

Table 1. Annotation of genes and protein coding regions in Antarctic fosmid ANT32C12

#	Nucleotide range	Dir.	Putative function	Closest BLASTP hit (E-value)	
1	1 - 1009	-	Predicted acyl-CoA transferases/carnitine dehydratase	CAB55821.1 (8e-51)	alpha
2	1160 - 2311	+	Predicted acyl-CoA dehydrogenases	ZP_00084445.1 (1e-151)	gamma
3	2314 - 3621	-	Predicted ATP-dependent exoDNase (exonuclease V), alpha subunit	NP_809634.1 (1e-65)	BCF
4	3744 - 4424	+	Predicted methylase	NP_796491.1 (1e-38)	gamma
5	4421 - 4855	-	Conserved hypothetical protein	ZP_00032675.1 (6e-11)	beta
6	4833 - 6035	+	Putative beta-lactamase class C	NP_250918.1 (1e-75)	gamma
7	6115 - 6684	+	Hypothetical protein	-	-
8	6759 - 7394	+	Conserved hypothetical protein	NP_798383.1 (3e-17)	gamma
9	7512 - 7817	+	Conserved hypothetical protein	AAO52198.1 (6e-27)	eucarya
10	7887 - 8393	+	Conserved hypothetical protein	NP_353310.1 (2e-11)	alpha
11	8383 - 9756	+	Predicted NAD-dependent aldehyde dehydrogenases	NP_534637.1 (1e-144)	alpha
12	9746 - 10753	+	Putative saccharopine dehydrogenase	NP_105333.1 (1e-74)	alpha
13	11063 - 11260	-	Predicted transcriptional regulators	NP_421035.1 (2e-11)	alpha
14	11270 - 11719	-	Hypothetical protein	-	-
15	11845 - 12336	+	Conserved hypothetical protein	ZP_00055759.1 (8e-07)	alpha
16	12360 - 13046	+	Conserved hypothetical protein	NP_654746.1 (4e-23)	LGC
17	13049 - 13672	+	Predicted 1-acyl-sn-glycerol-3-phosphate acyltransferase	ZP_00064877.1 (2e-25)	gamma
18	13669 - 15954	-	Conserved hypothetical protein	NP_710310.1 (1e-117)	spirochaetales
19	15641 - 16333	+	Predicted enoyl-CoA hydratase/carnitine racemase	NP_250439.1 (2e-35)	gamma
20	16351 - 16857	+	Predicted acetyltransferase, GNAT superfamily	ZP_00100576.1 (2e-11)	LGC
21	16905 - 17789	+	Conserved hypothetical protein	NP_207712.1 (1e-06)	epsilon
22	18003 - 18695	-	Hypothetical protein	-	-
23	18787 - 19512	-	Conserved hypothetical protein	ZP_00126659.1 (2e-05)	gamma
24	19612 - 21402	-	Predicted TypA membrane GTPase	ZP_00065644.1 (0.0)	gamma
25	21443 - 22723	+	Predicted metal-dependent amidase/aminoacylase/carboxypeptidase	NP_639131.1 (1e-106)	gamma
26	22795 - 23760	+	Predicted dioxygenase related to 2-nitropropane dioxygenase	NP_421175.1 (1e-111)	alpha
27	24302 - 25231	+	Predicted oxidoreductase	NP_250267.1 (1e-84)	gamma
28	25228 - 25596	-	Hypothetical protein	-	-
29	25776 - 26192	-	Conserved hypothetical protein	NP_203440.1 (4e-08)	bacteriophage
30	26247 - 27233	-	Conserved hypothetical protein	ZP_00115177.1 (9e-33)	cyanobacteria
31	27351 - 27911	+	Conserved hypothetical protein	ZP_00065866.1 (2e-41)	gamma
32	28050 - 30164	+	Predicted TonB-dependent receptor protein	AAG10467.1 (0.0)	gamma
33	30154 - 30750	+	Putative nicotinamide mononucleotide transporter	AAG10468.1 (5e-59)	gamma
34	30728 - 31570	+	Predicted LicA, choline kinase	AAG10469.1 (1e-37)	gamma
35	31572 - 32369	-	Predicted oxidoreductase	AAG10472.1 (1e-110)	gamma
36	32446 - 33162	+	Predicted dehydrogenase	AAG10473.1 (2e-86)	gamma
37	33226 - 33978	-	Proteorhodopsin	AAK30197.1 (1e-131)	gamma
38	34092 - 36389	-	Predicted TonB receptor protein	NP_419273.1 (1e-42)	alpha
39	36504 - 36986	+	Predicted phosphopantetheine adenyltransferase	AAG10476.1 (3e-73)	gamma
40	36983 - 37792	-	Predicted formamidopyrimidine-DNA glycosylase	AAG10477.1 (1e-105)	gamma
41	37796 - 39130	-	Predicted outer membrane protein TolC	AAG10478.1 (0.0)	gamma