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Table S1. Proteomic analysis of *Campylobacter jejuni* 11168H outer membrane vesicles.

Locus tag	gene	Protein	Peptides ^a			Sequence coverage			Mass	LipoP ^b	COG ^c
Cj0087	aspA	aspartate ammonia-lyase	3	5	/	6.6	10.9	/	52132		AATM
Cj0269c	ilvE	branched-chain amino acid aminotransferase	4	2	2	17.1	11.8	9.9	34008		AATM
Cj0415	-	putative GMC oxidoreductase subunit	24	20	22	41.4	33.5	42.6	64101		AATM
Cj0632	ilvC	ketol-acid reductoisomerase	8	/	2	35.3	/	8.2	37139		AATM
Cj0734c*	hisJ	histidine-binding protein precursor	8	5	9	50.2	25.9	39.4	27839	LSP	AATM
Cj0817	glnH	putative glutamine binding periplasmic protein	9	8	7	46.1	41	35.9	28896	SP	AATM
Cj0921c	peb1A	bifunctional adhesin/ABC transporter aspartate/glutamate-binding protein	9	10	11	44	51.4	52.1	28217	SP	AATM
Cj0922c	pebC	ABC-type amino-acid transporter ATP-binding protein	4	5	3	31	31	21.5	27439		AATM
Cj0982c*	cjaA	putative amino-acid transporter periplasmic solute-binding protein	14	14	15	51.3	51.3	51.6	31005	LSP	AATM
Cj1018c	livK	branched-chain amino-acid ABC transport system,periplasmic binding protein	3	3	5	15.4	13.3	23.3	39862	SP	AATM
Cj1503c	putA	putative proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase	24	12	19	27.7	14.6	19.7	132893		AATM
Cj1584c	-	putative peptide ABC-transport system periplasmic peptide-binding protein	3	3	3	9.2	8.8	9.2	58820		
Cj1014c	livF	branched-chain amino-acid ABC transport system ATP-binding protein	5	/	1	24.2	/	5.2	25578		AATM / PM
Cj1672c	eno	phosphopyruvate hydratase	3	/	5	12.8	/	23.2	45253		CTM
Cj0276	mreB	homolog of E. coli rod shape-determining protein	12	6	6	34.7	26.6	22.5	37671		CCC
Cj0695	ftsA	cell division protein FtsA	13	7	10	32.7	24.2	24.9	51100		CCC
Cj0886c	ftsK	putative cell division protein	3	8	9	4.9	12.2	13.2	107853		CCC
Cj1276c	-	putative integral membrane protein	3	2	3	13.4	8.6	13.4	31714	SP	CCC
Cj0019c	-	putative MCP-domain signal transduction protein	7	3	7	20.3	7.4	21.3	66860	SP	CM
Cj0144	-	putative methyl-accepting chemotaxis signal transduction protein	22	24	19	46.1	52.8	43.6	72546		CM
Cj0262c	-	putative methyl-accepting chemotaxis signal transduction protein	28	26	28	56.7	55.2	58.6	72901		CM
Cj0283c	cheW	chemotaxis protein	7	6	8	37	25.4	41.6	19504		CM
Cj0284c	cheA	chemotaxis histidine kinase	29	33	33	44.7	50.3	48.1	85361		CM
Cj0337c	motA	flagellar motor protein MotA	2	2	2	7.8	7.8	7.8	28279		CM
Cj0448c	-	putative MCP-type signal transduction protein	12	12	15	49.3	46.6	50.1	40605		CM
Cj1110c	-	putative MCP-type signal transduction protein	12	12	16	33.6	29.8	40.3	48548		CM
Cj1190c	cetA	bipartate energy taxis response protein cetA	14	13	16	35.3	31.4	38.6	51156		CM
Cj1338c	flaB	flagellin	7	/	7	15.9	/	14.9	59150		CM
Cj1339c	flaA	flagellin	10	12	14	24.5	25.7	32.7	59003		CM
Cj1506c	-	putative MCP-type signal transduction protein	19	22	23	40.7	48.3	48	77277		CM
Cj1564	-	putative methyl-accepting chemotaxis signal transduction protein	26	24	22	53.3	48.5	45.2	73191	SP	CM
Cj0113	pal	peptidoglycan associated lipoprotein (omp18)	3	5	5	17.6	33.9	33.9	18046	LSP	CEB
Cj0129c	-	outer membrane protein	8	7	12	15.6	13.4	20.6	83204	SP	CEB
Cj0131	-	putative peptidase M23 family protein	7	7	3	17.7	22.1	7.9	51749		CEB
Cj0365c*	cmeC	outer membrane channel protein CmeC (multidrug efflux system CmeABC)	2	2	3	5.5	5.3	8.5	55441	LSP	CEB
Cj0511*	-	putative secreted protease	5	4	5	18	14	18.7	48903	SP	CEB
Cj0646	-	putative lipoprotein	5	6	6	18.9	24.7	22.2	29414	LSP	CEB
Cj1235	-	putative peptidase M23 family protein	2	/	2	9.5	/	9.5	30640		CEB
Cj1427c	-	putative sugar-nucleotide epimerase/dehydratase	4	/	5	17.6	/	25.9	35864		CEB
Cj1444c*	kpsD	capsule polysaccharide export system periplasmic protein	12	6	9	26.6	13.4	16.3	60918	SP	CEB
Cj1478c	cadF	outer membrane fibronectin-binding protein	11	7	8	43.3	27.6	34.5	36146	SP	CEB
Cj1096c	metK	S-adenosylmethionine synthetase	3	/	3	8.8	/	10.6	44083		CoTM
Cj1540	-	putative periplasmic protein	9	7	12	40.5	32	49.8	29897	SP	CoTM

Cj0366c*	cmeB	inner membrane efflux transporter CmeB (multidrug efflux system CmeABC)	3	/	6	6.9	/	9.9	114066		DM
Cj0074c	-	putative iron-sulfur protein	1	7	4	5.8	21.3	12.5	54870		EPC
Cj0105	atpA	F0F1 ATP synthase subunit alpha	6	13	11	12.2	27.9	23.2	54824		EPC
Cj0107	atpD	F0F1 ATP synthase subunit beta	15	11	10	41.9	32.5	24.5	50875		EPC
Cj0264c	-	molybdopterin containing oxidoreductase	7	6	6	11.6	9.2	10	93788	SP	EPC
Cj0265c	-	putative cytochrome C-type haem-binding periplasmic protein	5	4	4	27.7	23	21.5	22270	SP	EPC
Cj0410	frdB	fumarate reductase iron-sulfur subunit	2	5	/	12.4	29.5	/	28282		EPC
Cj0531	icd	isocitrate dehydrogenase	7	9	11	13.6	15.9	24.7	82565		EPC
Cj0534	sucD	succinyl-coA synthetase alpha chain	6	7	7	28	37.7	37.7	30230		EPC
Cj0780	napA	nitrate reductase	31	29	33	33.1	33	38.1	105561	SP	EPC
Cj0835c	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	10	8	9	18.4	15	15.2	93476		EPC
Cj0932c	pckA	phosphoenolpyruvate carboxykinase	3	2	/	11.8	8.4	/	59530		EPC
Cj1184c	petC	putative ubiquinol-cytochrome C reductase cytochrome C subunit	5	3	4	17.4	13.1	13.4	41645		EPC
Cj1186c	petA	putative ubiquinol-cytochrome C reductase iron-sulfur subunit	4	5	5	32.3	32.3	32.3	18332	SP	EPC
Cj1265c	hydC	Ni/Fe-hydrogenase B-type cytochrome subunit	4	/	2	12.2	/	9.1	26894		EPC
Cj1266c	hydB	Ni/Fe-hydrogenase large subunit	24	16	13	52.2	34.3	29.2	64157		EPC
Cj1267c	hydA	Ni/Fe-hydrogenase small chain	5	4	5	20.3	12.9	17.9	41982		EPC
Cj1364c	fumC	fumarate hydratase	3	3	2	8	8	5.6	50963		EPC
Cj1382c	fldA	flavodoxin FldA	3	5	6	28.8	59.5	59.5	17224		EPC
Cj1476c	-	pyruvate-flavodoxin oxidoreductase	11	8	14	14.8	11.7	15.6	132357		EPC
Cj1487c	ccoP	cb-type cytochrome C oxidase subunit III	6	4	8	36.6	20.6	40.8	31370		EPC
Cj1489c	ccoO	cb-type cytochrome C oxidase subunit II	7	5	6	34.8	29	34.4	25048		EPC
Cj1511c	fdhA	putative formate dehydrogenase large subunit (Selenocysteine containing)	20	18	16	23.8	23.3	23.9	104573	SP	EPC
Cj0034c	-	putative periplasmic protein	4	4	7	20.6	24.9	34.8	26440	SP	FU
Cj0073c	-	conserved hypothetical protein Cj0073c	7	/	4	40.8	/	30.7	24695		FU
Cj0089*	-	putative lipoprotein	5	4	7	13	13.2	18.8	51607	LSP	FU
Cj0114*	-	putative periplasmic protein	6	5	7	27.6	19.7	30.2	35396	SP	FU
Cj0152c*	-	hypothetical protein Cj0152c	3	3	2	14.4	16.7	9	35536		FU
Cj0420	-	putative periplasmic protein	10	11	9	49.5	46.8	45.3	21025	SP	FU
Cj0926	-	hypothetical protein Cj0926	2	2	2	22.7	26.4	22.7	13124		FU
Cj1026c	-	putative lipoprotein	2	/	2	18.7	/	18.7	18570	LSP	FU
Cj0091	-	putative lipoprotein	7	6	6	36.2	26.1	26.1	22490	LSP	GF
Cj0289c*	peb3	major antigenic peptide PEB3	4	6	4	21.6	30.4	17.2	27576	SP	GF
Cj0393c	mqo	putative malate:quinone oxidoreductase	3	/	4	10.5	/	11.2	50953		GF
Cj0715	-	transthyretin-like periplasmic protein	/	2	3	/	18.2	24.1	15910	SP	GF
Cj0778	peb2	major antigenic peptide PEB2	6	6	7	29.4	29.4	38.8	27304	SP	GF
Cj1279c	-	putative fibronectin domain-containing lipoprotein	15	11	18	53.8	36.7	52.3	46152	LSP	GF
Cj0020c	-	cytochrome C551 peroxidase	6	4	4	23.4	18.4	18.4	34632	SP	IITM
Cj0143c*	-	putative periplasmic solute binding protein for ABC transport system	4	4	7	17.2	18.9	27.7	34613	SP	IITM
Cj0175c	cfbpA	putative iron-uptake ABC transport system, periplasmic iron-binding protein	5	3	/	18.6	12.3	/	37452		IITM
Cj0303c	modA	putative molybdate-binding lipoprotein	4	3	4	20.5	14.5	24.9	27705	LSP	IITM
Cj0358	-	putative cytochrome C551 peroxidase	6	2	3	17.9	8.5	12.6	37051	SP	IITM
Cj0612c	cft	ferritin	/	4	2	/	26.3	9.6	19531		IITM
Cj0613	pstS	putative periplasmic phosphate binding protein	7	6	9	33.2	29.3	40.5	36286	SP	IITM
Cj0772c	-	putative NLPA family lipoprotein	5	7	4	22.2	31.5	16.7	28621	SP	IITM
Cj1534c	-	putative bacterioferritin	3	2	3	28.2	19.5	29.5	17422		IITM
Cj0112	tolB	translocation protein TolB	9	9	13	33.3	27.4	42.3	44750	SP	ITSVT
Cj0598	-	hypothetical protein Cj0598	5	7	7	14.2	17.5	17.1	55634		ITSVT
Cj0127c	accD	acetyl-CoA carboxylase subunit beta	5	3	5	28.2	11.4	30	31274		LTM
Cj0443	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	3	5	6	14.7	18.3	26	34346		LTM
Cj0804	pyrD	dihydroorotate dehydrogenase 2	3	/	2	13.6	/	10.2	39114		NTM
Cj0918c	prsA	ribose-phosphate pyrophosphokinase	2	3	7	10	14.2	34	33848		NTM
Cj1274c	pyrH	uridylylate kinase	4	3	5	34.7	16.7	33.9	26174		NTM

Cj0017c*	dsbI	disulphide bond formation protein	11	7	8	29.5	19.1	21.5	56904		PM
Cj0146c	trxB	thioredoxin reductase	/	2	2	/	9.6	12.8	33496		PM
Cj0147c	trxA	thioredoxin	5	6	5	56.7	77.9	56.7	11517		PM
Cj0334	ahpC	alkyl hydroperoxide reductase	8	6	8	56.1	50	56.1	22047		PM
Cj0596	peb4cbf2	major antigenic peptide PEB-cell binding factor	9	7	10	35.9	26	30.8	30499	SP	PM
Cj0759	dnaK	molecular chaperone DnaK	3	3	2	10.6	10.1	8	67491		PM
Cj0779	tpx	thiol peroxidase	6	6	8	46.3	46.3	64	18771		PM
Cj0950c	-	putative lipoprotein	6	3	3	36.8	23.6	23.6	16323	LSP	PM
Cj1013c*	-	putative cytochrome C biogenesis protein	3	5	/	4.3	5.2	/	123789		PM
Cj1221	groEL	chaperonin GroEL	24	19	15	53.2	45.1	31.7	57991		PM
Cj1228c	htrA	serine protease (protease DO)	13	8	11	39.2	24.2	32.6	50976	SP	PM
Cj1289	-	possible periplasmic protein	5	3	4	25.1	13.3	17.7	30982	SP	PM
Cj1380	-	putative periplasmic protein	9	11	10	34.3	53.8	45.8	26751	SP	PM
Cj1725	-	putative periplasmic protein	4	/	2	27.1	/	13.6	21393	SP	PM
Cj0913c	hupB	DNA-binding protein HU homolog	3	3	2	52	37.8	34.7	10268		RRR
Cj1420c	-	putative methyltransferase	5	2	3	30	13.2	14.8	29837		SMB
Cj1516	-	putative periplasmic oxidoreductase	7	4	2	17.2	14.6	7.4	59096	SP	SMB
Cj1219c	-	putative periplasmic protein	17	12	12	30	20.3	20.8	92233		SMB / STM
Cj0285c	cheV	chemotaxis protein	21	19	20	60.4	58.5	58.8	35836		STM
Cj1118c	cheY	chemotaxis regulatory protein	3	3	8	21.5	21.5	76.9	14428		STM
Cj1189c	cetB	bipartate energy taxis response protein cetB	6	5	5	39.4	36.4	35.2	19358		STM
Cj1191c	-	putative PAS domain containing signal-transduction sensor protein	8	6	8	51.2	41.5	47	19036		STM
Cj0311	-	50S ribosomal protein L25/general stress protein Ctc	2	2	3	14	20.2	23	19506		TRB
Cj0470	tuf	elongation factor Tu	20	15	15	58.6	42.9	47.6	43623		TRB
Cj0493	fusA	elongation factor G	2	4	3	3.9	8	7.5	77013		TRB
Cj0884	rpsO	30S ribosomal protein S15	2	2	2	28.9	28.9	28.9	10220		TRB
Cj1695c	rplE	50S ribosomal protein L5	/	3	4	/	21	28.7	20201		TRB
Cj1708c	rpsJ	30S ribosomal protein S10	2	3	2	21.4	37.9	21.4	11665		TRB
Cj0077c	cdtC	Cytolethal distending toxin C	/	5	4	/	36	29.6	21372	SP	/
Cj0078c	cdtB	Cytolethal distending toxin B	4	4	5	24.9	25.7	20.4	29012	SP	/
Cj0079c	cdtA	Cytolethal distending toxin A	/	2	6	/	7.8	20.9	30299	LSP	/
Cj0090	-	putative lipoprotein	2	2	2	17.2	17.2	17.2	14104	LSP	/
Cj0092	-	putative periplasmic protein	13	10	8	40.4	32.8	29.7	49210	SP	/
Cj0124c	-	hypothetical protein Cj0124c	7	5	6	27.1	23.5	21	38604		/
Cj0151c	-	putative periplasmic protein	7	4	5	32.5	16.8	27.2	30602		/
Cj0352	-	putative transmembrane protein	8	7	8	38.9	35.8	38.9	31075		/
Cj0396c	-	putative lipoprotein	5	7	6	22.6	25	22.9	37532	LSP	/
Cj0399*	-	colicin V production protein homolog	3	3	5	17.6	24.6	29.4	20760		/
Cj0404	-	putative transmembrane protein	6	6	5	17.6	21.2	23.4	30755		/
Cj0406c	-	putative lipoprotein	9	11	7	28.8	38.1	26.4	33189	LSP	/
Cj0414	-	putative oxidoreductase subunit	23	18	22	69	51.2	70.2	26963	SP	/
Cj0530*	-	putative periplasmic protein	9	7	6	16.2	10	9.1	97660		/
Cj0700	-	hypothetical protein Cj0700	3	4	3	19	32.5	19	26007		/
Cj0776c	-	putative periplasmic protein	9	8	8	26.2	25.3	19.7	39544	SP	/
Cj0944c	-	putative periplasmic protein	/	3	2	/	14.3	10.7	27961	SP	/
Cj0998c	-	putative periplasmic protein	7	6	6	43.2	43.2	39.5	20593	SP	/
Cj1029c	mapA	putative lipoprotein	5	2	5	25.2	13.6	32.2	24311	LSP	/
Cj1041c	-	putative periplasmic ATP/GTP-binding protein	6	/	7	26.9	/	29.7	31719	SP	/
Cj1090c	-	putative lipoprotein	3	3	2	25.3	23.5	15.9	19107	LSP	/
Cj1170c	omp50	50 kda outer membrane protein precursor	14	14	13	33.6	30.2	33.6	53363	SP	/
Cj1178c	-	highly acidic protein	7	4	5	19.7	10.7	15.1	61669		/
Cj1214c	-	putative exporting protein	5	3	2	24.9	17	10.4	27462	SP	/
Cj1259	porA	major outer membrane protein	15	15	16	55.2	49.1	57.1	45660	SP	/

Cj1460	-	hypothetical protein Cj1460	3	2	2	27.6	20.5	20.5	14771		/
Cj1621*	-	putative periplasmic protein	4	4	3	20.4	20	14.8	28602	SP	/

*Glycosylated.

^aRefers to the number of peptides identified per protein.

^bLipoP predictions: SP; signal peptide LSP; lipoprotein signal peptide.

^cCOG assignments: AATM; Amino acid transport and metabolism, CTM; Carbohydrate transport and metabolism, CCC; Cell cycle control, cell division, chromosome partitioning, CM; Cell motility, CEB; Cell wall/membrane/envelope biogenesis, CoTM; Coenzyme transport and metabolism, DM; Defense mechanisms, EPC; Energy production and conversion, FU; Function unknown, GF; General function prediction only, IITM; Inorganic ion transport and metabolism, ITSVT; Intracellular trafficking, secretion, and vesicular transport, LTM; Lipid transport and metabolism, NTM; Nucleotide transport and metabolism, PM; Posttranslational modification, protein turnover, chaperones, RRR; Replication, recombination and repair, SMB; Secondary metabolites biosynthesis, transport and catabolism, STM; Signal transduction mechanisms, TRB; Translation, ribosomal structure and biogenesis, /; No assigned COG.