

Supporting Information

Comprehensive proteomic profiling of outer membrane vesicles from *Campylobacter jejuni*

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Table S1. Summary of proteins identified from the OMVs of *C. jejuni*.

Uniprot accession	Description	Gene	No. of peptides	Sequence coverage (%)	PEP ^a	Subcellular localization	Signal peptid ^e _b	COG ^c	Related to ^d
Q9PNB3	30S ribosomal protein S2	rpsB	23	77.2	4.37E-290	Cytoplasm		J	
Q9PI34	50S ribosomal protein L1	rplA	25	84.5	0	Cytoplasm		J	
O69289	60 kDa chaperonin	groL	70	92.5	0	Cytoplasm		O	
Q9PPL8	Acetate kinase	ackA	29	88.4	0	Cytoplasm		C	
Q0PA55	Aconitate hydratase 2	acnB	67	73.6	0	Cytoplasm		C	
Q0PBU3	Amidophosphoribosyltransferase	purF	19	53.5	7.35E-92	Cytoplasm		F	
Q9PHK7	Argininosuccinate synthase	argG	40	81.3	0	Cytoplasm		E	
Q0PC50	Aspartate ammonia-lyase	aspA	36	56.4	0	Cytoplasm		E	
Q59291	Aspartate-semialdehyde dehydrogenase	asd	20	56.6	8.13E-246	Cytoplasm	Sec	E	
Q9PN98	Aspartyl/glutamyl-tRNA amidotransferase subunit B	gatB	25	45.1	3.14E-269	Cytoplasm		E	
Q9PM78	ATP phosphoribosyltransferase	hisG	17	54.2	2.64E-102	Cytoplasm		E	
Q9PIM0	ATP-dependent Clp protease ATP-binding subunit ClpX	clpX	19	45.1	3.13E-125	Cytoplasm		OU	Proteolysis ^[1]
Q0PBM2	Chemotaxis histidine kinase	cheA	42	56.7	0	Cytoplasm		NT	
Q0PBM1	Chemotaxis protein	cheV	25	69.5	0	Cytoplasm		NT	
Q0P7U8	Citrate synthase	gltA	36	85.1	0	Cytoplasm		C	
Q0P9Q7	Delta-aminolevulinic acid dehydratase	hemB	25	67	3.67E-225	Cytoplasm		H	
Q0P891	DNA protection during starvation protein	dps	19	92.6	0	Cytoplasm		T	
Q9PM80	DNA-directed RNA polymerase subunit alpha	rpoA	25	77.4	0	Cytoplasm		K	
Q46124	DNA-directed RNA polymerase subunit beta	rpoB	100	63.5	0	Cytoplasm		K	
Q9PI30	DNA-directed RNA polymerase subunit beta'	rpoC	94	65.8	0	Cytoplasm		K	
Q9PI16	Elongation factor G	fusA	54	74.5	0	Cytoplasm		J	
O69303	Elongation factor Tu	tuf	43	95.2	0	Cytoplasm		J	
P42448	Enolase	eno	19	52.4	0	Cytoplasm		G	

Q0PBU4	Flagellum-specific ATP synthase	fliI	5	10.2	9.31E-08	Cytoplasm		N	
O69294	Fumarate hydratase class II	fumC	38	78	0	Cytoplasm		C	
Q9PMT4	Glucosamine--fructose-6-phosphate aminotransferase	glmS	27	41.1	1.19E-163	Cytoplasm		M	
Q9PP70	Glutamate-1-semialdehyde 2,1-aminomutase	hemL	25	62.5	9.01E-252	Cytoplasm	Sec	H	
Q0PAI0	Glutamine synthetase	glnA	28	55.3	6.73E-231	Cytoplasm		E	
Q0P8L1	Glyceraldehyde 3-phosphate dehydrogenase	gapA	22	64.8	2.82E-248	Cytoplasm		G	
Q0P9J4	Inosine-5'-monophosphate dehydrogenase	guaB	48	85.8	0	Cytoplasm		F	
Q0PAY5	Isocitrate dehydrogenase	icd	66	69.6	0	Cytoplasm		C	
Q9PIH0	Phosphate acyltransferase	plsX	12	36.6	2.86E-34	Cytoplasm		I	
Q9PP04	Probable cytosol aminopeptidase	pepA	29	55.9	2.22E-276	Cytoplasm		E	
Q9PHX1	Proline-tRNA ligase	proS	29	49	6.02E-141	Cytoplasm		J	
Q0P7V6	Protein RecA	recA	16	43.4	1.22E-141	Cytoplasm		L	
Q0P8I7	Putative sugar-nucleotide epimerase/dehydratase	Cj1427c	27	73.8	0	Cytoplasm		MG	
Q0PBB8	Pyruvate kinase	pyk	43	70.6	0	Cytoplasm		G	
Q9PP15	Ribose-phosphate pyrophosphokinase	prs	16	54.7	7.48E-246	Cytoplasm		G	
Q0P9F8	S-adenosylmethionine synthetase	metK	26	56.5	4.15E-241	Cytoplasm		H	
P24531	Serine hydroxymethyltransferase	glyA	28	58.9	0	Cytoplasm		E	
Q46108	Trigger factor	tig	66	85.4	0	Cytoplasm		O	
Q0P9C3	UDP-GlcNAc/Glc 4-epimerase	gne	24	62.8	9.80E-188	Cytoplasm		M	Glycoconjugate synthesis ^[2]
Q0P8W4	UDP-GlcNAc-specific C4,6 dehydratase/C5 epimerase	pseB	26	83.8	1.09E-184	Cytoplasm		M	
Q0P7Q2	Flagellar hook subunit protein	flgE2	23	36.2	9.37E-278	Extracellular	Sec	N	
Q9PHW6	Flagellar hook-associated protein 2	fliD	25	44.9	4.48E-250	Extracellular	Sec	N	
P56963	Flagellin A	flaA	34	72	0	Extracellular		N	Cell adhesion and immune stimulating activity ^[3]
P56964	Flagellin B	flaB	27	54.7	0	Extracellular		N	Cell adhesion and immune stimulating

										activity ^[3]
Q0P8E9	Putative flagellar hook-associated protein	flgK	7	12	5.70E-14	Extracellular	Sec	N		
Q0PA11	Putative flagellin	flaD	19	30.7	7.63E-100	Extracellular		N		
Q0PB04	Putative secreted protease	Cj0511	35	61.3	6.83E-252	Extracellular	Sec	O	Proteolysis ^[1]	
Q0PA10	ABC transport system ATP-binding protein	Cj0888c	6	8.7	3.19E-15	Inner membrane		R		
Q9PJ21	ATP synthase subunit alpha	atpA	35	61.1	4.13E-184	Inner membrane		C		
Q0PC30	ATP synthase subunit beta	atpD	33	70.8	0	Inner membrane		C		
Q0P8D0	Cbb3-type cytochrome c oxidase subunit	ccoP	14	46.7	0	Inner membrane	TM	P	Host colonization ^[4]	
Q0PA12	DNA translocase FtsK	ftsK	22	27.8	7.45E-181	Inner membrane	TM	L		
O52908	Flagellar biosynthesis protein flhF	flhF	22	51	1.97E-229	Inner membrane		NU		
Q0PBA1	Fumarate reductase flavoprotein subunit	frdA	65	82.4	0	Inner membrane	Sec	C		
Q0P9C5	GalNAc transferase/polymerase	pglH	17	49	5.98E-63	Inner membrane		M	N-linked glycan synthesis ^[5]	
Q0P9V7	Protein translocase subunit SecA	secA	56	60.1	0	Inner membrane		U		
Q0P8E1	Pyruvate-flavodoxin oxidoreductase	Cj1476c	94	74.3	0	Inner membrane		C		
Q0PB73	Succinate dehydrogenase flavoprotein subunit	sdhA	41	70.5	0	Inner membrane	Tat	C		
Q0P970	Ubiquinol-cytochrome c reductase iron-sulfur subunit	petA	13	68.9	1.92E-85	Inner membrane	Tat	C		
Q0P9A5	ADP-glyceromanno-heptose 6-epimerase	hldD	22	73.5	1.73E-153	Membrane		M		
Q0PC49	Anaerobic C4-dicarboxylate transporter	dcuA	7	12.1	3.09E-17	Membrane	TM	R		
Q0P8H0	Capsule polysaccharide export system periplasmic protein	kpsD	22	40.2	1.10E-194	Membrane	Sec	M		
Q0PCA8	Disulphide bond formation protein	dsbl	30	54.9	3.39E-251	Membrane	TM	O		
Q0PBA0	Fumarate reductase iron-sulfur protein	frdB	24	67.2	0	Membrane		C		
Q0PBM9	Homolog of E. coli rod shape-determining protein	mreB	22	56.1	1.78E-172	Membrane		N		

Q0P8Z0	Ni/Fe-hydrogenase large subunit	hydB	47	83.7	0	Membrane		C	
Q0P8Y9	Ni/Fe-hydrogenase small chain	hydA	18	60.7	6.28E-302	Membrane	Tat	C	
Q0PBW4	Putative iron-uptake ABC transport system	cfbpA	11	35.6	2.26E-70	Membrane	Sec	P	
Q0PB16	Putative lipoprotein	Cj0497	15	37.9	5.96E-170	Membrane	Sec	M	
Q0PBA4	Putative lipoprotein	Cj0406c	20	53.8	1.64E-191	Membrane	Sec	M	
Q0PBB4	Putative lipoprotein	Cj0396c	20	49.4	5.38E-62	Membrane	Sec	M	
Q0PC48	Putative lipoprotein	Cj0089	17	41.7	9.46E-126	Membrane	Sec	M	
Q0PCA6	Putative MCP-domain signal transduction protein	Cj0019c	32	53.5	0	Membrane	Sec	NT	
Q0P8B2	Putative MCP-type signal transduction protein	Cj1506c	48	63.6	0	Membrane	TM	NT	
Q0P9E4	Putative MCP-type signal transduction protein	Cj1110c	35	70.4	0	Membrane		NT	
Q0PB65	Putative MCP-type signal transduction protein	Cj0448c	34	90.4	0	Membrane		NT	
Q0PBY5	Putative membrane protein	Cj0152c	14	32.4	1.76E-65	Membrane		X	
Q0P864	Putative methyl-accepting chemotaxis signal transduction protein	Cj1564	44	61.3	0	Membrane	Sec	NT	
Q0PBA6	Putative transmembrane protein	Cj0404	13	40.3	7.98E-79	Membrane	TM	M	
Q0PBN7	Putative transmembrane protein	Cj0268c	23	57.2	1.08E-286	Membrane	TM	M	
Q0P986	50 kDa outer membrane protein	omp50	24	54.8	0	Outer membrane	Sec	MU	
P80672	Major outer membrane protein (Porin)	porA	29	63.9	0	Outer membrane	Sec	MU	Pore-forming activity ^[6]
Q0P8D9	Outer membrane fibronectin-binding protein	cadF	17	42.9	6.61E-96	Outer membrane	Sec	P	Binding to cell membrane ^[7]
Q0PC08	Outer membrane protein	Cj0129c	32	39.8	8.06E-246	Outer membrane	Sec	M	
Q0P9S0	Putative amino-acid transporter periplasmic solute-binding protein	cjaA	31	82.1	5.07E-279	Outer membrane	Sec	E	Highly immunogenic
Q0P8X7	Putative fibronectin domain-containing lipoprotein	Cj1279c	30	68.1	0	Outer membrane	Sec	P	Binding to cell membrane ^[7]
Q0PAS1	Putative peptidyl-prolyl cis-trans isomerase Cbf2	cbf2	35	77.7	9.91E-284	Outer membrane	Sec	J	Cell binding and amino acid transport ^[8]

Q0PC44	Putative periplasmic protein	Cj0093	8	21	2.86E-19	Outer membrane	Sec	X	
Q0P9N3	Branched-chain amino-acid ABC transport system	livJ	14	36.7	2.51E-101	Periplasm	Sec	E	
Q0P9N4	Branched-chain amino-acid ABC transport system	livK	9	35.2	2.43E-68	Periplasm	Sec	E	
Q9PPD9	Periplasmic nitrate reductase	napA	103	77.5	0	Periplasm	Tat	P	Host colonization ^[4]
Q9PJ14	Protein TolB	tolB	21	56.7	5.86E-193	Periplasm	Sec	E	
Q0PC89	Putative cytochrome C	Cj0037c	14	38.9	1.85E-74	Periplasm	Sec	C	
Q0PBF1	Putative cytochrome C551 peroxidase	Cj0358	32	69.5	9.37E-272	Periplasm	Sec	C	
Q0P8A7	Putative formate dehydrogenase large subunit	fdhA	63	63.6	0	Periplasm	Tat	C	
Q0P8Q2	Putative periplasmic cytochrome C	nrfA	53	72.5	0	Periplasm	TM	C	Host colonization ^[4]
Q0P8A3	Putative periplasmic oxidoreductase	Cj1516	19	39	9.44E-118	Periplasm	Tat	C	
Q0P9Q4	Putative periplasmic protein	Cj0998c	21	63.7	6.63E-262	Periplasm	Sec	M	
Q0P9T5	Putative periplasmic protein	Cj0964	9	24.2	3.83E-64	Periplasm	Sec	M	
Q0PAI5	Putative periplasmic protein	Cj0694	33	58.9	0	Periplasm	TM	M	
Q0PC23	Putative periplasmic protein	Cj0114	19	52.1	3.02E-199	Periplasm	Sec	M	
Q0PC45	Putative periplasmic protein	Cj0092	21	58.4	3.29E-267	Periplasm	Sec	M	
Q0P928	Serine protease	htrA	38	73.3	0	Periplasm	Sec	O	Proteolysis ^[1]
Q0PCA2	Adenylosuccinate lyase	purB	24	55	7.70E-125	Unknown		F	
Q9PM68	Bifunctional enzyme IspD/IspF	ispDF	13	38.8	1.93E-112	Unknown		M	
Q0P8W7	Biotin carboxylase	accC	24	56.4	5.73E-174	Unknown		I	
Q0PBN6	Branched-chain amino acid aminotransferase	ilvE	22	68.1	4.73E-229	Unknown		EH	
Q0PCB8	Glutamate synthase (NADPH) large subunit	gltB	51	39.8	0	Unknown		E	
Q0PCB6	Glutamate synthase (NADPH) small subunit	gltD	11	25.2	1.29E-195	Unknown		E	
Q9PHN5	Ketol-acid reductoisomerase	ilvC	27	70.9	4.83E-269	Unknown		EH	
Q0P804	L-serine dehydratase	sdaA	21	41.2	2.46E-227	Unknown		E	
Q0PAY0	OORA subunit of 2-oxoglutarate:acceptor oxidoreductase	oorA	27	59.1	0	Unknown		C	

Q0PAX5	Polyprenyl synthetase	Cj0541	5	13.1	3.79E-14	Unknown		I
Q0P8Y6	Putative 2-nitropropane dioxygenase	Cj1270c	22	66.9	0	Unknown		R
Q7BC55	Putative glycosyltransferase		10	25.1	1.07E-45	Unknown		
Q0PB95	Putative GMC oxidoreductase subunit	Cj0415	25	51.7	2.05E-165	Unknown (signal)	Sec	C
Q0PC61	Putative iron-sulfur protein	Cj0074c	34	63.7	0	Unknown		H
Q0P8J4	Putative methyltransferase	Cj1420c	26	85.2	0	Unknown		R
Q0P9W6	Putative pyruvate carboxylase B subunit	pycB	37	65.3	0	Unknown		IG
Q0P8B1	Putative regulatory protein	Cj1507c	19	67.3	1.43E-188	Unknown		X
Q0PB72	Putative succinate dehydrogenase iron-sulfur protein	sdhB	28	76	0	Unknown		C
Q0PB71	Putative succinate dehydrogenase subunit C	sdhC	20	77.9	0	Unknown (signal)	Sec	C
Q0P7V5	Putative uncharacterized protein	Cj1674	9	34.6	1.34E-48	Unknown		X
Q0P8T3	Putative uncharacterized protein	Cj1324	40	80.2	0	Unknown		X
Q0PC64	Putative uncharacterized protein	Cj0069	30	66.2	1.48E-284	Unknown		X
Q0PCB0	Putative uncharacterized protein	Cj0015c	20	52	1.74E-117	Unknown		X
Q0P9L5	Pyruvate carboxylase A subunit	pycA	40	79	0	Unknown		IG
Q9PHY1	Succinyl-CoA ligase [ADP-forming] subunit beta	sucC	34	74.4	0	Unknown		IQ
Q0PBP1	Molybdopterin containing oxidoreductase	Cj0264c	54	67.4	0	Unknown (signal)	Tat	H
Q0PCC0	Molybdopterin containing oxidoreductase	Cj0005c	13	31.6	1.64E-42	Unknown (signal)	Tat	H
Q0P972	Putative ubiquinol-cytochrome C reductase cytochrome C subunit	petC	27	59.6	0	Unknown (signal)	TM	C

^aPosterior error probability indicating how the observed peptide spectrum match (PSM) is incorrect.

^bSignal peptide motifs of the vesicular proteins were predicted using PRED-TAT. Sec, a signal peptide for the general secretory pathway; Tat, a signal peptide for the twin-arginine translocation pathway; TM, transmembrane domain.

^cClusters of orthologous groups of proteins. E, amino acid transport and metabolism; G, carbohydrate transport and metabolism; N, cell motility; M, cell wall/membrane/envelope biogenesis; H, coenzyme transport and metabolism; C, energy production and conversion; R, general function prediction only; P, inorganic ion transport and metabolism; U, intracellular trafficking, secretion and vesicular transport; I, lipid transport and metabolism; F, nucleotide transport and metabolism; O, posttranslational modification, protein turnover, chaperones; L, replication, recombination and repair; Q, secondary metabolites biosynthesis, transport and catabolism; T, signal transduction mechanisms; K, transcription; J, translation, ribosomal structure and biogenesis; X, poorly characterized.

^dKnown functions related to bacterial virulence or survival.

The list contains the vesicular proteins that were observed at least twice among triplicate experiments. N-glycoproteins, which were reported in literature [9,10], were written in bold and italics.

Table S2. Functional annotation terms by DAVID functional annotations tools for genes identified in the OMVs of *C. jejuni*.

Category	Term	Count	% ^a	P-value ^b	List Total	Fold Enrichment	Benjamini ^c
INTERPRO	IPR020003:ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain, active site	3	2.24	0.002493	122	33.93	0.244547
INTERPRO	IPR004489:Succinate dehydrogenase/fumarate reductase iron-sulphur protein	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR000793:ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR018951:Fumarase C, C-terminal	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR003953:Fumarate reductase/succinate dehydrogenase flavoprotein, N-terminal	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR006058:2Fe-2S ferredoxin, iron-sulphur binding site	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR004100:ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal	2	1.49	0.057607	122	33.93	0.691546
INTERPRO	IPR004112:Fumarate reductase/succinate dehydrogenase flavoprotein, C-terminal	2	1.49	0.057607	122	33.93	0.691546
SP_PIR_KEYWORDS	2Fe-2S	2	1.49	0.063953	134	30.37	0.306668
SP_PIR_KEYWORDS	dna-directed rna polymerase	3	2.24	0.004512	134	27.34	0.042052
PIR_SUPERFAMILY	PIRSF001274:F-type ATP synthase, alpha/beta subunits/V-type ATPase, subunit B	3	2.24	0.003989	79	26.58	0.318667
PIR_SUPERFAMILY	PIRSF000171:succinate dehydrogenase, flavoprotein subunit (SDHA/APRA/LASPO)	2	1.49	0.072923	79	26.58	0.973603
PIR_SUPERFAMILY	PIRSF500078:succinate dehydrogenase, flavoprotein subunit	2	1.49	0.072923	79	26.58	0.973603
SP_PIR_KEYWORDS	Secreted	4	2.99	3.32E-04	134	26.03	0.007331
INTERPRO	IPR000583:Glutamine amidotransferase, class-II	3	2.24	0.004891	122	25.45	0.281425
INTERPRO	IPR017932:Glutamine amidotransferase, type II	3	2.24	0.004891	122	25.45	0.281425
INTERPRO	IPR000194:ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain	3	2.24	0.004891	122	25.45	0.281425
SP_PIR_KEYWORDS	tricarboxylic acid cycle	3	2.24	0.006672	134	22.78	0.054125
SP_PIR_KEYWORDS	periplasm	2	1.49	0.084355	134	22.78	0.352157
INTERPRO	IPR002545:CheW-like protein	2	1.49	0.085163	122	22.62	0.811086

GOTERM_CC_FAT	GO:0045281~succinate dehydrogenase complex	3	2.24	0.005448	38	22.24	0.050574
GOTERM_CC_FAT	GO:0045282~plasma membrane succinate dehydrogenase complex	3	2.24	0.005448	38	22.24	0.050574
GOTERM_BP_FAT	GO:0017038~protein import	2	1.49	0.088	96	21.99	0.630219
SP_PIR_KEYWORDS	metalloprotein	4	2.99	7.71E-04	134	20.25	0.014555
GOTERM_MF_FAT	GO:0000104~succinate dehydrogenase activity	5	3.73	3.80E-05	97	20.04	0.008654
GOTERM_CC_FAT	GO:0045273~respiratory chain complex II	5	3.73	4.41E-05	38	18.53	0.002509
GOTERM_CC_FAT	GO:0045274~plasma membrane respiratory chain complex II	5	3.73	4.41E-05	38	18.53	0.002509
SP_PIR_KEYWORDS	pyruvate	4	2.99	0.001084	134	18.22	0.017877
SP_PIR_KEYWORDS	Molybdenum	3	2.24	0.012103	134	17.08	0.090868
INTERPRO	IPR003031:Delta crystallin	3	2.24	0.011767	122	16.97	0.485627
GOTERM_CC_FAT	GO:0070470~plasma membrane respiratory chain	5	3.73	9.96E-05	38	15.88	0.002835
INTERPRO	IPR010810:Flagellin hook, IN motif	4	2.99	0.001799	122	15.08	0.454843
GOTERM_BP_FAT	GO:0046356~acetyl-CoA catabolic process	10	7.46	2.08E-09	96	14.66	1.12E-07
GOTERM_BP_FAT	GO:0006099~tricarboxylic acid cycle	10	7.46	2.08E-09	96	14.66	1.12E-07
INTERPRO	IPR000362:Fumarate lyase	3	2.24	0.01616	122	14.54	0.49657
GOTERM_CC_FAT	GO:0070469~respiratory chain	5	3.73	1.93E-04	38	13.90	0.00366
GOTERM_BP_FAT	GO:0009060~aerobic respiration	12	8.96	4.83E-11	96	13.89	6.52E-09
GOTERM_BP_FAT	GO:0006084~acetyl-CoA metabolic process	10	7.46	9.38E-09	96	12.94	4.22E-07
GOTERM_BP_FAT	GO:0051187~cofactor catabolic process	10	7.46	9.38E-09	96	12.94	4.22E-07
GOTERM_BP_FAT	GO:0009109~coenzyme catabolic process	10	7.46	9.38E-09	96	12.94	4.22E-07
INTERPRO	IPR006657:Molydopterin dinucleotide-binding region	3	2.24	0.021139	122	12.73	0.550675
GOTERM_CC_FAT	GO:0005576~extracellular region	4	2.99	0.0024	38	12.71	0.027026
SP_PIR_KEYWORDS	electron transport	3	2.24	0.022779	134	12.43	0.148962
KEGG_PATHWAY	cju03020:RNA polymerase	3	2.24	0.020621	77	12.05	0.165218
KEGG_PATHWAY	cjr03020:RNA polymerase	3	2.24	0.020621	77	12.05	0.165218
KEGG_PATHWAY	cjj03020:RNA polymerase	3	2.24	0.020621	77	12.05	0.165218
KEGG_PATHWAY	cje03020:RNA polymerase	3	2.24	0.020621	77	12.05	0.165218
GOTERM_MF_FAT	GO:0046961~proton-transporting ATPase activity, rotational mechanism	3	2.24	0.022559	97	12.03	0.525962

INTERPRO	IPR009010:Aspartate decarboxylase-like fold	3	2.24	0.026664	122	11.31	0.597792
GOTERM_CC_FAT	GO:0009898~internal side of plasma membrane	3	2.24	0.025052	38	11.12	0.134643
GOTERM_CC_FAT	GO:0009424~flagellin-based flagellum hook	3	2.24	0.025052	38	11.12	0.134643
KEGG_PATHWAY	cje00020:Citrate cycle (TCA cycle)	13	9.70	1.04E-10	77	10.44	2.15E-08
GOTERM_MF_FAT	GO:0019829~cation-transporting ATPase activity	3	2.24	0.030745	97	10.31	0.448946
GOTERM_MF_FAT	GO:0016840~carbon-nitrogen lyase activity	3	2.24	0.030745	97	10.31	0.448946
INTERPRO	IPR013816:ATP-grasp fold, subdomain 2	3	2.24	0.032702	122	10.18	0.638903
KEGG_PATHWAY	cju00020:Citrate cycle (TCA cycle)	12	8.96	1.17E-09	77	10.15	1.21E-07
KEGG_PATHWAY	cjr00650:Butanoate metabolism	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cjj00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cje00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cju00650:Butanoate metabolism	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cjr00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cje00650:Butanoate metabolism	5	3.73	7.64E-04	77	10.04	0.011294
KEGG_PATHWAY	cjj00650:Butanoate metabolism	5	3.73	7.64E-04	77	10.04	0.011294
GOTERM_BP_FAT	GO:0045333~cellular respiration	14	10.45	1.44E-10	96	9.93	9.75E-09
KEGG_PATHWAY	cjj00020:Citrate cycle (TCA cycle)	11	8.21	1.25E-08	77	9.82	8.70E-07
KEGG_PATHWAY	cjr00020:Citrate cycle (TCA cycle)	11	8.21	1.25E-08	77	9.82	8.70E-07
SP_PIR_KEYWORDS	bacterial flagellum	3	2.24	0.036121	134	9.76	0.207849
KEGG_PATHWAY	cju00910:Nitrogen metabolism	6	4.48	1.52E-04	77	9.64	0.003947
GOTERM_CC_FAT	GO:0033178~proton-transporting two-sector ATPase complex, catalytic domain	3	2.24	0.034112	38	9.53	0.164603
GOTERM_BP_FAT	GO:0009061~anaerobic respiration	3	2.24	0.036305	96	9.42	0.444191
KEGG_PATHWAY	cje00910:Nitrogen metabolism	7	5.22	3.05E-05	77	9.37	0.001055
INTERPRO	IPR006656:Molybdopterin oxidoreductase	3	2.24	0.039217	122	9.25	0.645513
INTERPRO	IPR003088:Cytochrome c, class I	3	2.24	0.039217	122	9.25	0.645513
INTERPRO	IPR017909:Twin arginine translocation signal, Tat	5	3.73	0.001915	122	8.93	0.275992
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	15	11.19	1.40E-10	96	8.91	1.26E-08
KEGG_PATHWAY	cjd00020:Citrate cycle (TCA cycle)	8	5.97	1.09E-05	77	8.57	5.66E-04
SP_PIR_KEYWORDS	Chaperone	3	2.24	0.046308	134	8.54	0.24922

INTERPRO	IPR006655:Molybdopterin oxidoreductase, prokaryotic, conserved site	3	2.24	0.046176	122	8.48	0.654287
INTERPRO	IPR006311:Twin-arginine translocation pathway signal	5	3.73	0.002826	122	8.08	0.212134
KEGG_PATHWAY	cjr00910:Nitrogen metabolism	6	4.48	4.33E-04	77	8.03	0.008164
KEGG_PATHWAY	cjj00910:Nitrogen metabolism	6	4.48	4.33E-04	77	8.03	0.008164
GOTERM_MF_FAT	GO:0009374~biotin binding	3	2.24	0.049958	97	8.02	0.519777
GOTERM_MF_FAT	GO:0016885~ligase activity, forming carbon-carbon bonds	3	2.24	0.049958	97	8.02	0.519777
GOTERM_MF_FAT	GO:0033293~monocarboxylic acid binding	3	2.24	0.049958	97	8.02	0.519777
INTERPRO	IPR012285:Fumarate reductase, C-terminal	4	2.99	0.012274	122	7.98	0.44819
GOTERM_BP_FAT	GO:0022610~biological adhesion	5	3.73	0.002722	96	7.85	0.070957
GOTERM_BP_FAT	GO:0007155~cell adhesion	5	3.73	0.002722	96	7.85	0.070957
INTERPRO	IPR001492:Flagellin, N-terminal	3	2.24	0.05355	122	7.83	0.686269
KEGG_PATHWAY	cje00250:Alanine, aspartate and glutamate metabolism	8	5.97	2.97E-05	77	7.56	0.001236
KEGG_PATHWAY	cju00250:Alanine, aspartate and glutamate metabolism	8	5.97	4.63E-05	77	7.14	0.001374
KEGG_PATHWAY	cjd00910:Nitrogen metabolism	4	2.99	0.014316	77	7.14	0.139263
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	25	18.66	4.06E-15	96	6.96	1.11E-12
KEGG_PATHWAY	cjr00250:Alanine, aspartate and glutamate metabolism	7	5.22	3.18E-04	77	6.61	0.007324
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	3	2.24	0.072372	97	6.56	0.615479
SP_PIR_KEYWORDS	oxidoreductase	25	18.66	2.89E-13	134	6.43	1.92E-11
GOTERM_BP_FAT	GO:0030031~cell projection assembly	6	4.48	0.001904	96	6.28	0.055574
GOTERM_BP_FAT	GO:0009296~flagellum assembly	6	4.48	0.001904	96	6.28	0.055574
KEGG_PATHWAY	cjj00250:Alanine, aspartate and glutamate metabolism	7	5.22	4.54E-04	77	6.25	0.007237
GOTERM_MF_FAT	GO:0003899~DNA-directed RNA polymerase activity	3	2.24	0.08458	97	6.01	0.655313
GOTERM_MF_FAT	GO:0034062~RNA polymerase activity	3	2.24	0.08458	97	6.01	0.655313
SP_PIR_KEYWORDS	nadp	3	2.24	0.088529	134	5.94	0.356159
SP_PIR_KEYWORDS	signal	37	27.61	9.37E-19	134	5.91	1.25E-16
SP_PIR_KEYWORDS	iron-sulfur	4	2.99	0.029131	134	5.88	0.17848
GOTERM_CC_FAT	GO:0044459~plasma membrane part	8	5.97	2.11E-04	38	5.74	0.003001

SP_PIR_KEYWORDS	iron	7	5.22	0.001269	134	5.69	0.018583
SP_PIR_KEYWORDS	flagellum	7	5.22	0.001269	134	5.69	0.018583
KEGG_PATHWAY	cjd00250:Alanine, aspartate and glutamate metabolism	6	4.48	0.002653	77	5.67	0.03394
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	3	2.24	0.097358	97	5.55	0.623691
GOTERM_BP_FAT	GO:0030030~cell projection organization	7	5.22	0.001195	96	5.50	0.039563
GOTERM_BP_FAT	GO:0043064~flagellum organization	7	5.22	0.001195	96	5.50	0.039563
GOTERM_BP_FAT	GO:0009082~branched chain family amino acid biosynthetic process	3	2.24	0.098654	96	5.50	0.619789
GOTERM_MF_FAT	GO:0030151~molybdenum ion binding	4	2.99	0.035169	97	5.34	0.443239
SP_PIR_KEYWORDS	magnesium	5	3.73	0.013777	134	5.30	0.097426
INTERPRO	IPR009056:Cytochrome c, monohaem	4	2.99	0.04276	122	5.03	0.650742
SP_PIR_KEYWORDS	metal-binding	16	11.94	1.19E-06	134	4.67	5.26E-05
SP_PIR_KEYWORDS	protein biosynthesis	4	2.99	0.059126	134	4.44	0.29702
KEGG_PATHWAY	cjr02020:Two-component system	8	5.97	0.001307	77	4.43	0.017971
GOTERM_BP_FAT	GO:0022900~electron transport chain	4	2.99	0.057763	96	4.40	0.518192
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	4	2.99	0.057763	96	4.40	0.518192
SP_PIR_KEYWORDS	ligase	8	5.97	0.002233	134	4.34	0.029301
COG_ONTOLOGY	Energy production and conversion	7	5.22	0.00358	32	4.32	0.062519
KEGG_PATHWAY	cje00620:Pyruvate metabolism	5	3.73	0.025184	77	4.23	0.191208
SP_PIR_KEYWORDS	nucleotidyltransferase	4	2.99	0.070131	134	4.14	0.320792
KEGG_PATHWAY	cju00190:Oxidative phosphorylation	10	7.46	3.66E-04	77	4.12	0.007583
SP_PIR_KEYWORDS	lyase	8	5.97	0.003308	134	4.05	0.036057
KEGG_PATHWAY	cjj00190:Oxidative phosphorylation	10	7.46	4.49E-04	77	4.02	0.007752
KEGG_PATHWAY	cje00190:Oxidative phosphorylation	10	7.46	4.49E-04	77	4.02	0.007752
KEGG_PATHWAY	cjr00190:Oxidative phosphorylation	10	7.46	4.49E-04	77	4.02	0.007752
SP_PIR_KEYWORDS	Isomerase	8	5.97	0.003742	134	3.96	0.037628
GOTERM_CC_FAT	GO:0044461~flagellin-based flagellum part	6	4.48	0.013416	38	3.92	0.091751
GOTERM_CC_FAT	GO:0044460~flagellum part	6	4.48	0.013416	38	3.92	0.091751
GOTERM_CC_FAT	GO:0044463~cell projection part	6	4.48	0.013416	38	3.92	0.091751
SP_PIR_KEYWORDS	Protease	4	2.99	0.081989	134	3.88	0.354414

INTERPRO	IPR004089:Chemotaxis methyl-accepting receptor, signalling	5	3.73	0.038344	122	3.86	0.666466
KEGG_PATHWAY	cje02020:Two-component system	8	5.97	0.003507	77	3.78	0.042076
KEGG_PATHWAY	cjd02020:Two-component system	6	4.48	0.018226	77	3.71	0.159628
SP_PIR_KEYWORDS	cytoplasm	18	13.43	5.33E-06	134	3.69	1.77E-04
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	4	2.99	0.090237	96	3.66	0.625472
GOTERM_MF_FAT	GO:0015078~hydrogen ion transmembrane transporter activity	6	4.48	0.022312	97	3.61	0.577345
KEGG_PATHWAY	cje02030:Bacterial chemotaxis	4	2.99	0.093471	77	3.57	0.493576
GOTERM_MF_FAT	GO:0016836~hydro-lyase activity	4	2.99	0.096849	97	3.56	0.637319
GOTERM_CC_FAT	GO:0009288~flagellin-based flagellum	7	5.22	0.009664	38	3.54	0.076028
KEGG_PATHWAY	cje02040:Flagellar assembly	7	5.22	0.011079	77	3.51	0.11482
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	5	3.73	0.052703	96	3.44	0.518538
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	5	3.73	0.057976	96	3.33	0.503967
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	6	4.48	0.032375	97	3.28	0.439949
KEGG_PATHWAY	cju00230:Purine metabolism	8	5.97	0.009007	77	3.21	0.099276
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	7	5.22	0.018826	96	3.21	0.326134
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	7	5.22	0.018826	96	3.21	0.326134
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	7	5.22	0.020692	96	3.14	0.331858
KEGG_PATHWAY	cjd00190:Oxidative phosphorylation	7	5.22	0.019561	77	3.12	0.163602
SMART	SM00283:MA	5	3.73	0.05938	23	3.12	0.706045
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	7	5.22	0.022681	96	3.08	0.338316
GOTERM_BP_FAT	GO:0055114~oxidation reduction	28	20.90	6.00E-08	96	3.06	2.31E-06
GOTERM_BP_FAT	GO:0006928~cell motion	8	5.97	0.013701	96	3.03	0.266847
GOTERM_BP_FAT	GO:0001539~ciliary or flagellar motility	8	5.97	0.013701	96	3.03	0.266847
GOTERM_BP_FAT	GO:0051674~localization of cell	8	5.97	0.013701	96	3.03	0.266847
GOTERM_BP_FAT	GO:0048870~cell motility	8	5.97	0.013701	96	3.03	0.266847
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	7	5.22	0.024796	96	3.02	0.345385
KEGG_PATHWAY	cjj02020:Two-component system	6	4.48	0.041821	77	3.01	0.289488
KEGG_PATHWAY	cju02020:Two-component system	6	4.48	0.041821	77	3.01	0.289488

KEGG_PATHWAY	cje00230:Purine metabolism	8	5.97	0.015169	77	2.92	0.14049
KEGG_PATHWAY	cjr02040:Flagellar assembly	6	4.48	0.046988	77	2.92	0.30059
SP_PIR_KEYWORDS	cell inner membrane	5	3.73	0.092927	134	2.88	0.36065
GOTERM_MF_FAT	GO:0009055~electron carrier activity	18	13.43	1.37E-04	97	2.78	0.015612
GOTERM_MF_FAT	GO:0015077~monovalent inorganic cation transmembrane transporter activity	6	4.48	0.059978	97	2.78	0.565335
GOTERM_MF_FAT	GO:0051539~4 iron, 4 sulfur cluster binding	8	5.97	0.024692	97	2.71	0.47068
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	11	8.21	0.006543	96	2.66	0.14882
GOTERM_CC_FAT	GO:0019861~flagellum	8	5.97	0.021706	38	2.66	0.129758
GOTERM_CC_FAT	GO:0042995~cell projection	8	5.97	0.021706	38	2.66	0.129758
KEGG_PATHWAY	cjr00230:Purine metabolism	7	5.22	0.043463	77	2.62	0.289878
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	7	5.22	0.04655	96	2.61	0.492063
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	7	5.22	0.04655	96	2.61	0.492063
SP_PIR_KEYWORDS	nucleotide-binding	19	14.18	2.90E-04	134	2.60	0.007679
GOTERM_MF_FAT	GO:0050662~coenzyme binding	11	8.21	0.008488	97	2.57	0.323223
KEGG_PATHWAY	cjj00230:Purine metabolism	7	5.22	0.04793	77	2.56	0.296922
GOTERM_BP_FAT	GO:0042330~taxis	7	5.22	0.057055	96	2.48	0.530141
GOTERM_BP_FAT	GO:0007626~locomotory behavior	7	5.22	0.057055	96	2.48	0.530141
GOTERM_BP_FAT	GO:0006935~chemotaxis	7	5.22	0.057055	96	2.48	0.530141
GOTERM_BP_FAT	GO:0007610~behavior	7	5.22	0.057055	96	2.48	0.530141
SP_PIR_KEYWORDS	atp-binding	16	11.94	0.002964	134	2.34	0.035251
INTERPRO	IPR016040:NAD(P)-binding domain	7	5.22	0.085359	122	2.26	0.794549
GOTERM_MF_FAT	GO:0051540~metal cluster binding	12	8.96	0.023844	97	2.09	0.498819
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	12	8.96	0.023844	97	2.09	0.498819
SP_PIR_KEYWORDS	transferase	21	15.67	0.005239	134	1.92	0.04551
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	9	6.72	0.091974	96	1.90	0.618949
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	9	6.72	0.095998	96	1.88	0.622126
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	13	9.70	0.0366	96	1.88	0.428386
GOTERM_MF_FAT	GO:0048037~cofactor binding	14	10.45	0.030184	97	1.87	0.47168
GOTERM_MF_FAT	GO:0005506~iron ion binding	11	8.21	0.090888	97	1.74	0.66413
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	19	14.18	0.025382	97	1.68	0.444977

GOTERM_MF_FAT	GO:0046872~metal ion binding	27	20.15	0.005656	97	1.67	0.351395
GOTERM_MF_FAT	GO:0043169~cation binding	27	20.15	0.005656	97	1.67	0.351395
GOTERM_MF_FAT	GO:0043167~ion binding	27	20.15	0.005859	97	1.67	0.285674
UP_SEQ_FEATURE	signal peptide	37	27.61	0.002436	74	1.49	0.187221
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	19	14.18	0.084115	96	1.46	0.627857
GOTERM_MF_FAT	GO:0000166~nucleotide binding	31	23.13	0.044781	97	1.37	0.503131
GOTERM_MF_FAT	GO:0001882~nucleoside binding	25	18.66	0.094656	97	1.34	0.644803
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	27	20.15	0.092177	97	1.32	0.651653

^aPercent of proteins in the term with the particular annotation.

^bProbability of enrichment level occurring in randomly constructed term.

^cProbability of enrichment level occurring in randomly constructed term adjusted for multiple hypothesis testing using the Benjamini-Hochberg method.

Table S3. Functional annotation clustering by DAVID annotations tools for genes identified in the OMVs of *C. jejuni*.

Cluster 1		Enrichment Score^a: 10.00					
Category	Term	Count	%^b	P-value^c	Genes	Benjamini^d	
GOTERM_BP_FAT	GO:0009060~aerobic respiration	12	8.96	4.83E-11	Q0PB71, Q0PA55, O69294, Q0P972, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q0P970, Q9PHY1, Q0PAY5, Q0PBA0	6.52E-09	
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	15	11.19	1.40E-10	Q0PA55, Q0P8A7, Q0P7U8, Q0P972, Q0PC50, Q0P970, Q9PHY1, Q0PAY5, Q0PBA1, Q0PBA0, Q0PB71, Q9PPL8, O69294, Q0PB73, Q0PB72	1.26E-08	
GOTERM_BP_FAT	GO:0045333~cellular respiration	14	10.45	1.44E-10	Q0PA55, Q0P8A7, Q0P7U8, Q0P972, Q0PC50, Q0P970, Q9PHY1, Q0PAY5, Q0PBA1, Q0PBA0, Q0PB71, O69294, Q0PB73, Q0PB72	9.75E-09	
Cluster 2		Enrichment Score: 7.51					
GOTERM_BP_FAT	GO:0009060~aerobic respiration	12	8.96	4.83E-11	Q0PB71, Q0PA55, O69294, Q0P972, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q0P970, Q9PHY1, Q0PAY5, Q0PBA0	6.52E-09	
KEGG_PATHWAY	cje00020:Citrate cycle (TCA cycle)	13	9.70	1.04E-10	Q0PAY0, Q0PA55, Q0P7U8, Q0P9W6, Q9PHY1, Q0PBA1, Q0PAY5, Q0PBA0, Q0PB71, O69294, Q0PB73, Q0PB72, Q0P9L5	2.15E-08	
KEGG_PATHWAY	cju00020:Citrate cycle (TCA cycle)	12	8.96	1.17E-09	Q0PB71, Q0PAY0, Q0PA55, O69294, Q0P7U8, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA1, Q0P9L5, Q0PBA0	1.21E-07	
GOTERM_BP_FAT	GO:0006099~tricarboxylic acid cycle	10	7.46	2.08E-09	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA0	1.12E-07	
GOTERM_BP_FAT	GO:0046356~acetyl-CoA catabolic process	10	7.46	2.08E-09	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA0	1.12E-07	
GOTERM_BP_FAT	GO:0006084~acetyl-CoA metabolic process	10	7.46	9.38E-09	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA0	4.22E-07	
GOTERM_BP_FAT	GO:0009109~coenzyme catabolic process	10	7.46	9.38E-09	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA0	4.22E-07	
GOTERM_BP_FAT	GO:0051187~cofactor catabolic process	10	7.46	9.38E-09	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA0	4.22E-07	
KEGG_PATHWAY	cjj00020:Citrate cycle (TCA cycle)	11	8.21	1.25E-08	Q0PB71, Q0PAY0, Q0PA55, O69294, Q0P7U8, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA1, Q0PBA0	8.70E-07	
KEGG_PATHWAY	cjr00020:Citrate cycle (TCA cycle)	11	8.21	1.25E-08	Q0PB71, Q0PAY0, Q0PA55, O69294, Q0P7U8, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q0PBA1, Q0PBA0	8.70E-07	
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	11	8.21	0.006543	Q0PB71, Q0PA55, O69294, Q0P7U8, Q0PC50, Q0PB73, Q0PB72, Q9PHY1, Q0PAY5, Q9PPD9, Q0PBA0	0.14882	
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	13	9.70	0.0366	Q0P9Q7, Q0PA55, Q9PP70, Q0P7U8, Q0PC50, Q9PHY1, Q9PPD9, Q0PAY5, Q0PBA0, Q0PB71, O69294, Q0PB73, Q0PB72	0.428386	
Cluster 3		Enrichment Score: 3.76					
Category	Term	Count	%	PValue	Genes	Benjamini	
KEGG_PATHWAY	cje00910:Nitrogen metabolism	7	5.22	3.05E-05	Q0PAI0, Q0P8Y6, Q0PCB6, Q0PC50, Q0PCB8, Q0P8Q2,	0.001055	

					Q9PPD9	
KEGG_PATHWAY	cju00910:Nitrogen metabolism	6	4.48	1.52E-04	Q0PAI0, Q0PCB6, Q0PC50, Q0PCB8, Q0P8Q2, Q9PPD9	0.003947
KEGG_PATHWAY	cjr00910:Nitrogen metabolism	6	4.48	4.33E-04	Q0PAI0, Q0PCB6, Q0PC50, Q0PCB8, Q0P8Q2, Q9PPD9	0.008164
KEGG_PATHWAY	cjj00910:Nitrogen metabolism	6	4.48	4.33E-04	Q0PAI0, Q0PCB6, Q0PC50, Q0PCB8, Q0P8Q2, Q9PPD9	0.008164
Cluster 4	Enrichment Score: 3.65					
KEGG_PATHWAY	cje00250:Alanine, aspartate and glutamate metabolism	8	5.97	2.97E-05	Q0PCA2, Q0PAI0, Q0PCB6, Q0PBU3, Q0PC50, Q9PHK7, Q9PMT4, Q0PCB8	0.001236
KEGG_PATHWAY	cju00250:Alanine, aspartate and glutamate metabolism	8	5.97	4.63E-05	Q0PCA2, Q0PAI0, Q0PCB6, Q0PBU3, Q0PC50, Q9PHK7, Q9PMT4, Q0PCB8	0.001374
KEGG_PATHWAY	cjr00250:Alanine, aspartate and glutamate metabolism	7	5.22	3.18E-04	Q0PAI0, Q0PCB6, Q0PBU3, Q0PC50, Q9PHK7, Q9PMT4, Q0PCB8	0.007324
KEGG_PATHWAY	cjj00250:Alanine, aspartate and glutamate metabolism	7	5.22	4.54E-04	Q0PAI0, Q0PCB6, Q0PBU3, Q0PC50, Q9PHK7, Q9PMT4, Q0PCB8	0.007237
KEGG_PATHWAY	cjd00250:Alanine, aspartate and glutamate metabolism	6	4.48	0.002653	Q0PAI0, Q0PCB6, Q0PBU3, Q0PC50, Q9PHK7, Q9PMT4	0.03394
Cluster 5	Enrichment Score: 3.55					
GOTERM_MF_FAT	GO:000104~succinate dehydrogenase activity	5	3.73	3.80E-05	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.008654
GOTERM_CC_FAT	GO:0045274~plasma membrane respiratory chain complex II	5	3.73	4.41E-05	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.002509
GOTERM_CC_FAT	GO:0045273~respiratory chain complex II	5	3.73	4.41E-05	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.002509
GOTERM_CC_FAT	GO:0070470~plasma membrane respiratory chain	5	3.73	9.96E-05	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.002835
GOTERM_CC_FAT	GO:0070469~respiratory chain	5	3.73	1.93E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.00366
KEGG_PATHWAY	cjr00650:Butanoate metabolism	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cju00650:Butanoate metabolism	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cjr00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cjj00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cjj00650:Butanoate metabolism	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cje00650:Butanoate metabolism	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
KEGG_PATHWAY	cje00632:Benzoate degradation via CoA ligation	5	3.73	7.64E-04	Q0PB71, Q0PB73, Q0PB72, Q0PBA1, Q0PBA0	0.011294
Cluster 6	Enrichment Score: 3.37					
KEGG_PATHWAY	cju00190:Oxidative phosphorylation	10	7.46	3.66E-04	Q0PC30, Q0PB71, Q9PJ21, Q0P972, Q0PB73, Q0P8D0, Q0PB72, Q0P970, Q0PBA1, Q0PBA0	0.007583
KEGG_PATHWAY	cjj00190:Oxidative phosphorylation	10	7.46	4.49E-04	Q0PC30, Q0PB71, Q9PJ21, Q0P972, Q0PB73, Q0P8D0, Q0PB72, Q0P970, Q0PBA1, Q0PBA0	0.007752

KEGG_PATHWAY	cje00190:Oxidative phosphorylation	10	7.46	4.49E-04	Q0PC30, Q0PB71, Q9PJ21, Q0P972, Q0PB73, Q0P8D0, Q0PB72, Q0P970, Q0PBA1, Q0PBA0	0.007752
KEGG_PATHWAY	cjr00190:Oxidative phosphorylation	10	7.46	4.49E-04	Q0PC30, Q0PB71, Q9PJ21, Q0P972, Q0PB73, Q0P8D0, Q0PB72, Q0P970, Q0PBA1, Q0PBA0	0.007752
Cluster 7	Enrichment Score: 2.51					
SP_PIR_KEYWORD S	Secreted	4	2.99	3.32E-04	P42448, Q9PHW6, P56963, P56964	0.007331
GOTERM_CC_FAT	GO:0005576~extracellular region	4	2.99	0.0024	P42448, Q9PHW6, P56963, P56964	0.027026
SP_PIR_KEYWORD S	bacterial flagellum	3	2.24	0.036121	Q9PHW6, P56963, P56964	0.207849
Cluster 8	Enrichment Score: 2.24					
GOTERM_MF_FAT	GO:0046872~metal ion binding	27	20.1 5	0.005656	Q0P9Q7, Q0P8A7, Q9PP15, Q0P972, Q0P8E1, Q0P8A3, Q0P970, Q9PM68, Q0PAY5, Q0PBB8, P42448, Q9PP04, Q0PC61, Q0PBP1, Q0P8D0, Q9PHY1, Q9PIM0, Q0P9V7, Q9PPD9, Q9PM78, Q0PBA0, Q0PCC0, Q0P9J4, Q0P891, Q0PC89, Q0P8Z0, Q0PBF1	0.351395
GOTERM_MF_FAT	GO:0043169~cation binding	27	20.1 5	0.005656	Q0P9Q7, Q0P8A7, Q9PP15, Q0P972, Q0P8E1, Q0P8A3, Q0P970, Q9PM68, Q0PAY5, Q0PBB8, P42448, Q9PP04, Q0PC61, Q0PBP1, Q0P8D0, Q9PHY1, Q9PIM0, Q0P9V7, Q9PPD9, Q9PM78, Q0PBA0, Q0PCC0, Q0P9J4, Q0P891, Q0PC89, Q0P8Z0, Q0PBF1	0.351395
GOTERM_MF_FAT	GO:0043167~ion binding	27	20.1 5	0.005859	Q0P9Q7, Q0P8A7, Q9PP15, Q0P972, Q0P8E1, Q0P8A3, Q0P970, Q9PM68, Q0PAY5, Q0PBB8, P42448, Q9PP04, Q0PC61, Q0PBP1, Q0P8D0, Q9PHY1, Q9PIM0, Q0P9V7, Q9PPD9, Q9PM78, Q0PBA0, Q0PCC0, Q0P9J4, Q0P891, Q0PC89, Q0P8Z0, Q0PBF1	0.285674
Cluster 9	Enrichment Score: 1.97					
KEGG_PATHWAY	cjr02020:Two-component system	8	5.97	0.001307	Q0PAI0, Q0PBM2, Q0PBA1, Q0PBM1, Q0PBA0, Q0P928, P56963, P56964	0.017971
KEGG_PATHWAY	cje02020:Two-component system	8	5.97	0.003507	Q0PAI0, Q0PBM2, Q0PBA1, Q0PBM1, Q0PBA0, Q0P928, P56963, P56964	0.042076
KEGG_PATHWAY	cjd02020:Two-component system	6	4.48	0.018226	Q0PAI0, Q0PBM2, Q0PBA1, Q0PBM1, Q0PBA0, Q0P928	0.159628
KEGG_PATHWAY	cju02020:Two-component system	6	4.48	0.041821	Q0PAI0, Q0PBM2, Q0PBA1, Q0PBM1, Q0PBA0, Q0P928	0.289488
KEGG_PATHWAY	cjj02020:Two-component system	6	4.48	0.041821	Q0PAI0, Q0PBM2, Q0PBA1, Q0PBM1, Q0PBA0, Q0P928	0.289488
Cluster 10	Enrichment Score: 1.92					
GOTERM_BP_FAT	GO:0030030~cell projection organization	7	5.22	0.001195	Q0P7Q2, O52908, Q0PBU4, Q9PHW6, P56963, Q0P8E9, P56964	0.039563
GOTERM_BP_FAT	GO:0043064~flagellum organization	7	5.22	0.001195	Q0P7Q2, O52908, Q0PBU4, Q9PHW6, P56963, Q0P8E9, P56964	0.039563
SP_PIR_KEYWORD S	flagellum	7	5.22	0.001269	Q0P7Q2, O52908, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.018583

GOTERM_BP_FAT	GO:0030031~cell projection assembly	6	4.48	0.001904	O52908, Q0PBU4, Q9PHW6, P56963, Q0P8E9, P56964	0.055574
GOTERM_BP_FAT	GO:0009296~flagellum assembly	6	4.48	0.001904	O52908, Q0PBU4, Q9PHW6, P56963, Q0P8E9, P56964	0.055574
GOTERM_CC_FAT	GO:0009288~flagellin-based flagellum	7	5.22	0.009664	Q0P7Q2, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.076028
KEGG_PATHWAY	cje02040:Flagellar assembly	7	5.22	0.011079	Q0P7Q2, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.11482
GOTERM_CC_FAT	GO:0044463~cell projection part	6	4.48	0.013416	Q0P7Q2, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.091751
GOTERM_CC_FAT	GO:0044461~flagellin-based flagellum part	6	4.48	0.013416	Q0P7Q2, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.091751
GOTERM_CC_FAT	GO:0044460~flagellum part	6	4.48	0.013416	Q0P7Q2, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.091751
GOTERM_BP_FAT	GO:0001539~ciliary or flagellar motility	8	5.97	0.013701	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.266847
GOTERM_BP_FAT	GO:0051674~localization of cell	8	5.97	0.013701	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.266847
GOTERM_BP_FAT	GO:0048870~cell motility	8	5.97	0.013701	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.266847
GOTERM_BP_FAT	GO:0006928~cell motion	8	5.97	0.013701	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.266847
GOTERM_CC_FAT	GO:0019861~flagellum	8	5.97	0.021706	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.129758
GOTERM_CC_FAT	GO:0042995~cell projection	8	5.97	0.021706	Q0P7Q2, O52908, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q0P8E9, P56964	0.129758
KEGG_PATHWAY	cjr02040:Flagellar assembly	6	4.48	0.046988	Q0P7Q2, Q0PBU4, Q9PHW6, P56963, Q0P8E9, P56964	0.30059
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	9	6.72	0.130606	Q0P7Q2, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q9PNB3, Q0P8E9, P56964, Q9PI34	0.485625
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	9	6.72	0.130606	Q0P7Q2, Q0PBU4, Q0PA11, Q9PHW6, P56963, Q9PNB3, Q0P8E9, P56964, Q9PI34	0.485625
GOTERM_MF_FAT	GO:0005198~structural molecule activity	8	5.97	0.158134	Q0P7Q2, Q0PA11, Q9PHW6, P56963, Q9PNB3, Q0P8E9, P56964, Q9PI34	0.780435
Cluster 11		Enrichment Score: 1.64				
KEGG_PATHWAY	cju00230:Purine metabolism	8	5.97	0.009007	Q9PM80, Q9PI30, Q9PP15, Q0PCA2, Q0P9J4, Q46124, Q0PBU3, Q0PBB8	0.099276
KEGG_PATHWAY	cje00230:Purine metabolism	8	5.97	0.015169	Q9PM80, Q9PI30, Q9PP15, Q0PCA2, Q0P9J4, Q46124, Q0PBU3, Q0PBB8	0.14049
KEGG_PATHWAY	cjr00230:Purine metabolism	7	5.22	0.043463	Q9PM80, Q9PI30, Q9PP15, Q0P9J4, Q46124, Q0PBU3, Q0PBB8	0.289878
KEGG_PATHWAY	cjj00230:Purine metabolism	7	5.22	0.04793	Q9PM80, Q9PI30, Q9PP15, Q0P9J4, Q46124, Q0PBU3, Q0PBB8	0.296922
Cluster 12		Enrichment Score: 1.56				
SP_PIR_KEYWORD S	Molybdenum	3	2.24	0.012103	Q0P8A7, Q0PBP1, Q9PPD9	0.090868
INTERPRO	IPR006657:Molydopterin dinucleotide-binding region	3	2.24	0.021139	Q0P8A7, Q0PBP1, Q9PPD9	0.550675

INTERPRO	IPR009010:Aspartate decarboxylase-like fold	3	2.24	0.026664	Q0P8A7, Q0PBP1, Q9PPD9	0.597792
GOTERM_MF_FAT	GO:0030151~molybdenum ion binding	4	2.99	0.035169	Q0P8A7, Q0PBP1, Q9PPD9, Q0PCC0	0.443239
INTERPRO	IPR006656:Molybdopterin oxidoreductase	3	2.24	0.039217	Q0P8A7, Q0PBP1, Q9PPD9	0.645513
INTERPRO	IPR006655:Molybdopterin oxidoreductase, prokaryotic, conserved site	3	2.24	0.046176	Q0P8A7, Q0PBP1, Q9PPD9	0.654287

Cluster 13 **Enrichment Score: 1.29**

GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	7	5.22	0.018826	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.326134
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	7	5.22	0.018826	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.326134
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	7	5.22	0.020692	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.331858
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	7	5.22	0.022681	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.338316
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	7	5.22	0.04655	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.492063
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	7	5.22	0.04655	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.492063
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	7	5.22	0.123516	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.694723
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	7	5.22	0.230529	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.837033
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	7	5.22	0.230529	Q0PC30, Q9PP15, Q0PCA2, Q9PJ21, Q0P9J4, Q0PBU3, Q0PBU4	0.837033

Cluster 14 **Enrichment Score: 1.24**

GOTERM_BP_FAT	GO:0007626~locomotory behavior	7	5.22	0.057055	Q0P8B2, Q0PCA6, Q0PBM2, Q0P864, Q0PBM1, Q0PB65, Q0P9E4	0.530141
GOTERM_BP_FAT	GO:0042330~taxis	7	5.22	0.057055	Q0P8B2, Q0PCA6, Q0PBM2, Q0P864, Q0PBM1, Q0PB65, Q0P9E4	0.530141
GOTERM_BP_FAT	GO:0006935~chemotaxis	7	5.22	0.057055	Q0P8B2, Q0PCA6, Q0PBM2, Q0P864, Q0PBM1, Q0PB65, Q0P9E4	0.530141
GOTERM_BP_FAT	GO:0007610~behavior	7	5.22	0.057055	Q0P8B2, Q0PCA6, Q0PBM2, Q0P864, Q0PBM1, Q0PB65, Q0P9E4	0.530141

Cluster 15 **Enrichment Score: 1.14**

GOTERM_MF_FAT	GO:0015078~hydrogen ion transmembrane transporter activity	6	4.48	0.022312	Q0PC30, Q9PJ21, Q0P972, Q0P8D0, Q0P970, Q0PBU4	0.577345
GOTERM_MF_FAT	GO:0015077~monovalent inorganic cation transmembrane transporter activity	6	4.48	0.059978	Q0PC30, Q9PJ21, Q0P972, Q0P8D0, Q0P970, Q0PBU4	0.565335

GOTERM_MF_FAT	GO:0022890~inorganic cation transmembrane transporter activity	6	4.48	0.278148	Q0PC30, Q9PJ21, Q0P972, Q0P8D0, Q0P970, Q0PBU4	0.909979
Cluster 16		Enrichment Score: 1.11				
SP_PIR_KEYWORD S	nucleotide-binding	19	14.18	2.90E-04	Q0PC30, O52908, Q9PN98, Q9PP15, Q9PJ21, O69289, Q9PHK7, Q9PIM0, Q9PHY1, Q0P9V7, Q9PI16, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, O69303, Q9PPL8, Q0PA10, Q0PBU4	0.007679
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	27	20.15	0.092177	Q0PC30, Q9PP15, Q0PBM9, O69289, Q0PBM2, Q9PI16, Q9PHX1, Q0P7V6, O52908, Q9PN98, Q0P8W7, Q9PJ21, Q0P9F8, Q9PHY1, Q9PHK7, Q9PIM0, Q0P9V7, Q0PB95, Q0PA12, Q9PM78, Q0PBA1, O69303, Q9PPL8, Q0PCB6, Q0PA10, Q0PBU4, Q0P9L5	0.651653
GOTERM_MF_FAT	GO:0001882~nucleoside binding	25	18.66	0.094656	Q0PC30, Q9PP15, Q0PBM9, Q0PBM2, O69289, Q9PHX1, Q0P7V6, Q9PN98, Q0P8W7, Q9PJ21, Q0P9F8, Q9PHY1, Q9PHK7, Q9PIM0, Q0P9V7, Q0PB95, Q9PM78, Q0PBA1, Q0PA12, Q9PPL8, Q0PCB6, Q46124, Q0PA10, Q0PBU4, Q0P9L5	0.644803
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	24	17.91	0.141594	Q0PC30, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q0PB95, Q9PM78, Q0PA12, Q0PBA1, Q9PHX1, Q0P7V6, Q9PPL8, Q0PCB6, Q0PA10, Q0PBU4, Q0P9L5	0.753042
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	24	17.91	0.141594	Q0PC30, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q0PB95, Q9PM78, Q0PA12, Q0PBA1, Q9PHX1, Q0P7V6, Q9PPL8, Q0PCB6, Q0PA10, Q0PBU4, Q0P9L5	0.753042
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	24	17.91	0.176649	Q0PC30, O52908, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q9PI16, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, O69303, Q9PPL8, Q0PA10, Q0PBU4, Q0P9L5	0.807675
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	24	17.91	0.176649	Q0PC30, O52908, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q9PI16, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, O69303, Q9PPL8, Q0PA10, Q0PBU4, Q0P9L5	0.807675
GOTERM_MF_FAT	GO:0005524~ATP binding	21	15.67	0.25701	Q0PC30, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, Q9PPL8, Q0PA10, Q0PBU4, Q0P9L5	0.896445
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	21	15.67	0.25701	Q0PC30, Q9PN98, Q9PP15, Q0P8W7, Q0PBM9, Q9PJ21, Q0P9F8, O69289, Q9PHY1, Q0PBM2, Q9PHK7, Q9PIM0, Q0P9V7, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, Q9PPL8, Q0PA10, Q0PBU4, Q0P9L5	0.896445
Cluster 17		Enrichment Score: 1.06				
GOTERM_MF_FAT	GO:0033293~monocarboxylic acid binding	3	2.24	0.049958	Q0P8W7, Q0P9W6, Q0P9L5	0.519777
GOTERM_MF_FAT	GO:0016885~ligase activity, forming	3	2.24	0.049958	Q0P8W7, Q0P9W6, Q0P9L5	0.519777

	carbon-carbon bonds						
GOTERM_MF_FAT	GO:0009374~biotin binding	3	2.24	0.049958	Q0P8W7, Q0P9W6, Q0P9L5		0.519777
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	3	2.24	0.468561	Q0P8W7, Q0P9W6, Q0P9L5		0.98207
Cluster 18	Enrichment Score: 0.93						
SP_PIR_KEYWORD S	dna-directed rna polymerase	3	2.24	0.004512	Q9PM80, Q9PI30, Q46124		0.042052
KEGG_PATHWAY	cjr03020:RNA polymerase	3	2.24	0.020621	Q9PM80, Q9PI30, Q46124		0.165218
KEGG_PATHWAY	cju03020:RNA polymerase	3	2.24	0.020621	Q9PM80, Q9PI30, Q46124		0.165218
KEGG_PATHWAY	cje03020:RNA polymerase	3	2.24	0.020621	Q9PM80, Q9PI30, Q46124		0.165218
KEGG_PATHWAY	cjj03020:RNA polymerase	3	2.24	0.020621	Q9PM80, Q9PI30, Q46124		0.165218
SP_PIR_KEYWORD S	nucleotidyltransferase	4	2.99	0.070131	Q9PM80, Q9PI30, Q46124, Q9PM68		0.331651
GOTERM_MF_FAT	GO:0003899~DNA-directed RNA polymerase activity	3	2.24	0.08458	Q9PM80, Q9PI30, Q46124		0.655313
GOTERM_MF_FAT	GO:0034062~RNA polymerase activity	3	2.24	0.08458	Q9PM80, Q9PI30, Q46124		0.655313
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	3	2.24	0.113285	Q9PM80, Q9PI30, Q46124		0.673525
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	3	2.24	0.176257	Q9PM80, Q9PI30, Q46124		0.775925
SP_PIR_KEYWORD S	Transcription	3	2.24	0.273122	Q9PM80, Q9PI30, Q46124		0.712876
KEGG_PATHWAY	cju00240:Pyrimidine metabolism	3	2.24	0.596528	Q9PM80, Q9PI30, Q46124		0.992099
KEGG_PATHWAY	cje00240:Pyrimidine metabolism	3	2.24	0.630269	Q9PM80, Q9PI30, Q46124		0.994338
KEGG_PATHWAY	cjj00240:Pyrimidine metabolism	3	2.24	0.630269	Q9PM80, Q9PI30, Q46124		0.994338
KEGG_PATHWAY	cjr00240:Pyrimidine metabolism	3	2.24	0.630269	Q9PM80, Q9PI30, Q46124		0.994338
GOTERM_MF_FAT	GO:0016779~nucleotidyltransferase activity	4	2.99	0.6316	Q9PM80, Q9PI30, Q46124, Q9PM68		0.99671
GOTERM_BP_FAT	GO:0006350~transcription	3	2.24	0.678502	Q9PM80, Q9PI30, Q46124		0.996914
Cluster 19	Enrichment Score: 0.91						
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	9	6.72	0.091974	Q0PAI0, Q0PCB6, Q9PHK7, Q0PBN6, P24531, Q9PM78, Q59291, Q0PCB8, Q9PHN5		0.63283
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	9	6.72	0.095998	Q0PAI0, Q0PCB6, Q9PHK7, Q0PBN6, P24531, Q9PM78, Q59291, Q0PCB8, Q9PHN5		0.635504
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	10	7.46	0.158662	Q0PAI0, Q0PCB6, Q9PHK7, Q9PIH0, Q0PBN6, P24531, Q9PM78, Q59291, Q0PCB8, Q9PHN5		0.756712
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	10	7.46	0.168724	Q0PAI0, Q0PCB6, Q9PHK7, Q9PIH0, Q0PBN6, P24531, Q9PM78, Q59291, Q0PCB8, Q9PHN5		0.769495
Cluster 20	Enrichment Score: 0.89						
INTERPRO	IPR003088:Cytochrome c, class I	3	2.24	0.039217	Q0P972, Q0PC89, Q0P8D0		0.645513

INTERPRO	IPR009056:Cytochrome c, monohaem	4	2.99	0.04276	Q0P972, Q0PC89, Q0P8D0, Q0PBF1	0.650742
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	4	2.99	0.407647	Q0P972, Q0PC89, Q0P8D0, Q0PBF1	0.967489
GOTERM_MF_FAT	GO:0020037~heme binding	4	2.99	0.407647	Q0P972, Q0PC89, Q0P8D0, Q0PBF1	0.967489
Cluster 21	Enrichment Score: 0.78					
KEGG_PATHWAY	cjj00630:Glyoxylate and dicarboxylate metabolism	3	2.24	0.165138	Q0P8A7, Q0PA55, Q0P7U8	0.702108
KEGG_PATHWAY	cjr00630:Glyoxylate and dicarboxylate metabolism	3	2.24	0.165138	Q0P8A7, Q0PA55, Q0P7U8	0.702108
KEGG_PATHWAY	cje00630:Glyoxylate and dicarboxylate metabolism	3	2.24	0.165138	Q0P8A7, Q0PA55, Q0P7U8	0.702108
Cluster 22	Enrichment Score: 0.77					
GOTERM_CC_FAT	GO:0009424~flagellin-based flagellum hook	3	2.24	0.025052	Q0P7Q2, Q9PHW6, Q0P8E9	0.134643
KEGG_PATHWAY	cju02040:Flagellar assembly	4	2.99	0.313381	Q0P7Q2, Q0PBU4, Q9PHW6, Q0P8E9	0.879197
KEGG_PATHWAY	cjd02040:Flagellar assembly	4	2.99	0.313381	Q0P7Q2, Q0PBU4, Q9PHW6, Q0P8E9	0.879197
KEGG_PATHWAY	cjj02040:Flagellar assembly	4	2.99	0.330769	Q0P7Q2, Q0PBU4, Q9PHW6, Q0P8E9	0.889017
Cluster 23	Enrichment Score: 0.71					
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	4	2.99	0.090237	Q0P804, Q0P8L1, P42448, Q0PBB8	0.639899
GOTERM_BP_FAT	GO:0006096~glycolysis	3	2.24	0.128434	Q0P8L1, P42448, Q0PBB8	0.69798
KEGG_PATHWAY	cju00010:Glycolysis / Gluconeogenesis	3	2.24	0.165138	Q0P8L1, P42448, Q0PBB8	0.702108
KEGG_PATHWAY	cje00010:Glycolysis / Gluconeogenesis	3	2.24	0.187746	Q0P8L1, P42448, Q0PBB8	0.730359
KEGG_PATHWAY	cjd00010:Glycolysis / Gluconeogenesis	3	2.24	0.187746	Q0P8L1, P42448, Q0PBB8	0.730359
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	3	2.24	0.209491	Q0P8L1, P42448, Q0PBB8	0.820115
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	3	2.24	0.209491	Q0P8L1, P42448, Q0PBB8	0.820115
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	3	2.24	0.209491	Q0P8L1, P42448, Q0PBB8	0.820115
KEGG_PATHWAY	cjj00010:Glycolysis / Gluconeogenesis	3	2.24	0.210756	Q0P8L1, P42448, Q0PBB8	0.764942
KEGG_PATHWAY	cjr00010:Glycolysis / Gluconeogenesis	3	2.24	0.210756	Q0P8L1, P42448, Q0PBB8	0.764942
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	3	2.24	0.22635	Q0P8L1, P42448, Q0PBB8	0.838534
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	3	2.24	0.243307	Q0P8L1, P42448, Q0PBB8	0.847697
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	3	2.24	0.328194	Q0P8L1, P42448, Q0PBB8	0.908069
Cluster 24	Enrichment Score: 0.70					
KEGG_PATHWAY	cju00260:Glycine, serine and threonine metabolism	3	2.24	0.187746	Q0P804, P24531, Q59291	0.730359

KEGG_PATHWAY	cjd00260:Glycine, serine and threonine metabolism	3	2.24	0.187746	Q0P804, P24531, Q59291	0.730359
KEGG_PATHWAY	cjj00260:Glycine, serine and threonine metabolism	3	2.24	0.210756	Q0P804, P24531, Q59291	0.764942
KEGG_PATHWAY	cje00260:Glycine, serine and threonine metabolism	3	2.24	0.210756	Q0P804, P24531, Q59291	0.764942
KEGG_PATHWAY	cjr00260:Glycine, serine and threonine metabolism	3	2.24	0.210756	Q0P804, P24531, Q59291	0.764942
Cluster 25 Enrichment Score: 0.68						
INTERPRO	IPR001509:NAD-dependent epimerase/dehydratase	3	2.24	0.114423	Q0P8I7, Q0P9C3, Q0P9A5	0.897208
GOTERM_MF_FAT	GO:0016857~racemase and epimerase activity, acting on carbohydrates and derivatives	3	2.24	0.228408	Q0P8I7, Q0P9C3, Q0P9A5	0.880052
GOTERM_MF_FAT	GO:0016854~racemase and epimerase activity	3	2.24	0.351992	Q0P8I7, Q0P9C3, Q0P9A5	0.946181
Cluster 26 Enrichment Score: 0.65						
INTERPRO	IPR020003:ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain, active site	3	2.24	0.002493	Q0PC30, Q9PJ21, Q0PBU4	0.244547
PIR_SUPERFAMILY	PIRSF001274:F-type ATP synthase, alpha/beta subunits/V-type ATPase, subunit B	3	2.24	0.003989	Q0PC30, Q9PJ21, Q0PBU4	0.318667
INTERPRO	IPR000194:ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain	3	2.24	0.004891	Q0PC30, Q9PJ21, Q0PBU4	0.281425
GOTERM_MF_FAT	GO:0046961~proton-transporting ATPase activity, rotational mechanism	3	2.24	0.022559	Q0PC30, Q9PJ21, Q0PBU4	0.525962
GOTERM_MF_FAT	GO:0019829~cation-transporting ATPase activity	3	2.24	0.030745	Q0PC30, Q9PJ21, Q0PBU4	0.448946
GOTERM_CC_FAT	GO:0033178~proton-transporting two-sector ATPase complex, catalytic domain	3	2.24	0.034112	Q0PC30, Q9PJ21, Q0PBU4	0.164603
GOTERM_CC_FAT	GO:0016469~proton-transporting two-sector ATPase complex	3	2.24	0.168133	Q0PC30, Q9PJ21, Q0PBU4	0.527387
GOTERM_BP_FAT	GO:0015986~ATP synthesis coupled proton transport	3	2.24	0.176257	Q0PC30, Q9PJ21, Q0PBU4	0.775925
GOTERM_BP_FAT	GO:0015985~energy coupled proton transport, down electrochemical gradient	3	2.24	0.176257	Q0PC30, Q9PJ21, Q0PBU4	0.775925
GOTERM_BP_FAT	GO:0015992~proton transport	3	2.24	0.192777	Q0PC30, Q9PJ21, Q0PBU4	0.799344
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	3	2.24	0.243307	Q0PC30, Q9PJ21, Q0PBU4	0.847697
GOTERM_BP_FAT	GO:0006818~hydrogen transport	3	2.24	0.294358	Q0PC30, Q9PJ21, Q0PBU4	0.887991

GOTERM_MF_FAT	GO:0042625~ATPase activity, coupled to transmembrane movement of ions	3	2.24	0.321395	Q0PC30, Q9PJ21, Q0PBU4	0.937625
GOTERM_BP_FAT	GO:0034220~ion transmembrane transport	3	2.24	0.328194	Q0PC30, Q9PJ21, Q0PBU4	0.908069
GOTERM_BP_FAT	GO:0006754~ATP biosynthetic process	3	2.24	0.378086	Q0PC30, Q9PJ21, Q0PBU4	0.93468
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	3	2.24	0.378086	Q0PC30, Q9PJ21, Q0PBU4	0.93468
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009145~purine nucleoside triphosphate biosynthetic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009201~ribonucleoside triphosphate biosynthetic process	3	2.24	0.394395	Q0PC30, Q9PJ21, Q0PBU4	0.940459
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	3	2.24	0.426424	Q0PC30, Q9PJ21, Q0PBU4	0.953249
GOTERM_BP_FAT	GO:0009142~nucleoside triphosphate biosynthetic process	3	2.24	0.426424	Q0PC30, Q9PJ21, Q0PBU4	0.953249
GOTERM_BP_FAT	GO:0055085~transmembrane transport	4	2.99	0.429865	Q0PC30, Q9PJ21, Q0PBU4, Q0P9V7	0.951885
GOTERM_MF_FAT	GO:0015399~primary active transmembrane transporter activity	5	3.73	0.714266	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4, Q0P9V7	0.999085
GOTERM_MF_FAT	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity	5	3.73	0.714266	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4, Q0P9V7	0.999085
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	5	3.73	0.768226	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4, Q0P7V6	0.999584
GOTERM_MF_FAT	GO:0042626~ATPase activity, coupled to transmembrane movement of substances	4	2.99	0.807281	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4	0.99981
GOTERM_MF_FAT	GO:0043492~ATPase activity, coupled to movement of substances	4	2.99	0.807281	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4	0.99981
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	3	2.24	0.839515	Q0PC30, Q9PJ21, Q0PBU4	0.999894
GOTERM_MF_FAT	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	4	2.99	0.850661	Q0PC30, Q0P8H0, Q9PJ21, Q0PBU4	0.999937
GOTERM_BP_FAT	GO:0006811~ion transport	4	2.99	0.98937	Q0PC30, P80672, Q9PJ21, Q0PBU4	1
GOTERM_BP_FAT	GO:0006812~cation transport	3	2.24	0.990622	Q0PC30, Q9PJ21, Q0PBU4	1
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Cluster 27	Enrichment Score: 0.65					
KEGG_PATHWAY	cjd00270:Cysteine and methionine	3	2.24	0.210756	Q0P804, Q0P9F8, Q59291	0.764942

	metabolism						
KEGG_PATHWAY	cju00270:Cysteine and methionine metabolism	3	2.24	0.210756	Q0P804, Q0P9F8, Q59291		0.764942
KEGG_PATHWAY	cje00270:Cysteine and methionine metabolism	3	2.24	0.234037	Q0P804, Q0P9F8, Q59291		0.794948
KEGG_PATHWAY	cjr00270:Cysteine and methionine metabolism	3	2.24	0.234037	Q0P804, Q0P9F8, Q59291		0.794948
KEGG_PATHWAY	cjj00270:Cysteine and methionine metabolism	3	2.24	0.234037	Q0P804, Q0P9F8, Q59291		0.794948
Cluster 28	Enrichment Score: 0.52						
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	6	4.48	0.290064	O52908, Q9PJ14, Q46108, Q0PBU4, Q9PIM0, Q0P9V7		0.889452
GOTERM_BP_FAT	GO:0015031~protein transport	6	4.48	0.290064	O52908, Q9PJ14, Q46108, Q0PBU4, Q9PIM0, Q0P9V7		0.889452
GOTERM_BP_FAT	GO:0008104~protein localization	6	4.48	0.335295	O52908, Q9PJ14, Q46108, Q0PBU4, Q9PIM0, Q0P9V7		0.909028
Cluster 29	Enrichment Score: 0.48						
SP_PIR_KEYWORD S	gtp-binding	3	2.24	0.109094	O52908, Q9PI16, O69303		0.422301
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	3	2.24	0.215577	O52908, Q9PI16, O69303		0.999967
GOTERM_MF_FAT	GO:0005525~GTP binding	3	2.24	0.559916	O52908, Q9PI16, O69303		0.991929
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	3	2.24	0.559916	O52908, Q9PI16, O69303		0.991929
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	3	2.24	0.559916	O52908, Q9PI16, O69303		0.991929
Cluster 30	Enrichment Score: 0.43						
GOTERM_BP_FAT	GO:0016310~phosphorylation	5	3.73	0.27298	Q0PC30, Q9PPL8, Q9PJ21, Q0PBM2, Q0PBU4		0.877473
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	5	3.73	0.439421	Q0PC30, Q9PPL8, Q9PJ21, Q0PBM2, Q0PBU4		0.953307
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	5	3.73	0.439421	Q0PC30, Q9PPL8, Q9PJ21, Q0PBM2, Q0PBU4		0.953307
Cluster 31	Enrichment Score: 0.30						
SP_PIR_KEYWORD S	Protease	4	2.99	0.081989	Q9PP04, Q9PIM0, Q0PB04, Q0P928		0.365616
GOTERM_MF_FAT	GO:0008233~peptidase activity	4	2.99	0.867084	Q9PP04, Q9PIM0, Q0PB04, Q0P928		0.999957
GOTERM_MF_FAT	GO:0070011~peptidase activity, acting on L-amino acid peptides	3	2.24	0.913876	Q9PP04, Q0PB04, Q0P928		0.999994
GOTERM_BP_FAT	GO:0006508~proteolysis	3	2.24	0.968477	Q9PP04, Q0PB04, Q0P928		1
Cluster 32	Enrichment Score: 0.14						
GOTERM_CC_FAT	GO:0044462~external encapsulating structure part	4	2.99	0.438078	P80672, Q0P8D9, Q0P928, Q0P9S0		0.871702

GOTERM_CC_FAT	GO:0031975~envelope	4	2.99	0.856157	P80672, Q0P8D9, Q0P928, Q0P9S0	0.997024
GOTERM_CC_FAT	GO:0030313~cell envelope	4	2.99	0.856157	P80672, Q0P8D9, Q0P928, Q0P9S0	0.997024
GOTERM_CC_FAT	GO:0030312~external encapsulating structure	4	2.99	0.874132	P80672, Q0P8D9, Q0P928, Q0P9S0	0.997279
Cluster 33	Enrichment Score: 0.05					
GOTERM_BP_FAT	GO:0000160~two-component signal transduction system (phosphorelay)	3	2.24	0.856183	Q0PBM2, Q0PBM1, Q0P9E4	0.999927
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	4	2.99	0.907676	Q0PBM2, Q9PIM0, Q0PBM1, Q0P9E4	0.99999
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	4	2.99	0.907676	Q0PBM2, Q9PIM0, Q0PBM1, Q0P9E4	0.99999
GOTERM_BP_FAT	GO:0045449~regulation of transcription	4	2.99	0.927248	Q0PBM2, Q9PIM0, Q0PBM1, Q0P9E4	0.999995

^aGeometric mean of all the enrichment P-values of each annotation term in the group.

^bPercent of proteins in the cluster with the particular annotation.

^cProbability of enrichment level occurring in randomly constructed cluster.

^dProbability of enrichment level occurring in randomly constructed cluster adjusted for multiple hypothesis testing using the Benjamini-Hochberg method.

Table S4. Annotated gene terms not clustered by DAVID annotations tools for genes identified in the OMVs of *C. jejuni*.

Category	Term	Count	% ^a	P-value ^b	Genes	Benjamini ^c
SP_PIR_KEYWORDS	signal	37	27.61	9.37E-19	Q0PC23, Q0P8X7, Q0P9Q4, Q0P972, Q0P8A3, Q9PJ14, Q0P970, Q0PC08, Q0PBB4, Q0P9S0, Q0PCA6, Q0PCA8, Q0PAS1, Q0PB16, Q0P8H0, Q0P9N4, Q0P986, P80672, Q0P9N3, Q0P8B2, Q0PBP1, Q0P8D9, Q0P864, Q9PPD9, Q0PBW4, Q0PCC0, Q0P9T5, Q0PBA4, Q0PC89, Q0PB73, Q0PC48, Q0P8Q2, Q0PB04, Q0P928, Q0PC44, Q0PC45, Q0PBF1	1.25E-16
UP_SEQ_FEATURE	signal peptide	37	27.61	0.002436	Q0PC23, Q0P8X7, Q0P9Q4, Q0P972, Q0P8A3, Q9PJ14, Q0P970, Q0PC08, Q0PBB4, Q0P9S0, Q0PCA6, Q0PCA8, Q0PAS1, Q0PB16, Q0P8H0, Q0P9N4, Q0P986, P80672, Q0P9N3, Q0P8B2, Q0PBP1, Q0P8D9, Q0P864, Q9PPD9, Q0PBW4, Q0PCC0, Q0P9T5, Q0PBA4, Q0PC89, Q0PB73, Q0PC48, Q0P8Q2, Q0PB04, Q0P928, Q0PC44, Q0PC45, Q0PBF1	0.187221
GOTERM_MF_FAT	GO:000166~nucleotide binding	31	23.13	0.044781	Q0PC30, Q9PP15, Q0PBM9, O69289, Q0PBM2, Q9PI16, Q0PAY5, Q9PHX1, Q0P7V6, Q0P9A5, Q59291, O52908, Q9PN98, Q0P8W7, Q9PJ21, Q0P9F8, Q9PHY1, Q9PHK7, Q9PIM0, Q0P9V7, Q0PB95, Q9PM78, Q0PBA1, Q0PA12, Q0P8L1, O69303, Q9PPL8, Q0PCB6, Q0PA10, Q0PBU4, Q0P9L5	0.503131
GOTERM_BP_FAT	GO:0055114~oxidation reduction	28	20.90	6.00E-08	Q0PAY0, Q0P8A7, Q0P972, Q0P8E1, Q0P970, Q0PAY5, Q9PHN5, Q0PCA8, Q59291, Q0P8Y6, Q0P8Y9, Q0PBP1, Q0P8D0, Q0PBA1, Q9PPD9, Q0PBA0, Q0P8L1, Q0PCC0, Q0PB71, Q0PCB6, Q0P9J4, Q0P891, Q0PB73, Q0PB72, Q0PCB8, Q0P8Q2, Q0P8Z0, Q0PBF1	2.31E-06
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	25	18.66	4.06E-15	Q0PC30, Q0P8A7, Q0P972, Q0PC50, Q0P970, Q0PAY5, Q0PBB8, O69294, Q0PCA8, P42448, Q0PA55, Q9PJ21, Q0P7U8, Q0P8Y9, Q9PHY1, Q0PBA1, Q9PPD9, Q0PBA0, Q0P8L1, Q0PB71, Q9PPL8, Q0PB73, Q0PB72, Q0PBU4, Q0P8Z0	1.11E-12
SP_PIR_KEYWORDS	oxidoreductase	25	18.66	2.89E-13	Q0PAY0, Q0P8A7, Q0P972, Q0P970, Q0PAY5, Q9PHN5, Q0PCA8, Q59291, Q0PBP1, Q0P8D0, Q0P8Y9, Q0PBA1, Q9PPD9, Q0PBA0, Q0P8L1, Q0PB71, Q0PCB6, Q0P9J4, Q0P891, Q0PB73, Q0PB72, Q0P8Q2, Q0PCB8, Q0P8Z0, Q0PBF1	1.92E-11
SP_PIR_KEYWORDS	transferase	21	15.67	0.005239	Q9PI30, Q9PP15, Q0P7U8, Q0PBU3, Q0P9F8, Q9PMT4, Q0PBM2, Q0PBN6, Q9PM68, Q0PAX5, Q9PM78, Q0PBM1, Q0P9C5, Q0PBB8, Q9PM80, Q9PPL8, Q0P8J4, Q46124, Q9PIH0, P24531, Q7BC55	0.04551
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	19	14.18	0.025382	Q9PP04, Q0P8A7, Q0PC61, Q0P8E1, Q0P972, Q0P8A3, Q0P8D0, Q0P970, Q0PBP1, Q9PHY1, Q9PIM0, Q0P9V7, Q9PPD9, Q0PBA0, Q0PCC0, Q0P891, Q0PC89,	0.444977

GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	19	14.18	0.084115	Q0P8Z0, Q0PBF1 Q0PC30, Q0P9Q7, Q9PP70, Q9PP15, Q9PJ21, Q0PBU3, Q0PBN6, Q9PHK7, Q9PM78, Q9PPD9, Q9PHN5, Q0PCA2, Q0PAI0, Q0PCB6, Q0P9J4, Q0PBU4, P24531, Q0PCB8, Q59291	0.627857
SP_PIR_KEYWORDS	cytoplasm	18	13.43	5.33E-06	Q9PP04, Q9PP70, Q9PP15, O69289, Q9PMT4, Q9PHK7, Q0P9V7, Q9P116, Q9PM78, Q9PHX1, O69303, Q0P7V6, Q9PPL8, O69294, Q0P891, Q9PIH0, P24531, P42448	1.77E-04
GOTERM_MF_FAT	GO:0009055~electron carrier activity	18	13.43	1.37E-04	Q0PAY0, Q0P8A7, Q0PC61, Q0P8E1, Q0P972, Q0P8D0, Q0P970, Q0PBP1, Q9PPD9, Q0PBA1, Q0PBA0, Q0PCC0, Q0PB71, Q0PCB6, Q0PB73, Q0PC89, Q0PB72, Q0PBF1	0.015612
SP_PIR_KEYWORDS	metal-binding	16	11.94	1.19E-06	Q9PP04, Q0P8A7, Q9PP15, Q0P970, Q0PBP1, Q9PIM0, Q9PHY1, Q0P9V7, Q9PM68, Q9PM78, Q9PPD9, Q0P9J4, Q0P891, Q0PB72, P42448, Q0P8Z0	5.26E-05
SP_PIR_KEYWORDS	atp-binding	16	11.94	0.002964	Q0PC30, Q9PN98, Q9PP15, Q9PJ21, O69289, Q9PHK7, Q9PIM0, Q9PHY1, Q0P9V7, Q9PM78, Q0PA12, Q9PHX1, Q0P7V6, Q9PPL8, Q0PA10, Q0PBU4	0.035251
GOTERM_MF_FAT	GO:0048037~cofactor binding	14	10.45	0.030184	Q9PP70, Q0P8E1, Q0P8Y9, Q0PB95, Q0PBA1, Q0PAY5, Q0P8L1, Q9PHN5, Q0P9A5, Q0P9C3, Q0PCB6, Q0P8I7, P24531, Q59291	0.47168
GOTERM_CC_FAT	GO:0005886~plasma membrane	13	9.70	0.781243	O52908, Q0PC30, P80672, Q9PJ21, Q0P8D9, Q0P9V7, Q0PA12, Q0PBA1, Q0PBA0, Q0PB71, Q0PB73, Q0PB72, Q0PCA8	0.991874
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	12	8.96	0.023844	Q0P804, Q0P8A7, Q0PA55, Q0PC61, Q0PCB6, Q0P8E1, Q0PB72, Q0PBP1, Q0P8Y9, Q0P970, Q9PPD9, Q0PBA0	0.498819
GOTERM_MF_FAT	GO:0051540~metal cluster binding	12	8.96	0.023844	Q0P804, Q0P8A7, Q0PA55, Q0PC61, Q0PCB6, Q0P8E1, Q0PB72, Q0PBP1, Q0P8Y9, Q0P970, Q9PPD9, Q0PBA0	0.498819
GOTERM_MF_FAT	GO:0050662~coenzyme binding	11	8.21	0.008488	Q0PCB6, Q0P8E1, Q0P8I7, Q0PB95, Q0PAY5, Q59291, Q0PBA1, Q0P8L1, Q9PHN5, Q0P9C3, Q0P9A5	0.323223
GOTERM_MF_FAT	GO:0005506~iron ion binding	11	8.21	0.090888	Q0P8A7, Q0PC61, Q0P8E1, Q0P972, Q0PC89, Q0P891, Q0P8D0, Q0P970, Q9PPD9, Q0PBA0, Q0PBF1	0.66413
SP_PIR_KEYWORDS	transport	9	6.72	0.188638	Q0PC30, O52908, P80672, Q9PJ21, Q9PJ14, Q0P970, Q0P9V7, Q0PCA8, Q9PPD9	0.592149
GOTERM_CC_FAT	GO:0016021~integral to membrane	9	6.72	1	P80672, Q0P8B2, Q0PCA6, Q0P8D9, Q0PCA8, Q0PA12, Q0PBN7, Q0PC49, Q0PBA6	1
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	9	6.72	1	P80672, Q0P8B2, Q0PCA6, Q0P8D9, Q0PCA8, Q0PA12, Q0PBN7, Q0PC49, Q0PBA6	1
KEGG_PATHWAY	cjd00020:Citrate cycle (TCA cycle)	8	5.97	1.09E-05	Q0PAY0, Q0PA55, O69294, Q0P7U8, Q9PHY1, Q0PAY5, Q0PBA1, Q0PBA0	5.66E-04
GOTERM_CC_FAT	GO:0044459~plasma membrane part	8	5.97	2.11E-04	O52908, Q0PB71, Q0PB73, Q0PB72, Q0P9V7, Q0PBA1, Q0PA12, Q0PBA0	0.003001
SP_PIR_KEYWORDS	ligase	8	5.97	0.002233	Q9PN98, Q0P8W7, Q0PAI0, Q0P9W6, Q9PHK7, Q9PHY1, Q0P9L5, Q9PHX1	0.029301
SP_PIR_KEYWORDS	lyase	8	5.97	0.003308	Q0P804, Q0P9Q7, Q0PA55, Q0PCA2, O69294, Q0PC50,	0.036057

					Q9PM68, P42448	
SP_PIR_KEYWORDS	Isomerase	8	5.97	0.003742	Q9PP70, Q46108, Q9PMT4, Q0P8I7, Q9PHN5, Q0PAS1, Q0P9C3, Q0P9A5	0.037628
GOTERM_MF_FAT	GO:0051539~4 iron, 4 sulfur cluster binding	8	5.97	0.024692	Q0P804, Q0P8A7, Q0PA55, Q0PC61, Q0P8E1, Q0PBP1, Q0P8Y9, Q9PPD9	0.47068
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	8	5.97	0.223265	Q0PC30, Q9PJ21, Q9PHK7, Q9PHY1, Q9PIM0, Q0P9V7, Q0PA12, Q0P7V6	0.999222
SP_PIR_KEYWORDS	cell membrane	8	5.97	0.467813	Q0PC30, O52908, P80672, Q9PJ21, Q0P8D9, Q0P9V7, Q0PCA8, Q0PA12	0.902734
SP_PIR_KEYWORDS	membrane	8	5.97	0.478504	Q0PC30, O52908, P80672, Q9PJ21, Q0P8D9, Q0P9V7, Q0PCA8, Q0PA12	0.903698
GOTERM_MF_FAT	GO:0016887~ATPase activity	8	5.97	0.749899	Q0PC30, Q0P8H0, Q9PJ21, Q0PA10, O69289, Q0PBU4, Q9PIM0, Q0P7V6	0.999477
SP_PIR_KEYWORDS	iron	7	5.22	0.001269	Q0P8A7, Q0P891, Q0P8D0, Q0PB72, Q0P970, Q9PPD9, Q0P8Z0	0.018583
COG_ONTOLOGY	Energy production and conversion	7	5.22	0.00358	Q0PB71, Q0PC61, Q0P9W6, Q0P972, Q0PC89, Q0PB72, Q0PAY5	0.062519
KEGG_PATHWAY	cjd00190:Oxidative phosphorylation	7	5.22	0.019561	Q0PC30, Q9PJ21, Q0P972, Q0P8D0, Q0P970, Q0PBA1, Q0PBA0	0.163602
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	7	5.22	0.024796	Q0P804, Q9PMT4, Q9PM68, Q0P8L1, P42448, Q0PBB8, Q0P9C3	0.345385
INTERPRO	IPR016040:NAD(P)-binding domain	7	5.22	0.085359	Q0P8W4, Q0PCB6, Q0P8I7, Q0P8L1, Q9PHN5, Q0P9C3, Q0P9A5	0.82945
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	6	4.48	0.032375	Q9PP15, Q9PHY1, Q0PAY5, Q9PM78, P42448, Q0PBB8	0.439949
GOTERM_MF_FAT	GO:0019842~vitamin binding	6	4.48	0.254145	Q9PP70, Q0P8W7, Q0P8E1, Q0P9W6, P24531, Q0P9L5	0.90128
INTERPRO	IPR003593:ATPase, AAA+ type, core	6	4.48	0.465459	Q0PC30, O52908, Q0PA10, Q0PBU4, Q9PIM0, Q0P7V6	0.999932
GOTERM_BP_FAT	GO:0006412~translation	6	4.48	0.591791	Q9PN98, Q9PI16, Q9PHX1, O69303, Q9PNB3, Q9PI34	0.990459
SMART	SM00382:AAA	6	4.48	0.648695	Q0PC30, O52908, Q0PA10, Q0PBU4, Q9PIM0, Q0P7V6	0.999971
SP_PIR_KEYWORDS	hydrolase	6	4.48	0.826471	Q0PC30, Q9PP04, Q9PJ21, Q0PBU4, Q0PB04, Q0P928	0.997823
INTERPRO	IPR017909:Twin arginine translocation signal, Tat	5	3.73	0.001915	Q0P8A7, Q0PB73, Q0PBP1, Q0P8Y9, Q0PCC0	0.275992
GOTERM_BP_FAT	GO:0007155~cell adhesion	5	3.73	0.002722	P80672, Q0P8D9, Q9PHW6, P56963, P56964	0.070957
GOTERM_BP_FAT	GO:0022610~biological adhesion	5	3.73	0.002722	P80672, Q0P8D9, Q9PHW6, P56963, P56964	0.070957
INTERPRO	IPR006311:Twin-arginine translocation pathway signal	5	3.73	0.002826	Q0P8A7, Q0P8A3, Q0PB73, Q0P8Y9, Q9PPD9	0.212134
SP_PIR_KEYWORDS	magnesium	5	3.73	0.013777	Q9PP15, Q9PHY1, Q9PM78, P42448, Q0PBB8	0.097426
KEGG_PATHWAY	cje00620:Pyruvate metabolism	5	3.73	0.025184	Q9PPL8, Q0P8W7, Q0P9W6, Q0P9L5, Q0PBB8	0.191208
INTERPRO	IPR004089:Chemotaxis methyl-accepting receptor, signalling	5	3.73	0.038344	Q0P8B2, Q0PCA6, Q0P864, Q0PB65, Q0P9E4	0.666466

GOTERM_BP_FAT	GO:0019318~hexose metabolic process	5	3.73	0.052703	Q0P804, Q0P8L1, P42448, Q0PBB8, Q0P9C3	0.518538
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	5	3.73	0.057976	Q0PAI0, Q0PCB6, Q9PHK7, Q9PMT4, Q0PCB8	0.503967
SMART	SM00283:MA	5	3.73	0.05938	Q0P8B2, Q0PCA6, Q0P864, Q0PB65, Q0P9E4	0.706045
SP_PIR_KEYWORDS	cell inner membrane	5	3.73	0.092927	Q0PC30, Q9PJ21, Q0P9V7, Q0PCA8, Q0PA12	0.381487
KEGG_PATHWAY	cjd00230:Purine metabolism	5	3.73	0.175348	Q9PM80, Q9PP15, Q0P9J4, Q0PBU3, Q0PBB8	0.7144
INTERPRO	IPR013785:Aldolase-type TIM barrel	5	3.73	0.192886	Q0P9Q7, Q0P8Y6, Q0P9J4, Q0P9W6, Q0PCB8	0.97297
SP_PIR_KEYWORDS	lipoprotein	5	3.73	0.433567	Q0PB16, Q0P8X7, Q0PC48, Q0PBB4, Q0PBA4	0.884664
SP_PIR_KEYWORDS	transmembrane	5	3.73	0.95492	P80672, Q0PCA8, Q0PA12, Q0PBN7, Q0PBA6	0.999974
GOTERM_MF_FAT	GO:0003677~DNA binding	5	3.73	0.995628	Q9PM80, Q9PI30, Q46124, Q0PA12, Q0P7V6	1
SP_PIR_KEYWORDS	metalloprotein	4	2.99	7.71E-04	Q0P8D0, Q0P8Y9, Q0P970, Q0P8Z0	0.014555
SP_PIR_KEYWORDS	pyruvate	4	2.99	0.001084	Q0P8E1, Q0P9W6, Q0P9L5, Q0PBB8	0.017877
INTERPRO	IPR010810:Flagellin hook, IN motif	4	2.99	0.001799	Q0P7Q2, Q9PHW6, P56963, P56964	0.454843
INTERPRO	IPR012285:Fumarate reductase, C-terminal	4	2.99	0.012274	Q0PC61, Q0PCB6, Q0PB72, Q0PBA0	0.44819
KEGG_PATHWAY	cjd00910:Nitrogen metabolism	4	2.99	0.014316	Q0PAI0, Q0PCB6, Q0PC50, Q0P8Q2	0.139263
SP_PIR_KEYWORDS	iron-sulfur	4	2.99	0.029131	Q0P8A7, Q0PB72, Q0P970, Q9PPD9	0.17848
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	4	2.99	0.057763	Q0PAI0, Q0PCB6, Q9PHK7, Q0PCB8	0.518192
GOTERM_BP_FAT	GO:0022900~electron transport chain	4	2.99	0.057763	Q0P970, Q0PCA8, Q0PBA1, Q9PPD9	0.518192
SP_PIR_KEYWORDS	protein biosynthesis	4	2.99	0.059126	Q9PN98, Q9PI16, Q9PHX1, O69303	0.29702
KEGG_PATHWAY	cje02030:Bacterial chemotaxis	4	2.99	0.093471	Q0P8B2, Q0PBM2, Q0PBM1, Q0P9E4	0.493576
GOTERM_MF_FAT	GO:0016836~hydro-lyase activity	4	2.99	0.096849	Q0P9Q7, Q0PA55, O69294, P42448	0.637319
SP_PIR_KEYWORDS	amino-acid biosynthesis	4	2.99	0.117379	Q9PHK7, Q9PM78, Q59291, Q9PHN5	0.435961
GOTERM_BP_FAT	GO:0006457~protein folding	4	2.99	0.139073	Q46108, O69289, Q9PIM0, Q0PAS1	0.717332
INTERPRO	IPR017896:4Fe-4S ferredoxin, iron-sulphur binding domain	4	2.99	0.150002	Q0PC61, Q0P8E1, Q0PB72, Q0PBA0	0.944012
GOTERM_CC_FAT	GO:0042597~periplasmic space	4	2.99	0.171298	Q9PJ14, Q9PPD9, Q0P928, Q0P9S0	0.510319
SP_PIR_KEYWORDS	kinase	4	2.99	0.252856	Q9PPL8, Q9PP15, Q0PBM2, Q0PBB8	0.691126
COG_ONTOLOGY	Amino acid transport and metabolism	4	2.99	0.317566	Q0P9N4, Q0P9N3, Q9PHK7, Q0PB95	0.967897
GOTERM_MF_FAT	GO:0016879~ligase activity, forming carbon-nitrogen bonds	4	2.99	0.339196	Q9PN98, Q0P8W7, Q0PAI0, Q9PHK7	0.943583

GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	4	2.99	0.910734	Q0P9Q7, Q9PP70, Q9PM78, Q9PPD9	0.999989
INTERPRO	IPR017932:Glutamine amidotransferase, type II	3	2.24	0.004891	Q0PBU3, Q9PMT4, Q0PCB8	0.281425
INTERPRO	IPR000583:Glutamine amidotransferase, class-II	3	2.24	0.004891	Q0PBU3, Q9PMT4, Q0PCB8	0.281425
GOTERM_CC_FAT	GO:0045281~succinate dehydrogenase complex	3	2.24	0.005448	Q0PB71, Q0PB73, Q0PB72	0.050574
GOTERM_CC_FAT	GO:0045282~plasma membrane succinate dehydrogenase complex	3	2.24	0.005448	Q0PB71, Q0PB73, Q0PB72	0.050574
SP_PIR_KEYWORDS	tricarboxylic acid cycle	3	2.24	0.006672	O69294, Q0P7U8, Q9PHY1	0.054125
INTERPRO	IPR003031:Delta crystallin	3	2.24	0.011767	Q0PCA2, O69294, Q0PC50	0.485627
INTERPRO	IPR000362:Fumarate lyase	3	2.24	0.01616	Q0PCA2, O69294, Q0PC50	0.49657
SP_PIR_KEYWORDS	electron transport	3	2.24	0.022779	Q0P970, Q0PCA8, Q9PPD9	0.148962
GOTERM_CC_FAT	GO:0009898~internal side of plasma membrane	3	2.24	0.025052	O52908, Q0P9V7, Q0PA12	0.134643
GOTERM_MF_FAT	GO:0016840~carbon-nitrogen lyase activity	3	2.24	0.030745	Q0P804, Q0PCA2, Q0PC50	0.448946
INTERPRO	IPR013816:ATP-grasp fold, subdomain 2	3	2.24	0.032702	Q0P8W7, Q9PHY1, Q0P9L5	0.638903
GOTERM_BP_FAT	GO:0009061~anaerobic respiration	3	2.24	0.036305	Q0P8A7, Q0PBA1, Q0PBA0	0.444191
SP_PIR_KEYWORDS	Chaperone	3	2.24	0.046308	Q46108, O69289, Q9PIM0	0.24922
INTERPRO	IPR001492:Flagellin, N-terminal	3	2.24	0.05355	Q0PA11, P56963, P56964	0.686269
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	3	2.24	0.072372	Q0P8A7, Q59291, Q0P8L1	0.615479
SP_PIR_KEYWORDS	nadp	3	2.24	0.088529	Q59291, Q9PHN5, Q0P9A5	0.377601
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	3	2.24	0.097358	Q9PM80, Q9PIM0, Q59291	0.623691
GOTERM_BP_FAT	GO:0009082~branched chain family amino acid biosynthetic process	3	2.24	0.098654	Q0PBN6, Q59291, Q9PHN5	0.632696
GOTERM_BP_FAT	GO:0009081~branched chain family amino acid metabolic process	3	2.24	0.113285	Q0PBN6, Q59291, Q9PHN5	0.673525
INTERPRO	IPR004090:Chemotaxis methyl-accepting receptor	3	2.24	0.114423	Q0PCA6, Q0PB65, Q0P9E4	0.897208
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	3	2.24	0.128434	Q0P804, Q9PM68, Q0P8L1	0.69798

GOTERM_CC_FAT	GO:0009420~flagellin-based flagellum filament	3	2.24	0.137	Q0PA11, P56963, P56964	0.475879
SP_PIR_KEYWORDS	ion transport	3	2.24	0.153325	Q0PC30, P80672, Q9PJ21	0.521873
KEGG_PATHWAY	cje00640:Propanoate metabolism	3	2.24	0.165138	Q9PPL8, Q0P8W7, Q9PHY1	0.702108
SP_PIR_KEYWORDS	protein transport	3	2.24	0.192357	O52908, Q9PJ14, Q0P9V7	0.58849
KEGG_PATHWAY	cju00620:Pyruvate metabolism	3	2.24	0.280951	Q9PPL8, Q0P9L5, Q0PBB8	0.851276
GOTERM_BP_FAT	GO:0009066~aspartate family amino acid metabolic process	3	2.24	0.311317	Q0PC50, Q0P9F8, Q59291	0.898602
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	3	2.24	0.321395	Q0PAY5, Q59291, Q0P8L1	0.937625
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	3	2.24	0.328194	Q9PIH0, Q9PM68, Q0P8L1	0.908069
GOTERM_MF_FAT	GO:0050660~FAD binding	3	2.24	0.351992	Q0PCB6, Q0PB95, Q0PBA1	0.946181
INTERPRO	IPR017900:4Fe-4S ferredoxin, iron-sulphur binding, conserved site	3	2.24	0.38076	Q0PC61, Q0P8E1, Q0PB72	0.999543
GOTERM_MF_FAT	GO:0008483~transaminase activity	3	2.24	0.482283	Q9PP70, Q9PMT4, Q0PBN6	0.982999
GOTERM_MF_FAT	GO:0016769~transferase activity, transferring nitrogenous groups	3	2.24	0.509075	Q9PP70, Q9PMT4, Q0PBN6	0.986261
GOTERM_CC_FAT	GO:0019867~outer membrane	3	2.24	0.56025	P80672, Q0P8D9, Q0PC08	0.936366
KEGG_PATHWAY	cje02010:ABC transporters	3	2.24	0.850836	Q0P9N4, Q0P9N3, Q0PBW4	0.999936
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	3	2.24	0.962921	Q9PIH0, Q0PAX5, Q9PM68	1
GOTERM_BP_FAT	GO:0051188~cofactor biosynthetic process	3	2.24	0.967167	Q0P9Q7, Q9PP70, Q9PPD9	1
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	3	2.24	0.982312	Q0P804, Q9PMT4, Q0P8L1	1

^aPercent of proteins in the cluster with the particular annotation.

^bProbability of enrichment level occurring in randomly constructed cluster.

^cProbability of enrichment level occurring in randomly constructed cluster adjusted for multiple hypothesis testing using the Benjamini-Hochberg method.

Table S5. Vesicular proteins identified with lower confidence from OMVs of *C. jejuni*.

Uniprot accession	Description	Gene	No. of peptides	Sequence coverage (%)	PEP ^a
Q9PM74	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	hisA	9	37	2.64E-28
Q0P823	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	dapD	17	37	3.10E-37
Q9PHU4	3,4-dihydroxy-2-butanone 4-phosphate synthase	ribB	22	71.1	8.89E-135
Q9PI17	30S ribosomal protein S7	rpsG	20	80.8	1.89E-195
Q9PNT2	3-dehydroquininate synthase	aroB	13	31.9	7.10E-43
Q9PIK1	3-methyl-2-oxobutanoate hydroxymethyltransferase	panB	15	62.4	1.99E-152
Q9PLX4	50S ribosomal protein L2	rplB	20	55.4	8.69E-123
Q9PLY3	50S ribosomal protein L5	rplE	22	85.6	0
Q0PAG4	5-hydroxyisourate hydrolase	Cj0715	14	67.9	6.42E-118
Q9PN94	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	metE	14	21.1	1.33E-50
Q9ZI13	Alkyl hydroperoxide reductase subunit C	ahpC	19	91.9	5.15E-280
Q0PAK3	Anaerobic C4-dicarboxylate transporter	dcuB	10	13.3	2.68E-38
Q0PA56	Ankyrin repeat-containing putative periplasmic protein	Cj0834c	8	22.8	2.09E-81
Q46104	Argininosuccinate lyase	argH	29	55.4	1.21E-171
Q0PAC8	Aspartate aminotransferase	aspB	22	57.6	0
Q9PNJ6	Aspartate carbamoyltransferase	pyrB	7	28.8	1.71E-105
Q9PHM7	Aspartate--tRNA ligase	aspS	40	64.2	0
Q0P9E6	ATP-dependent Clp protease ATP-binding subunit^[1]	clpA	30	43.9	3.36E-224
Q9PHL0	ATP-dependent protease ATPase subunit HslU	hslU	41	72.2	0
Q0P9D8	ATP-dependent zinc metalloprotease FtsH^[1]	ftsH	41	50.2	0
Q0P8I3	Capsular polysaccharide heptosyltransferase	hddC	23	36.8	8.08E-119
Q0P8G9	Capsule polysaccharide export system inner membrane protein	kpsE	25	59.9	0
Q9PIL7	Carbamoyl-phosphate synthase large chain	carB	53	42.7	3.19E-209
Q9PMG8	Carbamoyl-phosphate synthase small chain	carA	18	49.7	5.29E-109
Q0P8C8	Cb-type cytochrome C oxidase subunit II	ccoO	19	77.8	2.42E-241
Q46101	CdtB (Cytolethal distending toxin B)^[11]	cdtB	6	31.3	1.08E-13
Q0PBB1	<i>Colicin V production protein homolog</i>	Cj0399	5	36.4	2.93E-40

Q9PJ84	CTP synthase	pyrG	23	47	7.43E-209
Q9PPB8	Cysteine--tRNA ligase	cysS	17	34.8	1.19E-51
Q0P971	Cytochrome b	petB	7	16.6	8.98E-42
Q0PC56	Cytolethal distending toxin subunit A^[11]	cdtA	8	28.7	2.20E-48
Q9PPB4	Dihydrodipicolinate synthase	dapA	20	75.5	3.02E-217
Q0PA86	Dihydroorotate dehydrogenase	pyrD	19	53.1	5.57E-257
Q0PBH1	DNA polymerase	polA	16	24.1	5.86E-110
Q0PCC3	DNA polymerase III subunit beta	dnaN	29	75.5	0
Q9PLZ2	DNA topoisomerase 1	topA	32	50.4	2.61E-173
Q9PNB4	Elongation factor Ts	tsf	32	83.5	0
Q0P8L4	Enoyl-[acyl-carrier-protein] reductase	fabI	17	55.8	3.61E-93
Q0P8Q4	Enterochelin uptake periplasmic binding protein	ceuE	13	44.2	4.49E-121
Q0PBG7	Excinuclease ABC subunit A	uvrA	23	26.5	7.21E-137
Q0PBJ1	Flagellar M-ring protein	fliF	15	28.2	9.12E-65
Q0PBA2	Fumarate reductase cytochrome B subunit	frdC	7	15.4	1.17E-14
Q0P8I6	GDP-L-fucose synthetase	fcl	19	56.4	1.38E-221
Q9PNN2	Glutamyl-tRNA(Gln) amidotransferase subunit A	gatA	21	54.3	2.82E-183
Q9PIA5	Glutamyl-tRNA(Gln) amidotransferase subunit C	gatC	6	63.8	5.43E-14
P51594	GTP cyclohydrolase 1	folE	9	43.7	1.19E-88
Q0PC87	GTP-binding protein TypA homolog	typA	28	52.2	4.49E-205
Q9PM76	Histidine biosynthesis bifunctional protein HisB	hisB	10	25.3	6.78E-42
Q46125	<i>Histidine-binding protein</i>	hisJ	18	43.8	2.11E-232
Q0PAP2	Hydrogenase isoenzymes formation protein	hypD	9	27.3	1.71E-22
Q0PC59	L-lactate permease	lctP	8	16.6	6.50E-168
Q9PMS2	L-seryl-tRNA(Sec) selenium transferase	selA	11	27	4.26E-29
Q9PPI1	Magnesium transport protein CorA	corA	13	42.2	2.84E-60
Q0PAB2	Major antigenic peptide PEB2^[12]	peb2	22	61.2	1.84E-286
Q0PBL7	Major antigenic peptide PEB3^[12]	peb3	14	50	6.11E-96
Q0P9X8	Major cell-binding factor (CBF1) (PEB1)^[12,13]	peb1A	30	72.2	6.79E-202
Q0P8X0	Malate oxidoreductase	Cj1287c	25	54.5	1.98E-185
Q0P7X7	Methionine aminopeptidase	map	11	51.6	2.21E-41
Q0P850	NADH-quinone oxidoreductase subunit B	nuoB	9	37.7	1.94E-32

Q9PM99	NADH-quinone oxidoreductase subunit D	nuoD	18	48.8	3.71E-129
Q0PCB3	Non-haem iron protein	rrc	30	84.2	0
Q0PAX9	OORB subunit of 2-oxoglutarate:acceptor oxidoreductase	oorB	28	81.5	0
Q9PNU6	Ornithine carbamoyltransferase	argF	18	62.7	2.42E-76
Q0P9M1	Outer membrane component of efflux system (Multidrug efflux system CmeDEF)^[14]	cmeD	10	27.4	2.03E-26
P0C633	Outer membrane lipoprotein mapA	mapA	9	51.9	1.49E-232
Q0P9F5	Peptidase	Cj1099	21	33.9	1.53E-207
Q9PMK5	Peptide chain release factor 2	prfB	8	31	2.83E-46
Q0PC22	Peptidyl-prolyl cis-trans isomerase	slyD	11	57.7	1.46E-232
Q0PBE3	Periplasmic fusion protein CmeA (Multidrug efflux system CmeABC)^[15]	cmeA	11	38.4	2.64E-136
Q0PAA7	<i>Periplasmic nitrate reductase small subunit (Cytochrome C-type protein)</i>	napB	12	73	1.53E-162
Q9PP34	Phenylalanine--tRNA ligase alpha subunit	pheS	21	66.7	2.12E-168
Q9PP35	Phenylalanine--tRNA ligase beta subunit	pheT	36	47	0
Q9PP01	Phosphoenolpyruvate carboxykinase	pckA	29	58.2	0
Q9PIE2	Phosphoglucosamine mutase	glmM	27	51.7	4.37E-183
Q9PMQ5	Phosphoglycerate kinase	pgk	25	57.8	0
Q9PHZ7	Phosphoribosylformylglycinamide synthase 1	purQ	8	37.2	1.31E-31
Q9PIH3	Phosphoserine aminotransferase	serC	17	50	8.01E-107
Q0P903	Polyribonucleotide nucleotidyltransferase	pnp	40	57.7	0
Q46123	Precursor of peptidoglycane associated lipoprotein	omp18	6	39.4	4.02E-144
Q9PPE0	Probable thiol peroxidase	tpx	15	89.1	0
Q0P8U0	Pse synthetase	pseI	16	50.1	6.65E-56
Q0P8S2	PseE protein	pseE	21	32.8	7.12E-123
Q0P8X9	Putative ABC transporter ATP-binding protein	Cj1277c	13	54.3	5.78E-75
Q0PB98	Putative ATP/GTP binding protein	Cj0412	20	38.3	0
Q0P875	Putative ATP/GTP-binding protein	rloH	12	21.4	2.77E-31
Q0P822	Putative ATP/GTP-binding protein (Mrp protein homolog)	mrp	21	61.1	2.76E-168
Q0P897	Putative CRISPR-associated protein	Cj1523c	23	23.5	3.17E-96
Q0PBP0	Putative cytochrome C-type haem-binding periplasmic protein	Cj0265c	14	49.7	1.26E-75
Q0P961	Putative dihydroorotase	pyrC2	25	61.5	0
Q0P8A8	Putative formate dehydrogenase iron-sulfur subunit	fdhB	21	89.2	3.46E-152

Q0PBD8	Putative glutathionylspermidine synthase	Cj0372	13	32.1	1.82E-67
Q0P8Y0	Putative integral membrane protein	Cj1276c	8	25	8.82E-37
Q0PC46	Putative lipoprotein	Cj0091	11	65.3	7.28E-167
Q0P9U9	Putative lipoprotein	Cj0950c	18	72.5	1.71E-290
Q0P7S1	Putative metallo-beta-lactamase family protein	Cj1710c	15	25	8.63E-152
Q0PBP3	Putative methyl-accepting chemotaxis signal transduction protein	Cj0262c	40	58.5	0
Q0PBZ3	Putative methyl-accepting chemotaxis signal transduction protein	Cj0144	38	54.9	0
Q0P8I8	Putative methyltransferase family protein	Cj1426c	9	34.3	1.74E-92
Q0P8A0	Putative molybdopterin biosynthesis protein	moeA2	13	34.6	1.50E-53
Q0P877	Putative NADP-dependent alcohol dehydrogenase	Cj1548c	13	50.8	1.08E-124
Q0P8T8	Putative nucleotide sugar dehydratase	Cj1319	6	18.3	4.89E-12
Q0P9R1	Putative oxidoreductase ferredoxin-type electron transport protein	Cj0991c	7	17.8	8.99E-34
Q0PC60	Putative oxidoreductase iron-sulfur subunit	Cj0075c	25	81.7	2.15E-266
Q0PC06	<i>Putative peptidase M23 family protein</i>	Cj0131	23	44	2.66E-133
Q0P844	Putative peptide ABC-transport system periplasmic peptide-binding protein	Cj1584c	10	24.5	2.88E-48
Q0P8Q1	Putative periplasmic cytochrome C	nrfH	7	41.5	4.00E-63
Q79JB5	Putative periplasmic protein		21	66	8.85E-211
Q0P885	Putative periplasmic protein	Cj1540	20	71.7	3.91E-203
Q0P8M9	Putative periplasmic protein	Cj1380	18	62.7	2.14E-185
Q0P937	Putative periplasmic protein	Cj1219c	44	57.8	0
Q0P807	<i>Putative periplasmic protein</i>	Cj1621	14	39.6	2.69E-142
Q0PBY6	Putative periplasmic protein	Cj0151c	17	76.8	1.12E-283
Q0PC92	Putative periplasmic protein	Cj0034c	17	58.9	1.58E-201
Q0PBZ4	<i>Putative periplasmic solute binding protein for ABC transport system</i>	Cj0143c	12	43.2	3.25E-120
Q0P9E8	Putative periplasmic thioredoxin	Cj1106	10	55.5	3.57E-159
Q0PAJ1	Putative phosphate acetyltransferase	pta	31	60.7	1.68E-259
Q0PAG3	Putative phospho-2-dehydro-3-deoxyheptonate aldolase	Cj0716	24	57.8	4.44E-287
Q0P912	Putative radical SAM domain protein	Cj1244	27	66.9	6.51E-158
Q0P8P1	Putative radical SAM domain protein	Cj1368	9	32.3	3.63E-23
Q0P8P4	Putative secreted serine protease	Cj1365c	9	9.9	5.95E-28
Q0PA47	<i>Putative secreted transglycosylase</i>	Cj0843c	7	11.5	9.54E-12
Q0P8I0	Putative sugar transferase	Cj1434c	24	46.5	7.86E-189

Q0PAW2	Putative uncharacterized protein	Cj0554	16	57.5	5.83E-274
Q0P8I5	Putative uncharacterized protein	Cj1429c	21	60.4	4.87E-142
Q0PC62	Putative uncharacterized protein	Cj0073c	10	24.4	8.73E-13
Q0PAH3	Putative uncharacterized protein	Cj0706	40	91.2	0
Q0P8W2	Putative uncharacterized protein	Cj1295	13	34.7	1.09E-94
Q0P8U8	Putative uncharacterized protein	Cj1309c	29	83	0
Q0PC82	Putative uncharacterized protein	Cj0044c	12	18.3	4.87E-21
Q0P9K1	Restriction modification enzyme	cjel	17	13.4	8.05E-35
Q9PM40	Ribonuclease 3	rnc	5	21	5.73E-19
Q9PIB3	Serine--tRNA ligase	serS	26	51.1	1.23E-239
Q0PAH0	Signal recognition particle protein	ffh	26	67.2	5.68E-139
Q0PAY2	Succinyl-CoA ligase [ADP-forming] subunit alpha	sucD	25	80.3	0
Q9PNP6	Thiazole synthase	thiG	19	70.9	8.28E-113
Q0PA78	Threonine synthase	thrC	18	40.6	3.46E-173
Q9PIL5	Transaldolase	tal	18	45.5	2.04E-119
Q9PI36	Transcription antitermination protein NusG	nusG	11	56.5	2.02E-45
Q0P7Y3	Transketolase	tkt	26	44.6	0
Q9PIZ1	Translation initiation factor IF-2	infB	35	38	2.09E-166
Q9PJ66	tRNA-specific 2-thiouridylase MnmA	mnmA	12	38.2	1.07E-58
Q0PBF4	Two-component regulator	Cj0355c	20	64.6	8.28E-280
Q9PHU0	UDP-3-O-acylglucosamine N-acyltransferase	lpxD	13	42.1	8.94E-126
Q0P8H5	UDP-galactopyranose mutase	glf	16	49.2	4.40E-121
Q0P9D4	UDP-GlcNAc C4,6 dehydratase^[16]	pglF	17	30	8.36E-53
Q9PI73	UDP-N-acetylmuramoylalanine--D-glutamate ligase	murD	5	15.9	2.18E-11
P45492	Uncharacterized lipoprotein	Cj0983	24	73.7	0
<i>Q9PID1</i>	<i>UPF0323 lipoprotein Cj0371</i>	<i>Cj0371</i>	10	38.3	1.92E-120
Q0PB50	Zinc protease-like protein	Cj0463	18	38.7	1.51E-69

^aPosterior error probability indicating how the observed peptide spectrum match (PSM) is incorrect.

Known virulence factors were referenced and written in bold.

Known N-glycoproteins were written in italics.

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