Claims

1. A polypeptide having an amino acid sequence comprising or consisting of:

    (a) FimH; or a variant, fragment and/or fusion of FimH, and

    (b) a donor-strand complementing amino acid sequence,

    wherein (b) is downstream of (a) and wherein (b) comprises or consists of an amino acid sequence according to SEQ ID NO: 5.

2. A polypeptide comprising or consisting of an amino acid sequence X-(a)- L-(b)-Y , wherein "(a)" is a FimH polypeptide; or a variant, fragment and/or fusion of FimH; "L" is a~~n optional~~ first linker; "(b)" is a donor-strand complementing amino acid sequence, wherein (b) comprises or consists of an amino acid sequence according to SEQ ID NO: 5, "X" is an optional N-terminal amino acid sequence; "Y is an optional C-terminal amino acid sequence, wherein "Y" is not derived from FimC or FimH or a fragment thereof.

3. The polypeptide of claim 1 or 2 wherein (a) comprises or consists of:

    (A) the amino acid sequence of SEQ ID NO: 1 (Genbank Accession no: ELL41155.1 (FimH of E. coli J96)), SEQ ID NO: 2, SEQ ID NO: 100 (Genbank Accession no: ABG72591.1 (FimH of UPEC 536)) , SEQ ID NO: 101, SEQ ID NO: 102 (Genbank Accession no: AAN83822.1 (FimH of CFT073)), SEQ ID NO: 103, SEQ ID NO: 104 (Genbank Accession no: AJE58925.1 (FimH of E. coli 789)), SEQ ID NO: 105, SEQ ID NO: 106 (Genbank Accession No. AAC35864.1, corresponding to nucleic acid sequence AF089840.1 (FimH of IHE3034), or SEQ ID NO: 107,

    (B) an amino acid sequence comprising from 1 to 10 single amino acid alterations compared to SEQ ID NO: 1 (Genbank Accession no: ELL41155.1 (FimH of E. coli J96)), SEQ ID NO: 2 , SEQ ID NO: 100 (Genbank Accession no: ABG72591.1 (FimH of UPEC 536)) , SEQ ID NO: 101, SEQ ID NO: 102 (Genbank Accession no: AAN83822.1 (FimH of CFT073)), SEQ ID NO: 103, SEQ ID NO: 104 (Genbank Accession no: AJE58925.1 (FimH of E. coli 789)), SEQ ID NO: 105, SEQ ID NO: 106 (Genbank Accession No. AAC35864.1, corresponding to nucleic acid sequence AF089840.1 (FimH of IHE3034), or SEQ ID NO: 107, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 single amino acid alterations,

    (C) an amino acid sequence with at least 70% sequence identity with SEQ ID NO: 1 (Genbank Accession no: ELL41155.1 (FimH of E. coli J96)), SEQ ID NO: 2 , SEQ ID NO: 100 (Genbank Accession no: ABG72591.1 (FimH of UPEC 536)) , SEQ ID NO: 101, SEQ ID NO: 102 (Genbank Accession no: AAN83822.1 (FimH of CFT073)), SEQ ID NO: 103, SEQ ID NO: 104 (Genbank Accession no: AJE58925.1 (FimH of E. coli 789)), SEQ ID NO: 105, SEQ ID NO: 106 (Genbank Accession No. AAC35864.1, corresponding to nucleic acid sequence AF089840.1 (FimH of IHE3034), or SEQ ID

NO: 107, for example, 80%, 85%, 90%, 91%. 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity, and/or

(D) a fragment of at least 10 consecutive amino acids from SEQ ID NO: 1 (Genbank Accession no: ELL41155.1 (FimH of E. coli J96)), SEQ ID NO: 2 , SEQ ID NO: 100 (Genbank Accession no: ABG72591.1 (FimH of UPEC 536)) , SEQ ID NO: 101, SEQ ID NO: 102 (Genbank Accession no: AAN83822.1 (FimH of CFT073)), SEQ ID NO: 103, SEQ ID NO: 104 (Genbank Accession no: AJE58925.1 (FimH of E. coli 789)), SEQ ID NO: 105, SEQ ID NO: 106 (Genbank Accession No. AAC35864.1, corresponding to nucleic acid sequence AF089840.1 (FimH of IHE3034), or SEQ ID NO: 107, for example, at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 275, 280, 290 or 300 consecutive amino acids.

~~4. The polypeptide of any one of the preceding claims wherein one or more amino acids known or predicted to be N-glycosylated or O-glycosylated are substituted with serine (S), alanine (A), aspartic acid (D) or glutamine (Q).~~

~~5. The polypeptide of claim 4 wherein (a) includes one or more of the following amino acid substitutions relative to SEQ ID NO: 2: N28S, N91D, N249D, N256D, or at the positions of SEQ ID NO: 101, 103 and 105 corresponding those positions of SEQ ID NO:2for example, one, two, three or four of the amino acid substitutions.~~

~~6. The polypeptide of any one of the preceding claims wherein (b) comprises or consists of:~~

~~6-28 amino acids of SEQ ID NO: 3; or a fragment and/or variant thereof, or~~

~~8-36 amino acids of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~7. The polypeptide of claim 6 wherein the 6-28 amino acids of SEQ ID NO: 3 correspond to the group consisting of:~~

~~(i) amino acids 1-28 of SEQ ID NO: 3,~~

~~(ii) amino acids 2-27 of SEQ ID NO: 3,~~

~~(iii) amino acids 3-26 of SEQ ID NO: 3,~~

~~(iv) amino acids 4-25 of SEQ ID NO: 3,~~

~~(v) amino acids 5-24 of SEQ ID NO: 3,~~

~~(vi) amino acids 6-23 of SEQ ID NO: 3,~~

~~(vii)amino acids 7-22 of SEQ ID NO: 3,~~

~~(viii) amino acids 8-21 of SEQ ID NO: 3,~~

~~(ix) amino acids 9-20 of SEQ ID NO: 3,~~

~~(x) amino acids 10-19 of SEQ ID NO: 3,~~

~~(xi) amino acids 11-18 of SEQ ID NO: 3, and~~

~~(xii) amino acids 12-17 of SEQ ID NO: 3.~~

~~8. The polypeptide of claim 6 wherein the 8-36 amino acids of SEQ ID NO: 4 correspond to the group consisting of:~~

~~(i) amino acids 1-36 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(ii) amino acids 2-35 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(iii) amino acids 3-34 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(iv) amino acids 4-33 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(v) amino acids 5-32 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(vi) amino acids 6-31 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(vii) amino acids 7-30 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(viii) amino acids 8-29 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(ix) amino acids 9-28 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(x) amino acids 10-27 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(xi) amino acids 11-26 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(xii) amino acids 12-25 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(xiii) amino acids 13-24 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(xiv) amino acids 14-23 of SEQ ID NO: 4; or a fragment and/or variant thereof,~~

~~(xv) amino acids 15-24 of SEQ ID NO: 4; or a fragment and/or variant thereof, and~~

~~(xvi) amino acids 16-23 of SEQ ID NO: 4; or a fragment and/or variant thereof.~~

~~9. The polypeptide of any one of the preceding claims wherein (b) comprises or consists of:~~

~~(A) the amino acid sequence of SEQ ID NO: 5 or SEQ ID NO: 6,~~

~~(B) an amino acid sequence comprising from 1 to 10 single amino acid alterations compared to SEQ ID NO: 5 or SEQ ID NO: 6, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 single amino acid alterations,~~

~~(C) a fragment of at least 7 consecutive amino acids from SEQ ID NO: 5, for example, at least 8, 9, 10, 11, 12, or 13 consecutive amino acids from SEQ ID NO: 5, or.~~

~~(D) a fragment of at least 7 consecutive amino acids from SEQ ID NO: 6, for example, at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18 consecutive amino acids from SEQ ID NO: 6.~~

~~10. The polypeptide of claim 1 or 2 wherein (b) comprises or consists of an amino acid sequence according to SEQ ID NO: 5.~~

~~11.~~4. The polypeptide of any one of the preceding claims wherein (b) is:

(i) directly joined to the C-terminus of (a), or

(ii) joined to the C-terminus of (a) via a first linker.

~~12.~~5. The polypeptide of any one of claims 2 or ~~4~~11, (ii) wherein the first linker or "L" comprises or consists of 2-20 amino acids, for example, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acids.

~~13.~~6. The polypeptide of any one of claims 2, or ~~5~~12 wherein the first linker begins with proline.

~~14.~~7. The polypeptide any one of claims 2, ~~11~~4 ~~13~~ 6 wherein the first linker comprises or consists of polar amino acids, for example, wherein the first linker is entirely comprised of polar amino acids or, if the first linker begins with proline, the remainder of the amino acids are polar.

~~15.~~8. The polypeptide of any one of claims 2, ~~11~~4 ~~14~~ 7 wherein the first linker comprises or consists of:

~~(i)~~ PGDGN **[SEQ ID NO: 7]**, or a variant or fusion thereof~~, or~~

~~(ii)~~(i) ~~DNKQ~~ **~~[SEQ ID NO: 8]~~**~~, or a variant or fusion thereof~~.

~~16. The polypeptide of any one of the preceding claims wherein the polypeptide comprises a protein purification affinity tag at the N-terminus, C-terminus and/or internally, for example, 6, 7, 8, 9 or 10 consecutive histidines.~~

~~17. The polypeptide of any one of the preceding claims wherein the polypeptide or "X" comprises a cell secretion leader sequence:~~

~~(i) upstream of (a), or~~

~~(ii) at the N-terminus of the polypeptide.~~

~~18. The polypeptide of claim 17 wherein the cell secretion leader sequence is selected from the group consisting of:~~

~~(i) METDTLLLWVLLLWVPGSTGD~~ **~~[SEQ ID NO: 9]~~**~~, or a variant or fusion thereof,~~

~~(ii) METDTLLLWVLLLWVPGSTGDAAQPARRARRTKLAL~~ **~~[SEQ ID NO: 10]~~**~~, or a variant or fusion thereof,~~

~~(iii) MRLLAKIICLMLWAICVA~~ **~~[SEQ ID NO: 11]~~**~~, or a variant or fusion thereof,~~

~~(iv) MGWSCIILFLVATATGVHS~~ **~~[SEQ ID NO: 12]~~**~~, or a variant or fusion thereof,~~

~~(v) METPAELLFLLLLWLPDTTG~~ **~~[SEQ ID NO: 13]~~**~~, or a variant or fusion thereof,~~

~~(vi) METDTLLLWVLLLWVPGSTG~~ **~~[SEQ ID NO: 108]~~**~~, or a variant or fusion thereof or~~

~~(vii)MEFGLSWVFLVAILEGVHC~~ **~~[SEQ ID NO: 14]~~**~~, or a variant or fusion thereof.~~

~~19.~~9. The polypeptide of any one of the preceding claims wherein the polypeptide comprises a nanoparticle domain at the N-terminus or C-terminus, optionally wherein "X" or "Y" comprise a nanoparticle domain.

~~20.~~10. The polypeptide of claim 9~~19~~ wherein the nanoparticle domain is selected from the group consisting of:

(i) ferritin (for example, **[SEQ ID NO: 15]** or [SEQ ID NO: 109] (*Helicobacter pylori*), **[SEQ ID NO: 16]** (*Escherichia coli*)), or any one of [SEQ ID NO: 149]- [SEQ ID NO: 152] (stabilized *Escherichia coli*)),or a variant and/or fragment thereof,

(ii) iMX313 (for example **[SEQ ID NO: 17]**), or a variant and/or fragment thereof,

(iii) mI3 (for example **[SEQ ID NO: 18]**), or a variant and/or fragment thereof,

(iv) encapsulin (for example **[SEQ ID NO: 19]**), or a variant and/or fragment thereof, or

(v) Self-assembling viral coat proteins, such as *Acinetobacter* phage AP205 coat protein (NCBI Reference Sequence: NP_085472.1), Hepatitis B virus core protein (HBc) **[SEQ ID NO: 110]**, or bacteriophage Qβ **[SEQ ID NO: 111]**, or a variant and/or fragment thereof.

~~21. The polypeptide of claim 19 or 20 wherein the nanoparticle domain is:~~

~~(i) directly joined to the polypeptide, or~~

~~(ii) joined to the polypeptide via a second linker.~~

~~22. The polypeptide of any one of claims 19-22 wherein the second linker comprises or consists of between 2-20 amino acids, for example, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acids.~~

~~23. The polypeptide of any one of claims 19-22 wherein the second linker comprises or consists glycines (G) and/or serines (S).~~

~~24. The polypeptide of any one of claims 19-23 wherein the second linker is selected from the group consisting of:~~

~~(i) GSSGSGSGS [SEQ ID NO: 112] or a variant or fusion thereof,~~

~~(ii) GGSGS [SEQ ID NO: 113] or a variant or fusion thereof,~~

~~(iii) GGS or a variant or fusion thereof,~~

~~(iv) SGSHHHHHHHHGGS [SEQ ID NO: 114], or a variant or fusion thereof,~~

~~(v) AKFVAAWTLKAAA [SEQ ID NO: 115] or a variant or a fusion thereof,~~

~~(vi) GGGGSLVPRGSGGGGS [SEQ ID NO: 116], or a variant or a fusion thereof,~~

~~(vii) EAAAKEAAAKEAAAKA [SEQ ID NO: 117], or a variant or a fusion thereof,~~

~~(viii) SGSFVAAWTLKAAAGGS [SEQ ID NO: 118] or a variant or a fusion thereof, and~~

~~(ix) SGSGSGGGGGGS [SEQ ID NO: 119] or a variant or a fusion thereof.~~

~~25. The polypeptide of any one of claims 19-24 wherein the nanoparticle domain is:~~

~~(i) upstream of (a),~~

~~(ii) at the N-terminus of the polypeptide,~~

~~(iii) downstream of (b), or~~

~~(iv) at the C-terminus of the polypeptide.~~

~~26. A polypeptide monomer comprising or consisting of an amino acid sequence that has:~~

~~(i) at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 16 and has one or more mutations from the group consisting of: glycine (G) at the position that aligns to residue 34 of SEQ ID NO: 16 (T34G mutation), aspartic acid (D) at the position that aligns to residue 70 of SEQ ID NO: 16 (N70D mutation), isoleucine (I) at the position that aligns to residue 72 of SEQ ID NO: 16 (V72I mutation) and alanine (A) at the position that aligns to residue 124 of SEQ ID NO: 16 (S124A mutation);~~

~~(ii) an amino acid sequence that has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 16 and has glycine (G) at the position that aligns to residue 34 of SEQ ID NO: 16 (T34G mutation), aspartic acid (D) at the position that aligns to residue 70 of SEQ ID NO: 16 (N70D mutation), isoleucine (I) at the position that aligns to residue 72 of SEQ ID NO: 16 (V72I mutation) and alanine (A) at the position that aligns to residue 124 of SEQ ID NO: 16 (S124A mutation), optionally wherein the polypeptide monomer comprises an amino acid sequence that has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 149.~~

~~(iii) has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 16 and has glycine (G) at the position that aligns to residue 34 of SEQ ID NO: 16 (T34G mutation), isoleucine (I) at the position that aligns to residue 72 of SEQ ID NO: 16 (V72I mutation) and alanine (A) at the position that aligns to residue 124 of SEQ ID NO: 16 (S124A mutation), optionally wherein the polypeptide monomer comprises an amino acid sequence that has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 150. .~~

~~(iv) has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 16 and has glycine (G) at the position that aligns to residue 34 of SEQ ID NO: 16 (T34G mutation), and alanine (A) at the position that aligns to residue 124 of SEQ ID NO: 16 (S124A mutation), optionally wherein the polypeptide monomer comprises an amino acid sequence that has at least 80%~~

sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 151.

(v) has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 16 and has glycine (G) at the position that aligns to residue 34 of SEQ ID NO: 16 (T34G mutation), optionally wherein the polypeptide monomer comprises an amino acid sequence that has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 152.

27. The polypeptide monomer of claim 26, comprising an amino acid sequence of selected from the group consisting of: SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, and SEQ ID NO: 152.

28. A nanoparticle comprising the polypeptide monomer of claims 26 or 27.

29. The nanoparticle of claim 29, wherein the nanoparticle is a homo-oligomer.

30. The nanoparticle of claims 28 or 29, wherein the exterior surface structure or interior surface structure of the nanoparticle carries one or more antigen and/or immunostimulant.

31. The nanoparticle of claim 30, wherein the antigen comprises or consists of the polypeptide of any one of claims 1 to 18.

32. The nanoparticle of claim 31, comprising or consisting of an amino acid sequence that has at least 80% sequence identity, for example at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence SEQ ID NO: 130 or 153.

33. The polypeptide of any one of the preceding claims wherein the polypeptide comprises or consists of an amino acid sequence corresponding to:

(i) SEQ ID NO: 20, or a variant and/or fragment thereof,

(ii) SEQ ID NO: 21, or a variant and/or fragment thereof,

(iii) SEQ ID NO: 22, or a variant and/or fragment thereof,

(iv) SEQ ID NO: 23, or a variant and/or fragment thereof,

(v) SEQ ID NO: 24, or a variant and/or fragment thereof,

(vi) SEQ ID NO: 25, or a variant and/or fragment thereof,

(vii) SEQ ID NO: 26, or a variant and/or fragment thereof,

(viii) SEQ ID NO: 27, or a variant and/or fragment thereof,

(ix) SEQ ID NO: 28, or a variant and/or fragment thereof,

(x) SEQ ID NO: 29, or a variant and/or fragment thereof,

(xi) SEQ ID NO: 30, or a variant and/or fragment thereof,

~~(xii) SEQ ID NO: 31, or a variant and/or fragment thereof,~~

~~(xiii) SEQ ID NO: 32, or a variant and/or fragment thereof,~~

~~(xiv) SEQ ID NO: 33, or a variant and/or fragment thereof,~~

~~(xv) SEQ ID NO: 34, or a variant and/or fragment thereof,~~

~~(xvi) SEQ ID NO: 35, or a variant and/or fragment thereof,~~

~~(xvii) SEQ ID NO: 36, or a variant and/or fragment thereof,~~

~~(xviii) SEQ ID NO: 37, or a variant and/or fragment thereof,~~

~~(xix) SEQ ID NO: 38, or a variant and/or fragment thereof,~~

~~(xx) SEQ ID NO: 39, or a variant and/or fragment thereof,~~

~~(xxi) SEQ ID NO: 40, or a variant and/or fragment thereof,~~

~~(xxii) SEQ ID NO: 41, or a variant and/or fragment thereof,~~

~~(xxiii) SEQ ID NO: 42, or a variant and/or fragment thereof,~~

~~(xxiv) SEQ ID NO: 43, or a variant and/or fragment thereof,~~

~~(xxv) SEQ ID NO: 44, or a variant and/or fragment thereof,~~

~~(xxvi) SEQ ID NO: 79, or a variant and/or fragment thereof,~~

~~(xxvii) SEQ ID NO: 80, or a variant and/or fragment thereof,~~

~~(xxviii) SEQ ID NO: 81, or a variant and/or fragment thereof,~~

~~(xxix) SEQ ID NO: 82, or a variant and/or fragment thereof,~~

~~(xxx) SEQ ID NO: 83, or a variant and/or fragment thereof,~~

~~(xxxi) SEQ ID NO: 84, or a variant and/or fragment thereof,~~

~~(xxxii) SEQ ID NO: 85, or a variant and/or fragment thereof,~~

~~(xxxiii) SEQ ID NO: 86, or a variant and/or fragment thereof,~~

~~(xxxiv) SEQ ID NO: 87, or a variant and/or fragment thereof,~~

~~(xxxv) SEQ ID NO: 88, or a variant and/or fragment thereof,~~

~~(xxxvi) SEQ ID NO: 89, or a variant and/or fragment thereof, and~~

~~(xxxvii) any one of SEQ ID NO: 120-124, SEQ ID NO: 129-143 and 153 or a variant and/or a fragment thereof.~~

~~34.~~11. The polypeptide of anyone of the preceding claims, wherein the polypeptide comprises or consists of an amino acid sequence with at least 70% sequence identity to SEQ ID NO: 123 or SEQ ID NO:124, for example, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO: 123 or SEQ ID NO:124.

~~35. The polypeptide of any one of the preceding claims wherein the mannose binding of the polypeptide is at least 20% lower than that of native FimH complexed with native FimC (FimHC complex), e.g., at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% lower.~~

~~36. The polypeptide of anyone of the preceding claims, wherein FimH is in the low affinity conformation, i.e. in the tense (T) state.~~

~~37. The polypeptide of any one of the preceding claims, wherein the auto-aggregation induced by the polypeptide is at least 20% lower than that of native FimH, e.g., at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% lower.~~

~~38. The polypeptide of any one of the preceding claims, wherein the polypeptide is capable of inhibiting bacterial adhesion by at least 20%, e.g., by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or by 100%.~~

~~39. The polypeptide of any one of the preceding claims, wherein the anti-FimH immunogenicity of the polypeptide is at least 20% higher than that of native FimH complexed with native FimC (in particular, we include FimH in the high-affinity conformation, relaxed (R) state (see above).), e.g., at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, 200%, 300%, 400% or 500% higher.~~

~~40. The polypeptide of any one of the preceding claims, wherein the polypeptide is capable of inhibiting hemagglutination of guinea pig red blood cells by at least 2-fold, e.g. by at least 3-fold, 4-fold, 5-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 40-fold, 50-fold, 60-fold, 70-fold, 80-fold, 90-fold, or 100-fold.~~

~~41.~~12. A nucleic acid encoding a polypeptide according to any one of claims 1-11~~40, for example, DNA or RNA encoded by any one of SEQ ID NOs: 45-77, 90-99 or a variant and/or fragment thereof~~.

~~42. The nucleic acid of claim 42 wherein the nucleic acid has been codon optimised for expression in a selected prokaryotic or eukaryotic cell, for example, a yeast cell (e.g., *Saccharomyces cerevisiae*, *Pichia pastoris*), an insect cell (e.g., *Spodoptera frugiperda* Sf21 cells, or Sf9 cells), or a mammalian cell (Expi293, Expi293GNTI, Chinese hamster ovary (CHO) cell, and Human embryonic kidney 293 cells (HEK 293)).~~

~~43. A vector comprising the nucleic acid of claim 41 or 42.~~

~~44. The vector of claim 43 wherein vector is a plasmid, for example, an expression plasmid.~~

~~45. The vector of claim 43 or 44 wherein the plasmid is selected from the group consisting of pCDNA3.1 (Life Technologies), pCDNA3.4 (Life Technologies), pFUSE, pBROAD, pSEC, pCMV, pDSG-IBA, and pHEK293 Ultra or is selected from the group of pACYCDuet-1, pTrcHis2A, pET21, pET15TEV, pET22b+, pET303/CT-HIS, PET303/CT, pBAD/Myc-His A, pET303, pET24b(+).~~

~~46. The vector of claim 43 wherein the vector is a viral vector, for example, an RNA viral vector.~~

~~47.~~13. A cell comprising a nucleic acid of claim 12~~41 or 42 or a vector of any one of claims 43-46~~.

~~48. The cell of claim 46 wherein the cell does not have N-acetylglucosaminyltransferase I (GnTI) activity.~~

~~49. The cell of claim 47 or 48 wherein the host cell is selected from the group consisting of Expi293, Expi293GNTI (Life Technologies), Chinese hamster ovary (CHO) cell, NIH-3T3 cells, 293-T cells, Vero cells, HeLa cells, PERC.6 cells (ECACC deposit number 96022940), Hep G2 cells, MRC-5 (ATCC CCL-171), WI-38 (ATCC CCL-75), fetal rhesus lung cells (ATCC CL-160), Madin-Darby bovine kidney ("MDBK") cells, Madin-Darby canine kidney ("MDCK") cells (e.g., MDCK (NBL2), ATCC CCL34; or MDCK 33016, DSM ACC 2219), baby hamster kidney (BHK) cells, such as BHK21-F, HKCC cells, and Human embryonic kidney 293 cells (HEK 293).~~

~~50. The cell of claim 47, wherein the host cells is selected from *Escherichia coli* from strains BL21(DE3), HMS174 (DE3), Origami 2 (DE3), BL21DE3T1r or T7shuffle express.~~

~~51. A cell culture comprising the cell of any one of claims 47-50.~~

~~52. A method of producing a polypeptide defined in any one of claims 1-40 by expressing the protein in a cell as defined in any one of claims 47-50 under suitable conditions and in a suitable medium, thereby expressing the encoded polypeptide.~~

~~53. The method of claim 52, further comprising collecting the expressed polypeptides from the cultured cell(s) and/or culture medium, and optionally purifying the collected polypeptides.~~

~~54. A pharmaceutical composition comprising the polypeptide of any one of claims 1-40, the nucleic acid of any one of claims 41 or42, or a vector of any one of claims 43-46.~~

~~55.~~14. A vaccine comprising the polypeptide of any one of claims 1-11~~40~~, or ~~a~~the nucleic acid of claim 12~~s~~ ~~41 or 42 or a vector of any one of claims 43-46~~.

~~56.~~ The vaccine of claim 14~~55~~ further comprising an adjuvant~~.~~,

~~57.~~15. ~~The vaccine of claim 56~~ wherein the adjuvant comprises any one of: 3D-MPL, QS21 and liposomes, for example liposomes comprising cholesterol.

~~58.~~16. The vaccine of claim 15~~57~~, wherein the adjuvant comprises 3D-MPL, QS21 and liposomes comprising cholesterol.

~~59. The vaccine of any one of claims 55-58, wherein the vaccine elicits a protective immune response after one or two doses.~~

~~60.~~17. The~~A~~ polypeptide of any one of claims 1-11~~40~~, the~~a~~ nucleic acid of claim 12~~41 or 42 or a vector of any one of claims 43-46~~, or ~~a~~the vaccine of claims ~~55-59~~14-16 for use in medicine.

~~61.~~18. The~~A~~ polypeptide of any one of claims 1-11~~40~~, the~~a~~ nucleic acid of claim 12~~41 or 42 or a vector of any one of claims 43-46~~, or the~~a~~ vaccine of claims ~~55-59~~ 14-16 for use in raising an immune response in

a mammal, for example, for treating and/or preventing one or more disease, optionally wherein the disease is a urinary tract infection.

~~62. Use of a polypeptide of any one of claims 1-40, a nucleic acid of claim 41 or 42 or a vector of any one of claims 43-46, or a vaccine of claim 55-59 for raising an immune response in a mammal, for example, for treating and/or preventing one or more disease.~~

~~63. Use of a polypeptide of any one of claims 1-40, a nucleic acid of claim 41 or 42 or a vector of any one of claims 43-46, or a vaccine of claim 55-59 for the manufacture of a medicament for raising an immune response in a mammal, for example, for treating and/or preventing one or more disease.~~

~~64. A method of raising an immune response in a mammal, the method comprising or consisting of administering the mammal with an effective amount of a polypeptide of any one of claims 1-40, a nucleic acid of claim 41 or 42 or a vector of any one of claims 43-46, or a vaccine of claim 55-59.~~