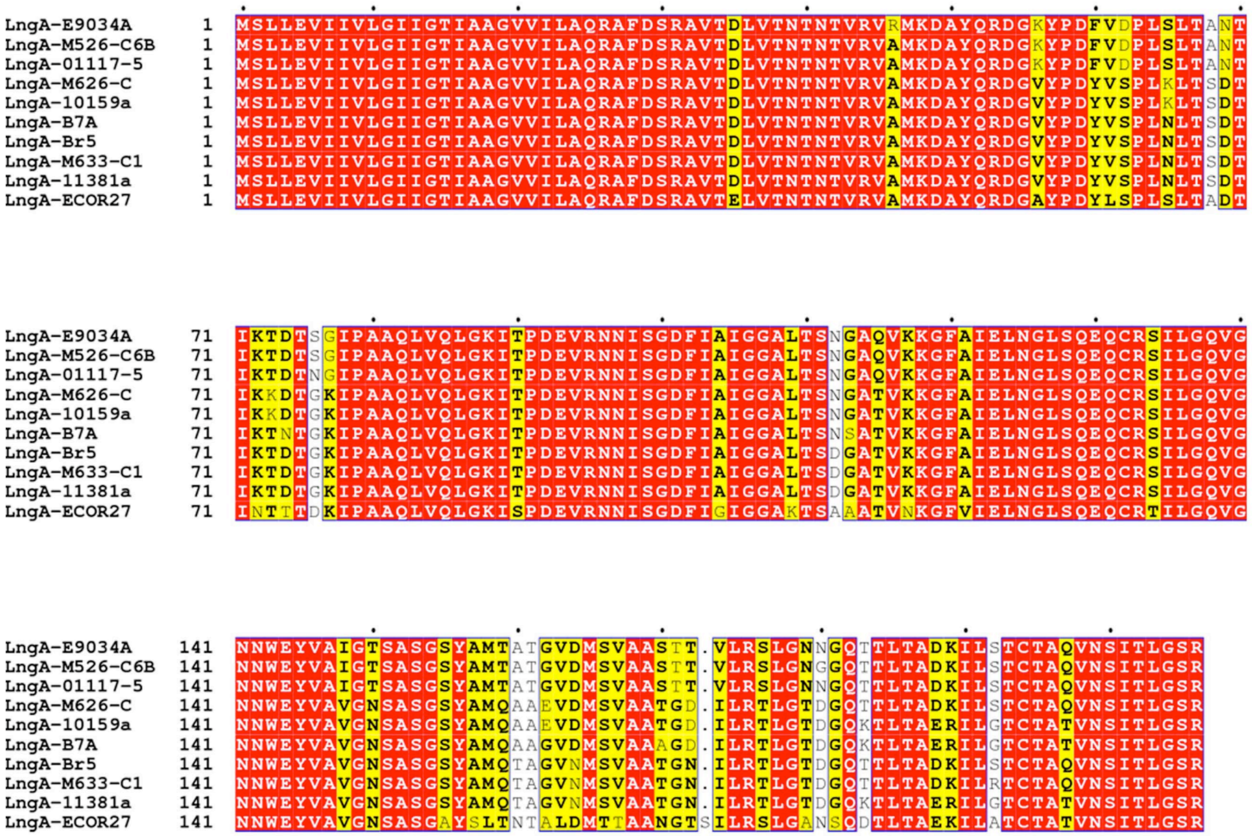

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LngA-01117-5    1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTDLVTNTNTVRVAMKDAYQRDGKYPDFVDPLSLTANT
LngA-M626-C     1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTDLVTNTNTVRVAMKDAYQRDGVYPDYVSPLKLTSDT
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LngA-B7A        1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTDLVTNTNTVRVAMKDAYQRDGVYPDYVSPLNLTSDT
LngA-Br5        1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTDLVTNTNTVRVAMKDAYQRDGVYPDYVSPLNLTSDT
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LngA-11381a     1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTDLVTNTNTVRVAMKDAYQRDGVYPDYVSPLNLTSDT
LngA-ECOR27     1  MSLLEVIIVLGIIGTIAAGVVILAQRAFDSRAVTELVTNTNTVRVAMKDAYQRDGAYPDYLSPLSLTADT

LngA-E9034A    71  IKTDTSGIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNGAQVKKGFAIELNGLSQEQCRSILGQVG
LngA-M526-C6B  71  IKTDTSGIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNGAQVKKGFAIELNGLSQEQCRSILGQVG
LngA-01117-5   71  IKTDTNGIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNGAQVKKGFAIELNGLSQEQCRSILGQVG
LngA-M626-C    71  IKKDTGKIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNGATVKKGFAIELNGLSQEQCRSILGQVG
LngA-10159a    71  IKKDTGKIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNGATVKKGFAIELNGLSQEQCRSILGQVG
LngA-B7A       71  IKTNTGKIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSNSATVKKGFAIELNGLSQEQCRSILGQVG
LngA-Br5       71  IKTDTGKIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSDGATVKKGFAIELNGLSQEQCRSILGQVG
LngA-M633-C1   71  IKTDTGKIPAAQLVQLGKITPDEVRNNISGDFIAIGGALTSDGATVKKGFAIELNGLSQEQCRSILGQVG
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LngA-ECOR27    71  INTTTDKIPAAQLVQLGKISPDEVRNNISGDFIGIGGAKTSAAATVNKGFVIELNGLSQEQCRTILGQVG

LngA-E9034A   141  NNWEYVAIGTSASGSYAMTATGVDMSVAASTT.VLRSLGNNGQTTLTADKILSTCTAQVNSITLGSR
LngA-M526-C6B 141  NNWEYVAIGTSASGSYAMTATGVDMSVAASTT.VLRSLGNGGQTTLTADKILSTCTAQVNSITLGSR
LngA-01117-5  141  NNWEYVAIGTSASGSYAMTATGVDMSVAASTT.VLRSLGNNGQTTLTADKILSTCTAQVNSITLGSR
LngA-M626-C   141  NNWEYVAVGNSASGSYAMQAAEVDMSVAATGD.ILRTLGTDGQTTLTADKILSTCTAQVNSITLGSR
LngA-10159a   141  NNWEYVAVGNSASGSYAMQAAEVDMSVAATGD.ILRTLGTDGQKTLTAERILGTCTATVNSITLGSR
LngA-B7A      141  NNWEYVAVGNSASGSYAMQAAGVDMSVAAAGD.ILRTLGTDGQKTLTAERILGTCTATVNSITLGSR
LngA-Br5      141  NNWEYVAVGNSASGSYAMQTAGVNMSVAATGN.ILRTLGTDGQTTLTADKILSTCTAQVNSITLGSR
LngA-M633-C1  141  NNWEYVAVGNSASGSYAMQTAGVNMSVAATGN.ILRTLGTDGQTTLTADKILRTCTAQVNSITLGSR
LngA-11381a   141  NNWEYVAVGNSASGSYAMQTAGVNMSVAATGN.ILRTLGTDGQKTLTAERILGTCTATVNSITLGSR
LngA-ECOR27   141  NNWEYVAVGNSASGAYSLTNTALDMTTAANGTSILRSLGANSQDTLTAEKILATCTATVNSITLGSR
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**Supplemental Figure S1. Amino acid sequence alignment of LngA variants.** Mature non-redundant LngA sequences from various ETEC strains: E9034A, GenBank Accession No. AAC33154; M526-C6B, ABV57880; 01117-5, ABV57862; M626-C, ABV57875; 10159a, ABV57868; B7A, ABV57871; Br5, ABV57878; M633-Cl, ABV57876; 11381a, ABV57869; and ECOR27, ABV57879. Identical residues are shown in white text with red shading; homologous residues have black text and yellow shading.