethyl, or Ts.

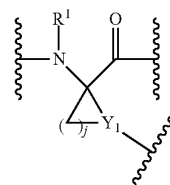
In certain embodiments, at least one instance of R^2 and R^3 together with the carbon atom to which they are attached, are joined to form a ring. In this instance, in certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} carbocyclyl or heterocyclyl. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} carbocyclyl. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl containing at least one O, N, or S atom. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl containing at least one nitrogen atom. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl containing one nitrogen atom. In certain embodiments, the ring formed by R^2 and R^3 together with the carbon atom to which they are attached is unsubstituted C_{3-6} heterocyclyl containing one nitrogen atom.

In certain embodiments, R^2 , R^3 , and the carbon to which R^2 and R^3 are attached are joined to form a ring. In certain embodiments, the ring formed by R^2 , R^3 , and the carbon to which R^2 and R^3 are attached is of the formula:

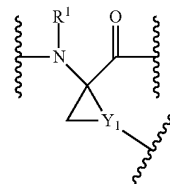


wherein Y_1 is $-CR^8-$ or $-N-$, each of j and j_1 is independently 0, 1, 2, 3, 4, 5, or 6. In certain embodiments, j_1 is zero, and the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:

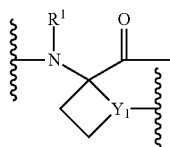
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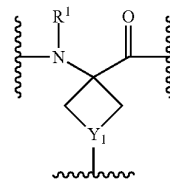
In certain embodiments, j is 0 and Y_1 is directly linked to the alpha-carbon of the amino acid. In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:



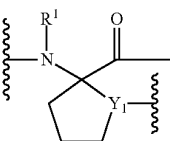
In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:



In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:

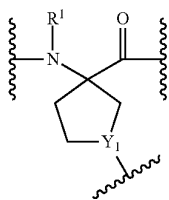


In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:

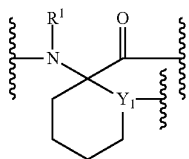


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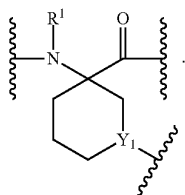
In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:



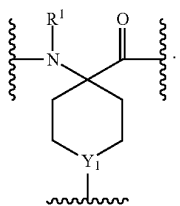
In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:



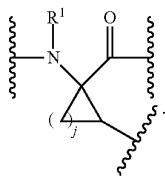
In certain embodiments, the ring formed by R^{2a} , R^{3a} and the carbon to which R^2 and R^3 are attached is of the formula:



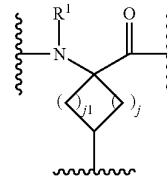
In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:



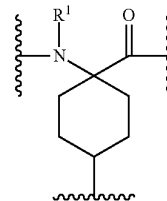
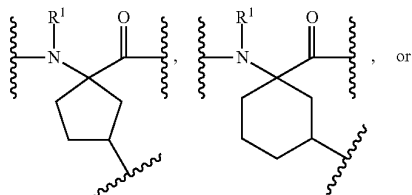
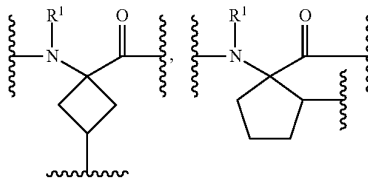
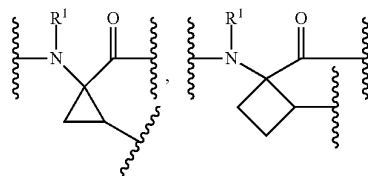
In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:

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In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^2 and R^3 are attached is of the formula:

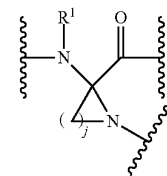


In certain embodiments, the ring formed by R^{2a} , R^{3a} and the carbon to which R^{2a} and R^{3a} are attached is of the formula:



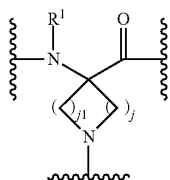
or stereoisomers thereof.

In certain embodiments, the ring formed by R^2 , R^3 and the carbon to which R^{2a} and R^{3a} are attached is of the formula:

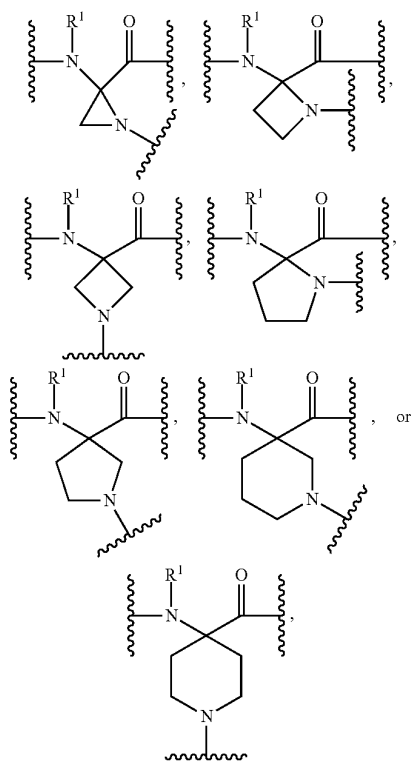


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In certain embodiments, the ring formed by R^{2a} , R^{3a} and the carbon to which R^{2a} and R^{3a} are attached is of the formula:



In certain embodiments, the ring formed by R^{2a} , R^{3a} and the carbon to which R^{2a} and R^{3a} are attached is of the formula:



or stereoisomers thereof.

As used herein, each of j and $j1$ is independently an integer between 1 and 10, inclusive. In some embodiments, j is 1. In some embodiments, j is 2. In some embodiments, j is 3. In some embodiments, j is 4. In some embodiments, j is 5. In some embodiments, j is 6. In some embodiments, j is 7. In some embodiments, j is 8. In some embodiments, j is 9. In some embodiments, j is 10. In some embodiments, $j1$ is 1. In some embodiments, $j1$ is 2. In some embodiments, $j1$ is 3. In some embodiments, $j1$ is 4. In some embodiments, $j1$ is 5. In some embodiments, $j1$ is 6. In some embodiments, $j1$ is 7. In some embodiments, $j1$ is 8. In some embodiments, $j1$ is 9. In some embodiments, $j1$ is 10.

In some embodiments, R^2 , R^3 and the carbon to which R^2 and R^3 are attached are not joined to form a ring. In this instance, R^3 is substituted or unsubstituted alkylene, substituted or unsubstituted alkenylene, substituted or unsubstituted alkynylene, substituted or unsubstituted heteroalkylene, or substituted or unsubstituted heterocyclylene. In

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some embodiments, R^3 is substituted or unsubstituted alkylene. In some embodiments, R^3 is substituted C_{1-10} alkylene. In some embodiments, R^3 is $-(CH_2)_j-$, wherein j is an integer between 0 and 10, inclusive.

In some embodiments, R^2 , R^3 and the carbon to which R^2 and R^3 are attached are not joined to form a ring. In this instance, R^2 is substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, substituted or unsubstituted heteroalkyl, or substituted or unsubstituted heterocyclyl. In some embodiments, R^2 is substituted or unsubstituted C_{1-10} alkyl. In some embodiments, R^2 is substituted methyl. In some embodiments, R^2 is unsubstituted methyl. In some embodiments, R^2 is substituted ethyl. In some embodiments, R^2 is unsubstituted ethyl. In some embodiments, R^2 is substituted or unsubstituted C_{2-6} alkyl.

As generally described above, R^3 is substituted or unsubstituted alkylene; substituted or unsubstituted heteroalkylene; substituted or unsubstituted carbocyclylene; or substituted or unsubstituted heterocyclylene; or optionally R^6 , R^7 and the carbon to which R^6 and R^7 are attached are joined to form a ring. In some embodiments, R^6 is substituted or unsubstituted C_{1-10} alkylene. In some embodiments, R^6 is substituted C_{1-10} alkylene. In some embodiments, R^6 is unsubstituted C_{1-10} alkylene. In some embodiments, R^6 is substituted or unsubstituted heteroalkylene. In some embodiments, R^6 is substituted heteroalkylene. In some embodiments, R^6 is unsubstituted heteroalkylene. In some embodiments, R^6 is substituted or unsubstituted heteroalkylene with at least one nitrogen. In some embodiments, R^6 is $-(CH_2)_k-Y_2-$, wherein k is an integer between 0 and 10, inclusive, and Y_2 is a bond, $-CR^8R^9-$, or $-NR^{10}-$, wherein R^8 , R^9 and R^{10} are as defined herein. In some embodiments, R^6 is $-(CH_2)_k-$. In some embodiments, R^6 is $-(CH_2)_k-NR^{10}-$. In some embodiments, R^6 is $-(CH_2)_k-NH-$. In some embodiments, R^6 is $-(CH_2)_{k+1}-$. In some embodiments, k is 0. In some embodiments, k is 1. In some embodiments, k is 2. In some embodiments, k is 3. In some embodiments, k is 4. In some embodiments, k is 5. In some embodiments, k is 6. In some embodiments, k is 7. In some embodiments, k is 8. In some embodiments, k is 9. In some embodiments, k is 10.

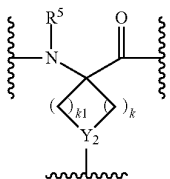
As generally described above, R^7 is substituted or unsubstituted alkyl; substituted or unsubstituted alkenyl; substituted or unsubstituted alkynyl; substituted or unsubstituted heteroalkyl; substituted or unsubstituted carbocyclyl; or substituted or unsubstituted heterocyclyl. In some embodiments, R^7 is substituted or unsubstituted C_{1-10} alkyl. In some embodiments, R^7 is substituted or unsubstituted heteroalkyl. In some embodiments, R^7 is substituted or unsubstituted heteroalkyl with at least one nitrogen atom. In some embodiments, R^7 is unsubstituted heteroalkyl with at least one nitrogen atom. In some embodiments, R^7 is substituted heteroalkyl with at least one nitrogen atom.

In some embodiments, for at least one instance, R^6 , R^7 and the carbon to which R^6 and R^7 are attached are joined to form a ring. In this instance, in some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} carbocyclyl or heterocyclyl. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} carbocyclyl. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or

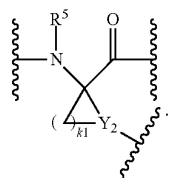
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unsubstituted C_{3-6} heterocyclyl with at least one O, N, or S atom. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl with at least one N. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is substituted or unsubstituted C_{3-6} heterocyclyl with one N. In some embodiments, the ring formed by R^6 and R^7 together with the carbon atom to which they are attached is unsubstituted C_{3-6} heterocyclyl with one N.

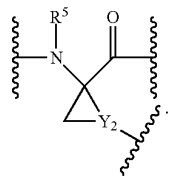
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formulae:



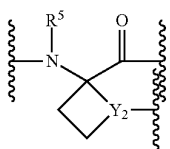
wherein Y_2 is $-CR^8-$ or $-N-$; k is 0, or an integer from 1 to 10, inclusive; and $k1$ is an integer from 1 to 10, inclusive. In some embodiments, $k1$ is zero, and the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



In some embodiments, the ring formed by R^2 , R^{3b} and the carbon to which R^2 and R^{3b} are attached is of the formula:

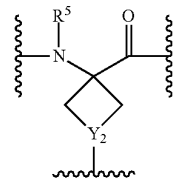


In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:

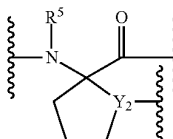


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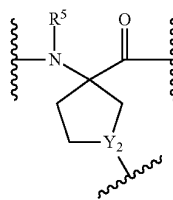
In some embodiments, the ring formed by R^2 , R^{3b} and the carbon to which R^2 and R^{3b} are attached is of the formula:



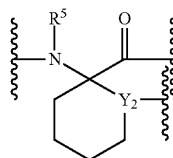
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



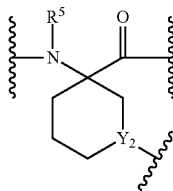
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:

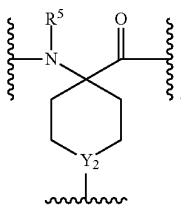


In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:

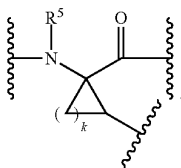


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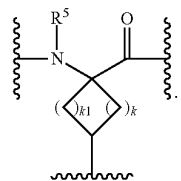
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



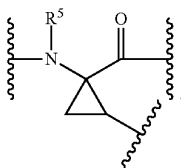
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



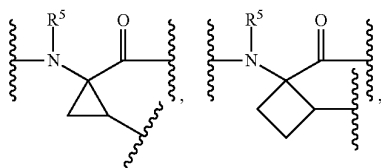
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



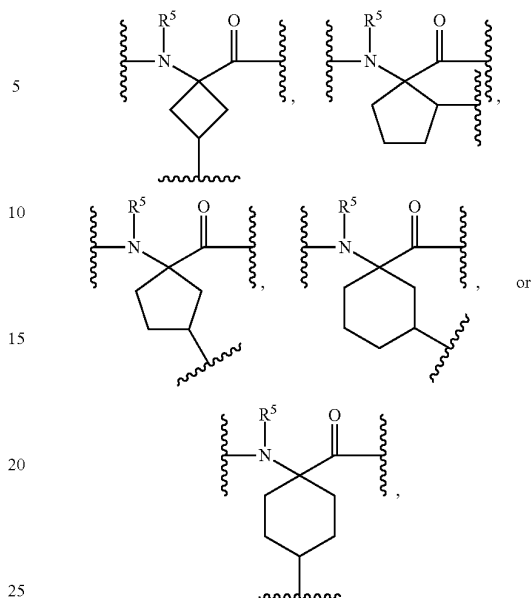
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



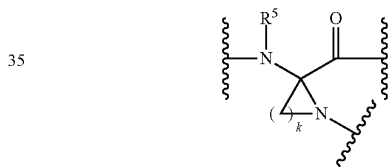
In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:

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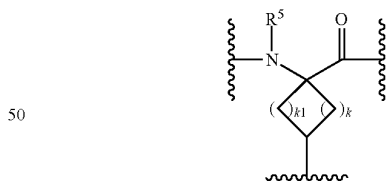
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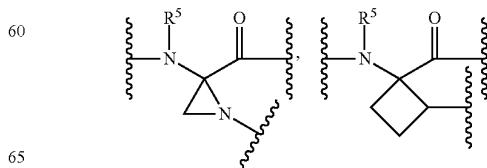
or stereoisomers thereof. In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:

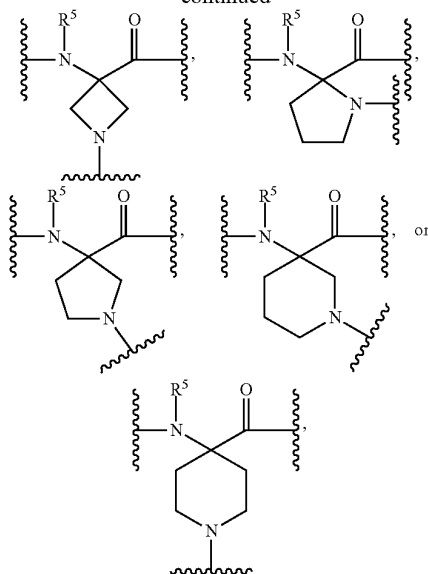


In some embodiments, the ring formed by R^6 , R^7 and the carbon to which R^6 and R^7 are attached is of the formula:



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-continued



or stereoisomers thereof, thereof.

As used herein, k is an integer between 0 and 10, inclusive; and k_1 is an integer between 1 and 10, inclusive. In some embodiments, k is 0. In some embodiments, k is 1. In some embodiments, k is 2. In some embodiments, k is 3. In some embodiments, k is 4. In some embodiments, k is 5. In some embodiments, k is 6. In some embodiments, k is 7. In some embodiments, k is 8. In some embodiments, k is 9. In some embodiments, k is 10. In some embodiments, k_1 is 1. In some embodiments, k_1 is 2. In some embodiments, k_1 is 3. In some embodiments, k_1 is 4. In some embodiments, k_1 is 5. In some embodiments, k_1 is 6. In some embodiments, k_1 is 7. In some embodiments, k_1 is 8. In some embodiments, k_1 is 9. In some embodiments, k_1 is 10.

In some embodiments, R^6 , R^7 and the carbon to which R^6 and R^7 are attached are not joined to form a ring. In this instance, R^6 is substituted or unsubstituted alkylene, substituted or unsubstituted alkenylene, substituted or unsubstituted alkynylene, substituted or unsubstituted heteroalkylene, or substituted or unsubstituted heterocyclylene. In some embodiments, R^6 is substituted or unsubstituted alkylene. In some embodiments, R^6 is substituted C_{1-10} alkylene. In some embodiments, R^6 is $-(CH_2)_k-$, wherein k is as defined above.

In some embodiments, R⁶, R⁷ and the carbon to which R⁶ and R⁷ are attached are not joined to form a ring. In this instance, in some embodiments, R⁷ is substituted or unsubstituted C₁₋₁₀ alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, substituted or unsubstituted heteroalkyl, or substituted or unsubstituted heterocyclyl. In some embodiments, R⁷ is substituted or unsubstituted C₁₋₁₀ alkyl. In some embodiments, R⁷ is substituted methyl. In some embodiments, R⁷ is unsubstituted methyl. In some embodiments, R⁷ is substituted ethyl. In some embodiments, R⁷ is unsubstituted ethyl. In some embodiments, R⁷ is substituted or unsubstituted C₂₋₆ alkyl.

In some embodiments, for at least one instance, R^2 , R^3 , and the carbon to which R^2 and R^3 are attached are not joined to form a ring, and R^6 , R^7 , and the carbon to which R^6 and R^7 are attached are not joined form a ring. In some embodiments, R^2 , R^3 and the carbon to which R^2 and R^3 are

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attached are not joined to form a ring, and R⁶, R⁷ and the carbon to which R⁶ and R⁷ are attached are joined form a ring. In some embodiments, R², R³ and the carbon to which R² and R³ are attached are joined to form a ring, and R⁶, R⁷ and the carbon to which R⁶ and R⁷ are attached are not joined form a ring. In some embodiments, for at least one instance, R², R³ and the carbon to which R² and R³ are attached are joined to form a ring, and R⁶, R⁷ and the carbon to which R⁶ and R⁷ are attached are joined form a ring.

In some embodiments, each instance of R^3 and R^6 are the same. In some embodiments, each instance of R^3 and R^6 are different.

As generally described above, L_1 is a bond, substituted or unsubstituted C_{1-10} alkylene, or $-C(=O)OR^{L1}-$, wherein R^{L1} is optionally substituted C_{1-10} alkylene. In some embodiments, L_1 is substituted or unsubstituted alkylene. In some embodiments, L_1 is substituted C_{1-10} alkylene. In some embodiments, L_1 is $-(CH_2)_g-$, wherein g is 0 or an integer between 1 and 10. In some embodiments, g is 0, and L_1 is a bond. In some embodiments, g is 1. In some embodiments, g is 2. In some embodiments, g is 3. In some embodiments, g is 4. In some embodiments, g is 5. In some embodiments, g is 6. In some embodiments, g is 7. In some embodiments, g is 8. In some embodiments, g is 9. In some embodiments, g is 10. In some embodiments, R^{L1} is substituted C_{1-10} alkylene. In some embodiments, R^{L1} is $-C(=O)O(CH_2)_{g1}-$, wherein $g1$ is an integer between 1 and 10 inclusive. In some embodiments, $g1$ is 1. In some embodiments, $g1$ is 2. In some embodiments, $g1$ is 3. In some embodiments, $g1$ is 4. In some embodiments, $g1$ is 5. In some embodiments, $g1$ is 6. In some embodiments, $g1$ is 7. In some embodiments, $g1$ is 8. In some embodiments, $g1$ is 9. In some embodiments, $g1$ is 10.

As generally described above, L_2 is a bond, substituted or unsubstituted C_{1-10} alkylene, or $-C(=O)OR^{L2}-$, wherein R^{L2} is optionally substituted C_{1-10} alkylene. In some embodiments, L_2 is substituted or unsubstituted alkylene. In some embodiments, L_2 is substituted C_{1-10} alkylene. In some embodiments, L_2 is $-(CH_2)_h-$, wherein h is 0 or an integer between 1 and 10 inclusive. In some embodiments, h is 0, and L_2 is a bond. In some embodiments, h is 1. In some embodiments, h is 2. In some embodiments, h is 3. In some embodiments, h is 4. In some embodiments, h is 5. In some embodiments, h is 6. In some embodiments, h is 7. In some embodiments, h is 8. In some embodiments, h is 9. In some embodiments, h is 10. In some embodiments, R^{L2} is substituted C_{1-10} alkylene. In some embodiments, R^{L2} is $-C(=O)O(CH_2)_{h1}-$, wherein $h1$ is an integer between 1 and 10 inclusive. In some embodiments, $h1$ is 1. In some embodiments, $h1$ is 2. In some embodiments, $h1$ is 3. In some embodiments, $h1$ is 4. In some embodiments, $h1$ is 5. In some embodiments, $h1$ is 6. In some embodiments, $h1$ is 7. In some embodiments, $h1$ is 8. In some embodiments, $h1$ is 9. In some embodiments, $h1$ is 10.

In some embodiments, each instance of L_1 and L_2 is the same. In some embodiments, each instance of L_1 and L_2 is different.

Group R^1 and R^5

As generally defined above, R¹ and R⁵ are, independently, hydrogen; acyl; optionally substituted C₁₋₆ alkyl; or an amino protecting group.

In some embodiments, R¹ is hydrogen. In some embodiments, R¹ is acyl; optionally substituted C₁₋₆ alkyl; or an amino protecting group. In some embodiments, R¹ is acyl or optionally substituted C₁₋₆ alkyl.

In some embodiments, R¹ is substituted or unsubstituted alkyl. In some embodiments, R¹ is substituted or unsubsti-

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tuted C₁₋₆ alkyl. In some embodiments, R¹ is unsubstituted C₁₋₆ alkyl. In some embodiments, R¹ is methyl, ethyl, or propyl.

In some embodiments, R¹ is acyl. In some embodiments, R¹ is acetyl (—C(=O)CH₃).

In some embodiments, R¹ is an amino protecting group. In some embodiments, R¹ is TBS, TBPS, Bn, BOC, Cbz, Fmoc, trifluoroacetyl, triphenylmethyl, or Ts.

In some embodiments, R⁵ is hydrogen. In some embodiments, R⁵ is acyl; optionally substituted C₁₋₆ alkyl; or an amino protecting group. In some embodiments, R⁵ is acyl or optionally substituted C₁₋₆alkyl.

In some embodiments, R⁵ is substituted or unsubstituted alkyl. In some embodiments, R⁵ is substituted or unsubstituted C₁₋₆ alkyl. In some embodiments, R⁵ is unsubstituted C₁₋₆ alkyl. In some embodiments, R⁵ is methyl, ethyl, or propyl.

In some embodiments, R⁵ is acyl. In some embodiments, R⁵ is acetyl (—C(=O)CH₃).

In some embodiments, R⁵ is an amino protecting group. In some embodiments, R⁵ is TBS, TBPS, Bn, BOC, Cbz, Fmoc, trifluoroacetyl, triphenylmethyl, or Ts.

In some embodiments, R¹ and R⁵ are, independently, hydrogen, C₁₋₆alkyl (e.g., methyl), or acyl. In some embodiments, R¹ and R⁵ are hydrogen.

In some embodiments, R¹ and R⁵ are, independently, hydrogen, optionally substituted C₁₋₆alkyl (e.g., methyl), or acyl. In some embodiments, R¹ and R⁵ are, independently, hydrogen, methyl, or acetyl. In some embodiments, R¹ and R⁵ are, independently, hydrogen or methyl. In some embodiments, R¹ and R⁵ are hydrogen. In some embodiments, R¹ and R⁵ are methyl.

Groups , R⁴ and P

As generally defined above, represents a single bond or a double bond. In some embodiments, is a single bond. In some embodiments, is a double bond.

As generally defined above, each instance of R⁴ is independently hydrogen; optionally substituted aliphatic; optionally substituted heteroaliphatic; substituted or unsubstituted aryl; optionally substituted heteroaryl; acyl; optionally substituted hydroxyl; optionally substituted thiol; optionally substituted amino; azido; cyano; isocyanato; halo; or nitro.

As generally defined above, p is 0, 1, or 2.

In some embodiments, each instance of p is 0, and thus each instance of R⁴ is absent to provide an unsubstituted crosslink. In some embodiments at least one instance of p is 1, and thus at least one instance of R⁴ is a non-hydrogen substituent.

In some embodiments, after stapling of an inventive polypeptide, the method further comprises additional synthetic modification of the unsaturated staple or stitch of the cross-linked peptides. Any chemical or biological modification to the stapled or stitched polypeptide may be made. In some embodiments, the modifications are carried out on the Alloc moiety of a polypeptide. In some embodiments, the modifications extrude CO₂ from the Alloc moiety from the stapled peptides. In some embodiments, the CO₂ extrusion is carried out in the presence of a palladium catalyst. In some embodiments, the CO₂ extrusion is carried out in the presence of Pd(PPh₃)₄. In some embodiments, the modification comprises alkylation on the amide group of the staple or stitch.

In some embodiments, additional modifications of the stapled or stitched peptides include reduction, oxidation, and nucleophilic or electrophilic additions to the double bond provided from a metathesis reaction to provide a syntheti-

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cally modified polypeptide. Other modifications may include conjugation of a stapled polypeptide, or a synthetically modifying the stapled polypeptide with a therapeutically active agent, label, or diagnostic agent anywhere on the stapled polypeptide scaffold, e.g., such as at the N-terminus of the stapled polypeptide, the C-terminus of the stapled polypeptide, on an amino acid side chain of the stapled polypeptide, or at one or more modified or unmodified stapled sites (i.e., to a staple). Such modification may be useful in delivery of the peptide or therapeutically active agent to a cell, tissue, or organ. Such modifications may, in some embodiments, allow for targeting to a particular type of cell or tissue.

The staples or stitches of the polypeptide may further comprise additional synthetic modification(s). Any chemical or biological modification may be made. In some embodiments, the staple or stitch has an Alloc group. In some embodiments, the modifications are carried out on the Alloc moiety of a polypeptide. In some embodiments, the modifications extrude CO₂ from the Alloc moiety from the stapled peptides. In some embodiments, the CO₂ extrusion is carried out in the presence of a palladium catalyst. In some embodiments, the CO₂ extrusion is carried out in the presence of Pd(PPh₃)₄. In some embodiments, such modifications include reduction, oxidation, and nucleophilic or electrophilic additions to the double bond provided from a metathesis reaction of the cross-link to provide a synthetically modified stapled or stitched polypeptide. One of ordinary skill in the art will appreciate that a wide variety of conditions may be employed to promote such transformations, therefore, a wide variety of conditions are envisioned; see generally, *March's Advanced Organic Chemistry: Reactions, Mechanisms, and Structure*, M. B. Smith and J. March, 5th Edition, John Wiley & Sons, 2001; *Advanced Organic Chemistry, Part B: Reactions and Synthesis*, Carey and Sundberg, 3rd Edition, Plenum Press, New York, 1993; and *Comprehensive Organic Transformations*, R. C. Larock, 2nd Edition, John Wiley & Sons, 1999, the entirety of each of which is hereby incorporated herein by reference. In other embodiments, the staple(s) of the polypeptide are not further modified.

In some embodiments, the staple or stitch has a double bond. In some embodiments, the modifications are carried out on the double bond of the stapled or stitched polypeptide. Exemplary conditions may be any reagent reactive with a double bond. In some embodiments, the reagent is able to react with a double bond, for example, via a hydrogenation, osmylation, hydroxylation (mono- or di-), amination, halogenation, cycloaddition (e.g., cyclopropanation, aziridination, epoxidation), oxy-mercuration, and/or a hydroboration reaction, to provide a functionalized single bond. As one of ordinary skill in the art will clearly recognize, these above-described transformations will introduce functionalities compatible with the particular stabilized structures and the desired biological interactions; such functionalities include, but are not limited to, hydrogen; substituted or unsubstituted aliphatic; substituted or unsubstituted heteroaliphatic; substituted or unsubstituted aryl; substituted or unsubstituted heteroaryl; acyl; substituted or unsubstituted hydroxyl; substituted or unsubstituted amino; substituted or unsubstituted thiol, halo; cyano; nitro; azido; imino; oxo; and thiooxo.

Other modifications may further include conjugation of the stapled or stitched polypeptide, or a synthetically modified stapled or stitched polypeptide, with a biologically active agent, label, targeting moiety, diagnostic agent, anywhere on the polypeptide scaffold, e.g., such as at the

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N-terminus of the polypeptide, the C-terminus of the polypeptide, on an amino acid side chain of the polypeptide, or at one or more modified or unmodified stapled sites. Such modification may be useful in delivery of the peptide or biologically active agent to a cell, tissue, or organ. Such modifications may allow for targeting of the stabilized polypeptide to a particular type of cell or tissue. Conjugation of an agent (e.g., a label, a diagnostic agent, a biologically active agent, a targeting moiety) to the stapled polypeptide may be achieved in a variety of different ways. The agent may be covalently conjugated, directly or indirectly, to the polypeptide at the site of stapling, or to the N-terminus or the C-terminus of the polypeptide. Alternatively, the agent may be noncovalently conjugated, directly or indirectly, to the polypeptide at the site of stapling, or to the N-terminus or the C-terminus of the polypeptide, or any other site on the polypeptide. Indirect covalent conjugation is by means of one or more covalent bonds. Indirect non-covalent conjugation is by means of one or more non-covalent interactions. Conjugation may also be via a combination of non-covalent and covalent interactions. The agent may also be conjugated to the polypeptide through a linker. Any number of covalent bonds may be used in the conjugation of a biologically active agent and/or diagnostic agent to the inventive polypeptide of the present invention. Such bonds include amide linkages, ester linkages, disulfide linkages, carbon-carbon bonds, carbamate linkages, carbonate linkages, urea linkages, hydrazide linkages, and the like. In some embodiments, the bond is cleavable under physiological conditions (e.g., enzymatically cleavable, cleavable at a high or low pH, with heat, light, ultrasound, x-ray, etc.). However, in some embodiments, the bond is not cleavable.

In some embodiments, the additional modification is PEGylation. The PEGylation of the stapled or stitched polypeptide can be carried out using any of the PEGylation reactions known in the art. Such reactions are described, for example, in the following references: Francis et al., (1992), Focus on Growth Factors 3: 4-10; European Patent Nos. 0 154 316 and 0 401 384; and U.S. Pat. No. 4,179,337. For example, PEGylation can be carried out via an acylation reaction or an alkylation reaction with a reactive polyethylene glycol molecule (or an analogous reactive water-soluble polymer) as described herein. For the acylation reactions, a selected polymer should have a single reactive ester group. For reductive alkylation, a selected polymer should have a single reactive aldehyde group. A reactive aldehyde is, for example, polyethylene glycol propionaldehyde, which is water stable, or mono C₁₋₁₀ alkoxy or aryloxy derivatives thereof (see, e.g., U.S. Pat. No. 5,252,714).

The stapled peptides of the invention may be synthesized using methods known in the art, e.g., general methods of preparing the stapled or stitched peptides and addition modifications are described in U.S. Pat. Nos. 7,192,713; 7,723,469; 7,786,072; 8,198,405; 8,324,428; 8,592,377; 8,796,418; 8,889,632; 8,895,699; 9,074,009; 9,273,099; 9,556,227; 9,617,309; U.S. Patent Application Publication Nos: 2010-0184645; 2010-0168388; 2010-0081611; 2009-0176964; 2009-0149630; 2006-0008848; 2014-0296160; 2014-162339; 2014-0011979; 2015-0239937; 2015-119951; 2016-0024153; 2016-0215036; 2016-0244494; 2017-0240604; 2017-0066799; PCT Application Publication Nos: WO 2010/011313; WO 2008/121767; WO 2008/095063; WO 2008/061192; WO2014/055564; and WO 2005/044839, as well as PCT Application No. PCT/US2014/025544; the synthetic methods of which are incorporated by references herein.

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Small Multidrug Resistance Transporters

The polypeptides of the invention include sequences of small multidrug resistance transporters of which two amino acids have been replaced with a cross-link. In some embodiments, the α -helix which is stabilized to produce the polypeptides of the invention is:

DLPATIGMMLICAGVLIINLLS (SEQ ID NO: 1)

Exemplary sequences of small multidrug resistance transporters which include an α -helix include:

Multidrug transporter EmrE (*Escherichia coli* (strain K12)):

MNPYIYLGGAAILAEVIGTTLMKFSEGFTDRWPSVGTIICYASFLLAQT (SEQ ID NO: 2)

LAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPATIGMMLICAGVLIINLLSRSTPH

Antiseptic-resistance protein (*Escherichia coli*): (SEQ ID NO: 3)

MKGWLFVLVIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYIAFYFLSLV

LKSIPVGVAYAVWSGLGVVITAIWLLHGGKLDAGFVGMGLIIAFLARSPSWKSLRRPTPW

Multidrug SMR transporter (*Escherichia coli*): (SEQ ID NO: 4)

MNPYIYLGGAAILAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQT

LAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPATIGMMLICAGVLVINLLSRSAHP

EmrE (*Mycobacterium tuberculosis*): (SEQ ID NO: 5)

MYIRTQGEVLTYFPLCAIAEAAATSLFKGSFGDFRVCSPGHDGAIAMP

SVLAASRIRSS

EmrE protein (*Mycobacterium orygis*): (SEQ ID NO: 6)

MIYLYLLCAIFAEVVATSLKSTEGFTRLWPTVGCIVGYIAFALLALSI

SHGMQTDVAYALWSAIGTAAIVLVAVLFLGSPISVMKVVGVLIVGVVTLNLAGAH

Ethidium bromide resistance protein (*Enterobacter cloacae*): (SEQ ID NO: 7)

MKGWLFVLVIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYIAFYFLSLV

LKSIPVGVAYAVWSGLGVVITAIWLLHGGKLDAGFVGMGLIIAFLARSPSWKSLRRPTPW

Orf3/QacEdelta1 fusion protein (*Klebsiella pneumoniae*): (SEQ ID NO: 8)

MKGWLFVLVIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYIAFYFLSLV

LKSIPVGVAYAVWSGLGVVITAIWLLHGGKLDAGFVGMGLIIAFLARSPSWKSLRRPTPW

Antiseptic-resistance protein (*Escherichia coli*): (SEQ ID NO: 9)

MKGWLFVLVIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYIAFYFLSLV

LKSIPVGVAYAVWSGLGVVITAIWLLHGGKLDAGFVGMGLIIAFLARSPSWKSLRRPTPW

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Ethidium bromide resistance protein (*Pseudomonas aeruginosa*):
(SEQ ID NO: 10)
MKGWLFVLVIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYIAFYFLSLV
LKSIPVGVAIVWSGLGVVITTAIAWLLHGQKLDAGFVGMGLIIAFL
ARSPSWKSLRRPTPW

Multidrug transporter (*Providencia rettgeri*):
(SEQ ID NO: 11)
MKGWLELVTAIVGEVIATSALKSSEGFTKLAPSAVVIIGYTAIFYFLSLV
LKSIPVGVAIVWSGLGVVITTAIAWLLHGQKLDAGFVGMGLIIAFL
ARSPSWKSLRRPTPW

Multidrug DMT transporter (*Pseudomonas citronellolis*):
(SEQ ID NO: 12)
MPGYLYLAIAIAEVIATSLKSVKGLSTPLPLLLVIVGYAISFWMLTV
VRSIPVGIAYAIWAGLGIVLVSAALVLYQQKLDAPALLGMGLIVSGVV
IQLFSGSVSH

Methyl viologen resistance protein C (*Pseudomonas aeruginosa*):
(SEQ ID NO: 13)
MTNYLYLAIAIAAEVVAATSLKAVAGFSKPLPLLLVVGYYLAFSMLVLV
MRTLPGVGVYAIWSGLGIVLVSLVAMFVYQRLDPAALLGIGLIIAGVLV
IQLFSRASGH

Methyl viologen resistance protein C (*Pseudomonas aeruginosa*):
(SEQ ID NO: 14)
MNPYIYLAAAIVLEVIATSLKASDGMSRLWPTVGALVGYGLCFYLLSVT
MKSVPPTGIAYAIWSGVGIVLISLIGLVVFKQRLDAPALIGIGLICAGVLV
INLFSRSSAH

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Membrane transport protein (*Bordetella pertussis*):
(SEQ ID NO: 15)
MNSWIHLMAIVAIEIATSALKSSEGFTRLPLSLVTAGYAIAPYFLALT
LRVIPVGVAIVWSGVGIVLISLVGALLFKQHLDLPAIIGIALILAGVVV
MNVFSKSVGH

Membrane transport protein (*Bordetella pertussis*):
(SEQ ID NO: 16)
MAGYAIAPYFTALTLRVIPVGVAIVWSGVGIVLISLVGALLFKQHLDLP
AIIGIALILAGVVMNVFSKSVGH

Membrane transport protein (*Bordetella pertussis*):
(SEQ ID NO: 17)
MGVAYAIWSGVGIVLISLVGALLFKQHLDLPAIIGIALILAGVVMNVFS
KSVGK

Ethidium bromide-methyl viologen resistance protein EmrE (*Neisseria meningitidis* serogroup B):
(SEQ ID NO: 18)
MPLATAYAIWAGVGINLTALVSVVFFGEKADFIGIVSIGLILLGVVLLNT
MSHMSGH

Quaternary ammonium compound-resistance protein, small multidrug resistance protein family (*Bacillus cereus* var. anthracis (strain Cl)):
(SEQ ID NO: 19)
MKNKAWLYVILTCEFEVFWVGFNTANTWWHWIIILGVIADVDFHFLSKAC
EHLATGTVYAVFAGAGTVGTFMLMDVFLFGGSFVSGKLFIVMVVAGVIGL
KLADNKEETVEGAA

Quaternary ammonium compound-resistance protein QacC (*Staphylococcus aureus*):
(SEQ ID NO: 20)
MPYIYLIIAISTEVIGSAFLKSSEGFSKFIPSLGTIISFGICFYFLSKTM
QHLPLNITYATWAGLGLVLTTVVSIIPKEQINLITIVSIVLIIIVGVVSL
NIFGTSH

Further exemplary polypeptides which include an α -helix include polypeptides which include a sequence at least 80% identical to SEQ ID NO:1:

Membrane transporters of cations and cationic drugs domain-containing protein (*Fundulus heteroclitus*):
(SEQ ID NO: 21)
MNPYIYLGGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2.3916):
(SEQ ID NO: 22)
MNPYIYLGGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMN18):
(SEQ ID NO: 23)
MNPYIYLGGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

QacE family quaternary ammonium compound efflux SMR transporter (*Escherichia coli*):
(SEQ ID NO: 24)
MNPYIYLGGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* (strain K12)): (SEQ ID NO: 25)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Hypothetical phage protein (*Escherichia coli* (strain SE11)): (SEQ ID NO: 26)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H591): (SEQ ID NO: 27)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE75): (SEQ ID NO: 28)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* B088): (SEQ ID NO: 29)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

EmrE protein (*Escherichia coli* (strain 55989/EAEC)): (SEQ ID NO: 30)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-427-07_S4_C3): (SEQ ID NO: 31)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 4.0967): (SEQ ID NO: 32)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 3-267-03_S4_C1): (SEQ ID NO: 33)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter (*Escherichia coli* O146:H21 str. 2010C-3325): (SEQ ID NO: 34)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* MS 145-7): (SEQ ID NO: 35)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-011-08_S1_C1): (SEQ ID NO: 36)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE66): (SEQ ID NO: 37)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* B185):
(SEQ ID NO: 38)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

EmrE protein (*Escherichia coli* O139:H28 (strain E24377A/ETEC)):
(SEQ ID NO: 39)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C3):
(SEQ ID NO: 40)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C1):
(SEQ ID NO: 41)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMEA 3718-1):
(SEQ ID NO: 42)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*):
(SEQ ID NO: 43)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug resistance protein DLP12 prophage (*Escherichia coli* NCCP15648):
(SEQ ID NO: 44)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* O83:H1 (strain NRG 857C/AIEC)):
(SEQ ID NO: 45)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli* O157):
(SEQ ID NO: 46)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE100):
(SEQ ID NO: 47)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia sp.* KTE159):
(SEQ ID NO: 48)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* Xuzhou21):
(SEQ ID NO: 49)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Ethidium bromide-methyl viologen resistance protein EmrE (*Escherichia coli* O157:H7 str. SS52):
(SEQ ID NO: 50)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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EmrE protein (*Escherichia coli* O157:H7 (strain EC869)): (SEQ ID NO: 51)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*): (SEQ ID NO: 52)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Integral membrane drug resistance protein EmrE (*Escherichia coli* O157:H7): (SEQ ID NO: 53)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli*): (SEQ ID NO: 54)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* HVH 70 (4-2963531)): (SEQ ID NO: 55)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* (strain UMEA 3162-1)): (SEQ ID NO: 56)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-005-03_S4_C3): (SEQ ID NO: 57)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H420): (SEQ ID NO: 58)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* DEC6A): (SEQ ID NO: 59)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 97.0246): (SEQ ID NO: 60)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* O104:H4 (strain 2011C-3493)): (SEQ ID NO: 61)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* O111:H8 sir. CVM9634): (SEQ ID NO: 62)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE73): (SEQ ID NO: 63)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* HVH 70 (4-2963531)): (SEQ ID NO: 64)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMNK88): (SEQ ID NO: 65)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia fergusonii*): (SEQ ID NO: 66)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* B088): (SEQ ID NO: 67)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Ethidium bromide-methyl viologen resistance protein EmrE
(*Escherichia coli* ISC7): (SEQ ID NO: 68)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* TA054): (SEQ ID NO: 69)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* ATCC BAA-2209): (SEQ ID NO: 70)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia sp.* KTE114): (SEQ ID NO: 71)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* HVH 25 (4-5851939)): (SEQ ID NO: 72)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H461): (SEQ ID NO: 73)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* M718): (SEQ ID NO: 74)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Methyl viologen resistance protein C (*Achromobacter sp.*): (SEQ ID NO: 75)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KOEGE 71 (186a)): (SEQ ID NO: 76)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* 2-427-07_S4_C3):
(SEQ ID NO: 77)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* O111:NM sir. K6722):
(SEQ ID NO: 78)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Quaternary ammonium transporter (*Escherichia coli* APEC O2-211):
(SEQ ID NO: 79)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE21):
(SEQ ID NO: 80)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug resistance protein (*Escherichia coli* (strain ATCC 9637/CCM
2024/DSM 1116/NCIMB 8666/NRRL B-766/W)): (SEQ ID NO: 81)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-177-06_S3_C3):
(SEQ ID NO: 82)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 3-267-03_S4_C1):
(SEQ ID NO: 83)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* HVH 50 (4-2593475)): (SEQ ID NO: 84)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1.2264):
(SEQ ID NO: 85)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* K-227): (SEQ ID NO: 86)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* 2a sir. 301): (SEQ ID NO: 87)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Methylviologen resistance (*Shigella sonnei* (strain Ss046)): (SEQ ID NO: 88)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* O174:H8 sir. 04-3038): (SEQ ID NO: 89)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* KTE108): (SEQ ID NO: 90)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Methylviologen resistance (*Escherichia coli* G3/10): (SEQ ID NO: 91)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Small Multidrug Resistance protein (*Escherichia coli* TW10509): (SEQ ID NO: 92)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 4.0522): (SEQ ID NO: 93)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Integral membrane drug resistance protein EmrE (*Escherichia coli* O111:H- (strain 11128/EHEC)): (SEQ ID NO: 94)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE20): (SEQ ID NO: 95)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-005-03_S4_C2): (SEQ ID NO: 96)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* M605): (SEQ ID NO: 97)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* TA447): (SEQ ID NO: 98)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli* O104:H4): (SEQ ID NO: 99)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMEA 3212-1): (SEQ ID NO: 100)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-177-06_S3_C2): (SEQ ID NO: 101)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 99.0741): (SEQ ID NO: 102)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* UMEA 3323-1): (SEQ ID NO: 103)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE10): (SEQ ID NO: 104)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE182): (SEQ ID NO: 105)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H386): (SEQ ID NO: 106)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* O83:H1 (strain NRG 857C/AIEC)): (SEQ ID NO: 107)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C3): (SEQ ID NO: 108)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C1): (SEQ ID NO: 109)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-176-05_S3_C2): (SEQ ID NO: 110)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* O25b:H4-ST131): (SEQ ID NO: 111)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* VA-6): (SEQ ID NO: 112)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H736): (SEQ ID NO: 113)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella flexneri* 4c): (SEQ ID NO: 114)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella flexneri*): (SEQ ID NO: 115)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

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Multidrug SMR transporter (*Escherichia coli*):
(SEQ ID NO: 116)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella sonnei*):
(SEQ ID NO: 117)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H605):
(SEQ ID NO: 118)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Quaternary ammonium transporter (*Escherichia coli* APEC O18):
(SEQ ID NO: 119)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N40513):
(SEQ ID NO: 120)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N40607):
(SEQ ID NO: 121)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug resistance protein DLP12 prophage (*Escherichia coli* NCCP15648):
(SEQ ID NO: 122)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N36254PS):
(SEQ ID NO: 123)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella boydii*):
(SEQ ID NO: 124)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella flexneri* 1a):
(SEQ ID NO: 125)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* MS 84-1):
(SEQ ID NO: 126)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* MS 124-1):
(SEQ ID NO: 127)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 110957):
(SEQ ID NO: 128)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* MS 85-1): (SEQ ID NO: 129)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* MS 117-3): (SEQ ID NO: 130)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 909945-2): (SEQ ID NO: 131)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 113290): (SEQ ID NO: 132)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* MS 115-1): (SEQ ID NO: 133)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* (strain MS 21-1)): (SEQ ID NO: 134)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGPFQQRDLPAIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia* sp. KTE52): (SEQ ID NO: 135)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

Uncharacterized protein (*Escherichia fergusonii* ECD227): (SEQ ID NO: 136)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

EmrE SMR transporter (*Escherichia coli* O55:H7 (strain CB9615/EPEC)): (SEQ ID NO: 137)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

SMR family multidrug resistance protein (*Klebsiella oxytoca*): (SEQ ID NO: 138)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* O128:H2 str. 2011C-3317): (SEQ ID NO: 139)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

Multidrug efflux protein (*Escherichia coli* O157:H7 str. SS52): (SEQ ID NO: 140)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 97.0259): (SEQ ID NO: 141)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG VGIVLIS
LLSWGLFGQRDLPAIIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* 9.0111): (SEQ ID NO: 142)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*): (SEQ ID NO: 143)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N37139PS): (SEQ ID NO: 144)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N36410PS): (SEQ ID NO: 145)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* N37122PS): (SEQ ID NO: 146)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE31): (SEQ ID NO: 147)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*): (SEQ ID NO: 148)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE33): (SEQ ID NO: 149)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* 2850-71): (SEQ ID NO: 150)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE11): (SEQ ID NO: 151)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE52): (SEQ ID NO: 152)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE96): (SEQ ID NO: 153)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE159): (SEQ ID NO: 154)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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QacE family quaternary ammonium compound efflux SMR transporter
(*Escherichia coli*): (SEQ ID NO: 155)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*): (SEQ ID NO: 156)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella sonnei*): (SEQ ID NO: 157)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella sonnei*): (SEQ ID NO: 158)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* E1118): (SEQ ID NO: 159)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGLFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE108): (SEQ ID NO: 160)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFVQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Shigella* sp. RAMC 28760): (SEQ ID NO: 161)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLLWGFFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli* BL21-DE3) (SEQ ID NO: 162)
MNPYIYLGGAIAEVI GTTLMKFSEGFTRLWPSVGTIICYCASFWLLAWLAYIPTGIAYAIWSGVGIVLIS
LLLWGFFGQRLDLP AIGMMLICAGVLVINLLSRSTPH

Multidrug transporter (*Escherichia coli* SE11) (SEQ ID NO: 163)
MNSFVSLGFLLLIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVI G
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLP AII
GMMLICAGVLVINLLSR SAPH

Methylviologen transporter EmrE (*Shigella flexneri* strain 8401) (SEQ ID NO: 164)
MNSFVSLGFLLLIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVI G
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLP AII
GMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* O1:K1) (SEQ ID NO: 165)
MNSFVSLGFLLLIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVI G
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLP AII
GMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Shigella flexneri* strain 2002017) (SEQ ID NO: 166)
MNSFVSLGFLLLIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVI G
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLP AII
GMMLICAGVLVINLLSR SAPH

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Multidrug transporter EmrE (*Shigella sonnei*) (SEQ ID NO: 167)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAILAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLP
GMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O45:K1) (SEQ ID NO: 168)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* strain 55989) (SEQ ID NO: 169)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O8 strain ED1a) (SEQ ID NO: 170)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* strain UT189/UPEC) (SEQ ID NO: 171)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O6:H1 strain CFT073) (SEQ ID NO: 172)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O25b:H4) (SEQ ID NO: 173)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O25b:H4-ST131) (SEQ ID NO: 174)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* TW10598) (SEQ ID NO: 175)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* 1.2741) (SEQ ID NO: 176)
MNPYIYLGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAIIGMMLICAGVLVINLLSRSAPH

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Multidrug SMR transporter (*Escherichia coli* M863)
(SEQ ID NO: 177)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Escherichia coli*)
(SEQ ID NO: 178)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Shigella sonnei*)
(SEQ ID NO: 179)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Escherichia coli*)
(SEQ ID NO: 180)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* DORA_B_14)
(SEQ ID NO: 181)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli*)
(SEQ ID NO: 182)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* 908573)
(SEQ ID NO: 183)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Shigella* sp. FC2928)
(SEQ ID NO: 184)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* HVH 41)
(SEQ ID NO: 185)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

QacE quaternary ammonium compound efflux SMR transporter
(*Escherichia coli*)
(SEQ ID NO: 186)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Shigella boydii*)
(SEQ ID NO: 187)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Shigella dysenteriae*)
(SEQ ID NO: 188)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Shigella dysenteriae*)
(SEQ ID NO: 189)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLPAAIGMMLICAGVLVINLLRSAPH

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Multidrug transporter EmrE (*Escherichia* sp. KTE11) (SEQ ID NO: 190)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia aibertii* B156) (SEQ ID NO: 191)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Escherichia* sp. KTE96) (SEQ ID NO: 192)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia* sp. KTE159) (SEQ ID NO: 193)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 194)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli*) (SEQ ID NO: 195)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Escherichia albertii*) (SEQ ID NO: 196)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Escherichia coli* E1118) (SEQ ID NO: 197)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Ethidium bromide-methyl viologen transporter EmrE (*Escherichia aibertii* KF1) (SEQ ID NO: 198)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Escherichia albertii*) (SEQ ID NO: 199)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Escherichia* sp. KTE52) (SEQ ID NO: 200)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFSQRLDLP AIIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia aibertii* strain TW07627) (SEQ ID NO: 201)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIANAIWSGVGIVLIS
LLSWGIFGQRLDLP AIIGMMLICAGVLVINLLRSATH

Multidrug transporter EmrE (*Shigella sonnei*) (SEQ ID NO: 202)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVNLGDAANLLI

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Multidrug transporter EmrE (*Shigella flexneri* 5a strain M90T)
 (SEQ ID NO: 203)
 MNSFVSLGFLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
 TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
 GMMLICAYYG

Multidrug transporter EmrE (*Citrobacter* sp. MGH106)
 (SEQ ID NO: 204)
 MNTYIYLGGAIAEVTGTTLMKFDTGFTRLWPSVGTIVCYCASFWLLSQTLAHIPTGIAYAIWSGVGIVLIS
 LLAWVIHQRLDLPAAIGMALICAGVLIINLLSRSAVH

Multidrug SMR transporter (*Escherichia coli*)
 (SEQ ID NO: 205)
 MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSAGTIIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFGQRLDLPAAIDTVMACKFFPGFVSR

Multidrug SMR transporter (*Paenibacillus* sp. VT-16-81)
 (SEQ ID NO: 206)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFGQRLDLPAAI

Ethidium bromide-methyl viologen EmrE transporter (*Klebsiella pneumoniae*)
 (SEQ ID NO: 207)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFLPTAGPASHYRHDVDLCRCVGY

Multidrug SMR transporter (*Shigella sonnei*)
 (SEQ ID NO: 208)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVRYCPD

Multidrug transporter EmrE (*Escherichia coli*)
 (SEQ ID NO: 209)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWYMRTFISCK
 R

Further exemplary polypeptides which include an α -helix include polypeptides which include a sequence at least 80% identical to PAIGMMLICAG (SEQ ID NO: 210):

Multidrug transporter EmrE (*Escherichia coli* O104:H4 strain 2011C-3493)
 (SEQ ID NO: 211)
 MNRKEYAMNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWYMR
 RTFISCKR

Membrane transporters of cations (*Fundulus heteroclitus*)
 (SEQ ID NO: 212)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2.3916)
 (SEQ ID NO: 213)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMN18)
 (SEQ ID NO: 214)
 MNPYIYLGGAIAEVIPTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
 LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

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QacE family quaternary ammonium compound efflux SMR transporter
(*Escherichia coli*) (SEQ ID NO: 215)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* strain K12) (SEQ ID NO: 216)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug SMR transporter (*Shigella sonnei*) (SEQ ID NO: 217)
MLSGQSGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* strain UMEA 3162-1) (SEQ ID NO: 218)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLIINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE11) (SEQ ID NO: 219)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE52) (SEQ ID NO: 220)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE52) (SEQ ID NO: 221)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli* strain SE11) (SEQ ID NO: 222)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 2-005-03_S4_C3) (SEQ ID NO: 223)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H420) (SEQ ID NO: 224)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* DEC6A) (SEQ ID NO: 225)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 97.0246) (SEQ ID NO: 226)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O104:H4 strain 2011C-3493) (SEQ ID NO: 227)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* H591)
(SEQ ID NO: 228)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia fergusonii* ECD227)
(SEQ ID NO: 229)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O111:H8 str. CVM9634)
(SEQ ID NO: 230)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O55:H7 strain CB9615/EPEC)
(SEQ ID NO: 231)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE73)
(SEQ ID NO: 232)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE75)
(SEQ ID NO: 233)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* HVH 70 4-2963531)
(SEQ ID NO: 234)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Klebsiella oxytoca*)
(SEQ ID NO: 235)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* HVH 70 4-2963531)
(SEQ ID NO: 236)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 1.2741)
(SEQ ID NO: 237)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMNK88)
(SEQ ID NO: 238)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia fergusonii*)
(SEQ ID NO: 239)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* B088)
(SEQ ID NO: 240)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* B088)
(SEQ ID NO: 241)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* strain 55989/EAEC)
(SEQ ID NO: 242)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRSTPH

Ethidium bromide-methyl viologen transporter EmrE (*Escherichia coli* ISC7)
(SEQ ID NO: 243)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* TA054)
(SEQ ID NO: 244)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* ATCC BAA-2209)
(SEQ ID NO: 245)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia albertii* B156)
(SEQ ID NO: 246)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia* sp, KTE96)
(SEQ ID NO: 247)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia* sp. KTE114)
(SEQ ID NO: 248)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* HVH 25 4-5851939)
(SEQ ID NO: 249)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* H461)
(SEQ ID NO: 250)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* M718)
(SEQ ID NO: 251)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Methyl viologen transporter EmrE (*Achromobacter* sp.)
(SEQ ID NO: 252)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* 2-427-07_S4_C3)
(SEQ ID NO: 253)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* KOEGE 71 186a)
(SEQ ID NO: 254)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 2-427-07_S4_C3)
(SEQ ID NO: 255)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug SMR transporter (*Escherichia coli* O111:NM strain K6722)
(SEQ ID NO: 256)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Quaternary ammonium transporter (*Escherichia coli* APEC O2-211)
(SEQ ID NO: 257)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* KTE21)
(SEQ ID NO: 258)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug SMR transporter (*Escherichia coli* O128:H2 strain 2011C-3317)
(SEQ ID NO: 259)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR STPH

Multidrug SMR transporter (*Shigella dysenteriae*)
(SEQ ID NO: 260)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 4.0967)
(SEQ ID NO: 261)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR STPH

Multidrug transporter EmrE (*Escherichia* sp. KTE159)
(SEQ ID NO: 262)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* strain ATCC 9637)
(SEQ ID NO: 263)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 3-267-03_S4_C1)
(SEQ ID NO: 264)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR STPH

Multidrug transporter EmrE (*Escherichia coli* 2-177-06_S3_C3)
(SEQ ID NO: 265)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

Multidrug transporter EmrE (*Escherichia coli* 3-267-03_S4_C1)
(SEQ ID NO: 266)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSR SAPH

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Multidrug transporter EmrE (*Escherichia coli* HVH 50 4-2593475)
(SEQ ID NO: 267)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* 1.2264)
(SEQ ID NO: 268)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSSPH

Multidrug transporter EmrE (*Shigella flexneri* K-227)
(SEQ ID NO: 269)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSSPH

Multidrug SMR transporter (*Escherichia coli* O146:H21 strain 2010C-3325)
(SEQ ID NO: 270)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* 2a strain 301)
(SEQ ID NO: 271)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Methylviologen resistance transporter EmrE (*Shigella sonnei* strain Ss046)
(SEQ ID NO: 272)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Escherichia coli* O174:H8 strain 04-3038)
(SEQ ID NO: 273)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* KTE108)
(SEQ ID NO: 274)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* O157:H7 strain SS52)
(SEQ ID NO: 275)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* MS 145-7)
(SEQ ID NO: 276)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella dysenteriae* 225-75)
(SEQ ID NO: 277)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* 908573)
(SEQ ID NO: 278)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Methylviologen transporter (*Escherichia coli* G3/10)
(SEQ ID NO: 279)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

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Multidrug transporter EmrE (*Escherichia coli* HVH 41 4-2677849)
(SEQ ID NO: 280)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFLFDQRLDLP AIIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli* M863)
(SEQ ID NO: 281)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug SMR transporter (*Escherichia coli* TW10509)
(SEQ ID NO: 282)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* 4.0522)
(SEQ ID NO: 283)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O111:H- strain 11128/EHEC)
(SEQ ID NO: 284)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* KTE20)
(SEQ ID NO: 285)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* 2-005-03_S4_C2)
(SEQ ID NO: 286)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia sp.* KTE31)
(SEQ ID NO: 287)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* M605)
(SEQ ID NO: 288)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* TA447)
(SEQ ID NO: 289)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug SMR transporter (*Escherichia coli* O104:H4)
(SEQ ID NO: 290)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia albertii* strain TW07627)
(SEQ ID NO: 291)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSAPH

Multidrug SMR transporter (*Shigella sp.* PAMC 28760)
(SEQ ID NO: 292)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLP AIIGMMLICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* 2-011-08_S1_C1)
(SEQ ID NO: 293)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMEA 3212-1)
(SEQ ID NO: 294)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* 2-177-06_S3_C2)
(SEQ ID NO: 295)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* 97.0259)
(SEQ ID NO: 296)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* 99.0741)
(SEQ ID NO: 297)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* KTE66)
(SEQ ID NO: 298)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* B185)
(SEQ ID NO: 299)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O139:H28 strain E24377A/ETEC)
(SEQ ID NO: 300)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* UMEA 3323-1)
(SEQ ID NO: 301)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* KTE10)
(SEQ ID NO: 302)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* 9.0111)
(SEQ ID NO: 303)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE182)
(SEQ ID NO: 304)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* H386)
(SEQ ID NO: 305)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

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Multidrug transporter EmrE (*Escherichia coli* O83:H1 strain NRG 857C/AIEC)
(SEQ ID NO: 306)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C3)
(SEQ ID NO: 307)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C1)
(SEQ ID NO: 308)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C3)
(SEQ ID NO: 309)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-392-07_S4_C1)
(SEQ ID NO: 310)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSSTPH

Multidrug transporter EmrE (*Escherichia coli* 1-176-05_S3_C2)
(SEQ ID NO: 311)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli* UMEA 3718-1)
(SEQ ID NO: 312)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSSTPH

Multidrug SMR transporter (*Escherichia coli* strain B/BL21-DE3)
(SEQ ID NO: 313)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSSTPH

Multidrug SMR transporter (*Escherichia coli*)
(SEQ ID NO: 314)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

QacE family quaternary ammonium compound efflux SMR transporter
(*Escherichia coli*)
(SEQ ID NO: 315)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

Multidrug transporter EmrE (*Escherichia coli*)
(SEQ ID NO: 316)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

QacE family quaternary ammonium compound efflux SMR transporter
(*Escherichia coli*)
(SEQ ID NO: 317)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSSTPH

Multidrug SMR transporter (*Escherichia coli* O25b:H4-ST131)
(SEQ ID NO: 318)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGIVGLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPH

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Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 319)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 320)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* KTE33) (SEQ ID NO: 321)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Shigella flexneri* VA-6) (SEQ ID NO: 322)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* H736) (SEQ ID NO: 323)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Shigella flexneri* 4c) (SEQ ID NO: 324)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Shigella flexneri*) (SEQ ID NO: 325)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 326)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EmrE (*Escherichia coli*) (SEQ ID NO: 327)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli*) (SEQ ID NO: 328)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EmrE (*Shigella sonnei*) (SEQ ID NO: 329)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* DORA_B_14) (SEQ ID NO: 330)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSAPN

Multidrug SMR transporter (*Escherichia coli* N37139PS) (SEQ ID NO: 331)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLRSRSTPH

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Multidrug transporter EmrE (*Escherichia coli* N36410PS) (SEQ ID NO: 332)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* H605) (SEQ ID NO: 333)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Quaternary ammonium transporter (*Escherichia coli* APEC O18) (SEQ ID NO: 334)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* N40513) (SEQ ID NO: 335)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia albertii*) (SEQ ID NO: 336)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia albertii*) (SEQ ID NO: 337)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug transporter EmrE (*Escherichia coli* N40607) (SEQ ID NO: 338)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug SMR transporter (*Escherichia coli* NCCP15648) (SEQ ID NO: 339)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug SMR transporter (*Escherichia coli* NCCP15648) (SEQ ID NO: 340)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* N36254PS) (SEQ ID NO: 341)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug SMR transporter (*Shigella sonnei*) (SEQ ID NO: 342)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug SMR transporter (*Shigella sonnei*) (SEQ ID NO: 343)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

Multidrug SMR transporter (*Shigella sonnei*) (SEQ ID NO: 344)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSA PH

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Multidrug transporter EmrE (*Escherichia coli* N37122PS) (SEQ ID NO: 345)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli*) (SEQ ID NO: 346)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPN

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 347)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* E1118) (SEQ ID NO: 348)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug SMR transporter (*Shigella boydii*) (SEQ ID NO: 349)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Shigella boydii*) (SEQ ID NO: 350)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug SMR transporter (*Shigella flexneri* 1a) (SEQ ID NO: 351)
MNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* MS 84-1) (SEQ ID NO: 352)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* MS 124-1) (SEQ ID NO: 353)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* 110957) (SEQ ID NO: 354)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* MS 85-1) (SEQ ID NO: 355)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* MS 117-3) (SEQ ID NO: 356)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

Multidrug transporter EmrE (*Escherichia coli* 909945-2) (SEQ ID NO: 357)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRAPH

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Multidrug transporter EmrE (*Escherichia coli* 113290)
(SEQ ID NO: 358)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O83:H1 strain NRG 857C/AIEC)
(SEQ ID NO: 359)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* MS 115-1)
(SEQ ID NO: 360)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* strain MS 21-1)
(SEQ ID NO: 361)
MNRKEYAMNPYIYLGGAIAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSG
VGIVLISLLSWGFFGQRLDLPAAIGMMLICAGVLVINLLSRSAPH

Multidrug SMR transporter (*Escherichia coli* strain SE11)
(SEQ ID NO: 362)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
GMLICAGVLVINLLSRSAPH

Methylviologen resistance transporter EmrE (*Shigella flexneri* serotype
5b strain 8401)
(SEQ ID NO: 363)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
GMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O1:K1/APEC)
(SEQ ID NO: 364)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
GMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Shigella flexneri* serotype X strain 2002017)
(SEQ ID NO: 365)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
GMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Shigella sonnei*)
(SEQ ID NO: 366)
MNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIAEVIG
TTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLDLPAAI
GMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* O45:K1 strain S88/ExPEC)
(SEQ ID NO: 367)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIA
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* strain 55989/EPEC)
(SEQ ID NO: 368)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGGAIA
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLSRSAPH

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Multidrug transporter EmrE (*Escherichia coli* O81 strain ED1a)
(SEQ ID NO: 369)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* strain UTI89/UPEC)
(SEQ ID NO: 370)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* O6:H1 strain CPT073)
(SEQ ID NO: 371)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* O25b:H4)
(SEQ ID NO: 372)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EntrE (*Escherichia coli* O25b:H4-ST131)
(SEQ ID NO: 373)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug transporter EmrE (*Escherichia coli* TW10598)
(SEQ ID NO: 374)
MLPGRVNSFVSLGFLLLIIIVPAFISCHARAPWIIHQDENGELCSNCSTILSSMNRKEYAMNPYIYLGAIL
AEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLISLLSWGFFGQRLD
LPAIIGMMLICAGVLVINLLRSRAPH

Multidrug SMR transporter (*Escherichia coli* O157)
(SEQ ID NO: 375)
MNPYIYLGAILAEVIGTTLMKFSEGPTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAVIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EntrE (*Escherichia coli* KTE100)
(SEQ ID NO: 376)
MNPYIYLGAILAEVIGTTLMKFSEGPTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAVIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EntrE (*Escherichia sp.* KTE159)
(SEQ ID NO: 377)
MNPYIYLGAILAEVIGTTLMKFSEGPTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAVIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EmrE (*Escherichia coli* Xuzhou21)
(SEQ ID NO: 378)
MNPYIYLGAILAEVIGTTLMKFSEGPTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAVIGMMLICAGVLVINLLRSRSTPH

Multidrug transporter EmrE (*Escherichia coli* KTE108)
(SEQ ID NO: 379)
MNPYIYLGAILAEVIGTTLMKFSEGPTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAVIGMMLICAGVLVINLLRSRSTPH

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Ethidium bromide-methyl viologen transporter EmrE (*Escherichia coli* O157:H7 strain SS52) (SEQ ID NO: 380)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O157:H7 strain EC869) (SEQ ID NO: 381)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 382)
MNPYIYEGGAIAEIVIGTTLMKSEGPTRLWPSVGTIICYASEWLLAOTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug SMR transporter (*Escherichia coli*) (SEQ ID NO: 383)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli* O157:H7) (SEQ ID NO: 384)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia coli*) (SEQ ID NO: 385)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Shigella flexneri* 2850-71) (SEQ ID NO: 386)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMMLICTGVLVINLLSRSTPH

Ethidium bromide-methyl viologen transporter EmrE (*Escherichia albertii* KF1) (SEQ ID NO: 387)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGIFGQRLDLPVIGMMLICAGVLVINLFSRSAPH

Multidrug SMR transporter (*Shigella* sp. FC2928) (SEQ ID NO: 388)
MNPYIYLGGAIAEIVIGTTLMKFSEGPTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLSAIGMMLICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Citrobacter* sp. MGH106) (SEQ ID NO: 389)
MNTYIYLGGAIAEIVGTTLMKFTDGFTRLWPSVGTIVCYASFWLLSQTLAHIPTGIAYAIWSGVGIVLIS
LLAWVIHGQRLDLPVIGMALICAGVLVINLLSRSAVH

Multidrug transporter EmrE (*Escherichia* sp. KTE11) (SEQ ID NO: 390)
MNPYIYLGGAIFAIVIGTTLMKFSDGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMILICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE52) (SEQ ID NO: 391)
MNPYIYLGGAIFAIVIGTTLMKFSDGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLFWGFFGQRLDLPVIGMILICAGVLVINLLSRSTPH

Multidrug transporter EmrE (*Escherichia* sp. KTE96) (SEQ ID NO: 392)
MNPYIYLGGAIFAIVIGTTLMKFSEGFTRLWPSVGTIICYASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPVIGMILICAGVLVINLLSRSTPH

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Multidrug transporter EmrE (*Escherichia* sp. KTE159) (SEQ ID NO: 393)
MNPYIYLGGAIFAEVIGTTLMKYSDGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMILICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Escherichia coli* E1118) (SEQ ID NO: 394)
MNPYIYLGGAIFAEVIGTTLMKYSDGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMILICAGVLVINLLSRSAPH

Multidrug transporter EmrE (*Shigella sonnei*) (SEQ ID NO: 395)
MNPYIYLGGAILAEVIGTTLMKFSEGFTRLWPSVGTIICYCASFWLLAQTLAYIPTGIAYAIWSGVGIVLIS
LLSWGFFGQRLDLPAAIGMMLICAGVLVINLGDAANLLI

Multidrug DMT transporter (*Shigella* sp. FC1967) (SEQ ID NO: 396)
MVFSRLYPSIVVVIGYCLSFWALSQVVRVMPGLIAYAIWSGLGIVLVSVAAVFLYQQKLDLPAAIGMSLIIA
GVLVINLLSKSASH

Multidrug DMT transporter (*Shigella* sp. FC130) (SEQ ID NO: 397)
MNGLTYLMLAIIEVIATTMLKASDGFSRLYPSIVVVIGYCLSFWALSQVVRVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAAIGMSLIAGVLVINLLSKSASH

Multidrug DMT transporter (*Shigella* sp. FC1655) (SEQ ID NO: 398)
MNGLTYLMLAIIEVIATTMLKASDGFSRLYPSIVVVIGYCLSFWALSQVVRVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAAIGMSLIAGVLVINLLSKSASH

Multidrug transporter EmrE (*Serratia plymuthica* 4Rx13) (SEQ ID NO: 399)
MSGFIYLTMAIVAIEVIATTMLKASEGFTRLWPSLVVVVG YAVAFWGLSMVVKTMPLGIVYAIWSGMGIVLVS
IAAVFVYQQKLDLPAVIGMVLIAGVLVINLLSKTAAH

Multidrug DMT transporter (*Serratia plymuthica* S13) (SEQ ID NO: 400)
MSGFIYLTMAIVAIEVIATTMLKASEGFTRLWPSLVVVVG YAVAFWGLSMVVKTMPLGIVYAIWSGMGIVLVS
IAAVFVYQQKLDLPAVIGMVLIAGVLVINLLSKTAAH

Multidrug transporter EmrE (*Proteus vulgaris*) (SEQ ID NO: 401)
MNGLTYLMLAIIEVIATTMLKASEGFRLYPSIVVVIGYCF SFWALSQVVRVMPGLIAYAIWSGLGIVLVS
VAAVFIYQQKLDLPAAIGMGLIAGVLVINLLSKSASH

Multidrug transporter EmrE (*Proteus vulgaris*) (SEQ ID NO: 402)
MNGLTYLMLAIIEVIATTMLKASEGFRLYPSIVVVIGYCF SFWALSQVVRVMPGLIAYAIWSGLGIVLVS
VAAVFIYQQKLDLPAAIGMGLIAGVLVINLLSKSASH

Multidrug transporter EmrE (*Proteus vulgaris*) (SEQ ID NO: 403)
MLAIIEVIATTMLKAEDGESRLYPSIVVVIGYCF SFWALSQVVKVMPGLIAYAIWEGLGIVLVSVAAVFLY
QQKLDLPAIVGMTLIIAGVLVINLLSKSASH

Multidrug transporter EmrE (*Proteus mirabilis* ATCC 29906) (SEQ ID NO: 404)
MNGLTYLILTIIEVIATTVLKASDGSRLYPSIVVVVG YCF SFWALSQVVKVMPGLIAYAIWSGLGIVLVS
VAAVFVYQQKLDLPAIVGMTLIIAGVLVINLLSNSTSH

Multidrug DMT transporter (*Proteus* sp. HMSC14B05) (SEQ ID NO: 405)
MNGLTYLILTIIEVIATTVLKASDGSRLYPSIVVVVG YCF SFWALSQVVKVMPGLIAYAIWSGLGIVLVS
VAAVFVYQQKLDLPAIVGMTLIIAGVLVINLLSNSTSH

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Methyl viologen transporter EmrE (*Proteus huseri* ZMd44)
(SEQ ID NO: 406)
MNGLTYLMLAIIEVIATTMLKASDGFSLYPSIVVVIGYCLSFWALSQVVRVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAIVGMTLIIAGVLVINLLSKSASH

Methyl viologen transporter EmrE (*Proteus mirabilis* strain HI4320)
(SEQ ID NO: 407)
MNGLTYLMLAIIEVIATTVLKASDGFSLYPSIVVVIGYCLSFWALSQVVKVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAIVGMTLIIAGVLVINLLSNSTSH

Multidrug SMR transporter (*Proteus penneri* ATCC 35198)
(SEQ ID NO: 408)
MNGLTYLMLAIIEVIATTMLKASDGFSLYPSIVVVIGYCLSFWALSQVVKVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAIVGMTLIIAGVLVINLLSKSASH

Multidrug DMT transporter (*Proteus mirabilis*)
(SEQ ID NO: 409)
MNGLTYLMLAIIEVIATTVLKASDGFSLYPSIVVVIGYCLSFWALSQVVKVMPGLIAYAIWSGLGIVLVS
VAAVFLYQQKLDLPAIVGMTLIIAGVLVINLLSNSTAH

Multidrug transporter EmrE (*Providencia rettgeri*)
(SEQ ID NO: 410)
MKGLSFLFISIIAEVIATTTLKASDGFSLYPSIVVVIGYAVSFWGLSQVVKVMPGLIAYAIWSGLGIVLVS
IAAIYIYNQKLDLPAIIGMLFIIVGVLIINLLSKSGTH

Multidrug SMR transporter (*Providencia rustigianii* DSM 4541)
(SEQ ID NO: 411)
MKGLGFLLSIAEVIATTTLKASDGFSLYPSIVVTGYATSFWGLSQVVKVMPGLIAYAIWSGLGIVLVS
VAAIYIYNQKLDLPAIIGMLLIIVGVLIINLFSKSGTH

Multidrug SMR transporter (*Xenorhabdus thuongxuanensis*)
(SEQ ID NO: 412)
MKFALSYNFGLVSNMNVWGYLFIALSEVIATTMLKSADGFTRLVPSIIVVTGYCLSFWALSQVVKVMPGLI
AYAVWSCLGIVLVSIAGIFLYQQKLDLPAIIGILLIIAGVLVINLLSKSAGH

Multidrug transporter EmrE (*Xenorhabdus doucetiae*)
(SEQ ID NO: 413)
MVNWAVFWKFGLSYHLGLVSNMNVWGYLFIALSEVIATTMLKTADGFTRLVPSIVVVLGYCLSFWALSQVV
KTMPGLIAYAVWSCLGIVLVSIAGIFLYQQKLDLPAIIGILLIIAGVLVINLLSKSAGH

Multidrug SMR transporter (*Enterobacter cancerogenus*)
(SEQ ID NO: 414)
MNTYFLGLGIAIAEVIATTFMKYSEGFTRLWPSLATLICFAAFYMLSQTLAHIPTGVAYAIWSGAGIVLIS
LVGWLVSQKLDLPAIIGMAFICIGVLIINVLFSKSGAH

Multidrug transporter EmrE (*Serratia plymuthica* PRI-2C)
(SEQ ID NO: 415)
MSGFIYLTMAIAEVIATTMLKASEGFTRLWPSLAVIVGYAVAFWGLSMVVKTMPLGIVYAIWSGMGIVLVS
IAAVFVYQQKLDLPAVIGMGLIIAGVLVINLLSKTAAH

Ethidium bromide-methyl viologen transporter EmrE (*Serratia fonticola*
AU-P3(3))
(SEQ ID NO: 416)
MTAFIYLAMAIIEVIATTLKASEGFTRLWPSVFFVVLGYAVAFWGLSMVVKTMPLGIVYAIWSGLGIVLVS
IAAVFIYQQKLDLPAVIGMGLIIAGVLVINLLSKSAGH

Multidrug transporter EmrE (*Escherichia vulneris* NBRC 102420)
(SEQ ID NO: 417)
MHAYVHLGIAIAEVIATTLRMRYSEGFTKLWPTVATLGCYAVAFWFLSQTLQYIPTGIAYAIWSGVGIVLIS
AAGWIFSGQKLDLPAIGGMALICAGVLVINLFSKSVAH

Ethidium bromide-methyl viologen transporter EmrE (*Serratia rubidaea*)
(SEQ ID NO: 418)
MYLTMAIIAEVIATTMLKASEGFTRLWPSLVVVLGYGVAFWGLSMVVKSMPLGIVYAIWSGMGVVLVSIAAV
FIYNQKLDWPAIIGMLIVAGVLVINLLSKTSAH

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Cation/cationic drug transporter (*Serratia marcescens* FGI94)

(SEQ ID NO: 419)

MTGLMYLTMAIIAEVIATTMLKASEGFTRLWPSLVVVLGYGVAFWGLSMVVKSMPLGIVYAIWSGMGVVLVS

IAAVFIYNQKLDWPAIIGMGLIVAGVLVINLLSKTSAH

Multidrug DMT transporter (*Serratia marcescens*)

(SEQ ID NO: 420)

MSGFMYLTMAIIAEVIATTMLKASEGFTRLWPSLVVVLGYGVAFWGLSMVVKSMPLGIVYAIWSGMGVVLVS

VAAVFVYQKLDWPAIIGMGLIAGVLVINLLSKASVH

Multidrug transporter EmrE (*Serratia odorifera* DSM 4582)

(SEQ ID NO: 421)

MNGFIYLTMAIIAEVIATTMLKASEGFTRWPSLVVVLGYGVAFWGLSMVVKTMPLGIVYAIWSGMGVVLVS

IAAVFVYNQKLDWPAIIGMGLIAGVLVINLLSKTSAH

Methods of Treatment

This invention describes peptides and methods of use for the treatment of bacterial infections. Pathogenic bacterial strains may become resistant to various treatments by developing a resistance to certain pharmaceutical agents. The resistance is conferred by small multidrug resistance (SMR) membrane-bound transporters. SMRs are a family of ubiquitous transporters in bacteria (e.g., *M. tuberculosis*, *P. aeruginosa*, *B. pertussis*, *N. meningitis*, *B. anthracis*, and *S. aureus*) that efflux a wide range of cytotoxic compounds through transmembrane pumps. SMRs include, for example, EmrE transporters and various quaternary ammonium compound (QAC) transporters. In an attempt to treat a bacterial infection, one might administer an antibiotic agent to combat the infection. However, an SMR transporter effluxes the antibiotic agent before it can kill the infection, thus conferring resistance to the antibiotic. Therefore, to effectively treat a drug resistant bacterial infection, one may need to inhibit one or more SMRs.

The peptides of the invention described herein include a C-terminal polypeptide of any one of an SMR transporter. SMRs exist as obligate dimers in their active form, with each monomer a ~110 residue four helix-bundle. The C-terminal polypeptide inhibits the dimerization of the SMR, thus preventing it from oligomerizing into its active state and reducing (e.g., by about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 99%, or about 100%) or completely eliminating its ability to efflux the antibiotic. Following administration of the peptide, one could then administer an antibiotic agent, to which the bacteria is now sensitive, in order to effectively treat the infection. Following treatment with a peptide of the invention with or without an antibiotic agent, the size of the bacterial infection, the bacterial load, or the total number of bacterial cells is reduced (e.g., by about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 99%, or about 100%) or completely eliminated relative to its initial size.

The polypeptides of the invention may be able to treat bacterial infections by preventing efflux of antibacterial agents administered in combination with a polypeptide of the invention. In some embodiments, the bacterial infection includes bacteria which express one or more small molecule resistance membrane-bound transporters.

"Antibacterial agents," also known as antibiotics, as used herein refer to agents used in the treatment and prevention of bacterial infections. Antibacterial agents include agents which kill the bacteria, known as "bactericidal agents" and agents which inhibit bacterial growth, known as "bacteriostatic agents." Antibacterial agents are generally classed

based on their mechanism of action, chemical structure, or spectrum of activity. Some antibacterial agents useful in combination with the polypeptides of the invention include (i) agents which target the bacteria cell wall (e.g., β -lactam antibiotics, cephalosporin antibiotics, carbapenem antibiotics), (ii) agents which target the cell membrane (e.g., polymyxin antibiotics), (iii) agents that interfere with bacterial enzymes (e.g., rifamycin antibiotics, lipiarmycin antibiotics, quinolone antibiotics, sulfonamide antibiotics), or (iv) agents which inhibit protein synthesis (e.g., macrolide antibiotics, lincosamide antibiotics, tetracycline antibiotics, aminoglycoside antibiotics).

In some embodiments, the method further includes administering one or more antibacterial agents (e.g., ampicillin, erythromycin, or tetracycline). In some embodiments, the one or more antibacterial agents is a β -lactam antibiotic such as a penicillin antibiotic (e.g., amoxicillin, ampicillin, bacampicillin, carbenicillin, cloxacillin, dicloxacillin, flucloxacillin, mexlocillin, nafcillin, oxacillin, penicillin G, penicillin V, piperacillin, pivampicillin, pivmecillinam, ticarcillin), a cephalosporin antibiotic (e.g., cefacetile, cefadroxil, cephalixin, cefaloglycin, cefalonium, cefaloridine, cefalotin, cefapirin, cefatrizine, cefazafur, cefazedone, cefazolin, cefradine, cefroxadine, ceftezole, cefaclor, cefamandole, cefmetazole, cefonicid, cefotetan, cefoxitin, cefprozil, cefuroxime, cefuzonam, cefcapene, cefdaloxime, cefdinir, cefditoren, cefetamet, cefixime, cefmenoxime, cefodizime, cefotaxime, cefpimizole, cefpodoxime, ceftieram, ceftibuten, ceftiofur, ceftiolene, ceftizoxime, ceftriaxone, cefoperazone, ceftazidime, cefclidine, cefepime, cefluprenam, cefoselis, cefozopran, cefpirome, cequinome, ceftobiprole, ceftaroline, cefaclomezine, cefaloram, cefapazole, cefcanel, cefedrolor, cefempidone, cefetizole, cefivritril, cefmatilen, cefmepidium, cefovecin, cefoxazole, ceftrotil, cefsumide, cefuracetime, ceftioxide), a monobactam antibiotic (e.g., aztreonam), or a carbapenem antibiotic (e.g., imipenem, doripenem, ertapenem, meropenem), a polymyxin antibiotic (e.g., polymyxin B), a rifamycin antibiotic (e.g., rifampin, rifabutin, rifapentine, rifalazil), a lipiarycin antibiotic, a quinolone antibiotic (e.g., flumequine, nalidixic acid, oxolinic acid, piromidic acid, pipemidic acid, rosoxacin, ciprofloxacin, enoxacin, lomefloxacin, nadifloxacin, norfloxacin, ofloxacin, pefloxacin, rifloxacin, balofloxacin, gatifloxacin, grepafloxacin, levofloxacin, moxifloxacin, pazufloxacin, sparfloxacin, temafloxacin, tosufloxacin, besifloxacin, delafloxacin, clinafloxacin, gemifloxacin, prulifloxacin, sitafloxacin, trovafloxacin), a fluoroquinolone antibiotic (e.g., delafloxacin), a sulfonamide antibiotic (e.g., sulfamethizole, sulfamethoxazole, trimethoprim-sulfamethoxazole), a macrolide antibiotic (e.g., fidaxomicin, azi-

thromycin, erythromycin, clarithromycin, roxithromycin, dirithromycin, telithromycin), a lincosamide antibiotic (e.g., clindamycin, lincomycin), a tetracycline antibiotic (e.g., demeclocycline, doxycycline, minocycline, oxytetracycline, tetracycline, tigecycline), a streptogramin antibiotic (e.g., pristinamycin, quipristin/dalfopristin), an aminoglycoside antibiotic (e.g., amikacin, gentamicin, kanamycin, neomycin, netilmicin, paromomycin, streptomycin, tobramycin), a cyclic lipopeptide antibiotic (e.g., daptomycin), a lipoglycopeptide antibiotic (e.g., telavancin), a glycopeptide antibiotic (e.g., vancomycin, teicoplanin), a glycylicycline antibiotic, an oxazolidinone antibiotic (e.g., linezolid, cycloserine), a tuberactinomycin antibiotic (e.g., viomycin, capreomycin), chloramphenicol, metronidazole, tinidazole, nitrofurantoin, or combinations thereof.

In some embodiments, the one or more antibacterial agent and any of the foregoing polypeptides or pharmaceutical compositions are administered within 28 days of each other (e.g., within 21, 14, 10, 7, 5, 4, 3, 2, or 1 days) or within 24 hours (e.g., 12, 6, 3, 2, or 1 hours; or concomitantly) each in an amount that together are effective to treat the subject.

Administration and Dosage

The present invention also features pharmaceutical compositions that contain a therapeutically effective amount of a polypeptide of the invention. The composition can be formulated for use in a variety of drug delivery systems. One or more physiologically acceptable excipients or carriers can also be included in the composition for proper formulation. Suitable formulations for use in the present invention are found in *Remington's Pharmaceutical Sciences*, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of methods for drug delivery, see, e.g., Langer (*Science* 249:1527-1533, 1990).

The pharmaceutical compositions are intended for parenteral, intranasal, topical, oral, or local administration, such as by a transdermal means, for prophylactic and/or therapeutic treatment. The pharmaceutical compositions can be administered parenterally (e.g., by intravenous, intramuscular, or subcutaneous injection), or by oral ingestion, or by topical application or intraarticular injection at areas affected by the vascular or cancer condition. Additional routes of administration include intravascular, intra-arterial, intratumor, intraperitoneal, intraventricular, intraepidural, as well as nasal, ophthalmic, intrascleral, intraorbital, rectal, topical, or aerosol inhalation administration. Sustained release administration is also specifically included in the invention, by such means as depot injections or erodible implants or components. Thus, the invention provides compositions for parenteral administration that include the above mentioned agents dissolved or suspended in an acceptable carrier, preferably an aqueous carrier, e.g., water, buffered water, saline, PBS, and the like. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents, detergents and the like. The invention also provides compositions for oral delivery, which may contain inert ingredients such as binders or fillers for the formulation of a tablet, a capsule, and the like. Furthermore, this invention provides compositions for local administration, which may contain inert ingredients such as solvents or emulsifiers for the formulation of a cream, an ointment, and the like.

These compositions may be sterilized by conventional sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile aqueous carrier prior to administration. The pH

of the preparations typically will be between 3 and 11, more preferably between 5 and 9 or between 6 and 8, and most preferably between 7 and 8, such as 7 to 7.5. The resulting compositions in solid form may be packaged in multiple single dose units, each containing a fixed amount of the above-mentioned agent or agents, such as in a sealed package of tablets or capsules. The composition in solid form can also be packaged in a container for a flexible quantity, such as in a squeezable tube designed for a topically applicable cream or ointment.

The compositions containing an effective amount can be administered for prophylactic or therapeutic treatments. In therapeutic applications, compositions are administered to a subject (e.g., a human) already suffering from a bacterial infection in an amount sufficient to cure or at least partially arrest the symptoms of the infection and its complications. An amount adequate to accomplish this purpose is defined as a "therapeutically effective amount," an amount of a polypeptide sufficient to substantially improve at least one symptom associated with the disease or a medical condition. For example, in the treatment of an infection, an agent or polypeptide that decreases, prevents, delays, suppresses, or arrests any symptom of the disease or condition would be therapeutically effective. A therapeutically effective amount of an agent or polypeptide is not required to cure a disease or condition but will provide a treatment for a disease or condition such that the onset of the disease or condition is delayed, hindered, or prevented, or the disease or condition symptoms are ameliorated, or the term of the disease or condition is changed or, for example, is less severe or recovery is accelerated in an individual.

Amounts effective for this use may depend on the severity of the disease or condition and the weight and general state of the subject. The therapeutically effective amount of the compositions of the invention and used in the methods of this invention applied to mammals (e.g., humans) can be determined by the ordinarily-skilled artisan with consideration of individual differences in age, weight, and the condition of the mammal. The agents of the invention are administered to a subject (e.g., a mammal, such as a human) in an effective amount, which is an amount that produces a desirable result in a treated subject. Therapeutically effective amounts can also be determined empirically by those of skill in the art.

Single or multiple administrations of the compositions of the invention including an effective amount can be carried out with dose levels and pattern being selected by the treating physician. The dose and administration schedule can be determined and adjusted based on the severity of the disease or condition in the subject, which may be monitored throughout the course of treatment according to the methods commonly practiced by clinicians or those described herein.

The polypeptides of the present invention may be used in combination with either conventional methods of treatment or therapy or may be used separately from conventional methods of treatment or therapy.

When the polypeptides of this invention are administered in combination therapies with other agents, they may be administered sequentially or concurrently to an individual. Alternatively, pharmaceutical compositions according to the present invention may be comprised of a combination of a polypeptide of the present invention in association with a pharmaceutically acceptable excipient, as described herein, and another therapeutic or prophylactic agent known in the art.

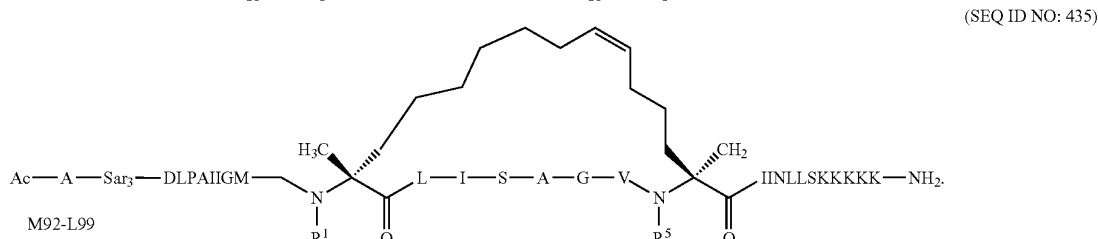
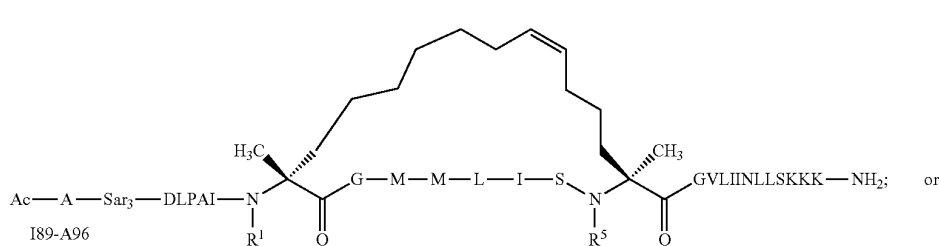
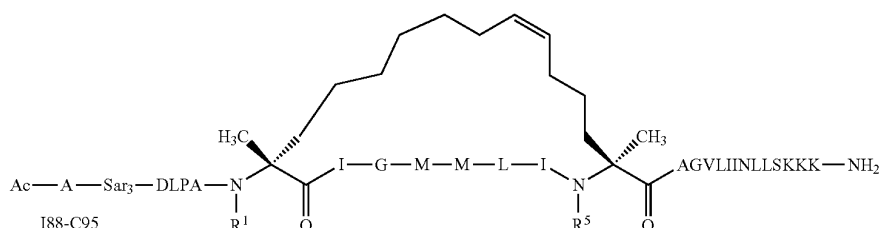
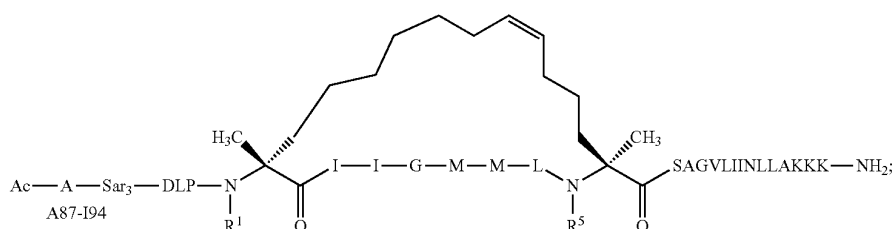
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EXAMPLES

Example 1. Liposome Preparation

1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC) and 1-palmitoyl-2-oleoyl-sn-glycero-3-phospho- (1'-rac-glycerol) (POPG) in chloroform (Avanti Polar Lipids Inc., AL, USA) were mixed in a 3:1 mol ratio (POPC:POPG) and dried into thin films. Lipid films were lyophilized overnight and brought up in 1 mL water, vortexed, frozen and lyophilized again. Lipids were then resuspended in 10 mM Tris buffer 10 mM NaCl pH 7.4 (5 mM) and freeze thawed 5× over dry ice and a water bath (50° C.). Lipids were then extruded using a 0.2 micron sized filter and left to equilibrate overnight. Samples were diluted further with buffer (2.5 mM) prior to addition to lyophilized peptide.

The lyophilized peptides added were:



Example 2. Determination of Helicity of Stapled Polypeptides by Circular Dichroism

The helicity of the polypeptides described in Example 1 were tested by circular dichroism (CD) spectroscopy. The helicity of the polypeptides was determined in SDS micelles and in lipid bilayers.

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The conditions in which the helicity in micelles were tested was stapled peptides (20 μM) in buffer (10 mM Tris HCl; 10 mM NaCl pH 7.4) and 140 mM SDS. The conditions in which the helicity in lipid bilayers were tested was 10 μM peptides in 2.5 mM POPC:POPG (3:1 mol ratio) (bacterial membrane mimetic lipid mixture).

As shown in FIGS. 1A and 1B, all of the tested polypeptides were found to be helical in both micelles and lipid bilayers.

Example 3. Determination of Cell Toxicity of Stapled Polypeptides

E. coli K12 cells were grown overnight to saturation in LB (Luria broth). Cells were harvested and resuspended in

fresh media to a final OD600 of 0.1. Cells were then grown in the presence of DMSO (dimethyl sulfoxide) alone or in DMSO-solubilized peptide (4 μM) over 1 hour, while OD600 was recorded in 15-minute intervals. *E. coli* growth curves were normalized to the starting OD600. Growth in the presence of peptide was normalized to the growth of cells with DMSO alone, using:

$$\text{Growth} = \frac{OD_{600}^{+peptide}}{OD_{600}^{-peptide}}.$$

As shown in FIG. 2, none of the four hydrocarbon-stapled peptides severely impact cell growth over the time tested. A dashed line at 1.0 represents the starting conditions of the cells. S-CAP-2G (sequence: KKKKKK-AGFAAWAAFGA (SEQ ID NO: 439), hydrocarbon staple indicated by underlined A) is a positive control for cell death. Data shown represents the average of at least 2 independent experiments. Error is indicated as SD.

Example 4. Inhibition of Efflux by Stapled Polypeptides

E. coli K12 cells were harvested by centrifugation, resuspended and diluted to an OD₆₀₀=0.1 in Minimal Medium A. Cells were then treated with 80 μM carbonyl cyanide m-chlorophenyl hydrazine (CCCP) for 5 min at room temperature, before adding 1 μg/mL EtBr and either DMSO (8 μl) or peptide (4 μM) from a concentrated DMSO stock (1000 μM peptide). Cells were incubated at 37° C. with shaking (250 rpm) for 30 min, centrifuged for 10 min, resuspended in fresh Minimal Medium A supplemented with 1 μg/mL EtBr (without CCCP). Fluorescence decay was immediately measured using a spectropolarimeter (Photon Technology International, NJ, USA) over 2200s with stirring (λ_{ex}=530 nm, slit width 2 nm, λ_{em}=600 nm, slit width 4 nm, 1s intervals). Background fluorescence intensity (ethidium alone, as well as final plateau values for *E. coli* cells alone) was subtracted from fluorescence values. Efflux experiments were repeated three times.

As shown in FIG. 3, M92-L99 inhibits efflux activity by 68%, A87-I94 by 60%, I89-A96 by 26%. I88-C95 does show any inhibition of efflux activity. A dashed line at 1.0 represents 100% inhibition.

OTHER EMBODIMENTS

It is to be understood that while the present disclosure has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the present disclosure, which is

defined by the scope of the appended claims. Other aspects, advantages, and alterations are within the scope of the following claims.

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the appended claims.

In the claims, articles such as “a,” “an,” and “the” may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include “or” between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention includes embodiments in which more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process.

It is also noted that the term “comprising” is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term “comprising” is used herein, the term “consisting of” is thus also encompassed and disclosed.

Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or subrange within the stated ranges in different embodiments of the invention, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from any one or more of the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the invention (e.g., any polynucleotide or protein encoded thereby; any method of production; any method of use) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 439

<210> SEQ ID NO 1

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 1

Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 2

-continued

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<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 2

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 3
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 3

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

Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
          20           25           30

Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
          35           40           45

Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
          50           55           60

Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
65           70           75           80

Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
          85           90           95

Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
          100          105          110

Thr Pro Trp
          115

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<210> SEQ ID NO 4
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 4

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

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-continued

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80
 Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95
 Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 5
 <211> LENGTH: 62
 <212> TYPE: PRT
 <213> ORGANISM: Mycobacterium tuberculosis

<400> SEQUENCE: 5

Met Tyr Ile Arg Thr Gln Gly Glu Val Leu Thr Tyr Leu Phe Pro Leu
 1 5 10 15
 Cys Ala Ile Ala Ala Glu Ala Ala Ala Thr Ser Leu Phe Lys Gly Ser
 20 25 30
 Phe Gly Asp Phe Arg Val Cys Ser Pro Gly His Asp Gly Ala Ile Thr
 35 40 45
 Ala Met Pro Ser Val Leu Ala Ala Ser Arg Ile Arg Ser Ser
 50 55 60

<210> SEQ ID NO 6
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Mycobacterium orygis

<400> SEQUENCE: 6

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

<210> SEQ ID NO 7
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: Enterobacter cloacae

<400> SEQUENCE: 7

Met Lys Gly Trp Leu Phe Leu Val Ile Ala Ile Val Gly Glu Val Ile
 1 5 10 15
 Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
 20 25 30
 Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
 35 40 45
 Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
 50 55 60

-continued

Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
 65 70 75 80

Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
 85 90 95

Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
 100 105 110

Thr Pro Trp
 115

<210> SEQ ID NO 8
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: *Klebsiella pneumoniae*

<400> SEQUENCE: 8

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

Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
 20 25 30

Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
 35 40 45

Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
 50 55 60

Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
 65 70 75 80

Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
 85 90 95

Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
 100 105 110

Thr Pro Trp
 115

<210> SEQ ID NO 9
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 9

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

Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
 20 25 30

Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
 35 40 45

Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
 50 55 60

Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
 65 70 75 80

Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
 85 90 95

Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
 100 105 110

Thr Pro Trp
 115

<210> SEQ ID NO 10

-continued

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<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 10
Met Lys Gly Trp Leu Phe Leu Val Ile Ala Ile Val Gly Glu Val Ile
1           5           10          15
Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
          20           25           30
Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
          35           40           45
Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
          50           55           60
Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
65           70           75           80
Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
          85           90           95
Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
          100          105          110
Thr Pro Trp
          115

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<210> SEQ ID NO 11
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Providencia rettgeri

<400> SEQUENCE: 11
Met Lys Gly Trp Leu Phe Leu Val Ile Ala Ile Val Gly Glu Val Ile
1           5           10          15
Ala Thr Ser Ala Leu Lys Ser Ser Glu Gly Phe Thr Lys Leu Ala Pro
          20           25           30
Ser Ala Val Val Ile Ile Gly Tyr Gly Ile Ala Phe Tyr Phe Leu Ser
          35           40           45
Leu Val Leu Lys Ser Ile Pro Val Gly Val Ala Tyr Ala Val Trp Ser
          50           55           60
Gly Leu Gly Val Val Ile Ile Thr Ala Ile Ala Trp Leu Leu His Gly
65           70           75           80
Gln Lys Leu Asp Ala Trp Gly Phe Val Gly Met Gly Leu Ile Ile Ala
          85           90           95
Ala Phe Leu Leu Ala Arg Ser Pro Ser Trp Lys Ser Leu Arg Arg Pro
          100          105          110
Thr Pro Trp
          115

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<210> SEQ ID NO 12
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas citronellolis

<400> SEQUENCE: 12
Met Pro Gly Tyr Leu Tyr Leu Ala Ile Ala Ile Val Ala Glu Val Ile
1           5           10          15
Ala Thr Ala Ser Leu Lys Ser Val Lys Gly Leu Ser Thr Pro Leu Pro
          20           25           30
Leu Leu Leu Val Ile Val Gly Tyr Ala Ile Ser Phe Trp Met Leu Thr
          35           40           45

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-continued

Leu Val Val Arg Ser Ile Pro Val Gly Ile Ala Tyr Ala Ile Trp Ala
 50 55 60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Leu Val Leu Tyr Gln
 65 70 75 80

Gln Lys Leu Asp Ala Pro Ala Leu Leu Gly Met Gly Leu Ile Val Ser
 85 90 95

Gly Val Val Val Ile Gln Leu Phe Ser Gly Ser Val Ser His
 100 105 110

<210> SEQ ID NO 13
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Pseudomonas aeruginosa*

<400> SEQUENCE: 13

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

Ala Thr Thr Ser Leu Lys Ala Val Ala Gly Phe Ser Lys Pro Leu Pro
 20 25 30

Leu Leu Leu Val Val Gly Gly Tyr Val Leu Ala Phe Ser Met Leu Val
 35 40 45

Leu Val Met Arg Thr Leu Pro Val Gly Val Val Tyr Ala Ile Trp Ser
 50 55 60

Gly Leu Gly Ile Val Leu Val Ser Leu Val Ala Met Phe Val Tyr Gly
 65 70 75 80

Gln Arg Leu Asp Pro Ala Ala Leu Leu Gly Ile Gly Leu Ile Ile Ala
 85 90 95

Gly Val Leu Val Ile Gln Leu Phe Ser Arg Ala Ser Gly His
 100 105 110

<210> SEQ ID NO 14
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Pseudomonas aeruginosa*

<400> SEQUENCE: 14

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

Ala Thr Ser Leu Leu Lys Ala Ser Asp Gly Met Ser Arg Leu Trp Pro
 20 25 30

Thr Val Gly Ala Leu Val Gly Tyr Gly Leu Cys Phe Tyr Leu Leu Ser
 35 40 45

Val Thr Met Lys Ser Val Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Ile Gly Leu Val Val Phe Lys
 65 70 75 80

Gln Arg Leu Asp Ala Pro Ala Leu Ile Gly Ile Gly Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Phe Ser Arg Ser Ser Ala His
 100 105 110

<210> SEQ ID NO 15
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Bordetella pertussis*

-continued

<400> SEQUENCE: 15

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

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<210> SEQ ID NO 16

<211> LENGTH: 74

<212> TYPE: PRT

<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 16

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Met Ala Gly Tyr Ala Ile Ala Phe Tyr Phe Leu Ala Leu Thr Leu Arg
1           5           10           15
Val Ile Pro Val Gly Val Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
          20           25           30
Val Leu Ile Ser Leu Val Gly Ala Leu Leu Phe Lys Gln His Leu Asp
          35           40           45
Leu Pro Ala Ile Ile Gly Ile Ala Leu Ile Leu Ala Gly Val Val Val
          50           55           60
Met Asn Val Phe Ser Lys Ser Val Gly His
65           70

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<210> SEQ ID NO 17

<211> LENGTH: 55

<212> TYPE: PRT

<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 17

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Met Gly Val Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile
1           5           10           15
Ser Leu Val Gly Ala Leu Leu Phe Lys Gln His Leu Asp Leu Pro Ala
          20           25           30
Ile Ile Gly Ile Ala Leu Ile Leu Ala Gly Val Val Val Met Asn Val
          35           40           45
Phe Ser Lys Ser Val Gly His
          50           55

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<210> SEQ ID NO 18

<211> LENGTH: 57

<212> TYPE: PRT

<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 18

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

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-continued

Leu Thr Ala Leu Val Ser Val Val Phe Phe Gly Glu Lys Ala Asp Phe
 20 25 30

Ile Gly Ile Val Ser Ile Gly Leu Ile Leu Leu Gly Val Val Leu Leu
 35 40 45

Asn Thr Met Ser His Met Ser Gly His
 50 55

<210> SEQ ID NO 19
 <211> LENGTH: 114
 <212> TYPE: PRT
 <213> ORGANISM: *Bacillus cereus*

<400> SEQUENCE: 19

Met Lys Asn Lys Ala Trp Leu Tyr Val Ile Leu Thr Cys Ile Phe Glu
 1 5 10 15

Val Phe Trp Val Phe Gly Phe Asn Thr Ala Asn Thr Trp Trp His Trp
 20 25 30

Ile Ile Ile Leu Gly Val Ile Ala Val Asp Phe His Phe Leu Ser Lys
 35 40 45

Ala Cys Glu His Leu Ala Thr Gly Thr Val Tyr Ala Val Phe Ala Gly
 50 55 60

Ala Gly Thr Val Gly Thr Phe Leu Met Asp Val Phe Leu Phe Gly Gly
 65 70 75 80

Ser Phe Ser Val Gly Lys Leu Phe Phe Ile Val Met Val Val Ala Gly
 85 90 95

Val Ile Gly Leu Lys Leu Ala Asp Asn Lys Glu Glu Thr Val Glu Gly
 100 105 110

Ala Ala

<210> SEQ ID NO 20
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: *Staphylococcus aureus*

<400> SEQUENCE: 20

Met Pro Tyr Ile Tyr Leu Ile Ile Ala Ile Ser Thr Glu Val Ile Gly
 1 5 10 15

Ser Ala Phe Leu Lys Ser Ser Glu Gly Phe Ser Lys Phe Ile Pro Ser
 20 25 30

Leu Gly Thr Ile Ile Ser Phe Gly Ile Cys Phe Tyr Phe Leu Ser Lys
 35 40 45

Thr Met Gln His Leu Pro Leu Asn Ile Thr Tyr Ala Thr Trp Ala Gly
 50 55 60

Leu Gly Leu Val Leu Thr Thr Val Val Ser Ile Ile Ile Phe Lys Glu
 65 70 75 80

Gln Ile Asn Leu Ile Thr Ile Val Ser Ile Val Leu Ile Ile Val Gly
 85 90 95

Val Val Ser Leu Asn Ile Phe Gly Thr Ser His
 100 105

<210> SEQ ID NO 21
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Fundulus heteroclitus*

-continued

<400> SEQUENCE: 21

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 22

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 22

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

```

<210> SEQ ID NO 23

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 23

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

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-continued

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 24
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 24

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 25
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 25

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 26
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 26

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 27
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 27

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 28
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 28

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 29
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 29

```

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

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<210> SEQ ID NO 30

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 30

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

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<210> SEQ ID NO 31

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 31

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 32
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 32

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 33
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 33

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 34
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 34

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 35
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 35

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 36
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 36

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 37
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 37

```

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

```

<210> SEQ ID NO 38

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 38

```

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

```

<210> SEQ ID NO 39

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 39

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 40
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 40

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 41
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 41

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 42
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 42

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 43
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 43

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 44
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 44

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 45
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 45

```

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

```

<210> SEQ ID NO 46

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 46

```

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

```

<210> SEQ ID NO 47

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 47

```

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1             5             10             15
Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20             25             30
Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35             40             45
Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50             55             60
Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65             70             75             80

```

-continued

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 48
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia sp.*

<400> SEQUENCE: 48

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 49
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 49

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 50
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 50

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

```

<210> SEQ ID NO 51
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 51

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

```

<210> SEQ ID NO 52
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 52

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

```

<210> SEQ ID NO 53
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

-continued

<400> SEQUENCE: 53

```

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

```

<210> SEQ ID NO 54

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 54

```

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

```

<210> SEQ ID NO 55

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 55

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 56
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 56

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

<210> SEQ ID NO 57
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 57

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

<210> SEQ ID NO 58
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 58

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 59
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 59

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 60
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 60

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 61
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 61

```

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

```

<210> SEQ ID NO 62

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 62

```

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

```

<210> SEQ ID NO 63

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 63

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 64
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 64

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 65
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 65

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 66
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia fergusonii

<400> SEQUENCE: 66

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 67
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 67

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 68
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 68

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 69
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 69

```

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

```

<210> SEQ ID NO 70

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 70

```

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

```

<210> SEQ ID NO 71

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 71

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 72
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 72

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 73
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 73

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 74
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 74

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 75
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Achromobacter sp.

<400> SEQUENCE: 75

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 76
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 76

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 77
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 77

```

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

```

<210> SEQ ID NO 78

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 78

```

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

```

<210> SEQ ID NO 79

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 79

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 80
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 80

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

<210> SEQ ID NO 81
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 81

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

<210> SEQ ID NO 82
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 82

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 83
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 83

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 84
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 84

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 85
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 85

```

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

```

<210> SEQ ID NO 86

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 86

```

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

```

<210> SEQ ID NO 87

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 87

```

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

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Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 88
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Shigella sunnier*

<400> SEQUENCE: 88

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 89
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 89

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 90
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 90

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 91
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 91

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 92
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 92

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 93
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 93

```

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

```

<210> SEQ ID NO 94

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 94

```

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

```

<210> SEQ ID NO 95

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 95

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 96
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 96

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

<210> SEQ ID NO 97
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 97

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

<210> SEQ ID NO 98
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 98

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 99
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 99

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 100
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 100

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 101
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 101

```

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

```

<210> SEQ ID NO 102

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 102

```

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

```

<210> SEQ ID NO 103

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 103

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 104
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 104

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

<210> SEQ ID NO 105
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 105

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

<210> SEQ ID NO 106
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 106

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 107
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 107

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 108
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 108

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 109
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 109

```

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

```

<210> SEQ ID NO 110

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 110

```

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

```

<210> SEQ ID NO 111

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 111

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 112
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Shigella flexneri*

<400> SEQUENCE: 112

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 113
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 113

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 114
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Shigella flexneri*

<400> SEQUENCE: 114

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 115
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 115

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 116
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 116

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 117
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

-continued

<400> SEQUENCE: 117

```

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

```

<210> SEQ ID NO 118

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 118

```

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

```

<210> SEQ ID NO 119

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 119

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 120
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 120

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 121
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 121

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 122
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 122

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 123
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 123

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 124
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella boydii

<400> SEQUENCE: 124

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 125
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

-continued

<400> SEQUENCE: 125

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
      20             25             30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
      35             40             45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
      50             55             60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
      65             70             75             80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
      85             90             95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
      100             105             110

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<210> SEQ ID NO 126

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 126

```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 1             5             10             15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
      20             25             30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
      35             40             45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
      50             55             60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
      65             70             75             80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
      85             90             95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
      100             105             110

Arg Ser Ala Pro His
      115

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<210> SEQ ID NO 127

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 127

```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 1             5             10             15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
      20             25             30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
      35             40             45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
      50             55             60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
      65             70             75             80

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-continued

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 128
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 128

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 129
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 129

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 130
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 130

```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1          5          10          15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
          20          25          30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          35          40          45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
          50          55          60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
65          70          75          80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
          85          90          95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
          100          105          110

Arg Ser Ala Pro His
          115

```

<210> SEQ ID NO 131

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 131

```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1          5          10          15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
          20          25          30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          35          40          45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
          50          55          60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
65          70          75          80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
          85          90          95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
          100          105          110

Arg Ser Ala Pro His
          115

```

<210> SEQ ID NO 132

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 132

```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1          5          10          15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
          20          25          30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          35          40          45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
          50          55          60

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Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
65          70          75          80
Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
85          90          95
Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
100         105         110
Arg Ser Ala Pro His
115

```

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<210> SEQ ID NO 133
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 133

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```

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

```

```

<210> SEQ ID NO 134
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 134

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```

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

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<210> SEQ ID NO 135

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<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 135

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 136
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia fergusonii

<400> SEQUENCE: 136

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

```

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<210> SEQ ID NO 137
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 137

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65           70           75           80

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Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 138
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Klebsiella oxytoca

<400> SEQUENCE: 138

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 139
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 139

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 140
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 140

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

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Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

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<210> SEQ ID NO 141
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 141

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

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<210> SEQ ID NO 142
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 142

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

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<210> SEQ ID NO 143
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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-continued

<400> SEQUENCE: 143

```

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

```

<210> SEQ ID NO 144

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 144

```

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

```

<210> SEQ ID NO 145

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 145

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 146
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 146

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 147
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 147

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

Gly Thr Thr Leu Met Lys Tyr Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 148
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 148

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ser
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 149
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 149

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

Gly Thr Thr Leu Met Lys Tyr Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 150
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 150

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Thr
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 151
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

-continued

<400> SEQUENCE: 151

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
          100          105          110

```

<210> SEQ ID NO 152

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 152

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
          100          105          110

```

<210> SEQ ID NO 153

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 153

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 154
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 154

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

<210> SEQ ID NO 155
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 155

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

<210> SEQ ID NO 156
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 156

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 157
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 157

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Gly Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 158
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 158

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 159
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 159

```

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

```

<210> SEQ ID NO 160

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 160

```

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

```

<210> SEQ ID NO 161

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella sp.

<400> SEQUENCE: 161

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 162
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli
 <400> SEQUENCE: 162

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

<210> SEQ ID NO 163
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli
 <400> SEQUENCE: 163

Met Asn Ser Phe Val Ser Leu Gly Phe Leu Leu Ile Ile Ile Val Pro
 1 5 10 15
 Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30
 Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45
 Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60
 Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 65 70 75 80
 Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 85 90 95
 Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 100 105 110
 Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 115 120 125
 Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 130 135 140
 Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 145 150 155 160
 Arg Ser Ala Pro His
 165

<210> SEQ ID NO 164
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

-continued

<400> SEQUENCE: 164

```

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
20           25           30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
35           40           45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
50           55           60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
65           70           75           80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
85           90           95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
115          120          125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
130          135          140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
145          150          155          160

Arg Ser Ala Pro His
165

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<210> SEQ ID NO 165

<211> LENGTH: 165

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 165

```

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
20           25           30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
35           40           45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
50           55           60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
65           70           75           80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
85           90           95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
115          120          125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
130          135          140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
145          150          155          160

Arg Ser Ala Pro His
165

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<210> SEQ ID NO 166

<211> LENGTH: 165

-continued

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<212> TYPE: PRT
<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 166

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
          20           25           30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
          35           40           45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
          50           55           60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
65           70           75           80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          85           90           95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
          115          120          125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
          130          135          140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
145          150          155          160

Arg Ser Ala Pro His
          165

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<210> SEQ ID NO 167
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 167

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
          20           25           30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
          35           40           45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
          50           55           60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
65           70           75           80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          85           90           95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
          115          120          125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
          130          135          140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
145          150          155          160

Arg Ser Ala Pro His
          165

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<210> SEQ ID NO 168
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 168
Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
 1             5             10             15
Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
          20             25             30
Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
          35             40             45
Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
          50             55             60
Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
          65             70             75             80
Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
          85             90             95
Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
          100            105            110
Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
          115            120            125
Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
          130            135            140
Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
          145            150            155            160
Ile Asn Leu Leu Ser Arg Ser Ala Pro His
          165            170

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<210> SEQ ID NO 169
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 169
Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
 1             5             10             15
Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
          20             25             30
Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
          35             40             45
Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
          50             55             60
Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
          65             70             75             80
Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
          85             90             95
Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
          100            105            110
Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
          115            120            125
Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
          130            135            140
Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
          145            150            155            160

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-continued

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 170
 <211> LENGTH: 170
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 170

Met Leu Ile Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15
 Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30
 Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35 40 45
 Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60
 Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80
 Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95
 Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110
 Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115 120 125
 Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130 135 140
 Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160
 Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 171
 <211> LENGTH: 170
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 171

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

-continued

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 172
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 172

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115 120 125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130 135 140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 173
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 173

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Ser Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115 120 125

-continued

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130 135 140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 174
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 174

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Ser Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115 120 125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130 135 140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 175
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 175

Met Leu Ile Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110

-continued

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
 115 120 125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
 130 135 140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
 145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 165 170

<210> SEQ ID NO 176
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 176

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Ser
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 177
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 177

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Ser
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 178
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 178

```

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

```

<210> SEQ ID NO 179

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 179

```

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

```

<210> SEQ ID NO 180

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 180

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 181
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 181

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

<210> SEQ ID NO 182
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 182

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

<210> SEQ ID NO 183
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 183

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 184
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sp.

<400> SEQUENCE: 184

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Ser Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 185
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 185

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 186
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 186

```

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

```

<210> SEQ ID NO 187

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella boydii

<400> SEQUENCE: 187

```

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

```

<210> SEQ ID NO 188

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella dysenteriae

<400> SEQUENCE: 188

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 189
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella dysenteriae

<400> SEQUENCE: 189

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

<210> SEQ ID NO 190
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 190

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

<210> SEQ ID NO 191
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 191

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 192
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 192

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 193
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 193

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 194
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 194

```

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

```

<210> SEQ ID NO 195

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 195

```

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

```

<210> SEQ ID NO 196

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 196

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 197
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 197

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 198
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 198

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Phe Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 199
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 199

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 200
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 200

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Phe Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 201
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 201

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Asn Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 202
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

-continued

<400> SEQUENCE: 202

```

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

```

<210> SEQ ID NO 203

<211> LENGTH: 154

<212> TYPE: PRT

<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 203

```

Met Asn Ser Phe Val Ser Leu Gly Phe Leu Leu Ile Ile Ile Val Pro
1           5           10           15
Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
          20           25           30
Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
          35           40           45
Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
          50           55           60
Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
          65           70           75           80
Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          85           90           95
Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
          100          105          110
Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
          115          120          125
Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
          130          135          140
Gly Met Met Leu Ile Cys Ala Tyr Tyr Gly
145          150

```

<210> SEQ ID NO 204

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Citrobacter sp.

<400> SEQUENCE: 204

```

Met Asn Thr Tyr Ile Tyr Leu Gly Ala Ala Ile Leu Ala Glu Val Thr
1           5           10           15
Gly Thr Thr Leu Met Lys Phe Thr Asp Gly Phe Thr Arg Leu Trp Pro
          20           25           30
Ser Val Gly Thr Ile Val Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ser
          35           40           45

```

-continued

Gln Thr Leu Ala His Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ala Trp Val Ile His Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ala Leu Ile Cys Ala
 85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Ala Val His
 100 105 110

<210> SEQ ID NO 205
 <211> LENGTH: 104
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 205

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Ala Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Asp Thr Val Met Ala Cys Lys
 85 90 95

Phe Phe Pro Gly Pro Val Ser Arg
 100

<210> SEQ ID NO 206
 <211> LENGTH: 82
 <212> TYPE: PRT
 <213> ORGANISM: Paenibacillus sp.

<400> SEQUENCE: 206

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg

<210> SEQ ID NO 207
 <211> LENGTH: 101
 <212> TYPE: PRT
 <213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 207

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Gly Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Leu
 65 70 75 80

Pro Thr Ala Gly Pro Ala Ser His Tyr Arg His Asp Val Asp Leu Cys
 85 90 95

Arg Cys Val Gly Tyr
 100

<210> SEQ ID NO 208
 <211> LENGTH: 71
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 208

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Arg Tyr Cys Pro Asp
 65 70

<210> SEQ ID NO 209
 <211> LENGTH: 73
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 209

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Tyr
 50 55 60

Met Arg Thr Phe Ile Ser Cys Lys Arg
 65 70

<210> SEQ ID NO 210
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 peptide

<400> SEQUENCE: 210

Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly
 1 5 10

<210> SEQ ID NO 211
 <211> LENGTH: 80

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<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 211

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1          5          10          15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
          20          25          30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
          35          40          45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
          50          55          60

Ile Ala Tyr Ala Ile Trp Tyr Met Arg Thr Phe Ile Ser Cys Lys Arg
65          70          75          80

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<210> SEQ ID NO 212
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Fundulus heteroclitus

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<400> SEQUENCE: 212

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20          25          30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35          40          45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50          55          60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65          70          75          80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85          90          95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 213
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 213

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20          25          30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35          40          45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50          55          60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65          70          75          80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85          90          95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 214
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 214

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 215
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 215

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

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<210> SEQ ID NO 216
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 216

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

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-continued

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 217
<211> LENGTH: 51
<212> TYPE: PRT
<213> ORGANISM: *Shigella sonnei*

<400> SEQUENCE: 217

Met Leu Ser Gly Gln Glu Ser Gly Ile Val Leu Ile Ser Leu Leu Ser
1 5 10 15

Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met
20 25 30

Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser
35 40 45

Thr Pro His
50

<210> SEQ ID NO 218
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 218

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 219
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia sp.*

<400> SEQUENCE: 219

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

-continued

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 220
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia sp.*

<400> SEQUENCE: 220

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 221
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia sp.*

<400> SEQUENCE: 221

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 222
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 222

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

-continued

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Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100                105                110

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<210> SEQ ID NO 223
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 223

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100                105                110

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<210> SEQ ID NO 224
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 224

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100                105                110

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<210> SEQ ID NO 225
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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-continued

<400> SEQUENCE: 225

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

```

<210> SEQ ID NO 226

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 226

```

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

```

<210> SEQ ID NO 227

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 227

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 228
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 228

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

<210> SEQ ID NO 229
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia fergusonii

<400> SEQUENCE: 229

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

<210> SEQ ID NO 230
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 230

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
 1 5 10 15
 Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30
 Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 231
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 231

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 232
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 232

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 233
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 233

```

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

```

<210> SEQ ID NO 234

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 234

```

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

```

<210> SEQ ID NO 235

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Klebsiella oxytoca

<400> SEQUENCE: 235

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

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Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 236
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 236

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Gln Val Ile
1 5 10 15

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 237
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 237

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Ser
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 238
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 238

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 239
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia fergusonii

<400> SEQUENCE: 239

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 240
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 240

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 241
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 241

```

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

```

<210> SEQ ID NO 242

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 242

```

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

```

<210> SEQ ID NO 243

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 243

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 244
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 244

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 245
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 245

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 246
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 246

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 247
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 247

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 248
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 248

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 249
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 249

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

<210> SEQ ID NO 250

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 250

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

<210> SEQ ID NO 251

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 251

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

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 252
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Achromobacter* sp.

<400> SEQUENCE: 252

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 253
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 253

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 254
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 254

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 255
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 255

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 256
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 256

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 257
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 257

```

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

```

<210> SEQ ID NO 258

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 258

```

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

```

<210> SEQ ID NO 259

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 259

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 260
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Shigella dysenteriae*

<400> SEQUENCE: 260

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Tyr Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 261
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 261

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 262
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Escherichia sp.*

<400> SEQUENCE: 262

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 263
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 263

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 264
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 264

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 265
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 265

```

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

```

<210> SEQ ID NO 266

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 266

```

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

```

<210> SEQ ID NO 267

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 267

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 268
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 268

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 269
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 269

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 270
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 270

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 271
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 271

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 272
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 272

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 273
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 273

```

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

```

<210> SEQ ID NO 274

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 274

```

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

```

<210> SEQ ID NO 275

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 275

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 276
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 276

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 277
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella dysenteriae

<400> SEQUENCE: 277

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Tyr Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 278
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 278

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 279
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 279

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 280
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 280

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 281
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 281

```

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

```

<210> SEQ ID NO 282

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 282

```

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

```

<210> SEQ ID NO 283

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 283

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 284
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 284

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 285
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 285

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 286
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 286

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 287
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 287

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

Gly Thr Thr Leu Met Lys Tyr Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 288
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 288

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 289
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 289

```

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

```

<210> SEQ ID NO 290

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 290

```

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

```

<210> SEQ ID NO 291

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 291

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
100 105 110

<210> SEQ ID NO 292
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Shigella* sp.

<400> SEQUENCE: 292

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Gly Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Leu Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 293
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 293

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
100 105 110

<210> SEQ ID NO 294
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 294

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

-continued

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 295
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 295

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 296
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 296

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 297
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 297

```

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

```

<210> SEQ ID NO 298

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 298

```

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

```

<210> SEQ ID NO 299

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 299

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 300
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 300

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 301
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 301

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 302
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 302

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 303
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 303

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 304
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 304

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 305
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

-continued

<400> SEQUENCE: 305

```

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

```

<210> SEQ ID NO 306

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 306

```

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

```

<210> SEQ ID NO 307

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 307

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 308
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 308

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 309
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 309

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 310
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 310

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

```

<210> SEQ ID NO 311
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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```

<400> SEQUENCE: 311

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 312
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 312

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100               105               110

```

```

<210> SEQ ID NO 313
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

-continued

<400> SEQUENCE: 313

```

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

```

<210> SEQ ID NO 314

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 314

```

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

```

<210> SEQ ID NO 315

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 315

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 316
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 316

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
 100 105 110

<210> SEQ ID NO 317
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 317

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 318
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 318

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 319
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 319

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Ser
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 320
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 320

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 321
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

-continued

<400> SEQUENCE: 321

```

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

```

<210> SEQ ID NO 322

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 322

```

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

```

<210> SEQ ID NO 323

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 323

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 324
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Shigella flexneri*

<400> SEQUENCE: 324

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 325
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Shigella flexneri*

<400> SEQUENCE: 325

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 326
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Escherichia coli*

<400> SEQUENCE: 326

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100                105                110

```

```

<210> SEQ ID NO 327
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 327

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100                105                110

```

```

<210> SEQ ID NO 328
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 328

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
   100                105                110

```

```

<210> SEQ ID NO 329
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

```

-continued

<400> SEQUENCE: 329

```

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

```

<210> SEQ ID NO 330

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 330

```

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

```

<210> SEQ ID NO 331

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 331

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 332
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 332

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 333
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 333

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 334
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 334

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 335
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 335

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 336
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia albertii

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<400> SEQUENCE: 336

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Thr His
   100               105               110

```

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<210> SEQ ID NO 337
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia albertii

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-continued

<400> SEQUENCE: 337

```

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

```

<210> SEQ ID NO 338

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 338

```

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

```

<210> SEQ ID NO 339

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 339

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 340
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 340

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 341
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 341

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 342
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 342

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35              40              45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50              55              60

Gly Val Gly Ile Val Leu Ile Gly Leu Leu Ser Trp Gly Phe Phe Gly
   65              70              75              80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85              90              95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100             105             110

```

```

<210> SEQ ID NO 343
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

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<400> SEQUENCE: 343

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20              25              30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35              40              45

Gln Thr Leu Ala Tyr Ile Pro Lys Gly Ile Ala Tyr Ala Ile Trp Ser
   50              55              60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65              70              75              80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85              90              95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100             105             110

```

```

<210> SEQ ID NO 344
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

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```

<400> SEQUENCE: 344

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20              25              30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
   35              40              45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50              55              60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65              70              75              80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85              90              95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100             105             110

```

```

<210> SEQ ID NO 345
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

-continued

<400> SEQUENCE: 345

```

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

```

<210> SEQ ID NO 346

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 346

```

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

```

<210> SEQ ID NO 347

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 347

```

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

```

-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 348
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 348

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Thr Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 349
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella boydii

<400> SEQUENCE: 349

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Leu Phe Asp
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 350
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella boydii

<400> SEQUENCE: 350

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 351
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Shigella flexneri

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```

<400> SEQUENCE: 351

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
   20                25                30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
   35                40                45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
   50                55                60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
   65                70                75                80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
   85                90                95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
   100               105               110

```

```

<210> SEQ ID NO 352
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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```

<400> SEQUENCE: 352

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```

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
  1                5                10                15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
   20                25                30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
   35                40                45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
   50                55                60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
   65                70                75                80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
   85                90                95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
   100               105               110

Arg Ser Ala Pro His
   115

```

```

<210> SEQ ID NO 353

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-continued

<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 353

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 354
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 354

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 355
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 355

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

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

-continued

Arg Ser Ala Pro His
115

<210> SEQ ID NO 358
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 358

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

<210> SEQ ID NO 359
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 359

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

<210> SEQ ID NO 360
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 360

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
1 5 10 15

-continued

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 361
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 361

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 1 5 10 15

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 20 25 30

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 35 40 45

Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala Tyr Ile Pro Thr Gly
 50 55 60

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 65 70 75 80

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 85 90 95

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 100 105 110

Arg Ser Ala Pro His
 115

<210> SEQ ID NO 362
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 362

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 65 70 75 80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 85 90 95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 115 120 125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 130 135 140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 145 150 155 160

Arg Ser Ala Pro His
 165

<210> SEQ ID NO 363
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: *Shigella flexneri*
 <400> SEQUENCE: 363

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 65 70 75 80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 85 90 95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 115 120 125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 130 135 140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 145 150 155 160

Arg Ser Ala Pro His
 165

<210> SEQ ID NO 364
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: *Escherichia coli*
 <400> SEQUENCE: 364

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 65 70 75 80

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Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 85 90 95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 115 120 125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 130 135 140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 145 150 155 160

Arg Ser Ala Pro His
 165

<210> SEQ ID NO 365
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 365

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
 65 70 75 80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
 85 90 95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
 115 120 125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
 130 135 140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
 145 150 155 160

Arg Ser Ala Pro His
 165

<210> SEQ ID NO 366
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 366

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

Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp Ile His Ile His Gln
 20 25 30

Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser Thr Ile Leu Ser Ser
 35 40 45

Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr Ile Tyr Leu Gly Gly
 50 55 60

-continued

Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu Met Lys Phe Ser Glu
65 70 75 80

Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr Ile Ile Cys Tyr Cys
85 90 95

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

Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile Val Leu Ile Ser Leu
115 120 125

Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp Leu Pro Ala Ile Ile
130 135 140

Gly Met Met Leu Ile Cys Ala Gly Val Leu Val Ile Asn Leu Leu Ser
145 150 155 160

Arg Ser Ala Pro His
165

<210> SEQ ID NO 367
 <211> LENGTH: 170
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 367

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50 55 60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65 70 75 80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85 90 95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100 105 110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115 120 125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130 135 140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145 150 155 160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165 170

<210> SEQ ID NO 368
 <211> LENGTH: 170
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 368

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35 40 45

Thr	Ile	Leu	Ser	Ser	Met	Asn	Arg	Lys	Glu	Tyr	Ala	Met	Asn	Pro	Tyr
50						55					60				
Ile	Tyr	Leu	Gly	Gly	Ala	Ile	Leu	Ala	Glu	Val	Ile	Gly	Thr	Thr	Leu
65					70					75					80
Met	Lys	Phe	Ser	Glu	Gly	Phe	Thr	Arg	Leu	Trp	Pro	Ser	Val	Gly	Thr
				85					90					95	
Ile	Ile	Cys	Tyr	Cys	Ala	Ser	Phe	Trp	Leu	Leu	Ala	Gln	Thr	Leu	Ala
			100					105					110		
Tyr	Ile	Pro	Thr	Gly	Ile	Ala	Tyr	Ala	Ile	Trp	Ser	Gly	Val	Gly	Ile
		115					120				125				
Val	Leu	Ile	Ser	Leu	Leu	Ser	Trp	Gly	Phe	Phe	Gly	Gln	Arg	Leu	Asp
	130					135					140				
Leu	Pro	Ala	Ile	Ile	Gly	Met	Met	Leu	Ile	Cys	Ala	Gly	Val	Leu	Val
145					150					155					160
Ile	Asn	Leu	Leu	Ser	Arg	Ser	Ala	Pro	His						
				165				170							

<400> SEQUENCE: 369

Met	Leu	Ile	Gly	Arg	Val	Asn	Ser	Phe	Val	Ser	Leu	Gly	Phe	Leu	Leu
1				5					10					15	
Ile	Ile	Ile	Val	Pro	Ala	Phe	Ile	Ser	Cys	His	Ala	Arg	Ala	Pro	Trp
			20					25					30		
Ile	His	Ile	His	Gln	Asp	Glu	Asn	Gly	Glu	Leu	Cys	Ser	Asn	Cys	Ser
	35					40					45				
Thr	Ile	Leu	Ser	Ser	Met	Asn	Arg	Lys	Glu	Tyr	Ala	Met	Asn	Pro	Tyr
	50				55						60				
Ile	Tyr	Leu	Gly	Gly	Ala	Ile	Leu	Ala	Glu	Val	Ile	Gly	Thr	Thr	Leu
65					70					75					80
Met	Lys	Phe	Ser	Glu	Gly	Phe	Thr	Arg	Leu	Trp	Pro	Ser	Val	Gly	Thr
				85					90					95	
Ile	Ile	Cys	Tyr	Cys	Ala	Ser	Phe	Trp	Leu	Leu	Ala	Gln	Thr	Leu	Ala
				100				105					110		
Tyr	Ile	Pro	Thr	Gly	Ile	Ala	Tyr	Ala	Ile	Trp	Ser	Gly	Val	Gly	Ile
	115					120						125			
Val	Leu	Ile	Ser	Leu	Leu	Ser	Trp	Gly	Phe	Phe	Gly	Gln	Arg	Leu	Asp
	130					135					140				
Leu	Pro	Ala	Ile	Ile	Gly	Met	Met	Leu	Ile	Cys	Ala	Gly	Val	Leu	Val
145					150					155					160
Ile	Asn	Leu	Leu	Ser	Arg	Ser	Ala	Pro	His						
				165				170							

<400> SEQUENCE: 370

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1 5 10 15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20 25 30

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Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
   35                               40               45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
   50                               55               60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
   65                               70               75               80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
   85                               90               95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
  100                               105              110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
  115                               120              125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
  130                               135              140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
  145                               150              155              160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
  165                               170

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<210> SEQ ID NO 371
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 371

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```

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
  1           5           10           15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
  20           25           30

Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
  35           40           45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
  50           55           60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
  65           70           75           80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
  85           90           95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
  100          105          110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
  115          120          125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
  130          135          140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
  145          150          155          160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
  165          170

```

```

<210> SEQ ID NO 372
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 372

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```

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
  1           5           10           15

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```

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
    20                      25                      30

Ile His Ile His Gln Asp Glu Asn Ser Glu Leu Cys Ser Asn Cys Ser
    35                      40                      45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
    50                      55                      60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
    65                      70                      75                      80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
    85                      90                      95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
    100                     105                     110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
    115                     120                     125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
    130                     135                     140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
    145                     150                     155                     160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
    165                     170

```

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<210> SEQ ID NO 373
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 373

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```

Met Leu Pro Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
  1          5          10          15

Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
    20                      25                      30

Ile His Ile His Gln Asp Glu Asn Ser Glu Leu Cys Ser Asn Cys Ser
    35                      40                      45

Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
    50                      55                      60

Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
    65                      70                      75                      80

Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
    85                      90                      95

Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
    100                     105                     110

Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
    115                     120                     125

Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
    130                     135                     140

Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
    145                     150                     155                     160

Ile Asn Leu Leu Ser Arg Ser Ala Pro His
    165                     170

```

```

<210> SEQ ID NO 374
<211> LENGTH: 170
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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-continued

<400> SEQUENCE: 374

```

Met Leu Ile Gly Arg Val Asn Ser Phe Val Ser Leu Gly Phe Leu Leu
1           5           10           15
Ile Ile Ile Val Pro Ala Phe Ile Ser Cys His Ala Arg Ala Pro Trp
20           25           30
Ile His Ile His Gln Asp Glu Asn Gly Glu Leu Cys Ser Asn Cys Ser
35           40           45
Thr Ile Leu Ser Ser Met Asn Arg Lys Glu Tyr Ala Met Asn Pro Tyr
50           55           60
Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile Gly Thr Thr Leu
65           70           75           80
Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Val Gly Thr
85           90           95
Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala Gln Thr Leu Ala
100          105          110
Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser Gly Val Gly Ile
115          120          125
Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly Gln Arg Leu Asp
130          135          140
Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala Gly Val Leu Val
145          150          155          160
Ile Asn Leu Leu Ser Arg Ser Ala Pro His
165          170

```

<210> SEQ ID NO 375

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 375

```

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

```

<210> SEQ ID NO 376

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 376

```

Met Asn Pro Tyr Ile Tyr Leu Gly Gly Ala Ile Leu Ala Glu Val Ile
1           5           10           15
Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
20           25           30

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-continued

```

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35                      40                      45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50                      55                      60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65                      70                      75                      80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
    85                      90                      95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
    100                      105                      110

```

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<210> SEQ ID NO 377
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 377

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```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
    20      25      30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35      40      45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50      55      60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65      70      75      80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
    85      90      95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
    100      105      110

```

```

<210> SEQ ID NO 378
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 378

```

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
    20      25      30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35      40      45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50      55      60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65      70      75      80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
    85      90      95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
    100      105      110

```

```

<210> SEQ ID NO 379
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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-continued

<400> SEQUENCE: 379

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Val
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

```

<210> SEQ ID NO 380

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 380

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
          100          105          110

```

<210> SEQ ID NO 381

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 381

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

```

-continued

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 382
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli
 <400> SEQUENCE: 382

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ser
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 383
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli
 <400> SEQUENCE: 383

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 384
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli
 <400> SEQUENCE: 384

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

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Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Val Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 385
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 385

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Met Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Thr Pro His
 100 105 110

<210> SEQ ID NO 386
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 386

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
 20 25 30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
 35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
 65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Thr
 85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
 100 105 110

<210> SEQ ID NO 387
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Escherichia albertii

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<400> SEQUENCE: 387

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Ile Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Phe Ser Arg Ser Ala Thr His
          100          105          110

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<210> SEQ ID NO 388

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella sp.

<400> SEQUENCE: 388

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Ser Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
          100          105          110

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<210> SEQ ID NO 389

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Citrobacter sp.

<400> SEQUENCE: 389

```

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

Gly Thr Thr Leu Met Lys Phe Thr Asp Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Val Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ser
          35           40           45

Gln Thr Leu Ala His Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ala Trp Val Ile His Gly
65           70           75           80

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-continued

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ala Leu Ile Cys Ala
85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Arg Ser Ala Val His
100 105 110

<210> SEQ ID NO 390
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 390

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 391
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 391

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
35 40 45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Phe Trp Gly Phe Phe Gly
65 70 75 80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
100 105 110

<210> SEQ ID NO 392
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

<400> SEQUENCE: 392

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

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

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Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35                      40                      45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50                      55                      60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65                      70                      75                      80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
    85                      90                      95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
    100                      105                      110

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<210> SEQ ID NO 393
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia sp.

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<400> SEQUENCE: 393

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```

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35          40          45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50          55          60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65          70          75          80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
    85          90          95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
    100          105          110

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<210> SEQ ID NO 394
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 394

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```

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

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

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
    35          40          45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
    50          55          60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
    65          70          75          80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Ile Leu Ile Cys Ala
    85          90          95

Gly Val Leu Val Ile Asn Leu Leu Ser Arg Ser Ala Pro His
    100          105          110

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<210> SEQ ID NO 395
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

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<400> SEQUENCE: 395

```

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

Gly Thr Thr Leu Met Lys Phe Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Val Gly Thr Ile Ile Cys Tyr Cys Ala Ser Phe Trp Leu Leu Ala
          35           40           45

Gln Thr Leu Ala Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Val Gly Ile Val Leu Ile Ser Leu Leu Ser Trp Gly Phe Phe Gly
65           70           75           80

Gln Arg Leu Asp Leu Pro Ala Ile Ile Gly Met Met Leu Ile Cys Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Gly Asp Ala Ala Asn Leu Leu Ile
          100          105          110

```

<210> SEQ ID NO 396

<211> LENGTH: 86

<212> TYPE: PRT

<213> ORGANISM: Shigella sp.

<400> SEQUENCE: 396

```

Met Val Phe Ser Arg Leu Tyr Pro Ser Ile Val Val Val Ile Gly Tyr
1           5           10           15

Cys Leu Ser Phe Trp Ala Leu Ser Gln Val Val Arg Val Met Pro Leu
          20           25           30

Gly Ile Ala Tyr Ala Ile Trp Ser Gly Leu Gly Ile Val Leu Val Ser
          35           40           45

Val Ala Ala Val Phe Leu Tyr Gln Gln Lys Leu Asp Leu Pro Ala Ile
          50           55           60

Ile Gly Met Ser Leu Ile Ile Ala Gly Val Leu Val Ile Asn Leu Leu
65           70           75           80

Ser Lys Ser Ala Ser His
          85

```

<210> SEQ ID NO 397

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Shigella sp.

<400> SEQUENCE: 397

```

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

Ala Thr Thr Met Leu Lys Ala Ser Asp Gly Phe Ser Arg Leu Tyr Pro
          20           25           30

Ser Ile Val Val Val Ile Gly Tyr Cys Leu Ser Phe Trp Ala Leu Ser
          35           40           45

Gln Val Val Arg Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Val Phe Leu Tyr Gln
65           70           75           80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Ser Leu Ile Ile Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Ser His
          100          105          110

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<210> SEQ ID NO 398
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Shigella* sp.

<400> SEQUENCE: 398

```

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

Ala Thr Thr Met Leu Lys Ala Ser Asp Gly Phe Ser Arg Leu Tyr Pro
          20           25           30

Ser Ile Val Val Val Ile Gly Tyr Cys Leu Ser Phe Trp Ala Leu Ser
          35           40           45

Gln Val Val Arg Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
          50           55           60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Val Phe Leu Tyr Gln
65           70           75           80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Ser Leu Ile Ile Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Ser His
          100          105          110

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<210> SEQ ID NO 399
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Serratia plymuthica*

<400> SEQUENCE: 399

```

Met Ser Gly Phe Ile Tyr Leu Thr Met Ala Ile Val Ala Glu Val Ile
1           5           10           15

Ala Thr Thr Met Leu Lys Ala Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Leu Val Val Val Val Gly Tyr Ala Val Ala Phe Trp Gly Leu Ser
          35           40           45

Met Val Val Lys Thr Met Pro Leu Gly Ile Val Tyr Ala Ile Trp Ser
          50           55           60

Gly Met Gly Ile Val Leu Val Ser Ile Ala Ala Val Phe Val Tyr Gln
65           70           75           80

Gln Lys Leu Asp Leu Pro Ala Val Ile Gly Met Val Leu Ile Ile Ala
          85           90           95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Thr Ala Ala His
          100          105          110

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<210> SEQ ID NO 400
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Serratia plymuthica*

<400> SEQUENCE: 400

```

Met Ser Gly Phe Ile Tyr Leu Thr Met Ala Ile Val Ala Glu Val Ile
1           5           10           15

Ala Thr Thr Met Leu Lys Ala Ser Glu Gly Phe Thr Arg Leu Trp Pro
          20           25           30

Ser Leu Val Val Val Val Gly Tyr Ala Val Ala Phe Trp Gly Leu Ser
          35           40           45

Met Val Val Lys Thr Met Pro Leu Gly Ile Val Tyr Ala Ile Trp Ser
          50           55           60

Gly Met Gly Ile Val Leu Val Ser Ile Ala Ala Val Phe Val Tyr Gln
65           70           75           80

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Gln Lys Leu Asp Leu Pro Ala Val Ile Gly Met Val Leu Ile Ile Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Thr Ala Ala His
100 105 110

<210> SEQ ID NO 401
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Proteus vulgaris*

<400> SEQUENCE: 401

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

Ala Thr Thr Met Leu Lys Ala Ser Glu Gly Phe Ser Arg Leu Tyr Pro
20 25 30

Ser Ile Val Val Val Ile Gly Tyr Cys Phe Ser Phe Trp Ala Leu Ser
35 40 45

Gln Val Val Arg Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Val Phe Ile Tyr Gln
65 70 75 80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Gly Leu Ile Ile Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Ser His
100 105 110

<210> SEQ ID NO 402
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Proteus vulgaris*

<400> SEQUENCE: 402

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

Ala Thr Thr Met Leu Lys Ala Ser Glu Gly Phe Ser Arg Leu Tyr Pro
20 25 30

Ser Ile Ile Val Val Ile Gly Tyr Cys Phe Ser Phe Trp Ala Leu Ser
35 40 45

Gln Val Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Leu Gly Ile Val Ser Val Ser Val Ala Ala Val Phe Ile Tyr Gln
65 70 75 80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Gly Leu Ile Ile Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Ser His
100 105 110

<210> SEQ ID NO 403
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: *Proteus vulgaris*

<400> SEQUENCE: 403

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

Ser Asp Gly Phe Ser Arg Leu Tyr Pro Ser Ile Val Val Val Ile Gly
20 25 30

-continued

Tyr Cys Phe Ser Phe Trp Ala Leu Ser Gln Val Val Lys Val Met Pro
 35 40 45
 Leu Gly Ile Ala Tyr Ala Ile Trp Ser Gly Leu Gly Ile Val Leu Val
 50 55 60
 Ser Val Ala Ala Val Phe Leu Tyr Gln Gln Lys Leu Asp Leu Pro Ala
 65 70 75 80
 Ile Val Gly Met Thr Leu Ile Ile Ala Gly Val Leu Val Ile Asn Leu
 85 90 95
 Leu Ser Lys Ser Ala Ser His
 100

<210> SEQ ID NO 404
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Proteus mirabilis*

<400> SEQUENCE: 404

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

<210> SEQ ID NO 405
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Proteus sp.*

<400> SEQUENCE: 405

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

<210> SEQ ID NO 406
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: *Proteus hauseri*

-continued

<400> SEQUENCE: 406

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

<210> SEQ ID NO 407

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: *Proteus mirabilis*

<400> SEQUENCE: 407

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

<210> SEQ ID NO 408

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: *Proteus penneri*

<400> SEQUENCE: 408

Met Asn Gly Leu Thr Tyr Leu Met Leu Ala Ile Ile Ser Glu Val Ile
1 5 10 15
Ala Thr Thr Met Leu Lys Ala Ser Asp Gly Phe Ser Arg Leu Tyr Pro
20 25 30
Ser Ile Val Val Val Ile Gly Tyr Cys Phe Ser Phe Trp Ala Leu Ser
35 40 45
Gln Val Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60
Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Val Phe Leu Tyr Gln
65 70 75 80

-continued

Gln Lys Leu Asp Leu Pro Ala Ile Val Gly Met Thr Leu Ile Ile Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Ser His
100 105 110

<210> SEQ ID NO 409
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Proteus mirabilis*

<400> SEQUENCE: 409

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

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

Ser Ile Val Val Val Val Gly Tyr Cys Phe Ser Phe Trp Ala Leu Ser
35 40 45

Gln Val Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Val Phe Val Tyr Gln
65 70 75 80

Gln Lys Leu Asp Leu Pro Ala Ile Val Gly Met Thr Leu Ile Ile Ala
85 90 95

Gly Val Leu Val Ile Asn Leu Leu Ser Asn Ser Thr Ala His
100 105 110

<210> SEQ ID NO 410
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Providencia rettgeri*

<400> SEQUENCE: 410

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

Ala Thr Thr Thr Leu Lys Ala Ser Asp Gly Phe Ser Arg Phe Trp Pro
20 25 30

Ser Leu Val Val Val Ile Gly Tyr Ala Val Ser Phe Trp Gly Leu Ser
35 40 45

Gln Val Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
50 55 60

Gly Leu Gly Ile Val Leu Val Ser Ile Ala Ala Ile Tyr Ile Tyr Asn
65 70 75 80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Leu Phe Ile Ile Val
85 90 95

Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Ser Gly Thr His
100 105 110

<210> SEQ ID NO 411
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: *Providencia rustigianii*

<400> SEQUENCE: 411

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

Ala Thr Thr Thr Leu Lys Ala Ser Asp Gly Phe Ser Arg Phe Trp Pro
20 25 30

-continued

Ser Leu Ile Val Val Ile Gly Tyr Ala Ile Ser Phe Trp Gly Leu Ser
 35 40 45

Gln Val Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Ile Trp Ser
 50 55 60

Gly Leu Gly Ile Val Leu Val Ser Val Ala Ala Ile Tyr Ile Tyr Asn
 65 70 75 80

Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Met Leu Leu Ile Ile Val
 85 90 95

Gly Val Leu Ile Ile Asn Leu Phe Ser Lys Ser Gly Thr His
 100 105 110

<210> SEQ ID NO 412
 <211> LENGTH: 124
 <212> TYPE: PRT
 <213> ORGANISM: Xenorhabdus thuongxuanensis
 <400> SEQUENCE: 412

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

Val Trp Gly Tyr Leu Phe Ile Ala Ile Leu Ser Glu Val Ile Ala Thr
 20 25 30

Thr Met Leu Lys Ser Ala Asp Gly Phe Thr Arg Leu Val Pro Ser Ile
 35 40 45

Ile Val Val Thr Gly Tyr Cys Leu Ser Phe Trp Ala Leu Ser Gln Val
 50 55 60

Val Lys Val Met Pro Leu Gly Ile Ala Tyr Ala Val Trp Ser Cys Leu
 65 70 75 80

Gly Ile Val Leu Val Ser Ile Ala Gly Ile Phe Leu Tyr Gln Gln Lys
 85 90 95

Leu Asp Leu Pro Ala Ile Ile Gly Ile Leu Leu Ile Ile Ala Gly Val
 100 105 110

Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Gly His
 115 120

<210> SEQ ID NO 413
 <211> LENGTH: 131
 <212> TYPE: PRT
 <213> ORGANISM: Xenorhabdus doucetiae
 <400> SEQUENCE: 413

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

Gly Leu Val Ser Asn Met Asn Val Trp Gly Tyr Leu Phe Ile Ala Ile
 20 25 30

Leu Ser Glu Val Ile Ala Thr Thr Met Leu Lys Thr Ala Asp Gly Phe
 35 40 45

Thr Arg Leu Val Pro Ser Ile Val Val Val Leu Gly Tyr Cys Leu Ser
 50 55 60

Phe Trp Ala Leu Ser Gln Val Val Lys Thr Met Pro Leu Gly Ile Ala
 65 70 75 80

Tyr Ala Val Trp Ser Cys Leu Gly Ile Val Leu Val Ser Ile Ala Gly
 85 90 95

Ile Phe Leu Tyr Gln Gln Lys Leu Asp Leu Pro Ala Ile Ile Gly Ile
 100 105 110

Leu Leu Ile Ile Ala Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser
 115 120 125

-continued

Ala Gly His
130

<210> SEQ ID NO 414
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Enterobacter cancerogenus

<400> SEQUENCE: 414

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

<210> SEQ ID NO 415
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Serratia plymuthica

<400> SEQUENCE: 415

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

<210> SEQ ID NO 416
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Serratia fonticola

<400> SEQUENCE: 416

Met Thr Ala Phe Ile Tyr Leu Ala Met Ala Ile Ile Ala Glu Val Ile
1 5 10 15
Ala Thr Thr Leu Leu Lys Ala Ser Glu Gly Phe Thr Arg Leu Trp Pro
20 25 30

-continued

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Ser Val Phe Val Val Leu Gly Tyr Ala Val Ala Phe Trp Gly Leu Ser
  35              40              45

Met Val Val Lys Thr Met Pro Leu Gly Ile Val Tyr Ala Ile Trp Ser
  50              55              60

Gly Leu Gly Ile Val Leu Val Ser Ile Ala Ala Val Phe Ile Tyr Gln
  65              70              75              80

Gln Lys Leu Asp Leu Pro Ala Val Ile Gly Met Gly Leu Ile Ile Ala
      85              90              95

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Ser Ala Gly His
      100              105              110

```

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<210> SEQ ID NO 417
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Escherichia vulneris

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<400> SEQUENCE: 417

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```

Met His Ala Tyr Val His Leu Gly Ile Ala Ile Val Ala Glu Val Ile
  1              5              10              15

Gly Thr Thr Leu Met Arg Tyr Ser Glu Gly Phe Thr Lys Leu Trp Pro
      20              25              30

Thr Val Ala Thr Leu Gly Cys Tyr Ala Val Ala Phe Trp Phe Leu Ser
      35              40              45

Gln Thr Leu Gln Tyr Ile Pro Thr Gly Ile Ala Tyr Ala Ile Trp Ser
      50              55              60

Gly Val Gly Ile Val Leu Ile Ser Ala Ala Gly Trp Ile Phe Ser Gly
      65              70              75              80

Gln Lys Leu Asp Leu Pro Ala Ile Gly Gly Met Ala Leu Ile Cys Ala
      85              90              95

Gly Val Leu Val Ile Asn Leu Phe Ser Lys Ser Val Ala His
      100              105              110

```

```

<210> SEQ ID NO 418
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Serratia rubidaea

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<400> SEQUENCE: 418

```

```

Met Tyr Leu Thr Met Ala Ile Ile Ala Glu Val Ile Ala Thr Thr Met
  1              5              10              15

Leu Lys Ala Ser Glu Gly Phe Thr Arg Leu Trp Pro Ser Leu Val Val
      20              25              30

Val Leu Gly Tyr Gly Val Ala Phe Trp Gly Leu Ser Met Val Val Lys
      35              40              45

Ser Met Pro Leu Gly Ile Val Tyr Ala Ile Trp Ser Gly Met Gly Val
      50              55              60

Val Leu Val Ser Ile Ala Ala Val Phe Ile Tyr Asn Gln Lys Leu Asp
      65              70              75              80

Trp Pro Ala Ile Ile Gly Met Gly Leu Ile Val Ala Gly Val Leu Val
      85              90              95

Ile Asn Leu Leu Ser Lys Thr Ser Ala His
      100              105

```

```

<210> SEQ ID NO 419
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Serratia marcescens

```

-continued

<400> SEQUENCE: 419

```

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

```

<210> SEQ ID NO 420

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Serratia marcescens

<400> SEQUENCE: 420

```

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

```

<210> SEQ ID NO 421

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Serratia odorifera

<400> SEQUENCE: 421

```

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

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-continued

Gly Val Leu Val Ile Asn Leu Leu Ser Lys Thr Ser Ala His
100 105 110

<210> SEQ ID NO 422
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(11)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 422

Asp Leu Pro Xaa Ile Ile Gly Met Met Leu Xaa Cys Ala Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 423
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (5)..(12)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 423

Asp Leu Pro Ala Xaa Ile Gly Met Met Leu Ile Xaa Ala Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 424
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(13)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES

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<222> LOCATION: (13)..(13)

<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 424

Asp Leu Pro Ala Ile Xaa Gly Met Met Leu Ile Cys Xaa Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 425

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (9)..(9)

<223> OTHER INFORMATION: Any crosslinked amino acid

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (9)..(16)

<223> OTHER INFORMATION: Crosslink between residues

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (16)..(16)

<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 425

Asp Leu Pro Ala Ile Ile Gly Met Xaa Leu Ile Cys Ala Gly Val Xaa
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 426

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (4)..(4)

<223> OTHER INFORMATION: Any crosslinked amino acid

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (4)..(11)

<223> OTHER INFORMATION: Crosslink between residues

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (11)..(11)

<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 426

Asp Leu Pro Xaa Ile Ile Gly Met Met Leu Xaa Ser Ala Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 427

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: MOD_RES

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<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(13)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 427

Asp Leu Pro Ala Ile Xaa Gly Met Met Leu Ile Ser Xaa Gly Val Leu
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 428
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (9)..(16)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 428

Asp Leu Pro Ala Ile Ile Gly Met Xaa Leu Ile Ser Ala Gly Val Xaa
1 5 10 15

Ile Ile Asn Leu Leu Ser
20

<210> SEQ ID NO 429
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Sarcosine
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (8)..(15)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Any crosslinked amino acid

-continued

<400> SEQUENCE: 429

Ala Xaa Xaa Xaa Asp Leu Pro Xaa Ile Ile Gly Met Met Leu Xaa Cys
1 5 10 15

Ala Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Lys Lys
20 25

<210> SEQ ID NO 430

<211> LENGTH: 29

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (2)..(4)

<223> OTHER INFORMATION: Sarcosine

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (9)..(9)

<223> OTHER INFORMATION: Any crosslinked amino acid

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (9)..(16)

<223> OTHER INFORMATION: Crosslink between residues

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (16)..(16)

<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 430

Ala Xaa Xaa Xaa Asp Leu Pro Ala Xaa Ile Gly Met Met Leu Ile Xaa
1 5 10 15

Ala Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Lys Lys
20 25

<210> SEQ ID NO 431

<211> LENGTH: 29

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (2)..(4)

<223> OTHER INFORMATION: Sarcosine

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (10)..(10)

<223> OTHER INFORMATION: Any crosslinked amino acid

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (10)..(17)

<223> OTHER INFORMATION: Crosslink between residues

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (17)..(17)

<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 431

Ala Xaa Xaa Xaa Asp Leu Pro Ala Ile Xaa Gly Met Met Leu Ile Cys
1 5 10 15

Xaa Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Lys Lys
20 25

<210> SEQ ID NO 432

<211> LENGTH: 31

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Sarcosine
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (13)..(20)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 432

Ala Xaa Xaa Xaa Asp Leu Pro Ala Ile Ile Gly Met Xaa Leu Ile Cys
1 5 10 15

Ala Gly Val Xaa Ile Ile Asn Leu Leu Ser Lys Lys Lys Lys Lys
20 25 30

<210> SEQ ID NO 433
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Sarcosine
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (8)..(15)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 433

Ala Xaa Xaa Xaa Asp Leu Pro Xaa Ile Ile Gly Met Met Leu Xaa Ser
1 5 10 15

Ala Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Lys Lys
20 25

<210> SEQ ID NO 434
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Sarcosine
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:

-continued

<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (10)..(17)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 434

Ala Xaa Xaa Xaa Asp Leu Pro Ala Ile Xaa Gly Met Met Leu Ile Ser
1 5 10 15

Xaa Gly Val Leu Ile Ile Asn Leu Leu Ser Lys Lys Lys
20 25

<210> SEQ ID NO 435
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Sarcosine
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Any crosslinked amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (13)..(20)
<223> OTHER INFORMATION: Crosslink between residues
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Any crosslinked amino acid

<400> SEQUENCE: 435

Ala Xaa Xaa Xaa Asp Leu Pro Ala Ile Ile Gly Met Xaa Leu Ile Ser
1 5 10 15

Ala Gly Val Xaa Ile Ile Asn Leu Leu Ser Lys Lys Lys Lys Lys
20 25 30

<210> SEQ ID NO 436
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 436

Ile Ile Asn Lys Lys Ser
1 5

<210> SEQ ID NO 437
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 437

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

<210> SEQ ID NO 438

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<211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 <400> SEQUENCE: 438

Asp Leu Pro Ala Ile Ile Gly Met
 1 5

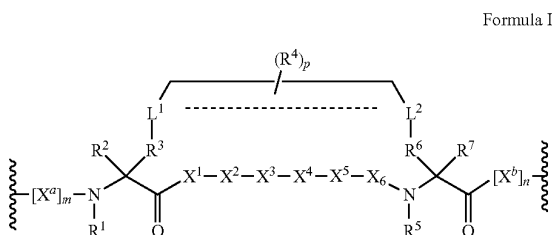
<210> SEQ ID NO 439
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (10)..(14)
 <223> OTHER INFORMATION: Hydrocarbon staple between residues
 <400> SEQUENCE: 439

Lys Lys Lys Lys Lys Lys Ala Gly Phe Ala Ala Trp Ala Ala Phe Gly
 1 5 10 15

Ala

The invention claimed is:

1. A polypeptide, or a pharmaceutically acceptable salt thereof, comprising a stabilized α -helix, wherein the polypeptide comprises the structure of Formula I:



wherein the dotted line represents an optional double bond;

m is 1, 2, 3, 4, 5, or 6;

n is 6-m;

p is 0, 1, or 2;

each of $[X^a]_m$, $[X^b]_n$, and X^1 - X^6 consist of consecutive amino acids of an α -helix of a monomer of a small multidrug resistance transporter, or conservative substitutions thereof;

R^1 and R^5 are, independently, hydrogen, optionally substituted acyl, or optionally substituted C_1 - C_6 alkyl;

R^2 and R^7 are, independently, optionally substituted C_1 - C_6 alkyl, optionally substituted C_2 - C_6 alkenyl, optionally substituted C_2 - C_6 alkynyl, optionally substituted C_1 - C_6 heteroalkyl, optionally substituted C_3 - C_6 carbocyclyl, or optionally substituted C_2 - C_9 heterocyclyl;

R^3 and R^6 are, independently, optionally substituted C_1 - C_6 alkylene, optionally substituted C_1 - C_6 heteroalkylene, optionally substituted C_3 - C_6 carbocyclyl, or optionally substituted C_2 - C_9 heterocyclyl, or R^1 and R^3

or R^5 and R^6 combine with the atoms to which they are attached to form an optionally substituted C_5 - C_6 heterocyclyl;

L^1 and L^2 are, independently, absent, optionally substituted C_1 - C_6 alkylene, or $-C(=O)OR^{L1}-$, wherein each R^{L1} is, independently, an optionally substituted C_1 - C_6 alkyl; and

each R^4 is, independently, optionally substituted C_1 - C_6 alkyl, or optionally substituted C_1 - C_6 heteroalkyl, wherein the polypeptide binds to the monomer of a small multidrug resistance transporter.

2. The polypeptide of claim 1, wherein R^2 is optionally substituted C_1 - C_6 alkyl.

3. The polypeptide of claim 2, wherein the optionally substituted C_1 - C_6 alkyl is methyl.

4. The polypeptide of claim 1, wherein R^7 is optionally substituted C_1 - C_6 alkyl.

5. The polypeptide of claim 4, wherein the optionally substituted C_1 - C_6 alkyl is methyl.

6. The polypeptide of claim 1, wherein R^1 is hydrogen.

7. The polypeptide of claim 1, wherein R^5 is hydrogen.

8. The polypeptide of claim 1, wherein p is 0.

9. The polypeptide of claim 1, wherein R^6 is optionally substituted C_1 - C_6 alkylene.

10. The polypeptide of claim 9, wherein the optionally substituted C_1 - C_6 alkylene is methylene.

11. The polypeptide of claim 1, wherein R^3 is optionally substituted C_1 - C_6 alkylene.

12. The polypeptide of claim 11, wherein the optionally substituted C_1 - C_6 alkylene is methylene.

13. The polypeptide of claim 1, wherein L^1 is optionally substituted C_1 - C_6 alkylene.

14. The polypeptide of claim 13, wherein optionally substituted C_1 - C_6 alkylene is pentylene.

15. The polypeptide of claim 1, wherein L^2 is optionally substituted C_1 - C_6 alkylene.

16. The polypeptide of claim 15, wherein optionally substituted C_1 - C_6 alkylene is ethylene.

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17. The polypeptide of claim 1, wherein the dotted line represents a double bond.

18. The polypeptide of claim 1, wherein X^1 is glycine, alanine, valine, leucine, or isoleucine.

19. The polypeptide of claim 18, wherein X^1 is glycine. 5

20. The polypeptide of claim 1, wherein each R^4 is, independently, optionally substituted C_1 - C_6 alkyl.

* * * * *

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