

Table 1. Genes containing associated elements and their predicted functions and functional categories.

Gene name	Alias	Predicted function ^a	Transcriptional unit number ^b	Genomic position ^c	Associated in	UniProt identifier	Gene ontology (GO)	Gene ontology (cellular component)	Gene ontology IDs
<i>cj0143c</i>	<i>znuA</i>	Putative periplasmic solute binding protein for ABC transport system	55	145,616	ST-21	Q0PBZ4	metal ion binding; metal ion transport	-	GO:0046872; GO:0030001
<i>cj0576</i>	<i>lpxD</i>	UDP-3-O-acylglucosamine N-acyltransferase (EC 2.3.1.-)	226	537,023	ST-21	Q9PHU0	lipid A biosynthetic process; transferase activity, transferring acyl groups other than amino-acyl groups	-	GO:0009245; GO:0016747
<i>cj0625</i>	<i>hypD</i>	Hydrogenase isoenzymes formation protein	238	585,102	ST-21	Q0PAP2	metal ion binding	-	GO:0046872
<i>cj0694</i>	<i>ppiD</i>	Putative periplasmic protein	264	651,043	ST-21	Q0PAI5	isomerase activity	-	GO:0016853
<i>cj1048c</i>	<i>dapE</i>	Succinyl-diaminopimelate desuccinylase (SDAP desuccinylase) (EC 3.5.1.18) (N-succinyl-L-L-2,6-diaminoheptanedioate amidohydrolase)	395	980,554	ST-21	Q0P9K4	cobalt ion binding; diaminopimelate biosynthetic process; lysine biosynthetic process via diaminopimelate; metalloproteinase activity; succinyl-diaminopimelate desuccinylase activity; zinc ion binding	-	GO:0050897; GO:0019877; GO:0009089; GO:0008237; GO:0009014; GO:0008270
<i>cj1049c</i>	-	Putative LysE family transporter protein	395	981,655	ST-21	Q0P9K3	amino acid transport; integral component of membrane; plasma membrane	integral component of membrane; plasma membrane	GO:0006865; GO:0016021; GO:0005886
<i>cj1051c</i>	<i>cjeI</i>	Restriction modification enzyme	395	982,991	ST-21	Q0P9K1	DNA binding; DNA methylation; N-methyltransferase activity	-	GO:0003677; GO:0006306; GO:0008170
<i>cj1161c</i>	-	Putative cation-transporting ATPase	428	1,091,795	ST-21	Q0P995	ATP binding; cation-transporting ATPase activity; integral component of membrane; metal ion binding; metal ion transport	integral component of membrane	GO:0005524; GO:0019829; GO:0016021; GO:0046872; GO:0030001
<i>cj1309c</i>	-	Uncharacterized protein	492	1,238,581	ST-45	Q0P8U8	-	-	0
<i>cj1364c</i>	<i>fumC</i>	Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	509	1,296,244	ST-45	Q69294	fumarate hydratase activity; fumarate metabolic process; tricarboxylic acid cycle; tricarboxylic acid cycle enzyme complex	tricarboxylic acid cycle enzyme complex	GO:0004333; GO:0006106; GO:0006099; GO:0045239
<i>cj1366c</i>	<i>glmS</i>	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	509	1,300,819	ST-45	Q9PMT4	carbohydrate binding; carbohydrate biosynthetic process; cytoplasm; glutamine-fructose-6-phosphate transaminase (isomerizing) activity; glutamine metabolic process	cytoplasm	GO:0030246; GO:0016051; GO:0005737; GO:0006541; GO:0004360
<i>cj1367c</i>	-	Putative nucleotidyltransferase	509	1,302,620	ST-45	Q0P8P2	transferase activity	-	GO:0016740
<i>cj1368</i>	-	Putative radical SAM domain protein	510	1,305,112	ST-45	Q0P8P1	4 iron, 4 sulfur cluster binding; menaquinone biosynthetic process; transferase activity, transferring alkyl or aryl (other than methyl) groups	-	GO:0051539; GO:0009234; GO:0016765
<i>cj1373</i>	-	Putative integral membrane protein	510	1,309,284	ST-45	Q0P8N6	integral component of membrane	integral component of membrane	GO:0016021
<i>cj1375</i>	-	Putative multidrug efflux transporter	512	1,312,555	ST-45	Q0P8N4	integral component of membrane; plasma membrane; transmembrane transport; transporter activity	integral component of membrane; plasma membrane	GO:0016021; GO:0005886; GO:0055085; GO:0005215
<i>cj1377c</i>	-	Putative ferredoxin	513	1,314,649	ST-45	Q0P8N2	iron-sulfur cluster binding	-	GO:0051536
<i>cj1378</i>	<i>selA</i>	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1) (Selenocysteine synthase) (Sec synthase) (Selenocysteinyl-tRNA(Sec) synthase)	514	1,316,388	ST-45	Q9PMS2	cytoplasm; L-seryl-tRNA(Sec) selenium transferase activity; pyridoxal phosphate binding; selenocysteine incorporation; selenocysteinyl-tRNA(Sec) biosynthetic process	cytoplasm	GO:0004125; GO:0005737; GO:0030170; GO:0001514; GO:0097056
<i>cj1414c</i>	<i>kpsC</i>	Capsule polysaccharide modification protein	529	1,346,283	ST-21	Q0P8K0	polysaccharide biosynthetic process; polysaccharide transport	-	GO:0000271; GO:0015774
<i>cj1444c</i>	<i>kpsD</i>	Capsule polysaccharide export system periplasmic protein	532	1,383,486	ST-21	Q0P8H0	membrane; polysaccharide transmembrane transporter activity	membrane	GO:0016020; GO:0015159
<i>cj1569c</i>	<i>nuoK</i>	NADH-quinone oxidoreductase subunit K (EC 1.6.99.5) (NADH dehydrogenase I subunit K) (NDH-1 subunit K)	578	1,501,081	ST-21	Q0P859	ATP synthesis coupled electron transport; integral component of membrane; NADH dehydrogenase (quinone) activity; plasma membrane; quinone binding; transport	integral component of membrane; plasma membrane	GO:0042773; GO:0005136; GO:0016021; GO:0005886; GO:0048038; GO:0006810

a. As defined on the UniProt database

b. In the *C. jejuni* NCTC11168 reference genome according to ProOpDB. Two identical numbers reflect co-transcription of the corresponding genes in the same transcriptional unit.

c. Starting position on the *C. jejuni* NCTC11168 genome sequence