

Supporting Information

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Table S1. IM proteins conserved in *E. coli*, *Bl. floridanus*, and *B. aphidicola* str. APS

Protein	Function*	Essential in <i>E. coli</i> [†]
AtpB	ATPase subunit	No
AtpE	ATPase subunit	No
AtpF	ATPase subunit	No
Cls	Phospholipid biosynthesis	No
CyoA	Ubiquinol oxidase subunit	No
CyoB	Ubiquinol oxidase subunit	No
CyoC	Ubiquinol oxidase subunit	No
CyoD	Ubiquinol oxidase subunit	No
CyoE	Ubiquinol oxidase subunit	No
FtsH	Protease	Yes
FtsI	Septal peptidoglycan biosynthesis	Yes
FtsL	Cell division	Yes
FtsW	Cell division protein; recruits FtsI to the cell division site	Yes
HflK	HflK-HflC membrane protein complex, regulator of FtsH	No
HflK	HflK-HflC membrane protein complex, regulator of FtsH	No
LepB	Signal peptidase	Yes
Lgt	Lipoprotein biogenesis	Yes
LoIC	Lipoprotein transport	Yes
LspA	Lipoprotein biogenesis	Yes
MraY	Peptidoglycan biosynthesis	Yes
MrcB	Peptidoglycan biosynthesis	No
MviN (MurJ)	Unknown	Yes
NuoA	NADH-ubiquinone oxidoreductase subunit	No
NuoH	NADH-ubiquinone oxidoreductase subunit	No
NuoJ	NADH-ubiquinone oxidoreductase subunit	No
NuoK	NADH-ubiquinone oxidoreductase subunit	No
NuoL	NADH-ubiquinone oxidoreductase subunit	No
NuoM	NADH-ubiquinone oxidoreductase subunit	No
NuoN	NADH-ubiquinone oxidoreductase subunit	No
PitA	Phosphate transporter	No
SecE	Protein transport across and insertion into IM	Yes
SecY	Protein transport across and insertion into IM	Yes
YajC	Protein transport across and insertion into IM	No
YajR	Unknown; major facilitator superfamily	No
YhgN	Unknown; predicted transporter (MarC family)	No
YibN	Unknown; predicted rhodanese-related sulfurtransferase	No
YidC	IM protein insertion	Yes
YoaE	Unknown; predicted transporter (TerC family)	No
YtfN	Unknown	No

*Functions according to EcoCyc and EcoGene (1, 2).

[†]According to Baba *et al.* (3).

1. Karp PD, Riley M, Paley SM, Pellegrini-Toole A, Krummenacker M (1999) Eco Cyc: Encyclopedia of *Escherichia coli* genes and metabolism. *Nucleic Acids Res* 27:55–58.
2. Rudd KE (2000) EcoGene: A genome sequence database for *Escherichia coli* K-12. *Nucleic Acids Res* 28:60–64.
3. Baba T, *et al.* (2006) Construction of *Escherichia coli* K-12 in-frame, single-gene knockout mutants: The Keio collection. *Mol Syst Biol* 2:2006 0008.

Table S2. STRING prediction of functional partners

Protein	Predicted functional partners*	Predicted topology†
MurJ	RodA, MurCDEZ, PbpA, FtsW, AmiC, NudH, GlmU	Integral
YajR	OxaA, PpdA, YjbD, PpnK	Integral
YhgN	None	Integral
YibN	PapD, HolA, GlpE, GrxC	Membrane-anchored
YoaE	None	Integral
YtfN	YtfM, MukEF, LolB, LptCD, SprT, YjaG, YajG	Membrane-anchored

*Using gene fusion, cooccurrence, textmining, and coexpression as prediction methods in STRING (1).

†Assigned by EchoLOCATION (2).

1. von Mering C, et al. (2007) STRING 7—Recent developments in the integration and prediction of protein interactions. *Nucleic Acids Res* 35:D358–D362.
2. Misra RV, Horler RS, Reindl W, Goryanin II, Thomas GH (2005) EchoBASE: An integrated post-genomic database for *Escherichia coli*. *Nucleic Acids Res* 33:D329–D333.