

APPENDIX 2: predicted CDSs and their protein similarities for the *C. jejuni* strain 81-176 plasmid pTet

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet1	382	Replication initiation protein	replication protein	<i>Selenomonas ruminantium</i> plasmid ps23	Q55007	1.9e-29	36.48
pTet2	126	Unknown	-	-			
pTet3	132	Unknown	Hypothetical cjp38	<i>C. jejuni</i>	Q8GJB7	1.6e-16	40
pTet4	170	Unknown	-	-			
pTet5	185	Unknown	-	-			
pTet6	88	Unknown	Hypothetical rgi82	<i>Oryza sativa</i>	Q944E8	5.2e-03	30.3
pTet7	186	Unknown	-	-			
pTet8	88	Unknown	-	-			
pTet9	1932	DNA methylase	Orf23	<i>Sinorhizobium meliloti</i> phage PBC5	Q8W6K4	3.7e-135	38.19
pTet10c	234	Unknown	-	-			
pTet11c	462	Nickase	MagA2	<i>Actinobacillus actinomycetemcomitans</i>	Q9F276	8.9e-25	32.26
pTet12c	183	unknown	-	-			
pTet13	93	Unknown	-	-			
pTet14	203	Unknown	-	-			
pTet15	217	Unknown	Hypothetical jhp0950	<i>H. pylori</i>	Q9ZK15	1.8e-19	39.63
pTet16	408	DNA primase	TraC	<i>E. coli</i>	P27189	4.1e-15	31.56
pTet17	87	Lipoprotein	MagB5	<i>Actinobacillus actinomycetemcomitans</i>	Q9F247	1.1e-02	37.7
pTet18c	85	Unknown	-	-			
pTet19c	61	Unknown	-	-			
pTet20	72	Unknown	Hypothetical jhp0960	<i>H. pylori</i>	Q9ZKH6	5.6e-10	52.77
pTet21	67	Unknown	Hypothetical jhp0961	<i>H. pylori</i>	Q9ZKH5	4.4e-13	68.42
pTet22	597	Unknown	Hypothetical amv156	<i>Amsacta moorei</i> entomopoxvirus	Q9EMP3	6.1e-04	22.74
pTet23c	204	Site-specific DNA recombinase	Soao172	<i>Shewanella oneidensis</i>	Q8E7Z6	1e-14	33.16

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet24c	125	Virulence-associated protein	Vap2	<i>Riemerella anatipestifer</i> pCFC1	O85171	1.9e-04	36.26
pTet25c	107	Unknown	-	-			
pTet26	87	Type IV secretion system protein	VirB2	<i>E. coli</i>	Q91UX6	1e-06	35.36
pTet27	922	ATPase	MagB3	<i>Actinobacillus actinomycetemcomitans</i>	Q9F245	1e-128	40.67
pTet28	188	Unknown	Hypothetical	<i>C. jejuni</i> pCjA13	Q847A4	1.3e-14	44.8
pTet29	221	Unknown	-	-			
pTet30	141	Single-strand DNA binding protein	Ssb-1	<i>Geobacter sulfurreducens</i>	AAR35527	5.3e-11	33.58
pTet31	86	Unknown	-	-			
pTet32	323	Unknown	MagB4	<i>Actinobacillus actinomycetemcomitans</i>	Q9F246	6e-19	32.66
pTet33	332	Unknown	MagB6	<i>Actinobacillus actinomycetemcomitans</i>	Q9F248	1.4e-15	25.93
pTet34	55	Lipoprotein	Cj1074c	<i>C. jejuni</i>	Q9PNM0	0.24	44.68
pTet35	220	Type IV secretion system protein	VirB8-like protein	<i>C. jejuni</i> pCjA13	Q847A8	1.1e-77	100
pTet36	295	Type IV secretion system protein	VirB9-like protein	<i>C. jejuni</i> pCjA13	Q847A7	3.7e-112	97.28
pTet37	391	Type IV secretion system protein	MagB10	<i>Actinobacillus actinomycetemcomitans</i>	Q9F252	5.7e-39	39.74
pTet38	330	Type IV secretion system protein	VirB11-like protein	<i>C. jejuni</i> pCjA13	Q847A5	4.6e-117	99.69
pTet39	603	Type IV secretion system protein	MagB12	<i>Actinobacillus actinomycetemcomitans</i>	Q9F254	4.9e-89	42.64
pTet40	145	Lipoprotein	MagB13	<i>Actinobacillus actinomycetemcomitans</i>	Q9F255	4.5e-03	26.57

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet41	254	Unknown	TrbM-like protein	<i>Haemophilus aegyptius</i> pF3031	Q8VRC6	4.5e-11	37.17
pTet42	265	Unknown	-	-			
pTet43	206	Unknown	-	-			
pTet44	730	Topoisomerase	TraE	<i>E. coli</i>	Q60215	1.8e-80	41.89
pTet45	473	Unknown	Hypothetical	<i>Plasmodium falciparum</i>	P21421	2.5e-03	25.39
pTet46	59	Unknown	Hypothetical cjp20	<i>C. jejuni</i>	Q8GJD3	3.1e-07	46.42
pTet47	639	Tetracycline resistance	TetO	<i>C. jejuni</i>	AAA23033	0	99.84
pTet48	57	Unknown	Hypothetical Orf6	<i>Enterococcus faecalis</i> transposon tn916	Q56396	4.3e-14	66.66
pTet49	222	Unknown	-	-			
pTet50	140	unknown	-	-			