

Supplemental table S1. Tryptophan-containing peptides identified by mass spectrometry.

Sequence	Protein accession	protein description	Trp Mascot Score	1-L-MT Mascot-Score
<i>Staphylococcus aureus</i>				
ANEDESQWNSLLEK	Q5HG77	Transketolase OS= <i>Staphylococcus aureus</i> (strain COL)	n.i.	102
VAAWYDNEMSYTAQLVR	Q5HHP5	Glyceraldehyde-3-phosphate dehydrogenase 1 OS= <i>Staphylococcus aureus</i>	73	98
WYVIDAEGQTLGR	A7X5B4	50S ribosomal protein L13 OS= <i>Staphylococcus aureus</i>	n.i.	68
SQQVWVESVQSSK	A7X659	Immunoglobulin-binding protein sbi OS= <i>Staphylococcus aureus</i>	56	59
NEDWQLYTAGK	Q5HCU5	Probable malate:quinone oxidoreductase 2 OS= <i>Staphylococcus aureus</i>	35	58
IGETHEGASQMDWMEQEQR	A6QEJ9	Elongation factor G OS= <i>Staphylococcus aureus</i>	n.i.	55
EATGDNWDGLGR	Q2FI18	Probable quinol oxidase subunit 1 OS= <i>Staphylococcus aureus</i>	45	53
SSIVVVGTTQWGDEGK	P65884	Adenylosuccinate synthetase OS= <i>Staphylococcus aureus</i>	n.i.	46
GAFPTWLAPK	A6U2F0	Threonyl-tRNA synthetase OS= <i>Staphylococcus aureus</i>	n.i.	46
VVYDITSKPPSTIEWE	A7WY93	GMP synthase [glutamine- hydrolyzing] OS= <i>Staphylococcus aureus</i>	45	45
YFDDDDMWNK	A6U2F0	Threonyl-tRNA synthetase OS= <i>Staphylococcus aureus</i>	n.i.	33
SVVIAYEPIWAIGTGK	A7WZS8	Triosephosphate isomerase OS= <i>Staphylococcus aureus</i>	63	n.i.
LGYDQVLWLDGVEQK	Q5HIC1	Probable branched-chain- amino-acid aminotransferase OS= <i>Staphylococcus aureus</i>	84	n.i.
VAAADTIYPFTQAENVWLPNK	P0A0A1	Pyruvate dehydrogenase E1 component subunit beta OS= <i>Staphylococcus aureus</i>	38	n.i.
<i>Streptococcus agalactiae</i>				
FSWISTGGGASMELEGK	A2RCM1	Phosphoglycerate kinase OS= <i>Streptococcus agalactiae</i>	n.i.	92
YADTDWGSINSMGLPNK	Q3K2G4	Dihydroorotate dehydrogenase OS= <i>Streptococcus agalactiae</i>	84	81
ADIDYAWEEADTTYGK	Q3K3W3	30S ribosomal protein S3 OS= <i>Streptococcus agalactiae</i>	n.i.	81
TSVVVVGTTQWGDEGK	C0ZA40	Adenylosuccinate synthetase	53	73

		OS= <i>Streptococcus agalactiae</i>		
NLGWDIISTGGTK	B5XJ20	Bifunctional purine biosynthesis protein purH OS= <i>Streptococcus agalactiae</i>	n.i.	65
AIGPEPWNAAYVEPSR	Q038U2	Glycyl-tRNA synthetase alpha subunit OS= <i>Streptococcus agalactiae</i> PE=3 SV=1 -	71	62
GQFGDVWIEFTPNEEGK	Q3JZB5	Elongation factor G OS= <i>Streptococcus agalactiae</i>	n.i.	57
WYVVDATDVPLGR	Q1WSC2	50S ribosomal protein L13 OS= <i>Streptococcus agalactiae</i>	46	56
VEADANNWETFVVPDNLVGGRR	Q3K2Y2	Glucose-6-phosphate isomerase OS= <i>Streptococcus agalactiae</i>	n.i.	54
GAPEGWVAPVK	Q3K3W2	50S ribosomal protein L16 OS= <i>Streptococcus agalactiae</i>	n.i.	52
QQAENLANWAK	Q8E0Z9	Single-stranded DNA-binding protein 3 OS= <i>Streptococcus agalactiae</i>	46	51
AFFEIINWVK	P0A4J3	Superoxide dismutase [Mn/Fe] OS= <i>Streptococcus agalactiae</i>	n.i.	49
WVNAAEVTEDNIK	Q3K3S2	CTP synthase OS= <i>Streptococcus agalactiae</i>	64	n.i.
SSIVVVGTTQWGDEGK	P65884	Adenylosuccinate synthetase OS= <i>Staphylococcus aureus</i>	53	n.i.

Protein extracts from bacteria were analyzed by LC-MS. Mascot-Scores for the identified tryptophan-containing peptides are given for bacteria grown in the presence of L-Tryptophan (Trp) and bacteria grown in the presence of 1-L-MT. n.i.: not identified. All searches were carried out with methylation of tryptophan residues as variable modifications. No peptide with tryptophan methylation was identified in any sample.