

Functional differences between *E. coli* and *ESKAPE* pathogen

GroES/GroEL

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TABLE S1. *E. coli* shares high amino acid similarity with ESKAPE pathogens ^a.

A

Bacterium	<i>Enterococcus faecium</i>	<i>Staphylococcus aureus</i>	<i>Klebsiella pneumoniae</i>	<i>Acinetobacter baumannii</i>	<i>Pseudomonas aeruginosa</i>	<i>Enterobacter cloacae</i>	<i>Escherichia coli</i>
<i>Enterococcus faecium</i>	-	83.5	75.5	76	76.1	75.5	75.2
<i>Staphylococcus aureus</i>	83.5	-	74.5	75.5	74.3	74.2	74
<i>Klebsiella pneumoniae</i>	75.5	74.5	-	85.6	87.4	95.5	98
<i>Acinetobacter baumannii</i>	76	75.5	85.6	-	88.1	85.6	85.4
<i>Pseudomonas aeruginosa</i>	76.1	74.3	87.4	88.1	-	87.3	87.3
<i>Enterobacter cloacae</i>	75.5	74.2	90.5	85.6	87.3	-	98
<i>Escherichia coli</i>	75.2	74	98	85.4	87.3	98	-

B

Bacterium	<i>Enterococcus faecium</i>	<i>Staphylococcus aureus</i>	<i>Klebsiella pneumoniae</i>	<i>Acinetobacter baumannii</i>	<i>Pseudomonas aeruginosa</i>	<i>Enterobacter cloacae</i>	<i>Escherichia coli</i>
<i>Enterococcus faecium</i>	-	75.3	62.9	66	70.1	62.9	62.9
<i>Staphylococcus aureus</i>	75.3	-	66	67	66	63.9	62.9
<i>Klebsiella pneumoniae</i>	62.9	66	-	77.6	76.3	100	97.9
<i>Acinetobacter baumannii</i>	66	67	77.6	-	86.7	77.6	78.6
<i>Pseudomonas aeruginosa</i>	70.1	66	76.3	86.7	-	77.3	78.4
<i>Enterobacter cloacae</i>	62.9	63.9	100	77.6	77.3	-	97.9
<i>Escherichia coli</i>	62.9	62.9	97.9	78.6	78.4	97.9	-

C

Bacterium	<i>Enterococcus faecium</i>	<i>Staphylococcus aureus</i>	<i>Klebsiella pneumoniae</i>	<i>Acinetobacter baumannii</i>	<i>Pseudomonas aeruginosa</i>	<i>Enterobacter cloacae</i>	<i>Escherichia coli</i>
<i>Enterococcus faecium</i>	-	84.9	77.7	77.8	77.1	77.7	77.4
<i>Staphylococcus aureus</i>	84.9	-	75.8	77	75.8	75.8	75.8
<i>Klebsiella pneumoniae</i>	77.7	75.8	-	87	89.4	95.5	98
<i>Acinetobacter baumannii</i>	77.8	77	87	-	88.3	87	86.7
<i>Pseudomonas aeruginosa</i>	77.1	75.8	89.4	88.3	-	89.1	88.9
<i>Enterobacter cloacae</i>	77.7	75.8	95.5	87	89.1	-	98
<i>Escherichia coli</i>	77.4	75.8	98	86.7	88.9	98	-

^a GroESL protein similarity (%) generated from EMBOSS Needle protein alignment of *E. coli* GroESL and ESKAPE pathogens. (A) GroESL protein similarity (%). (B) GroES protein similarity (%). (C) GroEL protein similarity (%). Color gradient demonstrates highest similarity highlighted in red, lowest similarity in white.