Supplementary Table 1. Proteins identified in *Mannheimia haemolytica* membrane vesicles. *M. haemolytica* vesicles were extracted and subjected to LC-MS/MS where proteins that constitute these structures were identified as described in the manuscript. Each protein was further analyzed with Bioinformatic Tools. A total of 226 proteins were identified from vesicles extracts. Predictions using bioinformatic tools indicate that 104 (46%) of these are of cytoplasmic origin, 58 (25.6%) are either periplasmic or outer membrane and one (0.4%) is the extracellular protein leukotoxin. The remaining 63 (27.8%) proteins are either of unknown locale or of cytoplasmic membrane.

	Protein name	**Protein GI number**	**PSORTb**	**LipoP**	**Protein molecular weight (Da)**	**Protein identification probability**	**Number of unique peptides**	**Number of unique spectra**	**Number of total spectra**	**Percentage of total spectra**	**Percentage sequence coverage**
1	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	254362937	Cytoplasmic 9.97	Cytoplasmic	29392.9	99.80%	2	2	4	0.05%	7.66%
2	2',3'-cyclic-nucleotide 2'-phosphodiesterase	254362830	Periplasmic 9.76	Signal peptide	72799.3	100.00%	3	3	5	0.07%	5.02%
3	3-deoxy-8-phosphooctulonate synthase	254362304	Cytoplasmic 9.97	Cytoplasmic	31101.9	100.00%	5	5	6	0.08%	16.20%
4	3-oxoacyl-[acyl-carrier-protein] reductase	254363104	Cytoplasmic 9.26	Cytoplasmic	25185.5	100.00%	3	3	6	0.08%	12.10%
5	6-phosphofructokinase	32035193	Cytoplasmic 9.26	Cytoplasmic	35105.5	99.80%	2	2	4	0.05%	8.39%
6	ABC superfamily ATP binding cassette transporter, binding protein	254361825	Cytoplasmic Membrane 9.97	lipoprotein signal peptide	29,974.30	100.00%	5	5	11	0.09%	24.90%
7	ABC superfamily ATP binding cassette transporter, binding protein	254362423	Unknown	Signal peptide	23162.8	99.80%	2	2	5	0.07%	9.00%
8	ABC superfamily ATP binding cassette transporter, binding protein	254362968	Periplasmic 10.00	Signal peptide	57975.8	100.00%	3	3	5	0.07%	5.12%
9	acetate kinase	254362831	Cytoplasmic 9.97	Cytoplasmic	43526.8	100.00%	3	3	5	0.07%	7.21%
10	ADP-glyceromanno-heptose 6-epimerase	254361453	Cytoplasmic 9.26	Cytoplasmic	34643.2	100.00%	3	3	5	0.07%	10.10%
11	alanine--tRNA ligase	254360816	Cytoplasmic 9.97	Cytoplasmic	96413.6	100.00%	7	7	13	0.17%	8.11%
12	aldehyde-alcohol dehydrogenase	254360511	Cytoplasmic 9.97	Cytoplasmic	95194.6	100.00%	8	8	13	0.17%	9.55%
13	amino acid ABC superfamily ATP binding cassette transporter, binding protein	254362204	Periplasmic 10.00	Signal peptide	28,024.10	100.00%	13	15	54	0.43%	56.40%
14	arginine ABC superfamily ATP binding cassette transporter, ABC protein	254360691	Cytoplasmic 9.97	Cytoplasmic	49676.3	99.80%	2	2	4	0.05%	4.09%
15	arginine ABC superfamily ATP binding cassette transporter, binding protein	254360693	Periplasmic 10.00	Signal peptide	26,659.40	100.00%	3	3	9	0.07%	18.90%
16	arginine ABC superfamily ATP binding cassette transporter, membrane protein	254360689	Cytoplasmic 9.26	Cytoplasmic	18799	99.90%	2	2	5	0.07%	8.67%
17	asparagine-tRNA ligase	254362094	Cytoplasmic 10.00	Cytoplasmic	52692.1	100.00%	4	4	8	0.11%	8.57%
18	aspartate--ammonia ligase	254361675	Cytoplasmic 10.00	Cytoplasmic	37439.6	100.00%	6	7	14	0.18%	16.10%
19	bacteriophage major capsid protein N	254360870	Cytoplasmic 8.96	Cytoplasmic	38628.5	100.00%	8	9	23	0.30%	23.10%
20	bacteriophage tail sheath protein FI	254360852	Unknown	Cytoplasmic	43114.4	100.00%	8	8	16	0.21%	20.40%
21	bacteriophage tail tube protein FII	254360851	Cytoplasmic 8.96	Cytoplasmic	18384.5	100.00%	3	3	8	0.11%	16.70%
22	biotin carboxylase	254362943	Cytoplasmic 9.97	Cytoplasmic	49240.8	100.00%	5	5	10	0.13%	13.40%
23	catalase	254361228	Periplasmic 10.00	Cytoplasmic	56868.5	100.00%	10	10	16	0.21%	24.50%
24	cell division protein FtsZ	254362457	Unknown	Cytoplasmic	43607.8	99.80%	2	2	5	0.07%	6.02%
25	cell division protein MukB	254360811	Cytoplasmic 9.94	Cytoplasmic	170217.2	99.70%	2	2	3	0.04%	1.21%
26	chaperone DnaK	254361232	Cytoplasmic 9.97	Cytoplasmic	68126.1	100.00%	3	3	4	0.05%	5.54%
27	chaperone GroEL	254362013	Cytoplasmic 9.97	Cytoplasmic	57558.6	100.00%	21	27	80	1.05%	38.30%
28	chaperone HtpG	254360944	Cytoplasmic 9.97	Cytoplasmic	71081.4	100.00%	8	8	13	0.17%	14.50%
29	CTP synthase	254363180	Cytoplasmic 9.97	Signal peptide	60060.8	100.00%	5	5	9	0.12%	9.17%
30	cysteine desulfurase	254361063	Cytoplasmic 9.97	Cytoplasmic	45380.1	99.80%	2	2	3	0.04%	5.17%
31	dihydrolipoyl dehydrogenase	254362994	Cytoplasmic 9.97	Cytoplasmic	50495.4	100.00%	8	8	25	0.33%	16.70%

	Protein name	Protein GI number	PSORTb	LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
32	dihydrolipoyllysine-residue acetyltransferase	254362996	Cytoplasmic 9.97	Cytoplasmic	66697.1	100.00%	16	18	44	0.58%	25.80%
33	DNA uptake lipoprotein ComL	254361950	Outermembrane 9.92	lipoprotein signal peptide	29,736.20	100.00%	6	7	18	0.14%	25.10%
34	DNA-binding protein H-NS	254361504	Cytoplasmic 9.26	Cytoplasmic	15053.9	99.80%	2	2	4	0.05%	14.30%
35	DNA-directed RNA polymerase subunit beta	254361140	Cytoplasmic 9.97	Cytoplasmic	149435.2	100.00%	9	9	16	0.21%	7.38%
36	DNA-directed RNA polymerase subunit beta prime	254361142	Cytoplasmic 9.97	Cytoplasmic	157920.3	100.00%	10	10	14	0.18%	6.66%
37	DPS family DNA-binding protein	254362225	Cytoplasmic 9.26	Cytoplasmic	18,838.50	99.90%	2	2	2	0.02%	26.80%
38	D-ribose ABC superfamily ATP binding cassette transporter, binding protein	254362593	Periplasmic 9.76	Signal peptide	30272.1	99.80%	2	2	6	0.08%	7.19%
39	ECA biosynthesis protein WecC	254360954	Cytoplasmic 9.97	Cytoplasmic	46531.5	99.80%	2	2	2	0.03%	4.49%
40	elongation factor EF1A	254362571	Cytoplasmic 9.97	Cytoplasmic	43263.3	100.00%	17	21	66	0.87%	45.20%
41	elongation factor EF1B	254360754	Cytoplasmic 9.97	Cytoplasmic	30190.2	100.00%	3	3	8	0.11%	10.60%
42	elongation factor EF2	254362572	Cytoplasmic 9.97	Cytoplasmic	76998	100.00%	12	13	31	0.41%	20.00%
43	enoyl-[acyl-carrier-protein] reductase (NADH)	254360820	Cytoplasmic 9.82	Cytoplasmic	28125.1	100.00%	3	3	8	0.11%	11.00%
44	exo-alpha-sialidase	254361924	Unknown	Signal peptide	65348.7	100.00%	11	11	26	0.34%	20.40%
45	formate C-acetyltransferase	254362619	Cytoplasmic 9.97	Cytoplasmic	86697.8	100.00%	9	9	18	0.24%	12.00%
46	fructose-bisphosphate aldolase	254360596	Cytoplasmic 8.96	Cytoplasmic	39120.6	100.00%	5	6	9	0.12%	20.90%
47	galactoside ABC superfamily ATP binding cassette transporter, binding protein	254361432	unknown	Cytoplasmic	33473.1	100.00%	11	11	22	0.29%	35.50%
48	glucose-6-phosphate isomerase	254361902	Cytoplasmic 9.97	Cytoplasmic	61112.2	99.70%	2	2	2	0.03%	5.49%
49	glutamate dehydrogenase (NADP(+)	254361731	Unknown	Cytoplasmic	36884.4	100.00%	6	6	14	0.18%	20.20%
50	glutamate--ammonia ligase	254361149	Cytoplasmic 9.97	Cytoplasmic	52405.5	100.00%	11	11	21	0.28%	20.30%
51	glyceraldehyde-3-phosphate dehydrogenase	254360874	Cytoplasmic 9.97	Cytoplasmic	35723.5	100.00%	10	10	22	0.29%	25.70%
52	glycerol kinase	254360701	Cytoplasmic 9.97	Cytoplasmic	56031.9	99.80%	2	2	4	0.05%	3.58%
53	glycerophosphodiester phosphodiesterase	254362648	Unknown	Signal peptide	37005	99.80%	2	2	2	0.03%	7.79%
54	H(+)-transporting two-sector ATPase, F(1) beta subunit	254361677	Cytoplasm 9.12	Cytoplasmic	49,767.00	100.00%	3	3	7	0.06%	9.63%
55	hypothetical bacteriophage protein	254362878	Unknown	Cytoplasmic	33660.8	100.00%	4	4	7	0.09%	15.20%
56	hypothetical bacteriophage protein	254361390	Unknown	lipoprotein signal peptide	12661.3	100.00%	3	3	6	0.08%	22.50%
57	hypothetical bacteriophage protein	254361480	Cytoplasmic 8.96	Cytoplasmic	29,800.90	99.80%	2	2	3	0.02%	10.90%
58	hypothetical protein MHA_0070	254360521	Unknown	Signal peptide	13994	99.80%	2	2	6	0.08%	17.10%
59	hypothetical protein MHA_0080	254360531	Unknown	Signal peptide	81245.3	100.00%	6	6	13	0.17%	8.25%
60	hypothetical protein MHA_0181	254360625	Unknown	lipoprotein signal peptide	19039.1	99.80%	2	2	4	0.05%	11.40%
61	hypothetical protein MHA_0367	254360803	Unknown	Signal peptide	11236.7	100.00%	4	4	9	0.12%	43.70%
62	hypothetical protein MHA_0410	254360844	Unknown	Signal peptide	12103.4	100.00%	6	7	14	0.18%	40.40%
63	hypothetical protein MHA_0488	254360922	Unknown	lipoprotein signal peptide	21298.9	100.00%	9	13	37	0.49%	41.70%
64	hypothetical protein MHA_0504	254360937	Unknown	lipoprotein signal peptide	22,488.60	100.00%	4	4	12	0.10%	17.70%
65	hypothetical protein MHA_0524	254360956	Unknown	Cytoplasmic	41120.1	100.00%	3	3	5	0.07%	10.10%
66	hypothetical protein MHA_0525	254360957	Cytoplasmic 8.96	Cytoplasmic	30536.8	100.00%	3	3	7	0.09%	8.96%
67	hypothetical protein MHA_0579	254361008	Unknown	Signal peptide	15,701.20	99.80%	2	2	10	0.08%	25.20%
68	hypothetical protein MHA_0680	254361100	Unknown	Signal peptide	17680.4	99.50%	2	2	4	0.05%	13.90%

	Protein name	Protein GI number	PSORTb	LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
69	hypothetical protein MHA_0690	254361110	OuterMembrane 9.93	Signal peptide	29,201.90	100.00%	6	7	17	0.14%	24.30%
70	hypothetical protein MHA_0837	254361251	CytoplasmicMembrane 7.88	lipoprotein signal peptide	35870	100.00%	4	4	13	0.17%	12.10%
71	hypothetical protein MHA_0861	254361274	Unknown	lipoprotein signal peptide	53013.8	100.00%	6	6	8	0.11%	12.80%
72	hypothetical protein MHA_0915	254361325	Unknown	Signal peptide	12,642.80	99.80%	2	3	11	0.09%	32.20%
73	hypothetical protein MHA_0965	254361375	Unknown	lipoprotein signal peptide	29719.5	100.00%	25	36	132	1.73%	53.60%
74	hypothetical protein MHA_1154	254361553	Periplasmic 9.84	lipoprotein signal peptide	27036.5	99.90%	2	3	9	0.12%	8.10%
75	hypothetical protein MHA_1406	254361799	OuterMembrane 9.92	lipoprotein signal peptide	43084.4	100.00%	9	12	31	0.41%	24.60%
76	hypothetical protein MHA_1610	254361999	Unknown	Signal peptide	22,270.80	100.00%	6	6	18	0.14%	27.70%
77	hypothetical protein MHA_1611	254362000	Unknown	lipoprotein signal peptide	15306.8	99.80%	2	2	3	0.04%	17.30%
78	hypothetical protein MHA_1671	254362061	Unknown	Signal peptide	16,049.80	100.00%	7	8	20	0.16%	52.00%
79	hypothetical protein MHA_1900	254362291	Unknown	lipoprotein signal peptide	20603.7	100.00%	4	4	10	0.13%	20.80%
80	hypothetical protein MHA_1915	254362307	Unknown	lipoprotein signal peptide	22783.6	100.00%	4	5	21	0.28%	17.50%
81	hypothetical protein MHA_1931	254362323	Unknown	lipoprotein signal peptide	10680.1	99.80%	2	2	5	0.07%	24.50%
82	hypothetical protein MHA_2025	254362418	Unknown	lipoprotein signal peptide	18490.8	100.00%	6	8	21	0.28%	37.70%
83	hypothetical protein MHA_2087	254362480	OuterMembrane 9.93	lipoprotein signal peptide	19,396.70	100.00%	7	8	22	0.18%	41.40%
84	hypothetical protein MHA_2126	254362519	Unknown	lipoprotein signal peptide	17,712.60	100.00%	4	4	12	0.10%	37.00%
85	hypothetical protein MHA_2237	254362641	Unknown	Signal peptide	18298.9	100.00%	9	10	24	0.32%	34.30%
86	hypothetical protein MHA_2300	254362706	Unknown	Cytoplasmic	11,908.60	99.80%	2	3	10	0.08%	20.40%
87	hypothetical protein MHA_2753	254363170	Unknown	lipoprotein signal peptide	14,117.90	99.70%	2	2	6	0.05%	20.30%
88	incomplete ribosomal protein L21	33147673	unknown	Cytoplasmic	7436	99.80%	2	3	5	0.07%	28.20%
89	initiation factor IF2-1	254361246	Cytoplasmic 9.97	Cytoplasmic	91804.6	99.80%	2	2	4	0.05%	2.37%
90	inorganic diphosphatase	254361193	Cytoplasmic 9.97	Cytoplasmic	19337.2	100.00%	3	3	5	0.07%	17.70%
91	iron (Fe3+) ABC superfamily ATP binding cassette transporter, binding protein	254360752	Unknown	Cytoplasmic	35641	100.00%	8	8	16	0.21%	23.00%
92	iron (Fe3+) ABC superfamily ATP binding cassette transporter, binding protein	254362568	Unknown	Cytoplasmic	26,886.00	99.70%	2	3	5	0.04%	9.09%
93	iron (Fe3+) ABC superfamily ATP binding cassette transporter, binding protein YfeA	254362889	Periplasmic 10.00	Signal peptide	32012.2	100.00%	9	9	15	0.20%	40.10%
94	iron-regulated outer membrane protein	254362499	OuterMembrane 10.00	Cytoplasmic	68970.4	100.00%	23	27	76	1.00%	39.80%

	Protein name	Protein GI number	PSORTb	LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
95	leukotoxin	254360695	Extracellular 10.00	Cytoplasmic	101983.4	100.00%	64	87	367	4.81%	58.80%
96	lipoprotein	254362686	Periplasmic 9.83	lipoprotein signal peptide	20666.6	100.00%	4	5	11	0.14%	27.80%
97	lipoprotein	254362006	Unknown	lipoprotein signal peptide	13891.2	99.80%	2	2	6	0.08%	21.80%
98	lipoprotein LppC	254363151	Unknown	lipoprotein signal peptide	63354.9	100.00%	21	23	62	0.81%	37.70%
99	lipoprotein PlpD	254361857	OuterMembrane 9.92	lipoprotein signal peptide	31,377.30	100.00%	3	3	11	0.09%	14.10%
100	lipoprotein VacJ	254363251	OuterMembrane 9.92	n-terminal transmembrane helix	14040.5	99.80%	2	2	5	0.07%	14.80%
101	lytic murein transglycosylase	254360683	unknown	lipoprotein signal peptide	39087.7	99.90%	2	2	3	0.04%	6.57%
102	M17 family leucyl aminopeptidase	254360526	Cytoplasmic 9.97	Cytoplasmic	54139.2	99.80%	2	2	3	0.04%	4.82%
103	M23B subfamily peptidase/lipoprotein	254362197	OuterMembrane 9.92	lipoprotein signal peptide	44631.6	100.00%	10	11	24	0.32%	28.20%
104	M48 family peptidase	254361194	Unknown	lipoprotein signal peptide	27129.8	99.80%	2	2	8	0.11%	9.16%
105	maltoporin	254360673	OuterMembrane 10.00	Signal peptide	47547.7	100.00%	6	6	12	0.16%	13.50%
106	maltose ABC superfamily ATP binding cassette transporter, binding protein MalE	254360675	Periplasmic 10.00	Signal peptide	43,380.80	100.00%	3	3	3	0.02%	7.58%
107	membrane-bound lytic murein transglycosylase	254361537	OuterMembra 9.93	lipoprotein signal peptide	40087.5	100.00%	4	4	9	0.12%	13.00%
108	Mu bacteriophage protein T	254361342	Unknown	Cytoplasmic	33948.3	100.00%	7	7	23	0.30%	24.90%
109	Mu bacteriophage tail sheath protein GpL	254361347	Unknown	Cytoplasmic	42692	99.80%	2	2	3	0.04%	5.26%
110	multicopper (Cu2+) oxidase	254361561	Unknown	Signal peptide	58,625.50	100.00%	3	3	4	0.03%	6.02%
111	N utilization substance A	254361245	Cytoplasmic 9.97	Cytoplasmic	55480.3	99.70%	2	2	3	0.04%	3.41%
112	N-acylneuraminate cytidylyltransferase	254360557	Cytoplasmic 9.97	Cytoplasmic	48190.5	99.80%	2	2	2	0.03%	4.77%
113	naphthoate synthase	254362223	Cytoplasmic 9.26	Cytoplasmic	31894.5	99.90%	2	2	4	0.05%	7.37%
114	nitrate reductase	254361386	Periplasmic 9.93	Signal peptide	94234.8	99.80%	2	2	2	0.03%	2.28%
115	oligopeptide ABC superfamily ATP binding cassette transporter, binding protein	254362033	Periplasmic 10.00	Cytoplasmic	58,479.80	99.80%	2	2	2	0.02%	3.28%
116	OMR family outer membrane iron receptor	254361273	OuterMembrane 9.52	Signal peptide	89700.1	100.00%	4	4	7	0.09%	5.19%
117	orotidine-5'-phosphate decarboxylase	254361241	Cytoplasmic 9.97	Cytoplasmic	25392.6	99.80%	2	2	3	0.04%	8.70%
118	outer membrane lipoprotein	254361177	OuterMembrane 9.93	lipoprotein signal peptide	15487.2	100.00%	3	3	11	0.14%	20.80%
119	outer membrane lipoprotein PlpE	254361907	Unknown	lipoprotein signal peptide	31006	100.00%	25	38	116	1.52%	48.60%
120	outer membrane protein D15	254361111	OuterMembrane 10.00	Signal peptide	88750.9	100.00%	18	19	41	0.54%	27.20%
121	outer membrane protein OmpA	254361457	OuterMembrane 10.00	Cytoplasmic	24721	100.00%	15	25	200	2.62%	70.40%

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122	outer membrane protein P1	254361061	OuterMembrane 10.00	Signal peptide	52807.2	100.00%	18	28	78	1.02%	37.30%
123	outer membrane protein P2	254361153	OuterMembrane 10.00	Signal peptide	41068.4	100.00%	19	21	57	0.75%	49.20%
124	oxoglutarate dehydrogenase (succinyl-transferring)	254361863	Cytoplasmic 9.97	Cytoplasmic	44912.4	100.00%	2	2	4	0.05%	9.05%
125	peptidoglycan-associated outer membrane lipoprotein	254360704	OuterMembrane 9.93	lipoprotein signal peptide	16792.8	100.00%	5	8	23	0.30%	44.10%
126	peptidylprolyl isomerase	254360924	Cytoplasmic 9.26	Cytoplasmic	22295.3	99.80%	2	2	3	0.04%	12.00%
127	peptidylprolyl isomerase	254361132	Periplasmic 9.76	Signal peptide	26333.7	100.00%	4	4	5	0.07%	15.40%
128	peptidylprolyl isomerase	254362982	Periplasmic 9.76	Signal peptide	34,444.50	100.00%	3	3	4	0.03%	10.20%
129	peroxiredoxin/glutaredoxin family protein	254363241	Unknown	Cytoplasmic	26920.2	100.00%	10	10	28	0.37%	43.40%
130	phosphate ABC superfamily ATP binding cassette transporter, binding protein	254361258	Periplasmic 9.76	Signal peptide	37410.5	100.00%	3	4	7	0.09%	9.83%
131	phosphate acetyltransferase	254362832	Cytoplasmic 9.97	Cytoplasmic	76550	100.00%	6	6	9	0.12%	9.28%
132	phosphoenolpyruvate--protein phosphotransferase	254362262	Cytoplasmic 9.97	Cytoplasmic	63111.8	100.00%	6	6	10	0.13%	11.20%
133	phosphogluconate 2-dehydrogenase	254362281	Cytoplasmic 8.96	Cytoplasmic	53547.6	99.80%	2	2	4	0.05%	4.96%
134	phosphoglycerate dehydrogenase	254362642	Cytoplasmic 9.97	Cytoplasmic	44356.7	99.80%	2	2	2	0.03%	5.87%
135	phosphoglycerate kinase	254360597	Cytoplasmic 9.97	Cytoplasmic	41548.2	100.00%	3	3	5	0.07%	7.42%
136	phosphoglycerate mutase	254360758	Cytoplasmic 8.96	Cytoplasmic	25965.6	100.00%	3	3	8	0.11%	12.30%
137	phosphopyruvate hydratase	254361471	Cytoplasmic 9.97	Cytoplasmic	46099.8	100.00%	6	6	16	0.21%	14.40%
138	pitrilysin	254361416	Periplasmic 9.76	signal peptide	110403	99.80%	2	2	4	0.05%	2.04%
139	polyribonucleotide nucleotidyltransferase	254361252	Cytoplasmic 9.97	Cytoplasmic	77834.8	99.80%	2	2	3	0.04%	3.49%
140	porin OmpW	254362806	Unknown	Cytoplasmic	5,814.90	100.00%	5	7	29	0.23%	77.40%
141	possible adhesin	254362666	Unknown	Signal peptide	14420.8	99.80%	2	2	4	0.05%	12.20%
142	possible arginine ABC superfamily ATP binding cassette transporter, binding protein	254360618	Periplasmic 10.00	Signal peptide	26,505.30	100.00%	3	3	13	0.10%	17.00%
143	possible cell division protein	254362934	CytoplasmicMembrane 9.82	Cytoplasmic	30656.8	99.80%	2	2	2	0.03%	6.47%
144	possible hemin ABC superfamily ATP binding cassette transporter, binding protein HbpA	254361671	Periplasmic 10.00	Signal peptide	59,616.20	100.00%	6	6	16	0.13%	22.80%
145	possible lipoprotein	254363154	Periplasmic 9.44	lipoprotein signal peptide	20924.4	100.00%	7	8	29	0.38%	44.40%
146	possible lipoprotein	254360821	Unknown	lipoprotein signal peptide	10341	99.50%	2	2	5	0.07%	16.30%
147	possible lipoprotein	254362041	Unknown	lipoprotein signal peptide	19301.8	100.00%	3	3	5	0.07%	13.90%
148	possible lipoprotein	254360822	Unknown	lipoprotein signal peptide	10104.9	99.80%	2	4	14	0.18%	20.70%
149	possible lipoprotein	254361089	OuterMembrane 9.92	lipoprotein signal peptide	18,211.80	100.00%	5	6	17	0.14%	37.00%
150	possible lipoprotein LolB	254362960	Unknown	lipoprotein signal peptide	24033.9	99.80%	2	2	8	0.11%	11.40%
151	possible LysM domain protein	254362289	Cytoplasmic 9.97	Cytoplasmic	15726.9	99.80%	2	2	2	0.03%	15.60%

	Protein name	Protein GI number	PSORTb	LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
152	possible molybdenum (Mo2+) ABC superfamily ATP binding cassette transporter, binding protein	254361790	Periplasmic 10.00	Signal peptide	27,590.10	100.00%	3	3	5	0.04%	11.20%
153	possible OMR family outer membrane hemoglobin receptor HmbR2	254362665	Outer membrane 10.00	Signal peptide	79464.7	99.60%	2	2	3	0.04%	2.36%
154	possible outer membrane protein	254361374	OuterMembrane 9.49	Signal peptide	37760.9	100.00%	5	5	12	0.16%	14.50%
155	possible outer membrane protein	254360920	Unknown	Signal peptide	56076	100.00%	13	14	31	0.41%	25.60%
156	possible outer membrane protein	254361137	Unknown	Signal peptide	37055.7	100.00%	8	8	15	0.20%	22.30%
157	possible protein-disulfide isomerase	254360996	Periplasmic 9.44	Signal peptide	23586.6	100.00%	3	3	3	0.04%	15.60%
158	possible rhodanese domain sulfurtransferase	254362707	Unknown	Signal peptide	12,810.90	99.50%	2	3	8	0.06%	23.10%
159	possible RND superfamily resistance-nodulation-cell division antiporter	254361802	OuterMembrane 9.92	lipoprotein signal peptide	51440.5	100.00%	11	11	20	0.26%	19.80%
160	possible secreted acid phosphatase	254362553	OuterMembrane 9.92	Cytoplasmic	23,073.40	100.00%	9	9	35	0.28%	48.30%
161	possible siderophore ABC superfamily ATP binding cassette transporter, binding protein	254362167	Cytoplasmic Membrane 9.97	Signal peptide	32,388.80	100.00%	5	5	15	0.12%	25.10%
162	possible thiamine ABC superfamily ATP binding cassette transporter, binding protein	254360649	Periplasmic 10.00	Signal peptide	33895	100.00%	3	3	7	0.09%	10.30%
163	possible transcriptional regulator	254361842	Unknown	Signal peptide	19885.5	99.70%	2	2	5	0.07%	11.40%
164	possible transglutaminase	254362485	Cytoplasmic 8.96	Signal peptide	40888.5	100.00%	4	4	8	0.11%	10.30%
165	preprotein translocase subunit SecA	254362009	Cytoplasmic 9.12	Cytoplasmic	102306.8	99.30%	2	2	3	0.04%	1.98%
166	protein disulfide-isomerase	254361859	Periplasmic 9.76	Signal peptide	25,110.20	100.00%	5	5	12	0.10%	26.90%
167	protein disulfide-isomerase	254363220	Periplasmic 10.00	Signal peptide	23,550.50	100.00%	5	6	22	0.18%	35.40%
168	pseudogene of conserved hypothetical protein	32034625	Unknown	Cytoplasmic	21410.8	100.00%	12	15	30	0.39%	52.50%
169	PTS family glucose porter component IIA	254362261	Cytoplasmic 9.97	Cytoplasmic	17812.6	99.80%	2	2	4	0.05%	10.80%
170	purine-nucleoside phosphorylase	254360546	Cytoplasmic 9.97	Cytoplasmic	25959.3	100.00%	3	3	8	0.11%	13.00%
171	pyruvate dehydrogenase (acetyl-transferring)	254362997	Cytoplasmic 9.97	Cytoplasmic	98900.9	100.00%	24	27	76	1.00%	28.10%
172	pyruvate kinase	254360636	Cytoplasmic 9.97	Cytoplasmic	50046.5	100.00%	4	4	10	0.13%	9.66%
173	recombinase RecA	254362313	Cytoplasmic 9.97	Cytoplasmic	39658.6	100.00%	3	3	9	0.12%	7.88%
174	riboflavin synthase beta subunit	254361996	Cytoplasmic 9.97	Cytoplasmic	16324.2	100.00%	3	3	6	0.08%	23.40%
175	ribose-phosphate diphosphokinase	254363000	Cytoplasmic 9.97	Cytoplasmic	34166.8	100.00%	4	4	6	0.08%	18.00%
176	ribosomal protein L1	254361444	Cytoplasmic 9.26	Cytoplasmic	23940.8	100.00%	4	4	7	0.09%	21.40%
177	ribosomal protein L10	254361436	Cytoplasmic 9.26	Cytoplasmic	17504.3	99.80%	2	2	6	0.08%	14.10%
178	ribosomal protein L11	254361445	Cytoplasmic 9.26	Cytoplasmic	14915.6	100.00%	4	4	10	0.13%	27.50%
179	ribosomal protein L14	254362787	Cytoplasmic 9.26	Cytoplasmic	11274.6	99.40%	2	2	5	0.07%	17.50%
180	ribosomal protein L15	254362778	Cytoplasmic 9.97	Cytoplasmic	15099.3	100.00%	6	6	11	0.14%	42.40%
181	ribosomal protein L16	254362067	Cytoplasmic 9.26	Cytoplasmic	15170.3	100.00%	3	3	6	0.08%	21.30%
182	ribosomal protein L17	254362771	Cytoplasmic 9.26	Cytoplasmic	14385	100.00%	3	3	9	0.12%	14.80%
183	ribosomal protein L19	254362948	Cytoplasmic 9.97	Cytoplasmic	13141.4	100.00%	5	5	8	0.11%	47.40%
184	ribosomal protein L2	254362071	Cytoplasmic 9.97	Cytoplasmic	29858.9	100.00%	7	9	22	0.29%	31.10%
185	ribosomal protein L22	254362069	Cytoplasmic 9.26	Cytoplasmic	12133.5	99.50%	2	2	4	0.05%	10.00%
186	ribosomal protein L3	254362074	Cytoplasmic 9.97	Cytoplasmic	22449.9	100.00%	7	8	22	0.29%	34.00%
187	ribosomal protein L4	254362073	Cytoplasmic 9.97	Cytoplasmic	22000.3	100.00%	3	3	6	0.08%	12.00%
188	ribosomal protein L5	254362785	Cytoplasmic 9.97	Cytoplasmic	20266.4	100.00%	5	5	15	0.20%	27.40%

	Protein name	Protein GI number	PSORTb	LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
189	ribosomal protein L6	254362782	Cytoplasmic 9.26	Cytoplasmic	18868.6	100.00%	4	4	10	0.13%	22.00%
190	ribosomal protein L7/L12	254361435	Cytoplasmic 9.26	Cytoplasmic	12301.3	99.80%	2	2	4	0.05%	20.50%
191	ribosomal protein L9	254361770	Cytoplasmic 9.26	Cytoplasmic	15179.9	100.00%	5	5	13	0.17%	37.60%
192	ribosomal protein S1	254361237	Cytoplasmic 9.97	Cytoplasmic	60160.3	100.00%	9	9	17	0.22%	16.60%
193	ribosomal protein S10	16272717	Cytoplasmic 9.26	Cytoplasmic	11748.8	100.00%	4	4	8	0.11%	41.70%
194	ribosomal protein S11	254362774	Cytoplasmic 9.26	Cytoplasmic	13885.1	99.80%	2	2	4	0.05%	15.50%
195	ribosomal protein S13	32034697	Cytoplasmic 9.97	Cytoplasmic	13251.2	100.00%	5	5	7	0.09%	43.20%
196	ribosomal protein S15	32033979	Cytoplasmic 9.26	Cytoplasmic	10162.3	99.90%	2	2	3	0.04%	15.70%
197	ribosomal protein S2	254360753	Cytoplasmic 9.97	Cytoplasmic	26311.9	100.00%	4	4	8	0.11%	17.10%
198	ribosomal protein S3	254362068	Cytoplasmic 9.97	Cytoplasmic	25779.6	100.00%	5	5	12	0.16%	23.80%
199	ribosomal protein S4	254362773	Cytoplasmic 9.97	Cytoplasmic	23805.9	100.00%	6	6	12	0.16%	25.00%
200	ribosomal protein S5	254362780	Cytoplasmic 9.97	Cytoplasmic	17488	99.90%	2	2	6	0.08%	12.70%
201	ribosomal protein S6***	53729064	Cytoplasmic 9.97	Cytoplasmic	14054.3	99.80%	2	2	7	0.09%	14.50%
202	ribosomal protein S7	254362573	Cytoplasmic 9.26	Cytoplasmic	17612.8	100.00%	5	5	14	0.18%	30.80%
203	ribosomal protein S8	254362783	Cytoplasmic 9.26	Cytoplasmic	14070.7	100.00%	4	5	11	0.14%	36.90%
204	ribosomal protein S9	254362052	Cytoplasmic 9.97	Cytoplasmic	14712.5	100.00%	5	6	15	0.20%	45.80%
205	S1C subfamily peptidase Do	254362428	Periplasmic 9.76	Signal peptide	49070.4	99.80%	2	2	5	0.07%	4.53%
206	S6 family IgA-specific metalloendopeptidase	254360993	OuterMembrane 9.83	Signal peptide	155611.7	100.00%	50	59	173	2.27%	36.00%
207	S6 family igA-specific metalloendopeptidase	254363217	OuterMembrane 9.82	Signal peptide	164482.9	100.00%	3	4	7	0.09%	3.46%
208	serotype 1-specific antigen	254362906	OuterMembrane 9.83	Signal peptide	103570.4	100.00%	69	110	672	8.82%	59.50%
209	SmpA family lipoprotein	254361732	OuterMembrane 9.93	lipoprotein signal peptide	12,919.40	100.00%	3	3	17	0.14%	33.60%
210	spermidine/putrescine ABC superfamily ATP binding cassette transporter, binding protein	254362547	Periplasmic 9.44	Cytoplasmic	36047.1	100.00%	3	3	7	0.09%	7.12%
211	succinate dehydrogenase	254362603	Cytoplasmic 7.88	Cytoplasmic	66123.9	99.80%	2	2	2	0.03%	5.33%
212	superoxide dismutase	254360578	Unknown	Cytoplasmic	23,793.80	99.90%	2	2	5	0.04%	8.45%
213	TonB family auxiliary protein TolB	254362584	Periplasmic 9.44	Signal peptide	41238.1	100.00%	13	15	39	0.51%	34.10%
214	TonB family auxiliary protein TolQ	254362581	Cytoplasmic Membrane 10.00	Cytoplasmic	25219.7	100.00%	3	3	7	0.09%	15.50%
215	transaldolase	254361180	Cytoplasmic 8.96	Cytoplasmic	35193.1	100.00%	3	3	4	0.05%	9.81%
216	transferrin binding protein A	254360640	OuterMembrane 10.00	Signal peptide	106470	100.00%	39	46	109	1.43%	37.60%
217	transferrin binding protein B	254360641	Outer Membrane 9.49	lipoprotein signal peptide	63734.4	100.00%	40	54	152	1.99%	67.90%
218	transketolase	254361985	Cytoplasmic9.97	Cytoplasmic	73480.8	100.00%	10	10	15	0.20%	15.90%
219	TRAP-T family tripartite ATP-independent periplasmic transporter, binding protein	254362109	Unknown	Signal peptide	34505.8	100.00%	5	5	8	0.11%	16.60%
220	TRAP-T family tripartite ATP-independent periplasmic transporter,binding protein	254361692	Periplasmic 9.76	Signal peptide	36,157.00	99.80%	2	2	5	0.04%	6.10%
221	trimethylamine-N-oxide reductase (cytochrome c)	254361297	Periplasmic 10.00	Signal peptide	91417.3	99.80%	2	2	4	0.05%	2.17%
222	triose-phosphate isomerase	254362191	Cytoplasmic 9.26	Cytoplasmic	27495.5	99.90%	2	2	5	0.07%	6.08%

	Protein name	Protein GI number	PSORTb		LipoP	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage
223	UDP-N-acetylglucosamine 2-epimerase	254360953	Cytoplasmic	9.97	Cytoplasmic	41406.6	100.00%	3	3	5	0.07%	9.43%
224	UDP-sugar diphosphatase	254361285	Periplasmic	9.76	Signal peptide	60961.4	100.00%	4	4	5	0.07%	7.68%
225	uracil phosphoribosyltransferase	254362984	Cytoplasmic	9.97	Cytoplasmic	22727.4	100.00%	3	3	8	0.11%	13.40%
226	uridine phosphorylase	254360938	Cytoplasmic	9.97	Cytoplasmic	27332.1	100.00%	5	5	12	0.16%	19.40%