

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

GroES/GroEL

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TABLE S2. *ESKAPE* pathogen GroES/GroEL is predicted to be structurally similar with comparable net charge in their respective cellular environments as compared to MG1655 GroES/GroEL^a.

Bacteria	Gram Stain	GroES kDa/Residues	GroES PI	GroEL kDa/Residues	GroEL PI
<i>Enterococcus faecium</i> ATCC 51559	(+)	10.0 / 94	5.03	57.2 / 541	4.66
<i>Staphylococcus aureus</i> ATCC 25923	(+)	10.4 / 94	4.87	57.6 / 538	4.56
<i>Klebsiella pneumoniae</i> ATCC 700603	(-)	10.4 / 97	5.38	57.1 / 548	4.84
<i>Acinetobacter baumannii</i> ATCC 19606	(-)	10.1 / 96	5.09	57.1 / 544	4.92
<i>Pseudomonas aeruginosa</i> ATCC 47085	(-)	10.3 / 97	5.17	57.1 / 547	5.04
<i>Enterobacter cloacae</i> ATCC 13047	(-)	10.4 / 97	5.38	57.1 / 548	4.85
<i>Escherichia coli</i> LG6	(-)	10.4 / 97	5.15	57.3 / 548	4.85

^a Isoelectric point and molecular weight data were generated using ExPASy Computer pI/MW data tool. Gram-positives (*E. faecium* and *S. aureus*) have overall fewer number of residues, lower isoelectric point, and are lacking C-terminal GGM repeat compared to Gram-negative bacteria (*K. pneumoniae*, *A. baumannii*, *P. aeruginosa*, *E. cloacae*, and *E. coli*).