UBA *Leptospirillum* group II 011206a assembly and the ordered 5-way CG assembly and used to analyze the ABend proteome

(Abend sample collected Jan 2004)

Fig. index	Gene # UBA	Preliminary annoation (FgenesB) of UBA	% cov UBA	UBA U_pep	% ID	Ordered JAZZ assembly 5-way CG	5-way CG annotation (Ram et al.	%cov 5way CG	5-way U_pep	Cov ratio
	8241									
1			NO GENE	-		5way_CG_42_GENE_1	hypo unique	NO DATA	-	-
2	UBA_8241_GENE_1	**Hypothetical**	22.5	0	100.00	5way_CG_42_GENE_2	**hypo unique**	22.5	0	1.00
3	UBA_8241_GENE_2	**Hemolysins and related containing CBS domai**	41.1	3	99.12	5way_CG_42_GENE_3	**hemolysin**	43.3	4	0.95
4	UBA_8241_GENE_3	**Hypothetical**	6.3	0	98.41	5way_CG_42_GENE_4	**hypo unique**	27.5	2	0.23
5	UBA_8241_GENE_4	**Hypothetical**	5.1	0	95.21	5way_CG_42_GENE_5	**hypo unique**	16.9	3	0.30
6	UBA_8241_GENE_5	Predicted transcriptional regulator	NO DATA	-	100.00	5way_CG_42_GENE_6	c hypo	NO DATA	-	-
7	UBA_8241_GENE_6	**Cysteine sulfinate desulfinase/cysteine desulfurase**	80.7	14	99.01	5way_CG_42_GENE_7	**cysteine desulfurase**	70.8	0	1.14
8	UBA_8241_GENE_7	**NifU homolog involved in Fe-S cluster formation**	76.6	10	97.81	5way_CG_42_GENE_8	**nifU homolog**	68.6	0	1.12
9	UBA_8241_GENE_8	**Uncharacterized conserved protein**	11.9	0	100.00	5way_CG_42_GENE_9	c hypo	11.9	0	1.00
10	UBA_8241_GENE_9	**DnaJ-domain-containing proteins 1**	66.7	31	91.11	5way_CG_42_GENE_10	**chaperone protein HscB**	25.8	0	2.59
11	UBA_8241_GENE_10	**Molecular chaperone**	73.8	52	98.51	5way_CG_42_GENE_11	**chaperone protein dnaK**	56.6	0	1.30
12	UBA_8241_GENE_11	**Ferredoxin**	36.9	6	97.09	5way_CG_42_GENE_13	**ferridoxin**	21.4	0	1.72
13	UBA_8241_GENE_12	**Uncharacterized protein conserved in bacteria**	83.6	13	97.01	5way_CG_42_GENE_14	**c hypo**	25.4	0	3.29
14	UBA_8241_GENE_12a	**hypothetical**	NO DATA	-	90.97	5way_CG_42_GENE_15	**hypo unique**	NO DATA	-	-
15	UBA_8241_GENE_13	**ATPases involved in chromosome partitioning**	73.2	0	99.16	5way_CG_42_GENE_16	**ATPase chromosome partitioning**	77.4	8	0.95
16	UBA_8241_GENE_14	Hypothetical	NO DATA	-	89.41	5way_CG_42_GENE_17	hypo unique	NO DATA	-	-
17	UBA_8241_GENE_15	Pseudouridylate synthase	NO DATA	-	93.28	5way_CG_42_GENE_18	tRNA pseudouridine synthase	NO DATA	-	-
18	UBA_8241_GENE_16	**conserved hypothetical protein [Solibacter usitatu**	50.5	0	100.00	5way_CG_42_GENE_19	**c hypo**	50.5	0	1.00
19	UBA_8241_GENE_17	**Glycerol-3-phosphate dehydrogenase**	25.8	0	97.45	5way_CG_42_GENE_20	**ycerol-3-phosph dehydrogenase**	42.5	13	0.61
20	UBA_8241_GENE_18	**Predicted phosphoribosyltransferases**	11.2	0	91.93	5way_CG_42_GENE_21	**c hypo**	42.6	5	0.26
21	UBA_8241_GENE_19	Hypothetical	NO DATA	-	92.31	5way_CG_42_GENE_22	hypo unique	NO DATA	-	-
22	UBA_8241_GENE_20	Predicted signal transduction protein containing a	NO DATA	-	94.80	5way_CG_42_GENE_23	GGDEF domain/EAL domain	NO DATA	-	-
23	UBA_8241_GENE_21	**Phospholipid-binding protein**	23.4	18	95.21	5way_CG_42_GENE_24	**phospholipid binding protein**	24.5	0	0.96
24	UBA_8241_GENE_22	**Seryl-tRNA synthetase**	35.1	0	93.41	5way_CG_42_GENE_25	**seryl tRNA synthetase**	59	59	0.59
25	UBA_8241_GENE_23	**Hypothetical**	52	9	94.31	5way_CG_42_GENE_26	**hypo unique**	38.2	0	1.36
26	UBA_8241_GENE_24	**Hypothetical**	58.3	17	95.02	5way_CG_42_GENE_27	**hypo unique**	38.2	0	1.53
27	UBA_8241_GENE_25	Hypothetical	NO DATA	-	92.86	5way_CG_42_GENE_27a		NO DATA	-	-
28	UBA_8241_GENE_27	**Hypothetical, split with above?**	12	0	98.26	5way_CG_42_GENE_29	**GTPases**	21.8	3	0.55
29	UBA_8241_GENE_28	Hypothetical	NO DATA	-	89.57	5way_CG_42_GENE_30	hypo unique	NO DATA	-	-
30	UBA_8241_GENE_29	Hypothetical	NO DATA	-	88.89	5way_CG_42_GENE_31	c hypo	NO DATA	-	-
31	UBA_8241_GENE_30	**Hypothetical**	52.1	0	97.14	5way_CG_42_GENE_32	**hypo unique**	85.7	30	0.61
32	UBA_8241_GENE_31	**Predicted Zn-dependent peptidases**	48.1	0	97.06	5way_CG_42_GENE_33	**peptidase**	65.1	52	0.74
33	UBA_8241_GENE_32	**Predicted Zn-dependent peptidases**	64.4	6	95.43	5way_CG_42_GENE_34	**zinc-dependent peptidase**	74.8	91	0.86
34	UBA_8241_GENE_33	Hypothetical	NO DATA	-	93.26	5way_CG_42_GENE_35	hypo unique	NO DATA	-	-
35	UBA_8241_GENE_34	NhaP-type Na+/H+ and K+/H+ antiporters	NO DATA	-	95.07	5way_CG_42_GENE_36	Na+/H+ antiporter	NO DATA	-	-
36	UBA_8241_GENE_35	77 Permeases of the major facilitator superfamily	NO DATA	-	93.71	5way_CG_42_GENE_37	metabolite transport protein	NO DATA	-	-
37	UBA_8241_GENE_37	hypothetical protein Mmc1DRAFT_0956 [Magneto	NO DATA	-	91.75	5way_CG_42_GENE_38	hypo unique	NO DATA	-	-
38			NO GENE	-		5way_CG_42_GENE_39	hypo unique	NO DATA	-	-
39			NO GENE	-		5way_CG_42_GENE_40	hypo unique	NO DATA	-	-
40			NO GENE	-		5way_CG_42_GENE_41	hypo unique	NO DATA	-	-
41			NO GENE	-		5way_CG_42_GENE_44	hypo unique	NO DATA	-	-
42			NO GENE	-		5way_CG_42_GENE_45	hypo unique	NO DATA	-	-
43			NO GENE	-		5way_CG_42_GENE_47	hypo unique	NO DATA	-	-
44			NO GENE	-		5way_CG_42_GENE_48	transposase	NO DATA	-	-
45			NO GENE	-		5way_CG_42_GENE_49	hypo unique	NO DATA	-	-
46			NO GENE	-		5way_CG_21_GENE_1	transposase	NO DATA	-	-
47			NO GENE	-		5way_CG_21_GENE_2	c hypo	NO DATA	-	-
48			NO GENE	-		5way_CG_21_GENE_3	c hypo	NO DATA	-	-
49			NO GENE	-		5way_CG_21_GENE_5	hypo unique	NO DATA	-	-
50			NO GENE	-		5way_CG_21_GENE_6	**integrase**	NO DATA	-	-
51		TRNA Arg ACG 34018..34094 (-)	-						-	
52	UBA_8241_GENE_38	**Leucyl-tRNA synthetase**	23.6	0	96.38	5way_CG_21_GENE_8	**leucyl tRNA synthetase**	39.7	21	0.59
53	UBA_8241_GENE_39	**lipoprotein, putative [Pelobacter carbinolicus DSM**	10.5	0	92.47	5way_CG_21_GENE_9	**c hypo**	10.5	0	1.00
54	UBA_8241_GENE_40	DNA polymerase III, delta subunit, putative [Geob	NO DATA	-	91.95	5way_CG_21_GENE_10	**DNA polymerase III, beta subunit**	6.6	2	0.06
55	UBA_8241_GENE_41	**Hypothetical**	86.2	0	98.85	5way_CG_21_GENE_11	**possible ribosomal protein S20**	86.2	0	1.00
56	UBA_8241_GENE_42	Uncharacterized membrane protein, putative viru	NO DATA	-	95.74	5way_CG_21_GENE_12	similar to virulence factor MviN	NO DATA	-	-
57	UBA_8241_GENE_43	**Restriction endonuclease**	12.9	0	99.46	5way_CG_21_GENE_13	**HNH endonuclease**	12.9	0	1.00
58	UBA_8241_GENE_44	**Uncharacterized conserved protein**	47.3	1	93.66	5way_CG_21_GENE_14	**c hypo**	69.2	52	0.68
59	UBA_8241_GENE_45a		NO DATA	-	88.34	5way_CG_21_GENE_15	c hypo	NO DATA	-	-
60	UBA_8241_GENE_46	Hypothetical	15.3	0	95.29	5way_CG_21_GENE_16	hypo unique	15.3	0	1.00
61	UBA_8241_GENE_47	**Predicted ATPase of the PP-loop superfamily implic**	22.1	0	95.11	5way_CG_21_GENE_17	**ATPase of the PP-loop superfamily**	31.6	2	0.70
62	UBA_8241_GENE_48	Hypothetical	NO DATA	-	95.67	5way_CG_21_GENE_18	**hypo unique**	9.6	1	0.06
63	UBA_8241_GENE_49	HD-GYP domain	NO DATA	-	94.81	5way_CG_21_GENE_19	**-GYP domain response regulator**	6.8	1	0.06
64	UBA_8241_GENE_50a		100	-	100.00	5way_CG_21_GENE_20	**hypo unique**	60	-	-
65		TRNA His GTG 48117..48191 (-)	-						-	
66	UBA_8241_GENE_51	Anthranilate/para-aminobenzoate synthases com	NO DATA	-	92.74	5way_CG_21_GENE_21	nthranilate synthase component	NO DATA	-	-
67	UBA_8241_GENE_52	Branched-chain amino acid aminotransferase/4-c	NO DATA	-	90.17	5way_CG_21_GENE_22	**ain amino acid aminotransferase**	9.8	2	0.06

68	UBA_8241_GENE_53	**Rubrerythrin**	92.1	0	100.00	5way_CG_21_GENE_23	**rubrerythrin**	92.1		0	1.00
69	UBA_8241_GENE_54	**Ribonucleotide reductase, alpha subunit**	65.8	0	99.04	5way_CG_21_GENE_24	**boncleotide-diphosphate reduct**	77.2		45	0.85
70	UBA_8241_GENE_55	**Uncharacterized protein conserved in bacteria**	36.2	0	96.49	5way_CG_21_GENE_25	**c hypo**	55.6		43	0.65
71	UBA_8241_GENE_56	**Collagen-binding surface adhesin SpaP (antigen I**	73.7	0	99.02	5way_CG_21_GENE_26	**c hypo**	73.7		0	1.00
72	UBA_8241_GENE_57	Cation/multidrug efflux pump - split??	NO DATA	-	91.69	5way_CG_21_GENE_27	cation efflux transporter	NO DATA	-	-	
73	UBA_8241_GENE_57	Cation/multidrug efflux pump - split??	NO DATA	-	88.94	5way_CG_21_GENE_28	cation efflux system protein	NO DATA	-	-	
74		TRNA Arg TCG 59936..60012 (-)		-					-		
75	UBA_8241_GENE_58	**Hypothetical**	15.1	1	96.05	5way_CG_21_GENE_31	**hypo unique**	10.5		5	1.44
76		TRNA Cys GCA 60793..60867 (+)		-					-		
77	UBA_8241_GENE_60	77 Permeases of the major facilitator superfamily	NO DATA	-	97.33	5way_CG_21_GENE_32	proline betaine transporter	NO DATA	-	-	
78	UBA_8241_GENE_61a		15	1	88.77	5way_CG_21_GENE_34	**inobutyric acid acetyltransferase**	23.5		6	0.64
79	UBA_8241_GENE_62	**4-aminobutyrate aminotransferase and related an**	14.8	0	97.88	5way_CG_21_GENE_35	**yrate pyruvate aminotransferase**	14.8		0	1.00
80	UBA_8241_GENE_63	: Uncharacterized conserved protein, contains do	NO DATA	-	96.95	5way_CG_21_GENE_36	**ectoine synthase**	22.1		1	0.06
81	UBA_8241_GENE_64	**phytanoyl-CoA deoxygenase family protein [Hahe**	10.5	0	94.43	5way_CG_21_GENE_37	**L-proline 4-hydroxylase**	38		18	0.28
82	UBA_8241_GENE_65	**Hypothetical**	36.1	0	87.07	5way_CG_21_GENE_38	**hypo**	49		6	0.74
83	UBA_8241_GENE_66	Hypothetical	NO DATA	-	95.42	5way_CG_21_GENE_39	hypo unique	NO DATA	-	-	
84	UBA_8241_GENE_67	Hypothetical	NO DATA	-	77.61	5way_CG_21_GENE_40	hypo unique	NO DATA	-	-	
85	UBA_8241_GENE_68	Ca2+/Na+ antiporter	NO DATA	-	90.43	5way_CG_21_GENE_41	Ca++/Na+ antiporter	NO DATA	-	-	
86	UBA_8241_GENE_69	77 Permeases of the major facilitator superfamily	NO DATA	-	91.13	5way_CG_21_GENE_42	major facilitator family permease	NO DATA	-	-	
87	UBA_8241_GENE_70	Hypothetical	NO DATA	-	97.20	5way_CG_21_GENE_43	ene call somewhere here c hypo	NO DATA	-	-	
88	UBA_8241_GENE_71	Putative proteasome component:Actinomycetale	NO DATA	-	99.33	5way_CG_21_GENE_44	ene call somewhere here c hypo	NO DATA	-	-	
89	UBA_8241_GENE_72	**20S proteasome, alpha and beta subunits**	17.5	0	99.13	5way_CG_21_GENE_45	**20S proteasome, alpha subunit**	35.4		4	0.49
90	UBA_8241_GENE_73	**20S proteasome, alpha and beta subunits**	42.5	0	96.43	5way_CG_21_GENE_46	**20S proteasome, beta subunit**	59.5		16	0.71
91	UBA_8241_GENE_74	Hypothetical	NO DATA	-	97.14	5way_CG_21_GENE_47	**hypo**	45.7		29	0.06
92	UBA_8241_GENE_75	**Putative proteasome component:Actinomycetale**	34.3	1	97.43	5way_CG_21_GENE_48	**c hypo**	47.3		9	0.73
93	UBA_8241_GENE_76	**ATPases of the AAA+ class**	50.6	0	99.14	5way_CG_21_GENE_49	**AAA family ATPase**	57		15	0.89
94	UBA_8241_GENE_77	**Peroxiredoxin**	57.6	0	98.73	5way_CG_21_GENE_51	**omigratory protein/peroxiredoxin**	86.1		64	0.67
95	UBA_8241_GENE_78	**Membrane protease subunits, stomatin/prohibitin**	74.8	1	99.30	5way_CG_21_GENE_52	**membrane protease**	75.5		2	0.99
96	UBA_8241_GENE_79	**Hypothetical**	43.1	0	93.07	5way_CG_21_GENE_53	**hypo unique**	74.8		75	0.58
97	UBA_8241_GENE_80	**Hypothetical**	28	0	96.77	5way_CG_21_GENE_54	**hypo unique**	51.6		16	0.54
98	UBA_8241_GENE_81	**Hypothetical**	31.3	0	97.39	5way_CG_21_GENE_56	**hypo unique**	31.3		0	1.00
99	UBA_8241_GENE_82	Zn-dependent alcohol dehydrogenases	4.8	0	92.22	5way_CG_21_GENE_57	**pendent alcohol dehydrogenase**	38.9		15	0.12
100	UBA_8241_GENE_83	**conserved hypothetical protein [Geobacter sulfur**	19.4	0	95.83	5way_CG_21_GENE_58	**odanese-related sulfurtransferase**	19.4		0	1.00
101	UBA_8241_GENE_84	**Cation/multidrug efflux pump**	17.4	0	97.70	5way_CG_21_GENE_59	**cation efflux pump**	34.9		46	0.50
102	UBA_8241_GENE_85	**Membrane-fusion protein**	25.2	0	89.68	5way_CG_32_GENE_53	**efflux transporter**	73.1		138	0.34
103	UBA_8241_GENE_86	**Outer membrane protein**	43.2	0	95.55	5way_CG_32_GENE_52	**outer membrane efflux protein**	51.1		26	0.85
104	UBA_8241_GENE_87	Predicted transcriptional regulators	NO DATA	-	96.43	5way_CG_32_GENE_51	transcriptional regulator	NO DATA	-	-	
105	UBA_8241_GENE_88	Hypothetical	NO DATA	-	98.88	5way_CG_32_GENE_50	hypo unique	NO DATA	-	-	
106	UBA_8241_GENE_89	**Helicase subunit of the DNA excision repair compl**	7.1	1	96.43	5way_CG_32_GENE_49	**excinuclease ABC, subunit B**	17.8		5	0.40
107	UBA_8241_GENE_90	Uncharacterized conserved protein	NO DATA	-	93.16	5way_CG_32_GENE_48	c hypo	NO DATA	-	-	
108	UBA_8241_GENE_91	**Predicted Rossmann fold nucleotide-binding prote**	21.8	0	96.65	5way_CG_32_GENE_47	**ybdenum cofactor carrier protein**	39.7		17	0.55
109	UBA_8241_GENE_92	**Hypothetical**	25.4	0	94.55	5way_CG_32_GENE_46	**aminopeptidase**	43.5		56	0.58
110	UBA_8241_GENE_93	**Thiol-disulfide isomerase and thioredoxins**	53.7	0	97.14	5way_CG_32_GENE_45	**thioldisulfide isomerase**	76.9		16	0.70
111	UBA_8241_GENE_94a		NO DATA	-	84.58	5way_CG_32_GENE_44	**endonuclease**	10.3		1	0.06
112	UBA_8241_GENE_95	Hypothetical	NO DATA	-	85.90	5way_CG_32_GENE_43	hypo unique	NO DATA	-	-	
113	UBA_8241_GENE_96	Cytochrome B561, bacterial [Shewanella baltica (	NO DATA	-	96.44	5way_CG_32_GENE_42	**hypo unique**	7.5		2	0.06
114	UBA_8241_GENE_97	FOG: EAL domain	NO DATA	-	95.66	5way_CG_32_GENE_41	GDEF domain/EAL domain protein	NO DATA	-	-	
115	UBA_8241_GENE_98	**Cation transport ATPase**	18.3	0	91.93	5way_CG_32_GENE_40	**cation transport ATPase**	47.6		61	0.38
116	UBA_8241_GENE_99	**Ammonia permease**	6.7	0	100.00	5way_CG_32_GENE_39	**ammonium transporter AMT2**	6.7		0	1.00
117	UBA_8241_GENE_100	**Nitrogen regulatory protein PII**	88.4	0	99.11	5way_CG_32_GENE_38	**tein PII (Gln synthetase regulator)**	98.2		26	0.90
118	UBA_8241_GENE_101	Ammonia permease	NO DATA	-	99.39	5way_CG_32_GENE_37	**ammonia permease**	8.2		14	0.06
119	UBA_8241_GENE_103	**Lfe107p1 [Leptospirillum ferrooxidans] induced unc**	12.5	0	96.46	5way_CG_32_GENE_36	**c hypo**	18.7		9	0.67
120	UBA_8241_GENE_104	Hypothetical	NO DATA	-	82.47	5way_CG_32_GENE_35	hypo unique	NO DATA	-	-	
121	UBA_8241_GENE_105	**Cystathionine beta-lyases/cystathionine gamma-**	31.4	0	94.01	5way_CG_32_GENE_34	**methionine gamma lyase**	48.6		9	0.65
122	UBA_8241_GENE_107	**Lfe126p - check for unique peptides**	30.4	0	96.71	5way_CG_32_GENE_33	**GGDEF domain protein**	44.7		16	0.68
123	UBA_8241_GENE_108	ABC-type dipeptide/oligopeptide/nickel transport	NO DATA	-	95.71	5way_CG_32_GENE_32	peptide ABC transporter	NO DATA	-	-	
124	UBA_8241_GENE_109	ABC-type dipeptide/oligopeptide/nickel transport	NO DATA	-	96.82	5way_CG_32_GENE_31	peptide ABC transporter	NO DATA	-	-	
125	UBA_8241_GENE_110	Hypothetical	NO DATA	-	82.22	5way_CG_32_GENE_29	hypo unique	NO DATA	-	-	
126	UBA_8241_GENE_111	**Hypothetical**	39.7	0	92.06	5way_CG_32_GENE_28	**hypo unique**	88.1		31	0.45
127	UBA_8241_GENE_112	**Hypothetical**	18.1	0	100.00	5way_CG_32_GENE_27	**in found in small soluble proteins**	18.1		0	1.00
128	UBA_8241_GENE_113	**Hypothetical**	33.7	0	94.71	5way_CG_32_GENE_26	**hypo unique**	61.5		36	0.55
129	UBA_8241_GENE_114	**Uncharacterized protein related to plant photosyst**	45.2	0	97.16	5way_CG_32_GENE_25	**c hypo**	55.7		2	0.81
130	UBA_8241_GENE_115	Hypothetical	NO DATA	-				NO GENE	-	-	
131	UBA_8241_GENE_116	Hypothetical	NO DATA	-	94.17	5way_CG_32_GENE_24	**hypo unique**	13		20	0.06
132	UBA_8241_GENE_117	**Predicted phosphatase/phosphohexomutase**	17.4	0	92.24	5way_CG_32_GENE_23	**/phosphoglycolate phosphatase**	38.8		12	0.45
133	UBA_8241_GENE_118	**Carbonic anhydrases/acetyltransferases, isoleuci**	22.6	0	97.18	5way_CG_32_GENE_22	**hexapeptide transferase**	35.6		3	0.63
134	UBA_8241_GENE_119	Signal transduction histidine kinase	NO DATA	-	97.44	5way_CG_32_GENE_21	sensor histidine kinase	NO DATA	-	-	
135	UBA_8241_GENE_120	**Response regulator containing CheY-like receiver,**	21.6	0	97.10	5way_CG_32_GENE_20	**DNA-binding response regulator**	45.9		4	0.47
136	UBA_8241_GENE_121	**Trypsin-like serine proteases, typically periplasmic**	69.2	0	97.00	5way_CG_32_GENE_19	**serine protease**	73		48	0.95
137	UBA_8241_GENE_122	**Holliday junction resolvasome, endonuclease sub**	53.8	0	94.30	5way_CG_32_GENE_18	**Holliday junction resolvase**	62		17	0.87
138	UBA_8241_GENE_123	**Holliday junction resolvasome, DNA-binding subu**	26	0	92.79	5way_CG_32_GENE_17	**Holliday junction helicase**	45.7		7	0.57
139	UBA_8241_GENE_124	**Holliday junction resolvasome, helicase subunit**	31.6	0	96.69	5way_CG_32_GENE_16	**Holliday junction helicase**	34		1	0.93

140	UBA_8241_GENE_125	**Hypothetical**	21.6	0	90.87	5way_CG_32_GENE_15	**hypo unique**	56.8		6	0.38
141	UBA_8241_GENE_126	**Periplasmic serine proteases (ClpP class)**	53.4	0	97.47	5way_CG_32_GENE_14	**periplasmic serine protease**	53.4		0	1.00
142	UBA_8241_GENE_127	**Hypothetical**	23.8	0	90.03	5way_CG_32_GENE_13	**hypo unique**	60.4		50	0.39
143	UBA_8241_GENE_128	PilT protein, N-terminal [Solibacter usitatus Ellin6076	NO DATA	-	91.43	5way_CG_32_GENE_12	be split with below?	hypo unique	NO DATA -	-	
144	UBA_8241_GENE_128	PilT protein, N-terminal [Solibacter usitatus Ellin6076	NO DATA	-	94.00	5way_CG_32_GENE_11	c hypo	NO DATA	-	-	
145	UBA_8241_GENE_129	hypothetical protein [Synechococcus elongatus P	NO DATA	-	98.44	5way_CG_32_GENE_10	c hypo	NO DATA	-	-	
146			NO GENE	-		5way_CG_32_GENE_9	hypo unique	NO DATA	-	-	
147	UBA_8241_GENE_130	**Uncharacterized enzyme involved in biosynthesis**	50	0	99.04	5way_CG_32_GENE_8	**TRAP signal transduction protein**	56.7		3	0.88
148	UBA_8241_GENE_131	Predicted tRNA(5-methylaminomethyl-2-thiouridylc	NO DATA	-	88.72	5way_CG_32_GENE_7	2-thiouridylate)-methyltransferase	NO DATA	-	-	
149	UBA_8241_GENE_132	Fe-S oxidoreductases	NO DATA	-	81.35	5way_CG_32_GENE_6	**similar to Fe-S oxidoreductase**	13.5		2	0.06
150	UBA_8241_GENE_133	hypothetical protein Bcep18194_B0330 [Burkholde	NO DATA	-				NO GENE	-	-	
151	UBA_8241_GENE_133a		NO DATA	-				NO DATA	-	-	
152	UBA_8241_GENE_134	Hypothetical	NO DATA	-				NO GENE	-	-	
153	UBA_8241_GENE_135	Hypothetical	NO DATA	-				NO GENE	-	-	
154	UBA_8241_GENE_136	**2-polyprenylphenol hydroxylase and related flava**	14	0				NO GENE	-		35.00
155	UBA_8241_GENE_137	77 Permeases of the major facilitator superfamily	NO DATA	-				NO GENE	-	-	
156	UBA_8241_GENE_138	Hypothetical	NO DATA	-				NO GENE	-	-	
157	UBA_8241_GENE_139a		NO DATA	-				NO GENE	-	-	
158	UBA_8241_GENE_140	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
159	UBA_8241_GENE_142	conserved domain protein [Coxiella burnetii RSA 4	NO DATA	-				NO GENE	-	-	
160	UBA_8241_GENE_143	Hypothetical	NO DATA	-				NO GENE	-	-	
161	UBA_8241_GENE_144	Hypothetical	NO DATA	-	77.48	5way_CG_32_GENE_5	c hypo	NO DATA	-	-	
162	UBA_8241_GENE_145	**2-polyprenylphenol hydroxylase and related flava**	14	-	100.00	5way_CG_32_GENE_4	**tiny, hypo unique**	27.5	-	-	
163	UBA_8241_GENE_145		14	-	88.08	5way_CG_32_GENE_3	heterdisulfide reductase	NO DATA	-	-	
164	UBA_8241_GENE_146	77 Permeases of the major facilitator superfamily	NO DATA	-	75.19	5way_CG_32_GENE_1	major facilitator family permease	NO DATA	-	-	
165	UBA_8241_GENE_147	Hypothetical	NO DATA	-				NO GENE	-	-	
166			NO GENE	-		5way_CG_630_GENE_2	hypo unique	NO DATA	-	-	
167	UBA_8241_GENE_148	Hypothetical	NO DATA	-	74.51	5way_CG_630_GENE_3	**hypo unique (630-3, 865-2)**	54.9		42	0.06
168			NO GENE	-		5way_CG_630_GENE_4	**transposase**	8.8	-	-	
169			NO GENE	-		5way_CG_630_GENE_5	hypo unique	NO DATA	-	-	
170	UBA_8241_GENE_149	**Hypothetical (cyt 575, see full length on7508)**	7.4	0	67.43	5way_CG_630_GENE_6	**hypo unique**	35.1		157	0.21
171			NO GENE	-		5way_CG_815_GENE_1	probable transposase	NO DATA	-	-	
172		TRNA Leu CAA 144961..145047 (+)	-						-		
173			NO GENE	-		5way_CG_815_GENE_2	integrase	NO DATA	-	-	
174			NO GENE	-		5way_CG_815_GENE_3	hypo unique	NO DATA	-	-	
175			NO GENE	-		5way_CG_815_GENE_4	hypo unique	NO DATA	-	-	
176			NO GENE	-		5way_CG_815_GENE_5	**hypo**	9.1	-	-	
177			NO GENE	-		5way_CG_478_GENE_8	c hypo	NO DATA	-	-	
178			NO GENE	-		5way_CG_478_GENE_7	hypo unique	NO DATA	-	-	
179			NO GENE	-		5way_CG_478_GENE_6	**hypo**	69.1	-	-	
180			NO GENE	-		5way_CG_478_GENE_5	hypo unique	NO DATA	-	-	
181			NO GENE	-		5way_CG_478_GENE_4	**TrwC plasmid prot/DNA helicase**	7.3		7	0.03
182			NO GENE	-		5way_CG_478_GENE_3	hypo unique	NO DATA	-	-	
183			NO GENE	-		5way_CG_478_GENE_1	hypo unique	NO DATA	-	-	
184			NO GENE	-		5way_CG_478_GENE_2	hypo unique	NO DATA	-	-	
185			NO GENE	-		5way_CG_600_GENE_1	DNA helicase	NO DATA	-	-	
186			NO GENE	-		5way_CG_600_GENE_2	hypo unique	NO DATA	-	-	
187			NO GENE	-		5way_CG_600_GENE_3	hypo unique	NO DATA	-	-	
188			NO GENE	-		5way_CG_600_GENE_4	hypo unique	NO DATA	-	-	
189			NO GENE	-		5way_CG_600_GENE_5	TrwB conjugal transfer protein	NO DATA	-	-	
190			NO GENE	-		5way_CG_185_GENE_1	plasmid coupling protein Trwb	NO DATA	-	-	
191			NO GENE	-		5way_CG_185_GENE_2	hypo unique	NO DATA	-	-	
192			NO GENE	-		5way_CG_185_GENE_3	hypo unique	NO DATA	-	-	
193			NO GENE	-		5way_CG_185_GENE_4	hypo unique	NO DATA	-	-	
194			NO GENE	-		5way_CG_185_GENE_5	hypo unique	NO DATA	-	-	
195			NO GENE	-		5way_CG_185_GENE_6	hypo unique	NO DATA	-	-	
196			NO GENE	-		5way_CG_185_GENE_7	hypo unique	NO DATA	-	-	
197			NO GENE	-		5way_CG_185_GENE_8	hypo unique	NO DATA	-	-	
198			NO GENE	-		5way_CG_185_GENE_9	**hypo unique**	46.7		2	0.03
199			NO GENE	-		5way_CG_185_GENE_10	hypo unique	NO DATA	-	-	
200			NO GENE	-		5way_CG_185_GENE_12	hypo unique	NO DATA	-	-	
201			NO GENE	-		5way_CG_185_GENE_13	**hypo**	93.5		123	0.03
202			NO GENE	-		5way_CG_185_GENE_14	hypo unique	NO DATA	-	-	
203			NO GENE	-		5way_CG_185_GENE_15	**biopolymer transport, ExbD**	51.7		28	0.03
204			NO GENE	-		5way_CG_185_GENE_16	**, links inner and outer membrane**	59.1		211	0.03
205			NO GENE	-		5way_CG_185_GENE_18	**biopolymer transport, TolQ**	44.1		90	0.03
206			NO GENE	-		5way_CG_185_GENE_19	**hypo unique**	26.2		117	0.03
207			NO GENE	-		5way_CG_185_GENE_20	hypo unique	NO DATA	-	-	
208			NO GENE	-		5way_CG_185_GENE_21	hypo unique	NO DATA	-	-	
209			NO GENE	-		5way_CG_185_GENE_22	**c hypo**	20.2		0	0.03
210			NO GENE	-		5way_CG_265_GENE_2	hypo unique	NO DATA	-	-	
211			NO GENE	-		5way_CG_265_GENE_3	hypo unique	NO DATA	-	-	

212			NO GENE	-		5way_CG_265_GENE_4	hypo unique	NO DATA	-	-		
213			NO GENE	-		5way_CG_265_GENE_5	phage-related integrase	NO DATA	-	-		
214			NO GENE	-		5way_CG_265_GENE_6	c hypo	NO DATA	-	-		
215			NO GENE	-		5way_CG_265_GENE_7	hypo unique	NO DATA	-	-		
216			NO GENE	-		5way_CG_265_GENE_8	hypo unique	NO DATA	-	-		
217			NO GENE	-		5way_CG_265_GENE_9	**hypo unique**	28.8	-	-		
218			NO GENE	-		5way_CG_265_GENE_10	**probable transposase**	62	-	-		
219			NO GENE	-		5way_CG_265_GENE_11	**transposase**	NO DATA	-	-		
220			NO GENE	-		5way_CG_265_GENE_12	hypo unique	NO DATA	-	-		
221			NO GENE	-		5way_CG_265_GENE_13	integrase	NO DATA	-	-		
222			NO GENE	-		5way_CG_265_GENE_14	**c hypo**	75.2		0	0.03	
223			NO GENE	-		5way_CG_265_GENE_15	hypo unique	NO DATA	-	-		
224			NO GENE	-		5way_CG_261_GENE_12	hypo unique	NO DATA	-	-		
225			NO GENE	-		5way_CG_261_GENE_11	transposase	NO DATA	-	-		
226			NO GENE	-		5way_CG_261_GENE_10	hypo unique	NO DATA	-	-		
227			NO GENE	-		5way_CG_261_GENE_9	**73-38, etc.) probable transposase**	62	-	-		
228			NO GENE	-		5way_CG_261_GENE_8	transposase	NO DATA	-	-		
229			NO GENE	-		5way_CG_261_GENE_7	transposase	NO DATA	-	-		
230			NO GENE	-		5way_CG_261_GENE_6	c hypo	NO DATA	-	-		
231			NO GENE	-		5way_CG_261_GENE_5	c hypo	NO DATA	-	-		
232			NO GENE	-		5way_CG_261_GENE_4	hypo unique	NO DATA	-	-		
233			NO GENE	-		5way_CG_261_GENE_3	**restriction endonuclease**	20.2		0	0.03	
234			NO GENE	-		5way_CG_261_GENE_2	hypo unique	NO DATA	-	-		
235			NO GENE	-		5way_CG_261_GENE_1	transposase	NO DATA	-	-		
236			NO GENE	-		5way_CG_173_GENE_18	hypo unique	NO DATA	-	-		
237			NO GENE	-		5way_CG_173_GENE_17	hypo unique	NO DATA	-	-		
238			NO GENE	-		5way_CG_173_GENE_16	**probable transposase**	62	-	-		
239			NO GENE	-		5way_CG_173_GENE_15	transposase	NO DATA	-	-		
240			NO GENE	-		5way_CG_173_GENE_14	**hypo unique**	36		97	0.03	
241			NO GENE	-		5way_CG_173_GENE_13	c hypo	NO DATA	-	-		
242			NO GENE	-		5way_CG_173_GENE_12	hypo unique	NO DATA	-	-		
243			NO GENE	-		5way_CG_173_GENE_11	IstB helper protein/transposase	NO DATA	-	-		
244			NO GENE	-		5way_CG_173_GENE_10	transposase	NO DATA	-	-		
245			NO GENE	-		5way_CG_173_GENE_9	**c hypo**	13.1		26	0.03	
246			NO GENE	-		5way_CG_173_GENE_7	hypo unique	NO DATA	-	-		
247			NO GENE	-		5way_CG_173_GENE_5	transposase	NO DATA	-	-		
248			NO GENE	-		5way_CG_173_GENE_4	transposase	NO DATA	-	-		
249			NO GENE	-		5way_CG_173_GENE_3	hypo unique	NO DATA	-	-		
250			NO GENE	-		5way_CG_173_GENE_2	**hypo unique**	NO DATA	-	-		
251			NO GENE	-		5way_CG_173_GENE_1	replication protein A	NO DATA	-	-		
252			NO GENE	-		5way_CG_374_GENE_1	hypo unique	NO DATA	-	-		
253			NO GENE	-		5way_CG_374_GENE_2	**hypo unique**	90.9		0	0.03	
254			NO GENE	-		5way_CG_374_GENE_3	**transposase**	73.3	-	-		
255	UBA_8241_GENE_150a		NO DATA	-	100.00	5way_CG_374_GENE_4a		NO DATA	-	-		
256	UBA_8241_GENE_151	Hypothetical	NO DATA	-	100.00	5way_CG_374_GENE_5	hypo unique	NO DATA	-	-		
257	UBA_8241_GENE_152	**Hypothetical**	12.4	0	100.00	5way_CG_374_GENE_6	**hypo unique**	12.4		0	1.00	
258	UBA_8241_GENE_153	**Hypothetical**	54	0	100.00	5way_CG_374_GENE_7	**hypo unique**	54		0	1.00	
259	UBA_8241_GENE_154	**Hypothetical**	15.9	0	100.00	5way_CG_374_GENE_8	**c hypo**	15.9		0	1.00	
260	UBA_8241_GENE_155	2 [Leptospirillum ferrooxidans]	NO DATA	-	100.00	5way_CG_374_GENE_9	hypo unique	NO DATA	-	-		
261	UBA_8241_GENE_156	**3 [Leptospirillum ferrooxidans]**	14.2	-	100.00	5way_CG_374_GENE_10	**ellulose synthase operon protein**	21	-	-		
262	UBA_8241_GENE_157a		80	0	100.00	5way_CG_4_GENE_100	**c hypo**	80		0	1.00	
263	UBA_8241_GENE_158	**Predicted amidohydrolase**	41.4	0	100.00	5way_CG_4_GENE_99	**trogen hydrolase domain protein**	41.4		0	1.00	
264	UBA_8241_GENE_159	**Panthothenate synthetase**	12.6	0	100.00	5way_CG_4_GENE_98	**pantoate-beta-alanine ligase**	12.6		0	1.00	
265	UBA_8241_GENE_160	**Predicted methyltransferases**	39.4	0	100.00	5way_CG_4_GENE_97	**orrin/porphyrin methyltransferase**	39.4		0	1.00	
266	UBA_8241_GENE_161	**dUTPase**	70.1	0	100.00	5way_CG_4_GENE_96	**deoxyuridinetriphosphatase**	70.1		0	1.00	
267	UBA_8241_GENE_162	**Hypothetical**	55.1	0	100.00	5way_CG_4_GENE_95	**hypo unique**	55.1		0	1.00	
268	UBA_8241_GENE_163	**Acetylglutamate kinase**	56.2	0	100.00	5way_CG_4_GENE_94	**acetyl glutamate kinase**	56.2		0	1.00	
269	UBA_8241_GENE_164	**ATP-dependent protease HslVU (ClpYQ), ATPase s**	32	0	100.00	5way_CG_4_GENE_93	**ATP-dependent HslU protease**	32		0	1.00	
270	UBA_8241_GENE_165	**ATP-dependent protease HslVU (ClpYQ), peptidas**	66.1	0	100.00	5way_CG_4_GENE_92	**heat shock protease**	66.1		0	1.00	
271	UBA_8241_GENE_166	**Integrase**	NO DATA	-	100.00	5way_CG_4_GENE_91	**integrase (domain complete)**	NO DATA	-	-		
272	UBA_8241_GENE_167	**NAD(FAD)-utilizing enzyme possibly involved in tra**	20.8	0	99.77	5way_CG_4_GENE_90	**ucose-inhibited division protein A**	20.8		0	1.00	
273	UBA_8241_GENE_168	**Topoisomerase IA**	45.3	0	99.76	5way_CG_4_GENE_89	**DNA topoisomerase I**	48.8		5	0.93	
274	UBA_8241_GENE_169	Predicted Rossmann fold nucleotide-binding prote	NO DATA	-	88.89	5way_CG_4_GENE_88	DNA processing protein DprA	NO DATA	-	-		
275	UBA_8241_GENE_170	Hypothetical	NO DATA	-	91.11	5way_CG_4_GENE_87	**hypo unique**	22.2		2	0.06	
276	UBA_8241_GENE_171	**Uncharacterized conserved protein**	66.2	0	98.75	5way_CG_4_GENE_86	**C transporter, ATP-binding protein**	81.2		17	0.82	
277	UBA_8241_GENE_172	ABC-type nitrate/sulfonate/bicarbonate transport	NO DATA	-	97.62	5way_CG_4_GENE_85	C transporter, ATP-binding protein	NO DATA	-	-		
278	UBA_8241_GENE_173	ABC-type anion transport system, duplicated pern	NO DATA	-	94.97	5way_CG_4_GENE_84	BC transporter, permease protein	NO DATA	-	-		
279	UBA_8241_GENE_174	Hypothetical	14.6	0	97.08	5way_CG_4_GENE_83	**hypo unique**	33.6		9	0.43	
280	UBA_8241_GENE_175	**Hypothetical**	43	0	96.26	5way_CG_4_GENE_82	**hypo unique**	54.2		5	0.79	
281	UBA_8241_GENE_176	**hypothetical protein SO0962 [Shewanella oneiden**	29.1	1	97.71	5way_CG_4_GENE_81	**c hypo**	40		13	0.73	
282	UBA_8241_GENE_177	**Transposase and inactivated derivatives**	31.4	-				NO GENE	-	-		
283	UBA_8241_GENE_178	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-		

284	UBA_8241_GENE_179	Hypothetical	NO DATA	-		95.87	5way_CG_4_GENE_80	c hypo	NO DATA	-	-	
285	UBA_8241_GENE_180	A/G-specific DNA glycosylase	NO DATA	-		89.86	5way_CG_4_GENE_79	adenine glycosylase	NO DATA	-	-	
286	UBA_8241_GENE_181	Hypothetical	NO DATA	-		96.73	5way_CG_4_GENE_78	hypo unique	NO DATA	-	-	
287	UBA_8241_GENE_181a		NO DATA	-		91.95	5way_CG_4_GENE_77	ylpterin-pyrophosphokinase FolK	NO DATA	-	-	
288	UBA_8241_GENE_182	**Aspartate/tyrosine/aromatic aminotransferase**	66		19	98.48	5way_CG_4_GENE_76	**aminotransferase**	67		34	0.99
289	UBA_8241_GENE_183	Hypothetical	NO DATA	-		90.72	5way_CG_4_GENE_75	hypo unique	NO DATA	-	-	
290	UBA_8241_GENE_184	Hypothetical	NO DATA	-		95.25	5way_CG_4_GENE_74	hypo unique	NO DATA	-	-	
291	UBA_8241_GENE_184a		NO DATA	-		63.76	5way_CG_4_GENE_73	hypo unique	NO DATA	-	-	
292	UBA_8241_GENE_186	Hypothetical	NO DATA	-		77.63	5way_CG_4_GENE_72	hypo unique	NO DATA	-	-	
293	UBA_8241_GENE_187	Hypothetical	NO DATA	-		68.29	5way_CG_4_GENE_70a		NO DATA	-	-	
294	UBA_8241_GENE_188	**8 Dehydrogenases with different specificities (relat**	20.4		0	93.62	5way_CG_4_GENE_70	**dehydrogenase**	75.3		56	0.27
295	UBA_8241_GENE_189	Flagellar biosynthesis pathway, component FlhB	NO DATA	-		95.00	5way_CG_4_GENE_69	flagellar biosynthetic protein, FlhB	NO DATA	-	-	
296	UBA_8241_GENE_190	Hypothetical	NO DATA	-		82.66	5way_CG_4_GENE_68	hypo unique	NO DATA	-	-	
297	UBA_8241_GENE_191	**Hypothetical**	21		0	89.25	5way_CG_4_GENE_67	**- probably chemotaxis/flagella**	46.2		14	0.45
298	UBA_8241_GENE_192	Hypothetical	NO DATA	-		89.58	5way_CG_4_GENE_66	hypo unique	NO DATA	-	-	
299	UBA_8241_GENE_193	**Flagellar motor protein**	16.5		0	97.32	5way_CG_4_GENE_65	**flagellar motor protein, MotB**	25.3		3	0.65
300	UBA_8241_GENE_194	**Flagellar motor component**	14.6		0	99.62	5way_CG_4_GENE_64	**flagellar motor protein, MotA**	14.6		0	1.00
301	UBA_8241_GENE_195	**Chemotaxis signal transduction protein**	57.3		0	95.91	5way_CG_4_GENE_63	**nding chemotaxis protein, CheW**	74.9		7	0.77
302	UBA_8241_GENE_196	**Methyl-accepting chemotaxis protein**	44		0	97.85	5way_CG_4_GENE_62	**yl-accepting chemotaxis protein**	51.7		14	0.85
303	UBA_8241_GENE_197	**Chemotaxis response regulator containing a CheY**	10.2		0	93.31	5way_CG_4_GENE_61	**rotein-glutamate methylesterase**	22.1		3	0.46
304	UBA_8241_GENE_198	**Chemotaxis protein histidine kinase and related ki**	41.9		1	95.99	5way_CG_4_GENE_60	**chemotaxis histidine kinase**	54.3		26	0.77
305	UBA_8241_GENE_199	**FOG: CheY-like receiver**	46.8		0	99.21	5way_CG_4_GENE_59	**chemotaxis protein CheY**	69		21	0.68
306	UBA_8241_GENE_200	Methylase of chemotaxis methyl-accepting protei	NO DATA	-		94.70	5way_CG_4_GENE_58	s protein methyltransferase CheR	NO DATA	-	-	
307	UBA_8241_GENE_201	**DNA-directed RNA polymerase specialized sigma**	19.9		0	98.41	5way_CG_4_GENE_57	**sigma factor for flagellar operon**	56.2		20	0.35
308	UBA_8241_GENE_202	**Lfe160p2 [Leptospirillum ferrooxidans]**	77.9	-		98.95	5way_CG_4_GENE_56	**chromosome partitioning ATPase**	63.7	-	-	
309		[redacted]	NO GENE	-			5way_CG_4_GENE_55	**flagellar biosynthesis protein FlhF**	13.5	-	-	
310			NO GENE	-			5way_CG_4_GENE_54	**agellar biosynthetic protein FlhA)**	19.9	-	-	
311			NO GENE	-			5way_CG_4_GENE_53	flagellar biosynthesis protein, FlhB	NO DATA	-	-	
312			NO GENE	-			5way_CG_4_GENE_52	flagellar biosynthesis protein, FliR	NO DATA	-	-	
313			NO GENE	-			5way_CG_4_GENE_51	axis/flagella (novel lepto genera)	NO DATA	-	-	
314	UBA_8241_GENE_203	Transposase and inactivated derivatives	NO DATA	-				[redacted]	NO GENE	-	-	
315	UBA_8241_GENE_204	Flagellar biosynthesis pathway, component FliP	NO DATA	-		97.74	5way_CG_4_GENE_50	flagellar biosynthetic protein, FliP	NO DATA	-	-	
316	UBA_8241_GENE_205	**Hypothetical**	12.1		0	90.17	5way_CG_4_GENE_49	**e flagellar assembly protein FliO)**	38.7		7	0.31
317	UBA_8241_GENE_206	**Flagellar motor switch/type III secretory pathway p**	64		0	100.00	5way_CG_4_GENE_48	**flagellar motor switch**	64		0	1.00
318	UBA_8241_GENE_207	**Flagellar basal body-associated protein**	50		0	100.00	5way_CG_4_GENE_47	**flagellar protein FliL**	50		0	1.00
319	UBA_8241_GENE_208	**Flagellar hook protein FlgE**	51.4		1	98.03	5way_CG_4_GENE_46	**flagellar hook protein**	63.5		37	0.81
320	UBA_8241_GENE_209	**Flagellar hook capping protein**	38.8		1	96.01	5way_CG_4_GENE_45	**flagellar hook protein**	51.1		14	0.76
321	UBA_8241_GENE_210	Hypothetical	NO DATA	-		77.37	5way_CG_4_GENE_44	**hypo unique**	20.2		9	0.06
322	UBA_8241_GENE_211	**Hypothetical**	20.7		0	87.57	5way_CG_4_GENE_43	**c hypo**	20.7		0	1.00
323	UBA_8241_GENE_212	Hypothetical	NO DATA	-		85.71	5way_CG_4_GENE_42	hypo unique	NO DATA	-	-	
324	UBA_8241_GENE_213	Flagellar biosynthesis/type III secretory pathway A	NO DATA	-		95.89	5way_CG_4_GENE_41	flagellar-type ATPase, FliI	NO DATA	-	-	
325	UBA_8241_GENE_214	**Hypothetical**	6.8		0	90.41	5way_CG_4_GENE_40	**hypo unique**	38.8		13	0.18
326	UBA_8241_GENE_215	**Flagellar motor switch protein**	40.1		0	99.70	5way_CG_4_GENE_39	**agellar motor switch protein, FliG**	40.1		0	1.00
327	UBA_8241_GENE_216	**Flagellar biosynthesis/type III secretory pathway I**	32.2		0	98.87	5way_CG_4_GENE_38	**flagellar M-ring protein, FliF**	38.6		4	0.83
328	UBA_8241_GENE_217	Hypothetical	NO DATA	-		96.33	5way_CG_4_GENE_37	flagellar basal body protein, FliE	NO DATA	-	-	
329	UBA_8241_GENE_218	Flagellar basal body rod protein	NO DATA	-		99.31	5way_CG_4_GENE_36	**lagellar basal body protein, FlgC**	20.7		1	0.06
330	UBA_8241_GENE_219	Flagellar basal body protein	NO DATA	-		93.55	5way_CG_4_GENE_35	flagellar basal body protein, FlgB	NO DATA	-	-	
331	UBA_8241_GENE_220	**Response regulator containing CheY-like receiver,**	7.2		0	95.09	5way_CG_4_GENE_34	**pendant response regulator, FleR**	14.7		2	0.49
332	UBA_8241_GENE_221	**Signal transduction histidine kinase**	26.6		0	94.09	5way_CG_4_GENE_33	**sensory box histidine kinase**	28.8		1	0.92
333	UBA_8241_GENE_222	**Lfe144p1 [Leptospirillum ferrooxidans]**	15.7		1	90.13	5way_CG_4_GENE_32	**c hypo**	33.5		12	0.47
334	UBA_8241_GENE_223	**Response regulator containing CheY-like receiver,**	23.8		0	95.35	5way_CG_4_GENE_31	**ein FleQ, transcriptional regulator**	37.2		6	0.64
335	UBA_8241_GENE_224	Uncharacterized Fe-S protein	NO DATA	-		90.06	5way_CG_4_GENE_30	Fe-S cluster binding protein	NO DATA	-	-	
336	UBA_8241_GENE_225	**Predicted signal transduction protein**	17.4		0	95.73	5way_CG_4_GENE_29	**c hypo (contains HD domain)**	28.1		4	0.62
337	UBA_8241_GENE_226	Predicted signal transduction protein	NO DATA	-		94.29	5way_CG_4_GENE_28	c hypo (contains HD domain)	NO DATA	-	-	
338	UBA_8241_GENE_227	**Hypothetical**	34.5		0	96.36	5way_CG_4_GENE_27	**hypo unique**	74.5		6	0.46
339	UBA_8241_GENE_228	Hypothetical	NO DATA	-		91.39	5way_CG_4_GENE_26	lipoate protein ligase	NO DATA	-	-	
340	UBA_8241_GENE_229	**Glycine cleavage system protein P (pyridoxal-bin**	47.4		0	97.38	5way_CG_4_GENE_25	**glycine dehydrogenase**	67.1		56	0.71
341	UBA_8241_GENE_230	**Glycine cleavage system protein P (pyridoxal-bin**	20.8		0	96.03	5way_CG_4_GENE_24	**avage system P protein, subunit 1**	59.4		47	0.35
342	UBA_8241_GENE_231	**Glycine cleavage system H protein (lipoate-bindir**	37.3		0	93.28	5way_CG_4_GENE_23	**glycine cleavage system protein**	93.3		40	0.40
343	UBA_8241_GENE_232	**Glycine cleavage system T protein (aminomethylt**	6.7		0	88.86	5way_CG_4_GENE_22	**lycine cleavage system T protein**	43.2		40	0.16
344	UBA_8241_GENE_234	**Hypothetical**	45.4		0	96.64	5way_CG_4_GENE_21	**eptidyl-prolyl cis-trans isomerase**	76.5		27	0.59
345	UBA_8241_GENE_235	Methyl-accepting chemotaxis protein	NO DATA	-		91.41	5way_CG_4_GENE_20	yl-accepting chemotaxis protein	NO DATA	-	-	
346	UBA_8241_GENE_235	Methyl-accepting chemotaxis protein	NO DATA	-		87.64	5way_CG_4_GENE_19	it gene with above	hypo unique	NO DATA	-	-
347	UBA_8241_GENE_236	**Hypothetical**	6		0	95.65	5way_CG_4_GENE_18	**hypo unique**	6		0	1.00
348	UBA_8241_GENE_237	**ABC-type sulfate transport system, periplasmic co**	37.8		0	95.28	5way_CG_4_GENE_17	**sporter, periplasmic component)**	51.6		41	0.73
349	UBA_8241_GENE_238	**Hypothetical**	61.9		1	96.79	5way_CG_4_GENE_16	**hypo unique**	84.4		170	0.73
350	UBA_8241_GENE_239	**Rhodanese-related sulfurtransferase**	66.7		0	100.00	5way_CG_4_GENE_15	**sulfurylase**	66.7		0	1.00
351	UBA_8241_GENE_240	**Hypothetical**	68.3		0	98.02	5way_CG_4_GENE_14	**hypo unique**	80.2		12	0.85
352	UBA_8241_GENE_242	**tRNA(1-methyladenosine) methyltransferase and r**	31.5		0	97.10	5way_CG_4_GENE_13	**AM-dependent methyltransferase**	46.4		12	0.68
353	UBA_8241_GENE_243	SAM-dependent methyltransferases	NO DATA	-		91.08	5way_CG_4_GENE_12	methyl transferase	NO DATA	-	-	
354	UBA_8241_GENE_244	**Thiol-disulfide isomerase and thioredoxins**	10.9		0	95.55	5way_CG_4_GENE_11	**chrome c biogenesis thioredoxin)**	39.9		18	0.27
355	UBA_8241_GENE_245	Hypothetical	3.7		2	88.25	5way_CG_4_GENE_10	hypo unique	NO DATA	-		20.00

356	UBA_8241_GENE_246	Hypothetical	NO DATA	-		94.03	5way_CG_4_GENE_9	hypo unique	NO DATA	-	-	
357	UBA_8241_GENE_247	**Diaminopimelate epimerase**	43.8	3		94.83	5way_CG_4_GENE_8	**diaminopimelate epimerase**	61.4		35	0.71
358	UBA_8241_GENE_248	**Hypothetical**	31	0		89.08	5way_CG_4_GENE_7	**hypo unique**	73.2		202	0.42
359	UBA_8241_GENE_249	8 Dehydrogenases with different specificities (relat	NO DATA	-		84.08	5way_CG_4_GENE_6	short chain dehydrogenase	NO DATA	-	-	
360	UBA_8241_GENE_250	**DnaK suppressor protein**	46.5	0		99.21	5way_CG_4_GENE_5	**DnaK suppressor protein**	52.8		2	0.88
361	UBA_8241_GENE_251	Uncharacterized conserved protein	NO DATA	-		91.41	5way_CG_4_GENE_4	oxidoreductase	NO DATA	-	-	
362	UBA_8241_GENE_252	**Putative silver efflux pump**	12.6	0		98.07	5way_CG_4_GENE_3	**metal efflux system protein**	14.1		1	0.89
363	UBA_8241_GENE_253	**Membrane-fusion protein**	42.6	1		95.26	5way_CG_4_GENE_2	**cation efflux protein**	58.7		35	0.73
364	UBA_8241_GENE_254	**Outer membrane protein**	30.1	0		98.91	5way_CG_59_GENE_29	**outer membrane efflux protein**	54.6		54	0.55
365	UBA_8241_GENE_255	Hypothetical	NO DATA	-					NO GENE	-	-	
366	UBA_8241_GENE_256	**Hypothetical**	45.1	0		94.66	5way_CG_59_GENE_28	**hypo unique**	68.9		45	0.65
367	UBA_8241_GENE_256a		NO DATA	-		87.14	5way_CG_59_GENE_27	**c hypo**	9.3		2	0.06
368	UBA_8241_GENE_258	**Hypothetical**	5.7	0		96.52	5way_CG_59_GENE_26	**hypo unique**	5.7		0	1.00
369	UBA_8241_GENE_259	**Predicted redox protein, regulator of disulfide bon**	63.4	0		97.56	5way_CG_59_GENE_24a		76.8		10	0.83
370	UBA_8241_GENE_260	**Hypothetical**	38	0		96.00	5way_CG_59_GENE_24	**hypo unique**	50		8	0.76
371	UBA_8241_GENE_261	**Transposase and inactivated derivatives, IS5 famil**	25.3	-					NO GENE	-	-	
372	UBA_8241_GENE_262	**Hypothetical**	42.4	0		95.08	5way_CG_59_GENE_23	**hypo unique**	44.3		4	0.96
373	UBA_8241_GENE_263	Hypothetical	NO DATA	-		89.16	5way_CG_59_GENE_22	**hypo unique**	66.3		18	0.06
374		TRNA Ser GGA 247314..247406 (+)	-							-		
375	UBA_8241_GENE_264	**DNA polymerase III, gamma/tau subunits**	15.2	1		95.00	5way_CG_59_GENE_21	**rase III, gamma and tau subunits**	42.2		19	0.36
376	UBA_8241_GENE_265	**Uncharacterized protein conserved in bacteria**	74	0		99.04	5way_CG_59_GENE_20	**c hypo**	74		41	1.00
377	UBA_8241_GENE_266	Recombinational DNA repair protein (RecF pathw	NO DATA	-		98.60	5way_CG_59_GENE_19	recombination protein, RecR	NO DATA	-	-	
378	UBA_8241_GENE_267	**Peptide chain release factor RF-3**	36.5	0		97.64	5way_CG_59_GENE_18	**peptide chain release factor 3**	51.2		11	0.71
379	UBA_8241_GENE_268	**Small-conductance mechanosensitive channel**	13.7	0		99.36	5way_CG_59_GENE_17	**potassium efflux system KefA**	13.7		0	1.00
380		TRNA Ser GCT 252853..252945 (-)	-							-		
381		TRNA Ser TGA 252964..253049 (-)	-							-		
382	UBA_8241_GENE_270	**FOG: TPR repeat**	35.7	0		92.57	5way_CG_59_GENE_16	**c hypo**	50.4		15	0.71
383	UBA_8241_GENE_271	Cytosine/adenosine deaminases check orf?	NO DATA	-		94.44	5way_CG_59_GENE_15	**dine/deoxycytidylate deaminase**	31.5		8	0.06
384		TRNA Ser CGA 254964..255053 (+)	-							-		
385	UBA_8241_GENE_273	**Transcriptional regulator containing PAS, AAA-typ**	31.1	1		96.25	5way_CG_59_GENE_14	**DNA-binding response regulator**	46.6		15	0.67
386	UBA_8241_GENE_274	**Hypothetical**	26.7	0		95.56	5way_CG_59_GENE_13	**hypo unique**	26.7		0	1.00
387	UBA_8241_GENE_276	**Protein containing tetrapyrrole methyltransferase**	30.6	0		95.68	5way_CG_59_GENE_12	**tetrapyrrole methylase family**	56.1		10	0.55
388	UBA_8241_GENE_277	**Anthranilate phosphoribosyltransferase**	30.5	1		91.02	5way_CG_59_GENE_11	**thranilate synthase component II**	59.3		17	0.51
389	UBA_8241_GENE_279	**HD-GYP domain**	15.7	-		97.09	5way_CG_59_GENE_10	**HD domain hydrolase**	28	-	-	
390	UBA_8241_GENE_280	**Predicted redox protein, regulator of disulfide bon**	80	0		98.75	5way_CG_59_GENE_9	**c hypo**	80		0	1.00
391	UBA_8241_GENE_281	**Uncharacterized conserved protein**	24.3	0		99.26	5way_CG_59_GENE_8	**c hypo**	33.8		23	0.72
392	UBA_8241_GENE_283	Hypothetical	NO DATA	-		94.44	5way_CG_59_GENE_7	hypo unique	NO DATA	-	-	
393	UBA_8241_GENE_284	**: Phospholipase C [Nostoc punctiforme PCC 73102**	26.1	0		96.66	5way_CG_59_GENE_6	**acid phosphatase**	46.2		16	0.56
394	UBA_8241_GENE_285	Hypothetical	NO DATA	-		95.91	5way_CG_59_GENE_5	**hypo unique**	11.4		3	0.06
395	UBA_8241_GENE_286	**Pyruvate/2-oxoglutarate dehydrogenase comple**	5.8	0		92.86	5way_CG_59_GENE_4	**DAHP synthase**	34.4		5	0.17
396	UBA_8241_GENE_287	Transposase, IS4 [Thermoanaerobacter ethanolicu	NO DATA	-					NO GENE	-	-	
397	UBA_8241_GENE_288	Hypothetical	NO DATA	-					NO GENE	-	-	
398			NO GENE	-			5way_CG_333_GENE_1	hypo unique - transposase	NO DATA	-	-	
399		TRNA Met CAT 266597..266673 (+)	-							-		
400	UBA_8241_GENE_289	Hypothetical	NO DATA	-		87.96	5way_CG_59_GENE_3	c hypo	NO DATA	-	-	
401	UBA_8241_GENE_290	Hypothetical	NO DATA	-		88.26	5way_CG_333_GENE_4	hypothetical	NO DATA	-	-	
402	UBA_8241_GENE_291	Hypothetical	NO DATA	-					NO GENE	-	-	
403	UBA_8241_GENE_292	Hypothetical	NO DATA	-		95.81	5way_CG_333_GENE_5		NO DATA	-	-	
404	UBA_8241_GENE_292a		NO DATA	-		93.12	5way_CG_333_GENE_6	uracil-DNA glycosylase	NO DATA	-	-	
405	UBA_8241_GENE_293	Hypothetical	NO DATA	-		100.00	5way_CG_333_GENE_7	hypo unique	NO DATA	-	-	
406	UBA_8241_GENE_294	**Hypothetical**	23.8	0		92.82	5way_CG_333_GENE_8	**hypo unique**	58.4		78	0.41
407	UBA_8241_GENE_295	**Hypothetical**	69.4	6		90.32	5way_CG_333_GENE_9	**hypo unique; (integral memb)**	60.5		54	1.15
408	UBA_8241_GENE_296	**Exoribonuclease R**	10.5	-		96.51	5way_CG_3_GENE_1	**exoribonuclease R**	13.2	-	-	
409	UBA_8241_GENE_297	**Hypothetical**	50	18		95.62	5way_CG_3_GENE_4	**hypo unique**	46.2		0	1.08
410	UBA_8241_GENE_298	**Outer membrane protein and related peptidoglyc**	62	6		98.32	5way_CG_3_GENE_5	**doglycan-associated lipoprotein**	57		0	1.09
411	UBA_8241_GENE_298a		67.7	48		92.64	5way_CG_3_GENE_6	**doglycan-associated lipoprotein)**	47.8		0	1.42
412	UBA_8241_GENE_299	Hypothetical	NO DATA	-		96.89	5way_CG_3_GENE_7	c hypo	NO DATA	-	-	
413	UBA_8241_GENE_300	**Thiamine monophosphate kinase**	14.3	1		89.55	5way_CG_3_GENE_8	**mine monophosphate kinase ThiL**	23.6		5	0.61
414	UBA_8241_GENE_301	**ATP-dependent Lon protease, bacterial type**	19.8	2		98.89	5way_CG_3_GENE_9	**ATP-dependant Lon protease**	24.4		9	0.81
415	UBA_8241_GENE_302	**UDP-glucose pyrophosphorylase**	44.1	0		97.31	5way_CG_3_GENE_10	**UDP-glucose pyrophosphorylase**	77.8		70	0.57
416	UBA_8241_GENE_303	**Dephospho-CoA kinase**	15.7	0		94.61	5way_CG_3_GENE_11	**dephospho-coA kinase**	54.4		14	0.29
417	UBA_8241_GENE_304	Hypothetical	NO DATA	-		96.86	5way_CG_3_GENE_12	hypo unique	NO DATA	-	-	
418	UBA_8241_GENE_305	**Chain B, Design Of Stable Alpha-Helical Arrays Fro**	10.9	0		98.25	5way_CG_3_GENE_13	**ble O-linked glycosyltransferase)**	22.3		1	0.49
419	UBA_8241_GENE_306	**DNA polymerase I - 3'-5' exonuclease and polym**	20.3	0		94.04	5way_CG_3_GENE_14	**DNA polymerase I**	27.5		16	0.74
420	UBA_8241_GENE_307	**Branched-chain amino acid aminotransferase/4-**	81	0		99.68	5way_CG_3_GENE_15	**ed-chain amino acid transferase**	88.1		1	0.92
421	UBA_8241_GENE_308	Integral membrane protein, interacts with FtsH	NO DATA	-		99.15	5way_CG_3_GENE_16	transport permease	NO DATA	-	-	
422	UBA_8241_GENE_309	Hypothetical	NO DATA	-		92.67	5way_CG_3_GENE_17	c hypo	NO DATA	-	-	
423	UBA_8241_GENE_310	Hypothetical possible split gene with below	NO DATA	-		86.79	5way_CG_3_GENE_18	c hypo	NO DATA	-	-	
424	UBA_8241_GENE_312	**Transcriptional regulator**	34.7	0		96.70	5way_CG_3_GENE_19	**transcriptional regulator**	59.1		17	0.59
425	UBA_8241_GENE_313	**Rad3-related DNA helicases**	6.5	0		94.99	5way_CG_3_GENE_20	**ATP-dependant helicase**	9.1		3	0.71
426	UBA_8241_GENE_314a		NO DATA	-		92.08	5way_CG_3_GENE_21	competent protein F	NO DATA	-	-	
427	UBA_8241_GENE_315	**IMP dehydrogenase/GMP reductase:TPR repeat [D**	27.6	0		97.22	5way_CG_3_GENE_22	**hypo**	50		20	0.55

428	UBA_8241_GENE_315a		20.5	0	96.22	5way_CG_3_GENE_23	c hypo	25.4		2	0.81
429	UBA_8241_GENE_316	Hypothetical	17	1	93.48	5way_CG_3_GENE_25	e-nucleotide adenylyltransferase	16.5		1	1.03
430	UBA_8241_GENE_317	Gamma-glutamyl phosphate reductase	24	0	95.72	5way_CG_3_GENE_26	a glutamyl phosphate reductase	56.3		29	0.43
431	UBA_8241_GENE_318	Glutamate 5-kinase	20.5	1	96.58	5way_CG_3_GENE_27	gamma glutamyl kinase	21.1		2	0.97
432	UBA_8241_GENE_319	Predicted GTPase	35.8	0	97.50	5way_CG_3_GENE_28	3-associated GTP-binding protein	61.1		12	0.59
433	UBA_8241_GENE_320	Ribosomal protein L27	56.5	2	97.83	5way_CG_3_GENE_29	ribosomal protein L27	58.7		36	0.96
434	UBA_8241_GENE_321	Ribosomal protein L21	23.6	0	97.17	5way_CG_3_GENE_30	ribosomal protein L21	70.8		31	0.33
435	UBA_8241_GENE_322	Fe2+/Zn2+ uptake regulation proteins	NO DATA	-	96.73	5way_CG_3_GENE_31	ferric uptake regulator	15.7		1	0.06
436	UBA_8241_GENE_323	BNR/Asp-box repeat protein [Azoarcus sp. EbN1]g	21.9	1	93.75	5way_CG_3_GENE_32	ytem II stability/assemby factor?	49.1		46	0.45
437		[redacted]	NO GENE	-		5way_CG_3_GENE_33	transposase	NO DATA	-	-	
438	UBA_8241_GENE_325	Hypothetical	NO DATA	-	96.42	5way_CG_3_GENE_34	hypo unique	NO DATA	-	-	
439	UBA_8241_GENE_326	6-pyruvoyl-tetrahydropterin synthase	38.3	0	97.66	5way_CG_3_GENE_36	voly tetrahydrobiopterin synthase	38.3		0	1.00
440	UBA_8241_GENE_327	ABC-type dipeptide/oligopeptide/nickel transport	17.9	4	95.24	5way_CG_3_GENE_37	C transporter ATP-binding protein	13.1		0	1.37
441	UBA_8241_GENE_328	ABC-type oligopeptide transport system, ATPase c	10.1	1	92.20	5way_CG_3_GENE_38	oligopeptide ABC transporter	NO DATA	-		20.00
442	UBA_8241_GENE_329	Phenylalanyl-tRNA synthetase alpha subunit	50.9	31	95.95	5way_CG_3_GENE_39	yl tRNa synthetase, alpha subunit	30.8		0	1.65
443	UBA_8241_GENE_330	Phenylalanyl-tRNA synthetase beta subunit	76.4	77	93.50	5way_CG_3_GENE_40	nyl tRNa synthetase, beta subunit	30.8		0	2.48
444	UBA_8241_GENE_331	Ribosomal protein L20	42.4	30	97.46	5way_CG_3_GENE_41	ribosomal protein L20	46.6		2	0.91
445	UBA_8241_GENE_332	Hypothetical	50.8	0	98.46	5way_CG_3_GENE_42	ribosomal protein L35	50.8		0	1.00
446	UBA_8241_GENE_333	Translation initiation factor 3 (IF-3)	72.6	13	97.14	5way_CG_3_GENE_43	Translation initiation factor	53.1		0	1.37
447	UBA_8241_GENE_334	Threonyl-tRNA synthetase	42.3	39	95.46	5way_CG_3_GENE_44	ossible threonyl tRNA synthetase	34.4		0	1.23
448	UBA_8241_GENE_335	FOG: GGDEF domain	29.5	19	91.40	5way_CG_3_GENE_45	GDEF domain/EAL domain protein	13.1		1	2.25
449	UBA_8241_GENE_336	Hydroxymethylpyrimidine/phosphomethylpyrimidi	57.8	21	87.99	5way_CG_3_GENE_46	oxymethylpyrimidine kinase ThiD	11.7		0	4.94
450	UBA_8241_GENE_337	Membrane proteins related to metalloendopeptid	41.6	21	90.54	5way_CG_3_GENE_47	peptidase, M23/M37 family	21.6		1	1.93
451	UBA_8241_GENE_338	Thiamine monophosphate synthase	49.8	6	96.74	5way_CG_3_GENE_48	osphate pyrophosphorylase ThiE	21.9		0	2.27
452	UBA_8241_GENE_339	Uncharacterized enzyme of thiazole biosynthesis	81.4	40	98.18	5way_CG_3_GENE_49	iamine biosynthesis protein ThiG	69.3		1	1.17
453	UBA_8241_GENE_340	Acyl-coenzyme A synthetases/AMP-(fatty) acid lig	45.9	17	97.19	5way_CG_3_GENE_50	acyl-coenzyme A synthetase	32.4		0	1.42
454	UBA_8241_GENE_341	Lactoylglutathione lyase and related lyases	28.9	0	98.97	5way_CG_3_GENE_51	lactoylglutathione lyase	28.9		0	1.00
455	UBA_8241_GENE_342a		NO DATA	-	83.70	5way_CG_3_GENE_52	hypo unique	NO DATA	-	-	
456	UBA_8241_GENE_343	UDP-N-acetylglucosamine:LPS N-acetylglucosamir	NO DATA	-	90.96	5way_CG_3_GENE_53	acylglycerol 3-glucosyltransferase	NO DATA	-	-	
457	UBA_8241_GENE_344	Uncharacterized protein conserved in bacteria	NO DATA	-	91.00	5way_CG_3_GENE_54	c hypo	NO DATA	-	-	
458	UBA_8241_GENE_345	77 Permeases of the major facilitator superfamily	NO DATA	-	94.07	5way_CG_3_GENE_55	multidrug efflux transporter	NO DATA	-	-	
459	UBA_8241_GENE_346	Dienelactone hydrolase and related enzymes	84.9	110	96.53	5way_CG_3_GENE_56	dienelactone hydrolase	64.9		1	1.31
460	UBA_8241_GENE_347	Hypothetical	NO DATA	-			[redacted]	NO GENE	-	-	
461	UBA_8241_GENE_348	FOG: WD40-like repeat	60.9	94	94.96	5way_CG_3_GENE_57	c hypo	42.5		0	1.43
462	UBA_8241_GENE_349	Hypothetical	66.1	147	96.36	5way_CG_3_GENE_58	hypo unique	41.8		0	1.58
463	UBA_8241_GENE_350	Signal transduction histidine kinase	22.4	1	99.37	5way_CG_3_GENE_59	omponent sensor histidine kinase	18.6		0	1.20
464	UBA_8241_GENE_351	Response regulators consisting of a CheY-like rece	NO DATA	-	98.65	5way_CG_3_GENE_60	o component response regulator	NO DATA	-	-	
465	UBA_8241_GENE_352	Hypothetical	87.4	17	96.69	5way_CG_3_GENE_61	hypo unique	49		0	1.78
466		TRNA Pro TGG 335638..335714 (-)		-					-		
467	UBA_8241_GENE_353	Hypothetical	16.7	0	96.23	5way_CG_3_GENE_62	hypo unique	16.7		0	1.00
468	UBA_8241_GENE_355	Zn-dependent hydrolases, including glyoxylases	57	34	90.78	5way_CG_3_GENE_63	zinc-dependant hydrolase	10.6		0	5.38
469	UBA_8241_GENE_356	F0F1-type ATP synthase, epsilon subunit (mitochon	76.2	18	98.60	5way_CG_3_GENE_64	ATP synthase, epsilon subunit	69.2		0	1.10
470	UBA_8241_GENE_357	F0F1-type ATP synthase, beta subunit	94.8	15	99.78	5way_CG_3_GENE_65	ATPsynth.	91.4		0	1.04
471	UBA_8241_GENE_358	F0F1-type ATP synthase, gamma subunit	76.3	38	98.97	5way_CG_3_GENE_66	ATP synthase, gamma subunit	64.6		0	1.18
472	UBA_8241_GENE_359	F0F1-type ATP synthase, alpha subunit	64.1	19	99.02	5way_CG_3_GENE_67	ATP synthase, alpha subunit	59.4		0	1.08
473	UBA_8241_GENE_360	Hypothetical	59.3	68	96.30	5way_CG_3_GENE_68	ATP synthase, delta subunit	35.4		0	1.68
474	UBA_8241_GENE_361	F0F1-type ATP synthase, subunit b	64.6	5	98.86	5way_CG_3_GENE_69	ATP synthase, beta subunit	61.1		0	1.06
475	UBA_8241_GENE_362	F0F1-type ATP synthase, subunit c/Archaeal/vacu	18.4	0	100.00	5way_CG_3_GENE_70	ATP synthase, subunit c	18.4		0	1.00
476	UBA_8241_GENE_363	F0F1-type ATP synthase, subunit a	NO DATA	-	96.72	5way_CG_3_GENE_71	ATP synthase, subunit a	NO DATA	-	-	
477	UBA_8241_GENE_364	Hypothetical	NO DATA	-	97.75	5way_CG_3_GENE_72	hypo unique	NO DATA	-	-	
478	UBA_8241_GENE_366	Hypothetical	NO DATA	-	96.95	5way_CG_3_GENE_73	c hypo	NO DATA	-	-	
479	UBA_8241_GENE_367	Predicted phosphatases	63.8	16	91.67	5way_CG_3_GENE_74	phosphoglycolate phosphatase	11.7		0	5.45
480	UBA_8241_GENE_368	ABC-type dipeptide/oligopeptide/nickel transport	NO DATA	-	95.00	5way_CG_3_GENE_75	peptide ABC transporter	NO DATA	-	-	
481	UBA_8241_GENE_369	ABC-type dipeptide/oligopeptide/nickel transport	NO DATA	-	95.99	5way_CG_3_GENE_76	peptide ABC transporter	NO DATA	-	-	
482	UBA_8241_GENE_370	ABC-type dipeptide transport system, periplasmic	33.1	9	95.88	5way_CG_3_GENE_77	binding protein of oligopeptide A	20.8		0	1.59
483	UBA_8241_GENE_371	Preprotein translocase SecG subunit [Syntrophoba	10.9	4	99.01	5way_CG_3_GENE_78	preprotein translocase SecG	NO DATA	-		20.00
484	UBA_8241_GENE_372	Triosephosphate isomerase	54.7	16	96.12	5way_CG_3_GENE_79	triosephosphate isomerase	29.1		0	1.88
485	UBA_8241_GENE_373	3-phosphoglycerate kinase	72.2	0	100.00	5way_CG_3_GENE_80	phosphoglycerate kinase	72.2		0	1.00
486	UBA_8241_GENE_374	Glyceraldehyde-3-phosphate dehydrogenase/er	81.6	70	98.25	5way_CG_3_GENE_81	de-3-phosphate dehydrogenase	56.4		0	1.45
487	UBA_8241_GENE_375	Membrane carboxypeptidase/penicillin-binding p	53.4	25	99.24	5way_CG_3_GENE_82	penicillin-binding protein	48.7		0	1.10
488	UBA_8241_GENE_376	Hypothetical	NO DATA	-	97.14	5way_CG_3_GENE_84	hypo unique	NO DATA	-	-	
489	UBA_8241_GENE_377	Orotate phosphoribosyltransferase	52.8	3	99.53	5way_CG_3_GENE_85	dine 5-monophosphate synthase	48.6		0	1.09
490	UBA_8241_GENE_378	Methyl-accepting chemotaxis protein	65.8	47	94.01	5way_CG_3_GENE_86	yl-accepting chemotaxis protein	41.8		0	1.57
491		TRNA Leu GAG 358476..358559 (-)		-					-		
492	UBA_8241_GENE_380	Siroheme synthase (precorrin-2 oxidase/ferrochel	53	5	93.06	5way_CG_3_GENE_89	siroheme synthase	15.7		0	3.38
493	UBA_8241_GENE_381	DNA uptake lipoprotein	36.6	14	97.12	5way_CG_3_GENE_90	competence protein ComL	28.4		0	1.29
494	UBA_8241_GENE_382	3-oxoacyl-[acyl-carrier-protein] synthase III	NO DATA	-	91.49	5way_CG_3_GENE_91	yl-(acyl-carrier-protein)synthase II	NO DATA	-	-	
495	UBA_8241_GENE_383	Response regulator containing CheY-like receiver,	27.1	5	98.47	5way_CG_3_GENE_92	nitrogen regulation protein NtrX	10.7		0	2.53
496	UBA_8241_GENE_384	Signal transduction histidine kinase involved in nit	18.5	1	98.00	5way_CG_3_GENE_93	gnal transduction histidine kinase	12.8		0	1.45
497	UBA_8241_GENE_385	Hypothetical	25.6	0	94.12	5way_CG_3_GENE_94	hypo unique	9.3		0	2.75
498	UBA_8241_GENE_386	Hypothetical	94.1	112	94.14	5way_CG_3_GENE_95	hypo unique	42.3		1	2.22
499	UBA_8241_GENE_387	Multiple antibiotic transporter	NO DATA	-	99.00	5way_CG_3_GENE_96	ntibiotic resistance protein MarC	NO DATA	-	-	

500	UBA_8241_GENE_387a		48.6	9	96.53	5way_CG_3_GENE_97	**hypo unique**	19.4		0	2.51
501	UBA_8241_GENE_389	**SAM-dependent methyltransferases**	25.4	5	90.87	5way_CG_3_GENE_98	ne biosynthesis methyltransferase	NO DATA	-		20.00
502	UBA_8241_GENE_390	**S-adenosylmethionine:tRNA-ribosyltransferase-iso**	9.1	1	90.86	5way_CG_3_GENE_99	ethionine tRNA ribosyl transferase	NO DATA	-		20.00
503	UBA_8241_GENE_391	**FOG: EAL domain**	26.5	9	94.80	5way_CG_3_GENE_100	**GDEF domain/EAL domain protein**	9.8		0	2.70
504	UBA_8241_GENE_392	**Hypothetical**	35.7	25	88.10	5way_CG_3_GENE_101	c hypo	NO DATA	-		20.00
505	UBA_8241_GENE_393	: Large exoproteins involved in heme utilization or	NO DATA	-	81.91	5way_CG_3_GENE_102	c hypo	NO DATA	-	-	
506	UBA_8241_GENE_394	**Uncharacterized NAD(FAD)-dependent dehydrog**	10.7	6	90.40	5way_CG_3_GENE_103	lfide-quinone reductase (147-16)	NO DATA	-		20.00
507	UBA_8241_GENE_395	**Carbonic anhydrase**	53.9	43	92.75	5way_CG_147_GENE_15	**carbonic anhydrase**	9.3		0	5.80
508	UBA_8241_GENE_396	**FOG: GGDEF domain**	50.5	15	93.75	5way_CG_147_GENE_14	**GDEF domain/EAL domain protein**	22		0	2.30
509	UBA_8241_GENE_396a		NO DATA	-	85.09	5way_CG_147_GENE_13	hypo unique	NO DATA	-	-	
510	UBA_8241_GENE_397	**Hypothetical**	59.7	0	98.39	5way_CG_147_GENE_11a		59.7		0	1.00
511	UBA_8241_GENE_399	DNA or RNA helicases of superfamily II	NO DATA	-	87.68	5way_CG_147_GENE_11	helicase	NO DATA	-	-	
512	UBA_8241_GENE_400	NTP pyrophosphohydrolases including oxidative d	NO DATA	-	81.34	5way_CG_147_GENE_10	NTP pyrophosphohydrolase	NO DATA	-	-	
513	UBA_8241_GENE_402	**HD-GYP domain**	18.3	8	93.28	5way_CG_147_GENE_9	o component response regulator	NO DATA	-		20.00
514	UBA_8241_GENE_403	Predicted esterase of the alpha-beta hydrolase su	NO DATA	-	94.55	5way_CG_147_GENE_8	serine protease	NO DATA	-	-	
515	UBA_8241_GENE_404	**NADPH:quinone reductase and related Zn-depend**	19.4	3	98.24	5way_CG_147_GENE_7	**alcohol dehydrogenase**	15.8		0	1.23
516	UBA_8241_GENE_405	Anti-sigma factor	NO DATA	-	100.00	5way_CG_147_GENE_6	allophanate hydrolase	NO DATA	-	-	
517	UBA_8241_GENE_406	Hypothetical	NO DATA	-	100.00	5way_CG_147_GENE_5	hypo unique	NO DATA	-	-	
518	UBA_8241_GENE_407	7 Permeases of the drug/metabolite transporter (D	NO DATA	-	100.00	5way_CG_147_GENE_4	transporter	NO DATA	-	-	
519	UBA_8241_GENE_408	**Uncharacterized protein conserved in bacteria**	42	0	100.00	5way_CG_147_GENE_3	**c hypo**	42		0	1.00
520	UBA_8241_GENE_409	**Predicted transcriptional regulator**	69.1	0	100.00	5way_CG_147_GENE_2	**redicted transcriptional regulator**	69.1		0	1.00
521		CRISPR tandem repeat region	NO GENE	-		CRISR tandem repeat	CRISPR	NO DATA	-	-	
522	UBA_8241_GENE_421	CRISPR-associated protein, Cas2 [Syntrophobacte	NO DATA	-		region		NO GENE	-	-	
523	UBA_8241_GENE_422	Uncharacterized protein predicted to be involved	NO DATA	-		(analysis to be reported separately) (continues below)		NO GENE	-	-	
524	UBA_8241_GENE_425	CRISPR-ssociated protein, Cas2 [Syntrophobacter	NO DATA	-	100.00	5way_CG_26_GENE_2	c hypo	NO DATA	-	-	
525	UBA_8241_GENE_426	**Uncharacterized protein**	NO DATA	-	100.00	5way_CG_26_GENE_3	**c hypo**	NO DATA	-	-	
526	UBA_8241_GENE_427	**CRISPR-associated protein, CT1974 [Pelobacter pro**	47.7	0	100.00	5way_CG_26_GENE_4	**c hypo**	47.7		0	1.00
527	UBA_8241_GENE_429	**CRISPR-associated protein, CT1976 [Pelobacter pro**	60.4	0	100.00	5way_CG_26_GENE_5	**c hypo**	60.4		0	1.00
528	UBA_8241_GENE_430	**CRISPR-associated protein, CT1975 [Pelobacter pro**	90.7	0	100.00	5way_CG_26_GENE_6	**c hypo**	90.7		0	1.00
529	UBA_8241_GENE_431	**hypothetical protein PproDRAFT_1803 [Pelobacter**	82.5	0	100.00	5way_CG_26_GENE_7	**c hypo**	82.5		0	1.00
530	UBA_8241_GENE_432	**hypothetical protein PproDRAFT_1802 [Pelobacter**	62.4	0	100.00	5way_CG_26_GENE_8	**c hypo**	62.4		0	1.00
531	UBA_8241_GENE_433	**Predicted helicases**	23.1	0	100.00	5way_CG_26_GENE_9	**RNA helicase**	23.1		0	1.00
532	UBA_8241_GENE_434	Hypothetical	NO DATA	-				NO GENE	-	-	
533	UBA_8241_GENE_436	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
534	UBA_8241_GENE_437	tmRNA-binding protein	NO DATA	-				NO GENE	-	-	
535	UBA_8241_GENE_438	**Transposase and inactivated derivatives, IS5 famil**	44.6	-	100.00	5way_CG_26_GENE_10	**transposase**	25.3	-	-	
536	UBA_8241_GENE_439	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_26_GENE_12	transposase	NO DATA	-	-	
537			NO GENE	-		5way_CG_26_GENE_13	hypo unique	NO DATA	-	-	
538			NO GENE	-		5way_CG_26_GENE_14	hypo unique	NO DATA	-	-	
539			NO GENE	-		5way_CG_26_GENE_15	**DNA methyltransferase/helicase**	18.2		15	0.03
540			NO GENE	-		5way_CG_26_GENE_16	c hypo	NO DATA	-	-	
541			NO GENE	-		5way_CG_26_GENE_17	c hypo	NO DATA	-	-	
542			NO GENE	-		5way_CG_26_GENE_18	hypo unique	NO DATA	-	-	
543			NO GENE	-		5way_CG_26_GENE_19	c hypo	NO DATA	-	-	
544			NO GENE	-		5way_CG_26_GENE_20	po, possibly virulence associated	NO DATA	-	-	
545			NO GENE	-		5way_CG_26_GENE_21	phage DNA binding protein	NO DATA	-	-	
546			NO GENE	-		5way_CG_26_GENE_22	hypo unique	NO DATA	-	-	
547			NO GENE	-		5way_CG_26_GENE_23	integrase INT P4	NO DATA	-	-	
548	UBA_8241_GENE_440	**tmRNA-binding protein**	47.2	0	100.00	5way_CG_26_GENE_24	**g protein/tmRNA-binding protein**	47.2		0	1.00
549	UBA_8241_GENE_441	**Leucyl aminopeptidase**	68.3	-	99.17	5way_CG_26_GENE_25	**leucyl aminopeptidase**	61.9	-	-	
550	UBA_8241_GENE_442	**Predicted PP-loop superfamily ATPase**	54.4	0	100.00	5way_CG_26_GENE_26	**an synthesis/transcription/ATPase**	54.4		0	1.00
551	UBA_8241_GENE_443	**Organic radical activating enzymes**	14.6	0	100.00	5way_CG_26_GENE_27	**SAM enzyme/Fe-S redox protein**	14.6		0	1.00
552	UBA_8241_GENE_444	**Hypothetical**	77.1	0	100.00	5way_CG_26_GENE_28	**c hypo**	77.1		0	1.00
553	UBA_8241_GENE_446	**Type IIA topoisomerase (DNA gyrase/topo II, topo**	36.3	0	100.00	5way_CG_26_GENE_29	**DNA gyrase**	36.3		0	1.00
554	UBA_8241_GENE_447	**Type IIA topoisomerase (DNA gyrase/topo II, topo**	40.8	0	100.00	5way_CG_26_GENE_30	**DNA gyrase, subunit B**	40.8		0	1.00
555	UBA_8241_GENE_448	**DNA polymerase sliding clamp subunit (PCNA hom**	75.7	2	99.48	5way_CG_26_GENE_31	**DNA polymerase III**	72.1		0	1.05
556	UBA_8241_GENE_449	**ATPase involved in DNA replication initiation**	36.1	0	100.00	5way_CG_26_GENE_32	**replication initiator protein DnaA**	36.1		0	1.00
557	UBA_8241_GENE_450	**Thiamine pyrophosphate-requiring enzymes [acet**	50.1	4	98.45	5way_CG_26_GENE_33	**acetolactate synthase**	46.5		0	1.08
558	UBA_8241_GENE_451	**Acetolactate synthase, small (regulatory) subunit**	63.6	16	98.37	5way_CG_26_GENE_34	**acetolactate synthase**	47.3		0	1.34
559	UBA_8241_GENE_452	**Ketol-acid reductoisomerase**	57.8	49	97.35	5way_CG_26_GENE_35	**ketol-acid reductoisomerase**	41.6		0	1.39
560	UBA_8241_GENE_453	**Phosphatidylserine decarboxylase**	25.8	2	96.31	5way_CG_26_GENE_36	**osphatidylserine decarboxylase**	22.1		0	1.17
561	UBA_8241_GENE_454a		NO DATA	-	99.28	5way_CG_26_GENE_37	serine O-phosphatidyltransferase	NO DATA	-	-	
562	UBA_8241_GENE_455	**Isopropylmalate/homocitrate/citramalate synthas**	38.3	3	96.99	5way_CG_26_GENE_38	**2-isopropylmalate synthase**	34.8		0	1.36
563	UBA_8241_GENE_456	**Isocitrate/isopropylmalate dehydrogenase**	78.1	49	96.49	5way_CG_26_GENE_39	**isocitrate dehydrogenase**	48.9		0	1.60
564	UBA_8241_GENE_457	**Aspartate-semialdehyde dehydrogenase**	83.4	13	97.13	5way_CG_26_GENE_40	**e semialdehyde dehydrogeanse**	64.2		0	1.30
565	UBA_8241_GENE_458	**Quinolinate synthase**	48.1	14	96.84	5way_CG_26_GENE_41	**quinolinate synthetase complex**	30.4		1	1.58
566	UBA_8241_GENE_458a		NO DATA	-	94.94	5way_CG_26_GENE_42	c hypo	NO DATA	-	-	
567	UBA_8241_GENE_459	Hypothetical	NO DATA	-	85.29	5way_CG_26_GENE_43	hypo unique	NO DATA	-	-	
568	UBA_8241_GENE_460	**putative protein [Aquifex aeolicus VF5]gi|1560641**	72.5	0	100.00	5way_CG_26_GENE_44	**ferridoxin oxidoreductase**	72.5		0	1.00
569	UBA_8241_GENE_461	**Hypothetical**	23.4	2	93.62	5way_CG_26_GENE_45	glutathione transferase	NO DATA	-		20.00
570	UBA_8241_GENE_462	**Hypothetical**	19.7	7	88.03	5way_CG_26_GENE_46	**hypo unique**	6.6		0	2.98
571	UBA_8241_GENE_463	Lfe123p2 [Leptospirillum ferrooxidans]	NO DATA	-	96.80	5way_CG_26_GENE_47	hypo unique	NO DATA	-	-	

572	UBA_8241_GENE_464	Lfe123p3 [Leptospirillum ferrooxidans]	NO DATA	-	93.72	5way_CG_26_GENE_48	c hypo	NO DATA	-	-	
573	UBA_8241_GENE_465	Hypothetical	NO DATA	-	89.01	5way_CG_80_GENE_26	dieneoate hydrolase/TPR domain	NO DATA	-	-	
574	UBA_8241_GENE_466	**Fe-S oxidoreductase**	11.6	3	94.58	5way_CG_80_GENE_25	nomethyl ester oxidative cyclase	4.3		0	2.70
575	UBA_8241_GENE_467	**Ribulose 1,5-bisphosphate carboxylase, large sub**	46.7	36	96.43	5way_CG_80_GENE_24	**RuBisCO-like protein**	53.3		34	0.88
576	UBA_8241_GENE_468	Hypothetical	NO DATA	-	81.27	5way_CG_80_GENE_23	hypo unique	NO DATA	-	-	
577	UBA_8241_GENE_469	**ABC-type phosphate transport system, periplasmi**	16.2	0	89.84	5way_CG_80_GENE_22	**Phos.binding.Perip.**	65.7		96	0.25
578	UBA_8241_GENE_470	7 Permeases of the drug/metabolite transporter (D	NO DATA	-	93.75	5way_CG_80_GENE_21	multidrug transporter	NO DATA	-	-	
579	UBA_8241_GENE_471a		32.8	5	76.73	5way_CG_80_GENE_20	c hypo	NO DATA	-		20.00
580	UBA_8241_GENE_472	**Hypothetical**	42.5	23	91.09	5way_CG_80_GENE_19	**thiol-disulfide isomerase**	20.1		0	2.11
581	UBA_8241_GENE_473	**Uncharacterized conserved protein**	24.6	5	96.38	5way_CG_80_GENE_18	c hypo	NO DATA	-		20.00
582	UBA_8241_GENE_474	Ribosomal protein L11 methylase	NO DATA	-	93.47	5way_CG_80_GENE_17	al protein L11 methyltransferase	NO DATA	-	-	
583	UBA_8241_GENE_475	**Orotidine-5'-phosphate decarboxylase**	47.8	13	90.80	5way_CG_80_GENE_16	**ine-5'-phosphate decarboxylase**	11.6		0	4.12
584	UBA_8241_GENE_476	**Transposase and inactivated derivatives**	31.7	-				NO GENE	-	-	
585	UBA_8241_GENE_477	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
586	UBA_8241_GENE_478	**N-formylmethionyl-tRNA deformylase**	78.3	0	100.00	5way_CG_80_GENE_15	**polypeptide deformylase**	78.3		0	1.00
587	UBA_8241_GENE_479	**ATP:corrinoid adenosyltransferase**	78.2	11	98.32	5way_CG_80_GENE_14	**cob(i)alamin adenosyltransferase**	70.9		0	1.10
588	UBA_8241_GENE_480	**Precorrin-3B methylase**	42.9	0	99.27	5way_CG_80_GENE_13	**genase (Cobalamin production)**	42.9		0	1.00
589	UBA_8241_GENE_481	**Cobalamin biosynthesis protein CbiG**	45	17	92.33	5way_CG_80_GENE_12	**aconitase**	15.6		1	2.88
590	UBA_8241_GENE_482	**Precorrin-6B methylase 2**	81	27	96.57	5way_CG_80_GENE_11	**precorrin-6Y methylase**	47.3		0	1.71
591	UBA_8241_GENE_482a		51.4	3	90.00	5way_CG_80_GENE_10	**precorrin-6y methylase**	31		0	1.66
592	UBA_8241_GENE_483	**Cobalamin biosynthesis protein CbiD**	30.4	5	93.60	5way_CG_80_GENE_9	**cobalamin biosynthesis protein**	15.7		1	1.94
593	UBA_8241_GENE_484	Predicted metal-dependent hydrolase	NO DATA	-	84.66	5way_CG_80_GENE_8	Zn metallo protease	NO DATA	-	-	
594	UBA_8241_GENE_485	Large-conductance mechanosensitive channel	NO DATA	-	96.67	5way_CG_80_GENE_7	ance mechanosensitive channel	NO DATA	-	-	
595	UBA_8241_GENE_486	Hypothetical, possible transposase?	NO DATA	-				NO GENE	-	-	
596	UBA_8241_GENE_487	Hypothetical, possible transposase?	NO DATA	-				NO GENE	-	-	
597			NO GENE	-		5way_CG_80_GENE_6	transposase	NO DATA	-	-	
598			NO GENE	-		5way_CG_80_GENE_5	hypo unique	NO DATA	-	-	
599			NO GENE	-		5way_CG_80_GENE_4	transposase	NO DATA	-	-	
600			NO GENE	-		5way_CG_80_GENE_3	transposase	NO DATA	-	-	
601			NO GENE	-		5way_CG_80_GENE_2	???	NO DATA	-	-	
602			NO GENE	-		5way_CG_80_GENE_1	???	NO DATA	-	-	
603			NO GENE	-		5way_CG_214_GENE_2	hypo unique	NO DATA	-	-	
604			NO GENE	-		5way_CG_214_GENE_4	DNA helicase	NO DATA	-	-	
605			NO GENE	-		5way_CG_214_GENE_5	transposase	NO DATA	-	-	
606			NO GENE	-		5way_CG_214_GENE_6	ment or transposase (Tn domain)	NO DATA	-	-	
607			NO GENE	-		5way_CG_214_GENE_7	hypo unique	NO DATA	-	-	
608			NO GENE	-		5way_CG_214_GENE_8	hypo unique	NO DATA	-	-	
609			NO GENE	-		5way_CG_214_GENE_9	probable transposase	NO DATA	-	-	
610			NO GENE	-		5way_CG_214_GENE_10	hypo unique	NO DATA	-	-	
611			NO GENE	-		5way_CG_214_GENE_12	transposase	NO DATA	-	-	
612			NO GENE	-		5way_CG_214_GENE_13	hypo unique	NO DATA	-	-	
613			NO GENE	-		5way_CG_150_GENE_16	transposase	NO DATA	-	-	
614	UBA_8241_GENE_488a		NO DATA	-	100.00	5way_CG_150_GENE_15a		NO DATA	-	-	
615	UBA_8241_GENE_488	**Ribosomal protein L9**	83.3	65	92.67	5way_CG_150_GENE_15	**ribosomal protein L9**	50.7		0	1.64
616	UBA_8241_GENE_489	**Hypothetical**	58.6	7	93.69	5way_CG_150_GENE_14a		NO DATA	-		20.00
617	UBA_8241_GENE_489a		NO DATA	-	100.00	5way_CG_150_GENE_13a		NO DATA	-	-	
618	UBA_8241_GENE_490	**Preprotein translocase subunit YidC**	32.1	21	95.30	5way_CG_150_GENE_13	**60kD inner membrane protein**	12.1		1	2.65
619	UBA_8241_GENE_491	Predicted GTPase	NO DATA	-	90.34	5way_CG_150_GENE_12	nene and furan oxidation protein	NO DATA	-	-	
620	UBA_8241_GENE_492	**NAD/FAD-utilizing enzyme apparently involved in**	8.4	2	93.06	5way_CG_150_GENE_11	se inhibited division protein, GidA	NO DATA	-		20.00
621	UBA_8241_GENE_493	**Predicted S-adenosylmethionine-dependent meth**	13.3	1	87.14	5way_CG_150_GENE_10	se inhibited division protein, GidB	NO DATA	-		20.00
622	UBA_8241_GENE_494	**ATPases involved in chromosome partitioning**	43.7	6	96.46	5way_CG_150_GENE_9	**osome partitioning protein, ParA**	33.9		0	1.29
623	UBA_8241_GENE_495	**Predicted transcriptional regulators**	82	49	92.96	5way_CG_150_GENE_8	**osome partitioning protein, ParB**	28.2		0	2.91
624	UBA_8241_GENE_496	**Integral membrane protein CcmA involved in cell**	91.7	8	97.73	5way_CG_150_GENE_7	**c hypo**	78		0	1.18
625	UBA_8241_GENE_497	Predicted tRNA(5-methylaminomethyl-2-thiouridyl	NO DATA	-	94.18	5way_CG_150_GENE_6	**-thiouridylate)-methyl transferase**	6.9		1	0.06
626	UBA_8241_GENE_498	**DNA polymerase III, epsilon subunit and related 3'**	50.6	23	93.21	5way_CG_150_GENE_5	**NA polymerase III, alpha subunit**	7.5		0	6.75
627	UBA_8241_GENE_499	**dsRNA-specific ribonuclease**	63.1	55	90.81	5way_CG_150_GENE_4	**ribonuclease III**	27.7		0	2.28
628	UBA_8241_GENE_501	**Predicted redox protein, regulator of disulfide bon**	92.2	24				NO GENE	-		35.00
629	UBA_8241_GENE_502	**Ferredoxin**	59.6	22				NO GENE	-		35.00
630			NO GENE	-		5way_CG_150_GENE_1	probable transposase	NO DATA	-	-	
631	UBA_8241_GENE_503	**Uncharacterized conserved protein**	60.8	-	98.65	5way_CG_6_GENE_88a		31.1	-	-	
632	UBA_8241_GENE_504	**Hypothetical**	79.5	102	94.41	5way_CG_6_GENE_88	**hypo unique**	23.6		0	3.37
633	UBA_8241_GENE_505	**UDP-3-O-acyl-N-acetylglucosamine deacetylase**	4.4	0	96.98	5way_CG_6_GENE_87	-acetylglucosamine deacetylase	4.4		0	1.00
634	UBA_8241_GENE_506a		NO DATA	-	100.00	5way_CG_6_GENE_85	hypo unique	NO DATA	-	-	
635	UBA_8241_GENE_507	**Uncharacterized protein conserved in archaea**	63.8	8	98.85	5way_CG_6_GENE_84	**c hypo**	51.3		0	1.24
636	UBA_8241_GENE_508	Hypothetical	NO DATA	-	99.44	5way_CG_6_GENE_83	hypo unique	NO DATA	-	-	
637	UBA_8241_GENE_509	**Archaeal fructose-1,6-bisphosphatase and relatec**	37.4	0	95.47	5way_CG_6_GENE_82	**inositol-1-monophosphatase**	17.7		0	2.11
638	UBA_8241_GENE_509a		NO DATA	-	93.94	5way_CG_6_GENE_81	zinc metalloprotease	NO DATA	-	-	
639	UBA_8241_GENE_510	Hypothetical	NO DATA	-	99.06	5way_CG_6_GENE_80	hypo unique	NO DATA	-	-	
640	UBA_8241_GENE_511	**Geranylgeranyl pyrophosphate synthase**	37.3	11	96.97	5way_CG_6_GENE_79	**ctaprenyl-diphosphate synthase**	22.4		0	1.67
641	UBA_8241_GENE_512	**Uncharacterized conserved protein**	84.7	63	97.65	5way_CG_6_GENE_78	**c hypo**	57.3		1	1.48
642	UBA_8241_GENE_513	Pseudouridylate synthases, 23S RNA-specific	NO DATA	-	90.77	5way_CG_6_GENE_77	ine synthase D, ribosomal subunit	NO DATA	-	-	
643	UBA_8241_GENE_514	**FOG: TPR repeat**	27.8	0	99.08	5way_CG_6_GENE_76	**N-acetylglucosamine transferase**	27.8		0	1.00

644	UBA_8241_GENE_515a		NO DATA	-	94.97	5way_CG_6_GENE_75	lipoprotein signal peptidase	NO DATA	-	-	
645	UBA_8241_GENE_516	Isoleucyl-tRNA synthetase	29.7	28	93.65	5way_CG_6_GENE_74	isoleucyl tRNA synthetase	11.8		0	2.52
646		TRNA Val CAC 493584..493658 (+)		-					-		
647	UBA_8241_GENE_517	Hypothetical	NO DATA	-	94.15	5way_CG_6_GENE_73	hypo unique	NO DATA	-	-	
648	UBA_8241_GENE_517a		NO DATA	-	89.35	5way_CG_6_GENE_72a		NO DATA	-	-	
649	UBA_8241_GENE_518	Predicted membrane protein	NO DATA	-	97.67	5way_CG_48_GENE_37	hypo unique	NO DATA	-	-	
650	UBA_8241_GENE_519	Hypothetical	43.4	21	90.70	5way_CG_48_GENE_36	Hypothetical	18		0	2.41
651	UBA_8241_GENE_520	Nucleoside-diphosphate-sugar pyrophosphorylase	NO DATA	-	92.08	5way_CG_48_GENE_35	Nucleoside-diphosphate-sugar p	NO DATA	-	-	
652	UBA_8241_GENE_520a		14.8	-	90.62	5way_CG_48_GENE_34	likely split gene	NO DATA	-	-	
653	UBA_8241_GENE_521	Predicted GTPase	60.8	35	93.87	5way_CG_48_GENE_33	GTP-binding protein	24.1		0	2.52
654	UBA_8241_GENE_522	Parvulin-like peptidyl-prolyl isomerase	67.9	16	96.76	5way_CG_48_GENE_32	ptidyl-prolyl cis-strans isomerase	65.9		1	1.03
655	UBA_8241_GENE_523	Parvulin-like peptidyl-prolyl isomerase	54.9	43	88.58	5way_CG_48_GENE_31	lin-like peptidyl-prolyl isomerase	24.4		1	2.25
656	UBA_8241_GENE_524	Parvulin-like peptidyl-prolyl isomerase	79.6	131	95.50	5way_CG_48_GENE_30	ptidyl-prolyl cis-strans isomerase	57.4		0	1.39
657	UBA_8241_GENE_525	Transcription-repair coupling factor (superfamily I	31.7	28	95.75	5way_CG_48_GENE_29	nscription-repair coupling factor	12.7		0	2.50
658	UBA_8241_GENE_526	ADP-heptose synthase, bifunctional sugar kinase/	52.5	0	91.62	5way_CG_48_GENE_28	ADP-heptose synthase	18.4		0	2.85
659	UBA_8241_GENE_527	Phosphoheptose isomerase	83.3	61	96.04	5way_CG_48_GENE_27	phosphoheptose isomerase	49.3		0	1.69
660	UBA_8241_GENE_528	Glutamate-1-semialdehyde aminotransferase	51.3	25	97.03	5way_CG_48_GENE_26	-semialdehyde aminotransferase	29.7		0	1.73
661	UBA_8241_GENE_529	Hypothetical	91.4	2	98.57	5way_CG_48_GENE_24	hypo unique	100		0	0.91
662	UBA_8241_GENE_530	Hypothetical	NO DATA	-	95.90	5way_CG_48_GENE_23	chaperone DnaJ	NO DATA	-	-	
663	UBA_8241_GENE_531	Pyruvate:ferredoxin oxidoreductase and related 2	82.8	22	99.03	5way_CG_48_GENE_21	ferredoxin oxidoreductase	71.4		0	1.16
664	UBA_8241_GENE_532	Pyruvate:ferredoxin oxidoreductase and related 2	83.7	16	99.31	5way_CG_48_GENE_20	ferredoxin oxidoreductase	75.3		0	1.11
665	UBA_8241_GENE_533	Pyruvate:ferredoxin oxidoreductase and related 2	92.2	0	99.57	5way_CG_48_GENE_19	uvate:ferredoxin oxidoreductase	92.2		0	1.00
666	UBA_8241_GENE_534	Pyruvate:ferredoxin oxidoreductase and related 2	79.2	12	96.04	5way_CG_48_GENE_18	ferredoxin oxidoreductase	41.6		0	1.90
667	UBA_8241_GENE_535	Hypothetical	62.8	11	95.74	5way_CG_48_GENE_17	hypo unique	36.2		0	1.73
668	UBA_8241_GENE_536	Hypothetical	27.1	4	97.86	5way_CG_48_GENE_16a	Hypothetical	19.3		0	1.40
669	UBA_8241_GENE_537	Pyruvate:ferredoxin oxidoreductase and related 2	72.2	31	98.77	5way_CG_48_GENE_16	ferredoxin oxidoreductase	66.5		0	1.09
670	UBA_8241_GENE_538	Pyruvate:ferredoxin oxidoreductase and related 2	62.5	0	100.00	5way_CG_48_GENE_15	below ferredoxin oxidoreductase	62.5		0	1.00
671	UBA_8241_GENE_539	Pyruvate:ferredoxin oxidoreductase and related 2	73.3	0	99.57	5way_CG_48_GENE_13	uvate ferredoxin oxidoreductase	73.3		0	1.00
672	UBA_8241_GENE_540	Hypothetical	81.3	24	90.67	5way_CG_48_GENE_12	hypo unique	40.8		0	1.99
673	UBA_8241_GENE_541	putative protein [Aquifex aeolicus VF5]gi|1560641	76.7	74	98.96	5way_CG_48_GENE_11	ferrodoxin oxidoreductase	50.8		0	1.51
674	UBA_8241_GENE_542	Hypothetical	88	62	93.23	5way_CG_48_GENE_10	hypo unique	13.5		0	6.52
675	UBA_8241_GENE_542a		NO DATA	-	98.86	5way_CG_48_GENE_9	c hypo	NO DATA	-	-	
676	UBA_8241_GENE_543	Glutamyl- and glutaminyl-tRNA synthetases	53.2	32	94.30	5way_CG_48_GENE_8	glutamyl tRNA synthetase	29.3		0	1.82
677	UBA_8241_GENE_544	Hypothetical	64.6	71	93.37	5way_CG_48_GENE_7	hypo unique	33.1		0	1.95
678	UBA_8241_GENE_545	Aspartate oxidase	26.7	9	98.25	5way_CG_48_GENE_6	L-aspartate oxidase	19.9		0	1.34
679	UBA_8241_GENE_546	DnaJ-class molecular chaperone	57	22	94.01	5way_CG_48_GENE_5	DnaJ protein	31.7		0	1.80
680	UBA_8241_GENE_547	Hypothetical	59.3	4	90.74	5way_CG_48_GENE_4	transcriptional regulator	NO DATA	-		20.00
681	UBA_8241_GENE_548	ATPases with chaperone activity, ATP-binding subu	82.2	27	98.96	5way_CG_48_GENE_3	Clp protease	74.2		1	1.11
682	UBA_8241_GENE_549	Hypothetical	16.3	1	94.94	5way_CG_48_GENE_2	hypo unique	NO DATA	-		20.00
683	UBA_8241_GENE_550	Bacterial nucleoid DNA-binding protein	87.9	-	98.67	5way_CG_48_GENE_1	histone-like	85.3	-	-	
684		TRNA Val GAC 529025..529099 (+)		-					-		
685	UBA_8241_GENE_552	Putative silver efflux pump	11.6	5	95.21	5way_CG_43_GENE_1	n/outer membrane efflux protein	NO DATA	-		20.00
686	UBA_8241_GENE_553	Membrane-fusion protein	43.6	7	94.41	5way_CG_43_GENE_2	cation efflux transporter	32.7		0	1.33
687	UBA_8241_GENE_554	Hypothetical	47.4	8	90.43	5way_CG_43_GENE_3	hypo unique	NO DATA	-		20.00
688	UBA_8241_GENE_555	Xaa-Pro aminopeptidase	60.1	11	96.59	5way_CG_43_GENE_4	Xaa-proline aminopeptidase	37.5		0	1.60
689	UBA_8241_GENE_556	Predicted O-methyltransferase	85.5	62	98.18	5way_CG_43_GENE_5	O-methyltransferase	54.5		0	1.57
690	UBA_8241_GENE_557	Ferredoxin subunits of nitrite reductase and ring-h	55.9	31	97.06	5way_CG_43_GENE_6	assimilatory nitrate reductase	31.4		0	1.78
691	UBA_8241_GENE_558	Hypothetical	NO DATA	-	100.00	5way_CG_43_GENE_7	sugar metabolism	NO DATA	-	-	
692	UBA_8241_GENE_559	ADP-glucose pyrophosphorylase	54.9	11	97.85	5way_CG_43_GENE_8	e-1-phosphate adenyltransferase	45.6		0	1.20
693	UBA_8241_GENE_560	Alpha-amylase/alpha-mannosidase	21.1	4	98.33	5way_CG_43_GENE_9	amylopullulanase	20.1		0	1.05
694	UBA_8241_GENE_561	Alpha-amylase/alpha-mannosidase	51.9	43	94.40	5way_CG_43_GENE_10	alpha-amylase	22.8		0	2.28
695	UBA_8241_GENE_562	Galactose-1-phosphate uridylyltransferase	62.9	0	100.00	5way_CG_43_GENE_11	e-1-phosphate uridylyltransferase	62.9		0	1.00
696	UBA_8241_GENE_563	Hypothetical	77.2	83	97.17	5way_CG_43_GENE_12	fructose bisphosphate aldolase)	56.7		1	1.36
697	UBA_8241_GENE_564	Uncharacterized conserved protein	32	23	96.22	5way_CG_43_GENE_13	c hypo	17.6		0	1.82
698	UBA_8241_GENE_565	Membrane-fusion protein	73.8	59	97.52	5way_CG_43_GENE_14	efflux transporter	60.3		0	1.22
699	UBA_8241_GENE_566	Cation/multidrug efflux pump	28.9	4	99.43	5way_CG_43_GENE_15	cation efflux transport	27.1		1	1.07
700	UBA_8241_GENE_567	Predicted aminomethyltransferase related to Gcv1	90.4	65	95.81	5way_CG_43_GENE_16	system; aminomethyltransferase	53.3		0	1.70
701	UBA_8241_GENE_568	Response regulator containing CheY-like receiver,	22.4	6	96.48	5way_CG_43_GENE_17	tabolism regulatory protein atoC	14.5		0	1.54
702	UBA_8241_GENE_569	Membrane-fusion protein	64	35	97.27	5way_CG_43_GENE_18	efflux transporter	50.6		0	1.26
703	UBA_8241_GENE_570	Outer membrane protein	46.5	44	98.16	5way_CG_43_GENE_19	efflux protein	39.4		0	1.18
704	UBA_8241_GENE_571	Thioredoxin reductase	59.4	18	97.74	5way_CG_43_GENE_20	thioredoxin reductase	39.8		0	1.49
705	UBA_8241_GENE_572	Hypothetical	29.8	3	94.05	5way_CG_43_GENE_21	hypo unique	8.9		0	3.35
706	UBA_8241_GENE_573	Hypothetical	78.7	84	95.83	5way_CG_43_GENE_22	hypo unique	58.6		1	1.34
707	UBA_8241_GENE_574	Highly conserved protein containing a thioredoxin	39.9	19	93.76	5way_CG_43_GENE_23	thymidylate kinase	15.8		0	2.53
708	UBA_8241_GENE_575	Predicted esterase	17.4	1	94.30	5way_CG_43_GENE_24	carboxylesterase	16.1		1	1.08
709	UBA_8241_GENE_576	Hypothetical	15.7	-	70.00	5way_CG_43_GENE_25	hypo unique	NO DATA	-	-	
710	UBA_8241_GENE_577	Transposase and inactivated derivatives	NO DATA	-				NO DATA	-	-	
711	UBA_8241_GENE_578	N-formylmethionyl-tRNA deformylase	NO DATA	-	94.92	5way_CG_43_GENE_26	peptide deformylase	19.8		1	0.06
712	UBA_8241_GENE_579	Methionyl-tRNA formyltransferase	73.4	58	94.04	5way_CG_43_GENE_27	methionyl tRNA formyltransferase	32.6		0	2.25
713	UBA_8241_GENE_580	Zn-dependent protease with chaperone function	31.5	0	98.64	5way_CG_43_GENE_28	otidase/Zn+-dependent protease	31.5		0	1.00
714	UBA_8241_GENE_581	Pentose-5-phosphate-3-epimerase	29.9	4	92.21	5way_CG_43_GENE_29	ribulose phosphate 3-epimerase	12.1		0	2.47
715	UBA_8241_GENE_582	Hypothetical	20.1	0	97.99	5way_CG_43_GENE_30	hypo unique	20.1		0	1.00

716	UBA_8241_GENE_583	Actin-like ATPase involved in cell morphogenesis	60.9	5	99.71	5way_CG_277_GENE_2	actin-like ATPase	56.6		0	1.08
717	UBA_8241_GENE_584	Cell shape-determining protein	17.1	1	95.73	5way_CG_277_GENE_3	shape determining protein MreC	7.5		0	2.28
718	UBA_8241_GENE_585	Hypothetical	NO DATA	-	97.45	5way_CG_277_GENE_4	hypo unique	NO DATA	-	-	
719	UBA_8241_GENE_586	Cell division protein FtsI/penicillin-binding protei	18.9	3	95.65	5way_CG_277_GENE_5	cell division protein FtsI	6.2		0	3.05
720	UBA_8241_GENE_587	Bacterial cell division membrane protein	NO DATA	-	98.07	5way_CG_277_GENE_6	shape determining protein RodA	NO DATA	-	-	
721	UBA_8241_GENE_588	Ribonucleases G and E	66.4	59	96.39	5way_CG_277_GENE_7	ribonuclease G	54.8		2	1.21
722	UBA_8241_GENE_589	Hypothetical	NO DATA	-	99.29	5way_CG_277_GENE_8	hypo unique	NO DATA	-	-	
723	UBA_8241_GENE_590	Hypothetical	23.5	2	93.13	5way_CG_277_GENE_9	7,8-dihydroneopterin aldolase	NO DATA	-		20.00
724	UBA_8241_GENE_591	Hypothetical	18	-	98.04	5way_CG_277_GENE_10	hypo unique	NO DATA	-	-	
725	UBA_8241_GENE_592	Ferredoxin	NO DATA	-	100.00	5way_CG_426_GENE_1	ferredoxin	NO DATA	-	-	
726	UBA_8241_GENE_593	Fe-S oxidoreductase	43.9	12	98.72	5way_CG_426_GENE_2	xidoreductase/methyltransferase	39.8		0	1.10
727	UBA_8241_GENE_594	Ribosomal protein L13	78.1	26	98.68	5way_CG_426_GENE_3	ribosomal protein L13	66.2		0	1.18
728	UBA_8241_GENE_595	Ribosomal protein S9	80	0	99.26	5way_CG_426_GENE_4	ribosomal protein S9	80		0	1.00
729	UBA_8241_GENE_596	Acetylglutamate semialdehyde dehydrogenase	32.9	-	92.67	5way_CG_426_GENE_5	e semialdehyde dehydrogenase	14.6	-	-	
730	UBA_8241_GENE_597	N-acetylglutamate synthase (N-acetylornithine ar	41.3	13	96.29	5way_CG_426_GENE_6	N-acetylglutamate synthase	29.5		0	1.40
731	UBA_8241_GENE_598	Ribosomal protein S2	81.4	-	96.91	5way_CG_13_GENE_68	ribosomal protein S2	78.4	-	-	
732	UBA_8241_GENE_599	Translation elongation factor Ts	90.9	42	98.48	5way_CG_13_GENE_67	ranslation elongation factor EF-Ts	85.4		0	1.06
733	UBA_8241_GENE_600	Uridylate kinase	67.4	1	98.73	5way_CG_13_GENE_66	uridylate kinase	58.1		0	1.16
734	UBA_8241_GENE_601	Ribosome recycling factor	97.3	129	97.28	5way_CG_13_GENE_65	ribosome recycling factor	62.5		0	1.56
735	UBA_8241_GENE_602	Alanine racemase	17.7	1	95.32	5way_CG_13_GENE_64	alanine racemase	14		0	1.26
736	UBA_8241_GENE_603	ABC-type transport system involved in resistance t	NO DATA	-	99.22	5way_CG_13_GENE_63	BC transporter, permease protein	NO DATA	-	-	
737	UBA_8241_GENE_604	ABC-type transport system involved in resistance t	31.8	3	96.97	5way_CG_13_GENE_62	C transporter, ATP-binding protein	16.3		0	1.95
738	UBA_8241_GENE_605	ABC-type transport system involved in resistance t	40.3	23	97.68	5way_CG_13_GENE_61	olute-binding periplasmic protein	36.1		0	1.12
739	UBA_8241_GENE_606	ResB protein required for cytochrome c biosynthes	20.5	10	97.46	5way_CG_13_GENE_60	e biosynthesis protein Ccs1/ResB	13.8		0	1.49
740	UBA_8241_GENE_608	ABC-type transport system involved in cytochrome	NO DATA	-	100.00	5way_CG_13_GENE_59	sis protein CcmF/ABC transporter	NO DATA	-	-	
741	UBA_8241_GENE_609	Thiol-disulfide isomerase and thioredoxins	34.2	3	98.99	5way_CG_13_GENE_58	in tlpA/cytochrome c biogenesis	24.1		0	1.42
742	UBA_8241_GENE_610	Thiol-disulfide isomerase and thioredoxins	33.9	6	89.47	5way_CG_13_GENE_57	hypo unique	NO DATA	-		20.00
743	UBA_8241_GENE_611	Cytochrome c biogenesis protein	NO DATA	-	98.80	5way_CG_13_GENE_56	rome c biogenesis protein CcdA	NO DATA	-	-	
744	UBA_8241_GENE_612	Dehydrogenases (flavoproteins)	NO DATA	-	93.99	5way_CG_13_GENE_55	geranylgeranyl reductase	NO DATA	-	-	
745	UBA_8241_GENE_613	protease family protein [Dehalococcoides etheno	15.2	6	95.27	5way_CG_13_GENE_54	Zn-dependant protease	NO DATA	-		20.00
746	UBA_8241_GENE_614	Primosomal protein N' (replication factor Y) - super	NO DATA	-	91.98	5way_CG_13_GENE_53	PriA (replication factor/helicase)	NO DATA	-	-	
747	UBA_8241_GENE_615	Predicted transcriptional regulator, consists of a Z	NO DATA	-	99.35	5way_CG_13_GENE_52	oate octaprenyltransferase UbiA	NO DATA	-	-	
748	UBA_8241_GENE_616	Glycine/serine hydroxymethyltransferase	60.6	45	98.31	5way_CG_13_GENE_51	hydroxymethyltransferase GlyA	44.2		0	1.37
749	UBA_8241_GENE_617	Ribose 5-phosphate isomerase RpiB	87.3	36	94.30	5way_CG_13_GENE_50	ribose-5-phosphate isomerase	59.5		0	1.47
750	UBA_8241_GENE_618	Hypothetical	18	1	93.44	5way_CG_13_GENE_49	possible exochitinase I precursor	NO DATA	-		20.00
751	UBA_8241_GENE_619	Thymidylate kinase	NO DATA	-	99.56	5way_CG_13_GENE_48	thymidylate kinase	NO DATA	-	-	
752	UBA_8241_GENE_620	Thymidylate kinase	NO DATA	-	99.54	5way_CG_13_GENE_47	thymidylate kinase	NO DATA	-	-	
753	UBA_8241_GENE_621	Exopolyphosphatase	4.4	1	96.33	5way_CG_13_GENE_46	exopolyphosphatase	NO DATA	-		20.00
754	UBA_8241_GENE_622	[Leptospirillum ferrooxidans]gi|62195101|ref|YP_2	32.9	6	90.72	5way_CG_13_GENE_45	t ubiquinone biosynthesis related	18.1		0	1.82
755	UBA_8241_GENE_623	Methylase involved in ubiquinone/menaquinone b	31.7	6	96.14	5way_CG_13_GENE_44	ne biosynthesis methyltransferase	8.1		1	3.91
756	UBA_8241_GENE_624	Fe-S oxidoreductase	39.6	0	99.06	5way_CG_13_GENE_43	Fe-S oxidoreductase	39.6		0	1.00
757	UBA_8241_GENE_625	Hypothetical	60.6	12	94.71	5way_CG_13_GENE_42	t ubiquinone biosynthesis related	42.4		0	1.43
758	UBA_8241_GENE_626	4-hydroxybenzoate polyprenyltransferase and relc	NO DATA	-	95.12	5way_CG_13_GENE_41	ybenzoate polyprenyltransferase	NO DATA	-	-	
759	UBA_8241_GENE_627	Hypothetical	NO DATA	-	100.00	5way_CG_13_GENE_39	hypo unique	NO DATA	-	-	
760	UBA_8241_GENE_628	Hypothetical	NO DATA	-	91.76	5way_CG_13_GENE_39a		NO DATA	-	-	
761	UBA_8241_GENE_629	77 Permeases of the major facilitator superfamily	14.8	4	99.13	5way_CG_13_GENE_37	permease	12.2		0	1.21
762	UBA_8241_GENE_630	Kef-type K+ transport systems, predicted NAD-bin	56.5	23	99.14	5way_CG_13_GENE_36	potassium uptake protein	40.1		0	1.41
763	UBA_8241_GENE_631	Ornithine/acetylornithine aminotransferase	62.8	52	96.92	5way_CG_13_GENE_35	acetylornithine aminotransferase	25.6		0	2.45
764	UBA_8241_GENE_632	Ornithine carbamoyltransferase	41.4	5	95.47	5way_CG_13_GENE_34	ornithine carbamoyltransferase	34.6		0	1.20
765	UBA_8241_GENE_633	Argininosuccinate synthase	65.7	2	99.02	5way_CG_13_GENE_33	arginosuccinate synthase	63.7		0	1.03
766	UBA_8241_GENE_634	Argininosuccinate lyase	54	32	98.07	5way_CG_13_GENE_32	arginosuccinate lyase	40		0	1.35
767	UBA_8241_GENE_635	Diaminopimelate decarboxylase	88.4	62	97.83	5way_CG_13_GENE_31	diaminopimelate decarboxylase	67.4		0	1.31
768	UBA_8241_GENE_636	Hypothetical	54.5	9	95.15	5way_CG_13_GENE_30	ique - suspect lysine biosynthesis	40		0	1.36
769	UBA_8241_GENE_637	Dihydrodipicolinate synthase/N-acetylneuraminal	84.4	19	98.64	5way_CG_13_GENE_29	dihydrodipicolinate synthase	80.7		1	1.05
770	UBA_8241_GENE_638	Dihydrodipicolinate reductase	79.6	37	96.23	5way_CG_13_GENE_28	dihydrodipicolinate reductase	46		1	1.73
771	UBA_8241_GENE_639	2-keto-4-pentenoate hydratase/2-oxohepta-3-en	88.8	32	94.76	5way_CG_13_GENE_27	atechol pathway acid hydratase	40.1		1	2.21
772	UBA_8241_GENE_640	Flagellar basal body rod protein	18.4	1	98.13	5way_CG_13_GENE_26	flagellar hook protein FlgG	13.5		0	1.36
773	UBA_8241_GENE_641	Flagellar basal body rod protein	62.1	1	99.23	5way_CG_13_GENE_25	lar hook basal-body protein FlgG	52.1		0	1.19
774	UBA_8241_GENE_642	Hypothetical	NO DATA	-	87.32	5way_CG_13_GENE_24	hypo unique	NO DATA	-	-	
775	UBA_8241_GENE_642a		48.6	10	98.08	5way_CG_13_GENE_23	nique - suspect flagellar related	29.3		0	1.66
776	UBA_8241_GENE_643	Flagellar basal-body P-ring protein	47.2	12	95.20	5way_CG_13_GENE_22	flagellar P-ring protein	35		0	1.35
777	UBA_8241_GENE_644	Hypothetical	NO DATA	-	88.43	5way_CG_13_GENE_21	peptidase-like	NO DATA	-	-	
778	UBA_8241_GENE_645	Flagellin and related hook-associated proteins	43	0	99.65	5way_CG_13_GENE_20	flagellin, FliC	43		0	1.00
779	UBA_8241_GENE_646	Hypothetical	45.4	46	94.96	5way_CG_13_GENE_19	hypo - suspect flagella related	27.7		0	1.64
780	UBA_8241_GENE_647	Hypothetical	NO DATA	-	91.46	5way_CG_13_GENE_18	hypo unique	NO DATA	-	-	
781	UBA_8241_GENE_648	Flagellar hook-associated protein	48.3	6	98.04	5way_CG_13_GENE_17	flagellar hook associated protein	40.5		0	1.19
782	UBA_8241_GENE_649	Flagellin and related hook-associated proteins	66	25	99.04	5way_CG_13_GENE_16	llar hook associated protein, FlgL	49.7		0	1.33
783	UBA_8241_GENE_650	Hypothetical	43.8	0	98.75	5way_CG_13_GENE_15	carbon storage regulator csrA	43.8		0	1.00
784	UBA_8241_GENE_651	Uncharacterized protein conserved in bacteria	31.5	9	97.20	5way_CG_13_GENE_14	c hypo	15.4		0	2.05
785	UBA_8241_GENE_652	Flagellin and related hook-associated proteins	91.3	86	98.91	5way_CG_13_GENE_13	gellin FliC-primary struct. Flagella	86.2		1	1.06
786	UBA_8241_GENE_653	Flagellar capping protein	62.2	20	98.96	5way_CG_13_GENE_12	flagellar hook-associated protein	45.9		0	1.36
787	UBA_8241_GENE_654	6 Flagellin-specific chaperone FliS	14.5	0	97.37	5way_CG_13_GENE_11	flagellar protein FliS	14.5		0	1.00

788	UBA_8241_GENE_655	Hypothetical	NO DATA	-		91.23	5way_CG_13_GENE_10	hypo unique	NO DATA	-	-	
789	UBA_8241_GENE_656	hypothetical protein Mmc1DRAFT_1954 [Magneto	NO DATA	-		94.48	5way_CG_13_GENE_9	c hypo	NO DATA	-	-	
790	UBA_8241_GENE_657	**SAM-dependent methyltransferases**	13.1		3	95.38	5way_CG_13_GENE_8	**glycosyl transferase**	5.5		0	2.38
791	UBA_8241_GENE_658	ADP-heptose:LPS heptosyltransferase	NO DATA	-		87.43	5way_CG_13_GENE_7	-heptose-LPS heptosyltransferase	NO DATA	-	-	
792	UBA_8241_GENE_659	Uncharacterized protein conserved in bacteria	NO DATA	-		91.99	5way_CG_13_GENE_6	c hypo	NO DATA	-	-	
793	UBA_8241_GENE_660	ADP-heptose:LPS heptosyltransferase	NO DATA	-		87.23	5way_CG_13_GENE_5	-heptose-LPS heptosyltransferase	NO DATA	-	-	
794	UBA_8241_GENE_661	Hypothetical	NO DATA	-		93.09	5way_CG_13_GENE_4	**c hypo**	28.1		3	0.06
795	UBA_8241_GENE_662	Hypothetical	NO DATA	-		94.27	5way_CG_13_GENE_3	embrane Fe III dicitrate receptor	NO DATA	-	-	
796	UBA_8241_GENE_663	Hypothetical likely split gene with above	NO DATA	-		99.14	5way_CG_13_GENE_3	embrane Fe III dicitrate receptor	NO DATA	-	-	
797		[redacted]	NO GENE	-			5way_CG_13_GENE_1	transposase	NO DATA	-	-	
798	UBA_8241_GENE_664	Hypothetical	NO DATA	-		95.68	5way_CG_22_GENE_48	**hypo unique**	58.3		11	0.06
799	UBA_8241_GENE_665	Hypothetical	NO DATA	-		88.35	5way_CG_22_GENE_46	**hypo unique**	25.2		11	0.06
800	UBA_8241_GENE_666	**Inorganic pyrophosphatase**	83		4	98.90	5way_CG_22_GENE_45	**pyrophosphatase**	67		0	1.24
801	UBA_8241_GENE_667	**ABC-type antimicrobial peptide transport system,**	47.9		0	99.15	5way_CG_22_GENE_44	**C transporter, ATP binding protein**	47.9		0	1.00
802	UBA_8241_GENE_668	ABC-type antimicrobial peptide transport system,	NO DATA	-		98.26	5way_CG_22_GENE_43	BC transporter, permease protein	NO DATA	-	-	
803	UBA_8241_GENE_669	**Membrane-fusion protein**	50		0	97.37	5way_CG_22_GENE_42	**efflux transporter**	68.2		20	0.73
804	UBA_8241_GENE_670	**Flagellar motor switch protein**	24.6		0	99.70	5way_CG_22_GENE_41	**lagellar motor switch protein FliM**	34.3		2	0.72
805	UBA_8241_GENE_671	**Transcriptional regulator containing GAF, AAA-typ**	23.9		0	95.66	5way_CG_22_GENE_39	**scriptional regulator (nifA family)**	35.5		7	0.67
806	UBA_8241_GENE_672	NADH:ubiquinone oxidoreductase subunit 5 (chair	NO DATA	-		94.18	5way_CG_22_GENE_38	NADH dehydrogenase, subunit 5	NO DATA	-	-	
807	UBA_8241_GENE_673	Hypothetical	NO DATA	-		90.62	5way_CG_22_GENE_37	NADH dehydrogenase, subunit 4	NO DATA	-	-	
808	UBA_8241_GENE_674	**Uncharacterized protein conserved in bacteria**	10.3		0	91.92	5way_CG_22_GENE_36	**c hypo**	18.8		17	0.55
809	UBA_8241_GENE_675	**Hypothetical**	57.9		0	99.12	5way_CG_22_GENE_35	**to nitrogen regulatory protein PII)**	57.9		0	1.00
810	UBA_8241_GENE_676	Hypothetical	NO DATA	-		94.49	5way_CG_22_GENE_34	major facilitator family permease	NO DATA	-	-	
811	UBA_8241_GENE_677	**FOG: TPR repeat split with below**	4.2	-		79.62	5way_CG_22_GENE_33	unit c: cleaves diGMP synthase...	59.6	-	-	
812		[redacted]	NO GENE	-			5way_CG_22_GENE_32	glycosyltransferase	NO DATA	-	-	
813		[redacted]	NO GENE	-			5way_CG_22_GENE_31	**cyclic di-GMP binding protein**	35		60	0.03
814	UBA_8241_GENE_678	Endoglucanase Y	3.8		0	84.70	5way_CG_22_GENE_30	**cellulase**	39.1		37	0.10
815	UBA_8241_GENE_680	**Membrane carboxypeptidase (penicillin-binding**	10.4		0	96.69	5way_CG_22_GENE_29	**membrane carboxypeptidase**	34.5		20	0.30
816		TRNA Gln CTG 668118..668191 (-)	-							-		
817	UBA_8241_GENE_681a		32.8		0	96.80	5way_CG_22_GENE_28	**hypo unique**	40.8		5	0.80
818	UBA_8241_GENE_682	outer membrane protein [Acidithiobacillus ferroox	NO DATA	-		91.99	5way_CG_22_GENE_27	c hypo	NO DATA	-	-	
819	UBA_8241_GENE_683	Hypothetical	NO DATA	-		88.26	5way_CG_22_GENE_26	**c hypo**	16.6		3	0.06
820	UBA_8241_GENE_683a		NO DATA	-		90.13	5way_CG_22_GENE_25	hypo unique	NO DATA	-	-	
821	UBA_8241_GENE_684	DNA repair proteins	NO DATA	-		97.47	5way_CG_22_GENE_24	DNA repair protein RadC	NO DATA	-	-	
822	UBA_8241_GENE_685	**Predicted unusual protein kinase**	12		0	97.49	5way_CG_22_GENE_23	**ubiquinone biosynthesis protein**	12		0	1.00
823	UBA_8241_GENE_686	**Nitroreductase**	12.8		0	97.71	5way_CG_22_GENE_22	**H oxidase (noxC)/nitroreductase**	22.6		4	0.57
824	UBA_8241_GENE_687	**Uncharacterized protein conserved in bacteria**	30.2		0	92.92	5way_CG_22_GENE_21	**c hypo**	63.7		12	0.47
825	UBA_8241_GENE_688	**Adenylosuccinate synthase**	66.4		0	99.31	5way_CG_22_GENE_20	**adenylosuccinate synthetase**	70.8		8	0.94
826	UBA_8241_GENE_689	**Uncharacterized conserved protein**	39.4		0	99.04	5way_CG_22_GENE_19	**c hypo**	39.4		0	1.00
827	UBA_8241_GENE_690	**Hypothetical**	20.5		0	96.53	5way_CG_22_GENE_18	**hypo**	34.2		68	0.60
828	UBA_8241_GENE_691	Response regulators consisting of a CheY-like rece	NO DATA	-		97.30	5way_CG_22_GENE_17	-binding response regulator PhoB	NO DATA	-	-	
829	UBA_8241_GENE_692	Hypothetical	NO DATA	-		91.07	5way_CG_22_GENE_15	hypo unique	NO DATA	-	-	
830	UBA_8241_GENE_693	**ABC-type phosphate transport system, periplasmic**	43.3		0	97.85	5way_CG_22_GENE_14	**rotein, ABC transporter Ab Ex. Fn**	61		86	0.71
831	UBA_8241_GENE_694	ABC-type phosphate transport system, permease	NO DATA	-		98.24	5way_CG_22_GENE_12	BC transporter, permease protein	NO DATA	-	-	
832	UBA_8241_GENE_695	ABC-type phosphate transport system, permease	NO DATA	-		98.02	5way_CG_22_GENE_11	BC transporter, permease protein	NO DATA	-	-	
833	UBA_8241_GENE_696	**ABC-type phosphate transport system, ATPase cor**	55.6		0	99.60	5way_CG_22_GENE_10	**transporter, ATP-binding domain**	64		3	0.87
834	UBA_8241_GENE_697	**Phosphate uptake regulator**	79.3		0	99.54	5way_CG_22_GENE_9	**nsporter transcriptional regulator**	79.3		0	1.00
835	UBA_8241_GENE_698	**Predicted alternative thymidylate synthase**	28.7		0	98.53	5way_CG_22_GENE_8	**thymidylate synthase**	35.3		2	0.81
836	UBA_8241_GENE_699	Hypothetical, likely split gene (check prot)>>>	24.8		1	90.93	5way_CG_22_GENE_7	**hypo unique**	38.7		12	0.64
837	UBA_8241_GENE_701	**NAD-dependent aldehyde dehydrogenases**	22.3		0	91.83	5way_CG_22_GENE_6	**aldehyde dehydrogenase**	51.4		42	0.43
838	UBA_8241_GENE_702	Hypothetical	NO DATA	-		96.08	5way_CG_22_GENE_5	hypo unique	NO DATA	-	-	
839	UBA_8241_GENE_705	Fructose-1,6-bisphosphatase, likely split?	8.4		0	91.59	5way_CG_22_GENE_4	**fructose bisphophatase**	67.8		88	0.12
840	UBA_8241_GENE_706	Hypothetical	NO DATA	-		98.56	5way_CG_22_GENE_3a		NO DATA	-	-	
841	UBA_8241_GENE_707	**Hypothetical**	45.3		0	97.99	5way_CG_22_GENE_3	**hypo unique**	45.3		0	1.00
842		[redacted]	NO GENE	-			5way_CG_22_GENE_2	**histone deacetylase**	9.6		3	0.03
843		[redacted]	NO GENE	-			5way_CG_22_GENE_1	transposase	NO DATA	-	-	
844	UBA_8241_GENE_708	Transposase and inactivated derivatives	NO DATA	-			[redacted]		NO GENE	-	-	
845												
846												
847		[redacted]	NO GENE	-			5way_CG_581_GENE_9	transposase	NO DATA	-	-	
848		[redacted]	NO GENE	-			5way_CG_581_GENE_8	transposase	NO DATA	-	-	
849		[redacted]	NO GENE	-			5way_CG_581_GENE_7	transposase	NO DATA	-	-	
850		[redacted]	NO GENE	-			5way_CG_581_GENE_6	transposase	NO DATA	-	-	
851		[redacted]	NO GENE	-			5way_CG_581_GENE_5	hypo unique	NO DATA	-	-	
852		[redacted]	NO GENE	-			5way_CG_581_GENE_4	transposase	NO DATA	-	-	
853		[redacted]	NO GENE	-			5way_CG_581_GENE_2	**k (possible carbonic anhydrase)**	15		-	-
854		[redacted]	NO GENE	-			5way_CG_581_GENE_1		47.5	-	-	
		8135										
1	UBA_8135_GENE_1	**Hypothetical**	71.4	-		97.57	5way_CG_62_GENE_1	**hypo**	48.9	-	-	
2	UBA_8135_GENE_2	ABC-type transport system involved in resistance t	NO DATA	-		98.85	5way_CG_62_GENE_2	BC transporter permease protein	NO DATA	-	-	

3	UBA_8135_GENE_3	ABC-type transport system involved in resistance t	7	0	97.67	5way_CG_62_GENE_3	C transporter ATP-binding protein	7		0	1.00
4	UBA_8135_GENE_4	ABC-type multidrug transport system substrate-bin	56.2	4	100.00	5way_CG_62_GENE_4	olasmic substrate binding protein	51		0	1.10
5	UBA_8135_GENE_5	FOG: TPR repeat	77.6	165	91.69	5way_CG_62_GENE_5	c hypo	26.2		0	2.96
6		[redacted]	NO GENE	-		5way_CG_62_GENE_6	oreductase/K+-channel protein?	NO DATA	-	-	
7	UBA_8135_GENE_6	Hypothetical	37.1	5	94.84	5way_CG_62_GENE_7	c hypo	25.4		0	1.46
8	UBA_8135_GENE_7	Hypothetical	NO DATA	-	83.59	5way_CG_62_GENE_8	c hypo	NO DATA	-	-	
9	UBA_8135_GENE_8	: Uncharacterized protein conserved in bacteria [I	NO DATA	-	90.03	5way_CG_62_GENE_9	c hypo	NO DATA	-	-	
10	UBA_8135_GENE_9	Uncharacterized conserved protein	87.1	81	92.03	5way_CG_62_GENE_10	Ab.AbMem (check annotation!)	68.4		0	1.27
11	UBA_8135_GENE_10a		12.2	8	80.75	5way_CG_62_GENE_11	hypo unique	NO DATA	-	20.00	
12	UBA_8135_GENE_13	Adenylate cyclase, family 3 (some proteins contai	6.6	1	97.36	5way_CG_62_GENE_12	adenylate cyclase	NO DATA	-	20.00	
13	UBA_8135_GENE_14	Hypothetical	93.4	53	89.71	5way_CG_62_GENE_13	hypo unique	36		1	2.59
14	UBA_8135_GENE_15	Hypothetical	58.4	34	94.12	5way_CG_62_GENE_14	possible thioredoxin	30.8		0	1.90
15	UBA_8135_GENE_16	Phosphoribosylaminoimidazole carboxylase (NCA	24.7	4	94.76	5way_CG_62_GENE_15	zole carboxylase, ATPase subunit	10.5		0	2.35
16	UBA_8135_GENE_17	Phosphoribosylcarboxyaminoimidazole (NCAIR) m	63.4	22	93.14	5way_CG_62_GENE_16	osylaminoimidazole carboxylase	40		0	1.59
17	UBA_8135_GENE_18	NADH:ubiquinone oxidoreductase, NADH-binding	49	20	97.79	5way_CG_62_GENE_17	reducing hydrogenase subunit C	38.9		0	1.26
18	UBA_8135_GENE_19	putative ferredoxin [Burkholderia pseudomallei K9	33.7	0	100.00	5way_CG_62_GENE_18	ferredoxin	33.7		0	1.00
19	UBA_8135_GENE_20	Hypothetical	64.8	61	96.59	5way_CG_62_GENE_19	c hypo (contains TPR domain)	47		1	1.38
20	UBA_8135_GENE_21	Soluble lytic murein transglycosylase and related	25.8	1	96.19	5way_CG_62_GENE_20	transglycosylase	22		0	1.17
21	UBA_8135_GENE_23	Transposase and inactivated derivatives	73.3	-			[redacted]	NO GENE	-	-	
22	UBA_8135_GENE_24	cAMP-binding proteins - catabolite gene activato	51.5	4	98.73	5way_CG_62_GENE_21	transcriptional regulator	36.7		0	1.40
23	UBA_8135_GENE_25	Hypothetical	NO DATA	-	97.78	5way_CG_62_GENE_22	hypo unique	NO DATA	-	-	
24		[redacted]	NO GENE	-		5way_CG_62_GENE_23	transposase	NO DATA	-	-	
25	UBA_8135_GENE_26	Glycogen synthase	15.6	6	90.06	5way_CG_62_GENE_24	glycogen synthase	NO DATA	-	20.00	
26	UBA_8135_GENE_27	hypothetical protein Franean1DRAFT_6268 [Frankic	45.4	0	100.00	5way_CG_62_GENE_25	acyl desaturase	45.4		0	1.00
27	UBA_8135_GENE_27a		NO DATA	-	95.24	5way_CG_62_GENE_26	hypo unique	NO DATA	-	-	
28	UBA_8135_GENE_28	Sulfite reductase, beta subunit (hemoprotein)	34.2	27	91.59	5way_CG_62_GENE_27	redoxin-nitrite / sulfite reductase	8		0	4.28
29	UBA_8135_GENE_29	Hypothetical	3	-	90.34	5way_CG_62_GENE_28	unique (identical is C-drift library)	NO DATA	-	-	
30	UBA_8135_GENE_30	Hypothetical	NO DATA	-	81.29	5way_CG_67_GENE_2	proteophosphoglycan	NO DATA	-	-	
31	UBA_8135_GENE_31	Site-specific recombinase XerD	7.6	-	92.36	5way_CG_67_GENE_3	integrase	7.6	-	-	
32	UBA_8135_GENE_32	Coproporphyrinogen III oxidase and related Fe-S c	8.5	1	83.80	5way_CG_67_GENE_4	n coproporphyrinogen III oxidase	NO DATA	-	20.00	
33	UBA_8135_GENE_33	Hypothetical	NO DATA	-	78.81	5way_CG_67_GENE_5	hypo unique	NO DATA	-	-	
34	UBA_8135_GENE_34	MoxR-like ATPases	NO DATA	-	93.62	5way_CG_67_GENE_6	MoxR-like ATPase	NO DATA	-	-	
35	UBA_8135_GENE_35	Hypothetical	NO DATA	-	86.71	5way_CG_67_GENE_7	hypo unique	NO DATA	-	-	
36	UBA_8135_GENE_36	Hypothetical	NO DATA	-	82.12	5way_CG_67_GENE_8	NA-dependent RNA polymerase	NO DATA	-	-	
37	UBA_8135_GENE_37	Hypothetical	NO DATA	-	92.58	5way_CG_67_GENE_9	hypo unique	NO DATA	-	-	
38	UBA_8135_GENE_38	Hypothetical	NO DATA	-	89.02	5way_CG_67_GENE_10	hypo unique	NO DATA	-	-	
39	UBA_8135_GENE_39	Hypothetical	NO DATA	-	91.67	5way_CG_67_GENE_11	hypo unique	NO DATA	-	-	
40	UBA_8135_GENE_40	tihypothecal protein ELI2158 [Erythrobacter litoralis	NO DATA	-	89.93	5way_CG_67_GENE_12	pilus biogenesis protein	NO DATA	-	-	
41	UBA_8135_GENE_40a		NO DATA	-	80.41	5way_CG_67_GENE_13	hypo unique	NO DATA	-	-	
42	UBA_8135_GENE_41	Hypothetical	NO DATA	-	97.70	5way_CG_67_GENE_14	gene with below; hypo unique	NO DATA	-	-	
43	UBA_8135_GENE_42	3-hydroxyisobutyrate dehydrogenase and related	53.8	16	96.77	5way_CG_67_GENE_16	3-hydroxyacid dehydrogenase	26		0	2.07
44	UBA_8135_GENE_43	ABC-type antimicrobial peptide transport system,	45.2	16	93.36	5way_CG_67_GENE_17	C transporter ATP-binding protein	20.7		0	2.18
45	UBA_8135_GENE_44	ABC-type antimicrobial peptide transport system,	NO DATA	-	95.19	5way_CG_67_GENE_18	BC transporter permease protein	NO DATA	-	-	
46	UBA_8135_GENE_45	Predicted secreted hydrolase	20	9	89.47	5way_CG_67_GENE_19	c hypo	NO DATA	-	20.00	
47	UBA_8135_GENE_46	Uncharacterized conserved protein	NO DATA	-	97.78	5way_CG_67_GENE_20	c hypo	NO DATA	-	-	
48	UBA_8135_GENE_47	Hypothetical	NO DATA	-	86.24	5way_CG_67_GENE_21	hypo unique	NO DATA	-	-	
49	UBA_8135_GENE_48	Predicted transcriptional regulator	NO DATA	-	98.58	5way_CG_67_GENE_22	transcriptional regulator	NO DATA	-	-	
50	UBA_8135_GENE_49	methyl-accepting chemotaxis protein [Vibrio parc	40.3	34	92.56	5way_CG_67_GENE_23	l-accepting chemotaxis protein)	20.5		0	1.97
51	UBA_8135_GENE_50a		NO DATA	-	98.90	5way_CG_67_GENE_24	protein diacylglycerol transferase	NO DATA	-	-	
52	UBA_8135_GENE_51	dnaK possibly split with above?	80.9	1	99.26	5way_CG_67_GENE_25	dnaK deletion suppressor protein	74.3		0	1.09
53	UBA_8135_GENE_52	Predicted EndoIII-related endonuclease	NO DATA	-	95.71	5way_CG_67_GENE_26	endonuclease III	NO DATA	-	-	
54	UBA_8135_GENE_53	NADH:ubiquinone oxidoreductase, NADH-binding	66.8	56	99.33	5way_CG_67_GENE_27	NADH dehydrogenase subunit F	57		0	1.17
55	UBA_8135_GENE_54	Hypothetical	NO DATA	-			[redacted]	NO DATA	-	-	
56		[D:1..115] # 5S ribosomal RNA # Thermoactinomyces	-						-		
57	UBA_8135_GENE_56	Cold shock proteins	61.5	-	100.00	5way_CG_140_GENE_1	cold shock protein	89.7	-	-	
58	UBA_8135_GENE_57	Hypothetical	NO DATA	-	96.10	5way_CG_140_GENE_2	eral secretion pathway protein H	18.5		0	0.06
59	UBA_8135_GENE_58	secretion system protein I/J:Bacterial type II secre	NO DATA	-	97.64	5way_CG_140_GENE_3	neral secretion pathway protein I	NO DATA	-	-	
60	UBA_8135_GENE_59	: Type II secretory pathway, component PulJ [Vibri	NO DATA	-	98.30	5way_CG_140_GENE_4	neral secretion pathway protein J	NO DATA	-	-	
61	UBA_8135_GENE_60	Replicative DNA helicase	33.7	2	99.14	5way_CG_140_GENE_5	replicative DNA helicase	31.7		0	1.06
62	UBA_8135_GENE_61	Histidyl-tRNA synthetase	49.7	27	92.20	5way_CG_140_GENE_6	histidyl tRNA synthetase	22.7		0	2.19
63	UBA_8135_GENE_62	Phosphoglycerate dehydrogenase and related de	89.9	0	99.07	5way_CG_140_GENE_7	osphoglycerate dehydrogenase	72		0	1.25
64	UBA_8135_GENE_63	Serine-pyruvate aminotransferase/archaeal aspar	70.1	21	98.95	5way_CG_140_GENE_8	aminotransferase	60.9		0	1.15
65	UBA_8135_GENE_64	ABC-type oligopeptide transport system, periplasn	30.5	11	92.84	5way_CG_140_GENE_9	ter, oligopeptide binding protein	12.4		0	2.46
66		5S_RRNA V5SRRNA 64059..64122 (-)	-						-		
67		TRNA Ala TGC 67323..67398 (-)	-						-		
68		TRNA Ile GAT 67404..67480 (-)	-				tRNA Ile		-		
69		SSU_RRNA AF356830 67606..69123 (-)	-						-		
70		[redacted]	NO GENE	-		5way_CG_120_GENE_1	transposase	NO DATA	-	-	
71	UBA_8135_GENE_69	GMP synthase - Glutamine amidotransferase dom	NO DATA	-	89.79	5way_CG_120_GENE_2	glutamine amidotransferase	NO DATA	-	-	
72	UBA_8135_GENE_70	Putative silver efflux pump	18.3	7	97.08	5way_CG_120_GENE_3	heavy metal efflux pump CzcA	14.1		0	1.30
73	UBA_8135_GENE_71	Membrane-fusion protein	66.8	61	93.05	5way_CG_120_GENE_4	efflux protein, CzcB	43.3		0	1.54
74	UBA_8135_GENE_72	Tyrosyl-tRNA synthetase	58.1	57	93.80	5way_CG_120_GENE_5	tyrosyl tRNA synthetase	23.1		0	2.52

75	UBA_8135_GENE_73	Hypothetical	50.6	21	90.68	5way_CG_120_GENE_6	hypo unique	9.1		0	5.56
76	UBA_8135_GENE_74	Nucleoside diphosphate kinase	97.1	58	97.83	5way_CG_120_GENE_7	nucleoside diphosphate kinase	76.8		0	1.26
77	UBA_8135_GENE_75	Predicted integral membrane protein	NO DATA	-	90.49	5way_CG_120_GENE_8	c hypo	NO DATA	-	-	
78	UBA_8135_GENE_76	Nucleoside-diphosphate-sugar epimerases	79	35	95.41	5way_CG_120_GENE_9	dTDP-glucose 4,6-dehydratase	27.9		0	2.83
79	UBA_8135_GENE_77	DNA-binding protein, stimulates sugar fermentatio	71.1	38	93.72	5way_CG_120_GENE_10	r fermentation stimulation protein	21.8		0	3.26
80	UBA_8135_GENE_78	Predicted UDP-glucose 6-dehydrogenase	62.5	40	96.84	5way_CG_120_GENE_11	UDP-glucose 6-dehydrogenase	44.5		1	1.40
81	UBA_8135_GENE_79	Glycine/D-amino acid oxidases (deaminating)	61.9	26	95.20	5way_CG_120_GENE_12	cine oxidase (sarcosine oxidase)	22.1		0	2.80
82	UBA_8135_GENE_80	Predicted membrane protein	NO DATA	-	93.71	5way_CG_120_GENE_13	c hypo	NO DATA	-	-	
83	UBA_8135_GENE_81	Cbb3-type cytochrome oxidase, cytochrome c su	71.6	0	100.00	5way_CG_120_GENE_14	e oxidase, cytochrome c subunit	71.6		0	1.00
84	UBA_8135_GENE_82	Uncharacterized conserved protein	55.2	29	98.02	5way_CG_57_GENE_2	c hypo	34.5		0	1.60
85	UBA_8135_GENE_83	Prephenate dehydratase	60.3	3	98.08	5way_CG_57_GENE_3	chorismate mutase	48.5		0	1.24
86	UBA_8135_GENE_84	3-deoxy-D-arabino-heptulosonate 7-phosphate (I	76.8	0	99.71	5way_CG_57_GENE_4	matic amino acid biosynthesis...	76.8		0	1.00
87	UBA_8135_GENE_85	Prephenate dehydrogenase	43	9	92.38	5way_CG_57_GENE_5	prephenate dehydrogenase	24.5		0	1.76
88	UBA_8135_GENE_86	5-enolpyruvylshikimate-3-phosphate synthase	44.7	30	94.05	5way_CG_57_GENE_6	lshikimate-3-phosphate synthase	10.1		0	4.43
89	UBA_8135_GENE_87	Cytidylate kinase	64.3	30	88.69	5way_CG_57_GENE_7	cytidylate kinase	15.4		0	4.18
90	UBA_8135_GENE_88a		50.9	23	93.86	5way_CG_57_GENE_8	acyltransferase	23.3		0	2.18
91	UBA_8135_GENE_89	Di- and tricarboxylate transporters chech ORF	NO DATA	-	97.00	5way_CG_57_GENE_9	ORF... sodium/sulfate transporter	NO DATA	-	-	
92	UBA_8135_GENE_90	5-formyltetrahydrofolate cyclo-ligase	NO DATA	-	88.35	5way_CG_57_GENE_10	rmyltetrahydrofolate cyclo-ligase	NO DATA	-	-	
93	UBA_8135_GENE_91	GTP cyclohydrolase I	24.6	1	96.34	5way_CG_57_GENE_11	GTP cyclohydrolase I	19.9		0	1.24
94	UBA_8135_GENE_92	5,10-methylene-tetrahydrofolate dehydrogenase/	87.8	21	98.30	5way_CG_57_GENE_12	ylenetetrahydrofolate reductase	79.9		0	1.10
95	UBA_8135_GENE_93	5,10-methylenetetrahydrofolate reductase	65.1	9	98.62	5way_CG_57_GENE_13	ylenetetrahydrofolate reductase	31.5		0	2.07
96	UBA_8135_GENE_94	Ketopantoate hydroxymethyltransferase	29.7	1	96.81	5way_CG_57_GENE_14	ntoate hydroxymethyltransferase	23.3		0	1.27
97	UBA_8135_GENE_95	Uncharacterized protein involved in cation transp	76.2	2	97.79	5way_CG_57_GENE_15	cation transport regulator	68.5		0	1.11
98	UBA_8135_GENE_96	Exonuclease III	27.9	20	93.21	5way_CG_57_GENE_16	exodeoxyribonuclease III	NO DATA	-		20.00
99	UBA_8135_GENE_97	hypothetical protein Francci3DRAFT_0099 [Frankia	7.7	0	96.15	5way_CG_57_GENE_17	similar to acyl-[ACP] desaturases	7.7		0	1.00
100	UBA_8135_GENE_98	Methyl-accepting chemotaxis protein	72.1	13	94.64	5way_CG_57_GENE_18	match is L. ferrooxidans protein)	50.5		1	1.43
101	UBA_8135_GENE_99	Hypothetical	29	27	91.43	5way_CG_57_GENE_19	glycolate oxidase	4.4		0	6.59
102	UBA_8135_GENE_100	Predicted HD-superfamily hydrolase	30.7	4	95.78	5way_CG_57_GENE_20	HD domain hydrolase	22.6		0	1.36
103	UBA_8135_GENE_101	Glutamate synthase domain 2	46.5	61	97.38	5way_CG_57_GENE_21	te synthase (NADPH) large chain	34.9		0	1.33
104	UBA_8135_GENE_102	Uncharacterized protein conserved in bacteria	77.3	5	99.09	5way_CG_57_GENE_22	c hypo	68.2		0	1.13
105	UBA_8135_GENE_103	DNA-directed RNA polymerase, sigma subunit (sig	70.1	1	99.00	5way_CG_57_GENE_23	RNA polymerase	69.9		1	1.00
106	UBA_8135_GENE_104	Acylphosphatases	86.9	6	98.99	5way_CG_57_GENE_24	possible acylphosphatase	55.6		0	1.56
107		TRNA Pro CGG 112701..112777 (-)		-					-		
108	UBA_8135_GENE_106	Fumarase	59.9	58	95.97	5way_CG_57_GENE_26	fumarase	30.6		1	1.96
109	UBA_8135_GENE_107	Predicted site-specific integrase-resolvase	21.9	-				NO GENE	-	-	
110	UBA_8135_GENE_108	Transposase, IS4 [Moorella thermoacetica ATCC 3	NO DATA	-				NO GENE	-	-	
111											
112											
113	8049										
114	UBA_8049_GENE_1	Hypothetical	NO DATA	-				NO GENE	-	-	
115	UBA_8049_GENE_2	Hypothetical	NO DATA	-	100.00	5way_CG_25_GENE_1	hypo unique	NO DATA	-	-	
116	UBA_8049_GENE_3	Cbb3-type cytochrome oxidase, cytochrome c su	71.6	0	100.00	5way_CG_25_GENE_2	tochrome c oxidase, fixO subunit	71.6		0	1.00
117	UBA_8049_GENE_4	Hypothetical	7.3	0	100.00	5way_CG_25_GENE_3	hypo unique	7.3		0	1.00
118	UBA_8049_GENE_6	Hypothetical	NO DATA	-	100.00	5way_CG_25_GENE_4	hypo unique	NO DATA	-	-	
119	UBA_8049_GENE_7	Hypothetical	35	0	100.00	5way_CG_25_GENE_5	cytochrome c	35		0	1.00
120	UBA_8049_GENE_8	Hypothetical	19.1	0	98.53	5way_CG_25_GENE_6	hypo unique	19.1		0	1.00
121	UBA_8049_GENE_9	Hypothetical	NO DATA	-	97.42	5way_CG_25_GENE_7	hypo unique	20.6		1	0.06
122	UBA_8049_GENE_10	Hypothetical	NO DATA	-	98.92	5way_CG_25_GENE_8	e c oxidase, cbb3 type, subunit I	NO DATA	-	-	
123	UBA_8049_GENE_11	Uncharacterized conserved protein	57.5	7	98.62	5way_CG_25_GENE_9	serine/threonine kinase	39.2		0	1.47
124	UBA_8049_GENE_12	Cbb3-type cytochrome oxidase, subunit 1	NO DATA	-	98.94	5way_CG_25_GENE_10	e c oxidase, cbb3 type, subunit I	NO DATA	-	-	
125	UBA_8049_GENE_13	Hypothetical	NO DATA	-	85.39	5way_CG_25_GENE_11	hypo unique	NO DATA	-	-	
126	UBA_8049_GENE_14	Hypothetical	9.5	5	97.96	5way_CG_25_GENE_12	Fe-S binding protein, FixG	5.4		1	1.76
127	UBA_8049_GENE_15	Hypothetical	43.9	27	94.84	5way_CG_25_GENE_13	hypo unique	NO DATA	-		20.00
128	UBA_8049_GENE_16	Hypothetical	NO DATA	-	90.74	5way_CG_25_GENE_13a		NO DATA	-	-	
129	UBA_8049_GENE_17	Hypothetical	NO DATA	-	98.51	5way_CG_25_GENE_15	c hypo	NO DATA	-	-	
130	UBA_8049_GENE_18	NTP pyrophosphohydrolases including oxidative d	49	18	91.41	5way_CG_25_GENE_16	ADP-ribose pyrophosphatase	6.6		0	7.42
131	UBA_8049_GENE_19	Hypothetical	NO DATA	-	92.06	5way_CG_25_GENE_17	polyferredoxin	NO DATA	-	-	
132	UBA_8049_GENE_20	Transcriptional regulator containing PAS, AAA-type	39.7	1	98.73	5way_CG_25_GENE_18	ma 54 dependent DNA-binding...	37.2		0	1.07
133	UBA_8049_GENE_22	Anthranilate/para-aminobenzoate synthases com	46.1	13	96.61	5way_CG_25_GENE_19	nthranilate synthase component I	27.5		0	1.68
134	UBA_8049_GENE_23	Anthranilate/para-aminobenzoate synthases com	22.7	4	96.97	5way_CG_25_GENE_20	thranilate synthase component II	4		0	5.68
135	UBA_8049_GENE_24	Anthranilate phosphoribosyltransferase	41.6	14	93.55	5way_CG_25_GENE_21	anilate phosphoribosyltransferase	15.5		0	2.68
136	UBA_8049_GENE_25	Indole-3-glycerol phosphate synthase	30.7	3	91.24	5way_CG_25_GENE_22	e-3-glycerol phosphate synthase	NO DATA	-		20.00
137	UBA_8049_GENE_26	Phosphoribosylanthranilate isomerase	57.1	28	93.87	5way_CG_25_GENE_23	horibosyl)anthranilate isomerase	NO DATA	-		20.00
138	UBA_8049_GENE_27	Tryptophan synthase beta chain	46.4	7	98.54	5way_CG_25_GENE_24	ryptophan synthase, beta subunit	42		0	1.10
139	UBA_8049_GENE_28	Tryptophan synthase alpha chain	53.8	17	95.45	5way_CG_25_GENE_25	tryptophan synthase alpha chain	26.1		0	2.06
140	UBA_8049_GENE_29	Acetyl-CoA carboxylase beta subunit	27	0	99.34	5way_CG_25_GENE_26	acetyl-CoA carboxylase	27		0	1.00
141	UBA_8049_GENE_30	Folylpolyglutamate synthase	26.8	4	93.47	5way_CG_25_GENE_27	folylpolyglutamate synthase	12.6		0	2.13
142	UBA_8049_GENE_31	Organic solvent tolerance protein OstA	12.7	1	97.92	5way_CG_25_GENE_28	organic solvent tolerance protein	16.3		3	0.78
143	UBA_8049_GENE_32	conserved hypothetical protein [Shewanella sp. M	62	56	95.09	5way_CG_25_GENE_29	similarity to carboxypeptidase D)	28.9		0	2.15
144	UBA_8049_GENE_33	Predicted sugar kinase	17.4	3	97.70	5way_CG_25_GENE_30	ATP/NAD kinase	10.5		0	1.66
145	UBA_8049_GENE_34	NADPH-dependent glutamate synthase beta chai	86.5	41	99.51	5way_CG_25_GENE_31	glutamate synthase	76.7		0	1.13
146	UBA_8049_GENE_34a		75.2	0	100.00	5way_CG_25_GENE_32	cyt b6 complex Rieske Fe-S	75.2		0	1.00

147	UBA_8049_GENE_35	Cytochrome b subunit of the bc complex	10.3	0	100.00	5way_CG_25_GENE_33	chrome b subunit of bc complex	10.3		0	1.00
148	UBA_8049_GENE_36	hypothetical protein AcidDRAFT_1459 [Solibacter u	12	1	97.83	5way_CG_25_GENE_34	aquinol-cytochrome c reductase	9.4		0	1.28
149	UBA_8049_GENE_36a		NO DATA	-	100.00	5way_CG_25_GENE_35	hypo unique	NO DATA	-	-	
150	UBA_8049_GENE_37	cytochrome c, class I [Geobacter metallireducens	42.4	27	99.69	5way_CG_25_GENE_36	ve cytochrome c oxidase subunit	38.6		0	1.10
151	UBA_8049_GENE_38	ABC-type multidrug transport system, ATPase com	35.5	1	95.72	5way_CG_25_GENE_37	C transporter, ATP-binding protein	23.2		1	1.53
152	UBA_8049_GENE_39	ABC-type multidrug transport system, permease c	NO DATA	-	96.34	5way_CG_25_GENE_38	BC transporter, permease protein	NO DATA	-	-	
153	UBA_8049_GENE_40	Uncharacterized protein conserved in bacteria	78.7	-	96.34	5way_CG_25_GENE_39	c hypo	39	-	-	
154	UBA_8049_GENE_41	Uncharacterized protein conserved in bacteria	78.7	-	96.34	5way_CG_25_GENE_39		39	-	-	
155	UBA_8049_GENE_42	Periplasmic serine proteases (ClpP class)	57.1	15	97.58	5way_CG_25_GENE_40	signal peptide peptidase	42.7		0	1.34
156	UBA_8049_GENE_42a		58	4	94.12	5way_CG_25_GENE_41	hypo unique	42		0	1.38
157	UBA_8049_GENE_43	Putative glycerate kinase	NO DATA	-	88.40	5way_CG_25_GENE_42	glycerate kinase	NO DATA	-	-	
158	UBA_8049_GENE_44	Hypothetical	NO DATA	-	97.70	5way_CG_25_GENE_43	hypo unique	NO DATA	-	-	
159	UBA_8049_GENE_45	Uncharacterized conserved protein	9.5	4	91.92	5way_CG_25_GENE_44	ynthase/transcription termination	NO DATA	-		20.00
160	UBA_8049_GENE_46	Hypothetical	27.8	15	95.65	5way_CG_25_GENE_45	hypo unique	NO DATA	-		20.00
161	UBA_8049_GENE_47	Hypothetical	52.7	48	93.64	5way_CG_25_GENE_46	hypo unique	35.9		0	1.47
162	UBA_8049_GENE_48	Hypothetical	63.5	24	87.83	5way_CG_25_GENE_47	hypo unique	21.7		0	2.93
163	UBA_8049_GENE_49	Predicted membrane protein	NO DATA	-	98.21	5way_CG_25_GENE_48	c hypo	NO DATA	-	-	
164	UBA_8049_GENE_50	77 Permeases of the major facilitator superfamily	NO DATA	-	93.07	5way_CG_25_GENE_49	multidrug efflux transporter	NO DATA	-	-	
165	UBA_8049_GENE_51	FOG: CBS domain	59.2	8	98.03	5way_CG_25_GENE_50	c hypo	53.9		0	1.10
166	UBA_8049_GENE_52	Hypothetical	18.9	2	88.17	5way_CG_25_GENE_51	ATP/GTP hydrolase	NO DATA	-		20.00
167	UBA_8049_GENE_54	7 Diadenosine tetraphosphate (Ap4A) hydrolase a	32.4	6	96.09	5way_CG_25_GENE_52	HIT family hydrolase	NO DATA	-		20.00
168	UBA_8049_GENE_55	Hypothetical	50.6	15	96.10	5way_CG_25_GENE_53	hypo unique	45		0	1.12
169	UBA_8049_GENE_56	Pyrimidine operon attenuation protein/uracil phos	61.8	12	96.48	5way_CG_25_GENE_54	uracil phosphoribosyltransferase	36.2		0	1.71
170	UBA_8049_GENE_57	Aspartate carbamoyltransferase, catalytic chain	51.9	2	98.70	5way_CG_25_GENE_55	aspartate carbamoyltransferase	43.8		0	1.18
171	UBA_8049_GENE_58	Dihydroorotase and related cyclic amidohydrolas	41.3	13	97.26	5way_CG_25_GENE_56	dihydroorotase	24.7		0	1.67
172	UBA_8049_GENE_59	Carbamoylphosphate synthase small subunit	45.2	25	96.71	5way_CG_25_GENE_57	osphate synthetase, small subunit	15.1		0	2.99
173	UBA_8049_GENE_60	Uncharacterized Fe-S protein PflX, homolog of pyr	6	0	96.99	5way_CG_25_GENE_58	rmate-lyase 1 activating enzyme	6		0	1.00
174	UBA_8049_GENE_61	Carbamoylphosphate synthase large subunit (split	44.5	35	97.78	5way_CG_25_GENE_59	osphate synthetase, large subunit	33		0	1.35
175	UBA_8049_GENE_62	Transcription elongation factor	81.2	0	100.00	5way_CG_25_GENE_60	transcription elongation factor	81.2		0	1.00
176	UBA_8049_GENE_63	Hypothetical	NO DATA	-	100.00	5way_CG_25_GENE_61	hypo unique	NO DATA	-	-	
177	UBA_8049_GENE_64	Hypothetical	NO DATA	-				NO GENE	-	-	
178	UBA_8049_GENE_65	Uncharacterized conserved protein	89.7	39				NO DATA	-		20.00
179	UBA_8049_GENE_66	Soluble lytic murein transglycosylase and related	62.7	-	94.59	5way_CG_1108_GENE_3	transglycosylase	27	-	-	
180	UBA_8049_GENE_67	Hypothetical	NO DATA	-	92.21	5way_CG_483_GENE_1	hypo unique	NO DATA	-	-	
181	UBA_8049_GENE_68	Pyruvate/2-oxoglutarate dehydrogenase complex	43.2	12	93.49	5way_CG_483_GENE_2	differs from others in community)	23		1	1.88
182	UBA_8049_GENE_69	Predicted signal transduction protein containing a	1.4	0	91.44	5way_CG_483_GENE_3	DEF domain/EAL domain protein	1.4		0	1.00
183			NO GENE	-		5way_CG_23_GENE_1	transposase - hypo unique	NO DATA	-	-	
184	UBA_8049_GENE_70	Glutamine synthetase	70	24	99.57	5way_CG_23_GENE_3	glutamine synthetase	70		1	1.00
185	UBA_8049_GENE_71	Aspartyl-tRNA synthetase	52.6	33	98.46	5way_CG_23_GENE_4	aspartyl tRNA synthetase	42.8		0	1.23
186	UBA_8049_GENE_72a		23.1	16	75.40	5way_CG_23_GENE_4a		7.9		0	2.92
187	UBA_8049_GENE_74	GMP synthase, PP-ATPase domain/subunit	44	32	96.51	5way_CG_23_GENE_6	GMP synthase	16.5		0	2.67
188	UBA_8049_GENE_75	IMP dehydrogenase/GMP reductase	70.1	24	99.39	5way_CG_23_GENE_7	monophosphate dehydrogenase	60.5		0	1.16
189	UBA_8049_GENE_76	Uncharacterized conserved protein	NO DATA	-	90.17	5way_CG_23_GENE_8	c hypo	NO DATA	-	-	
190	UBA_8049_GENE_77	Predicted ATPase (AAA+ superfamily)	51.7	28	93.33	5way_CG_23_GENE_9	one activity, ATP-binding domain	34		1	1.52
191	UBA_8049_GENE_78	Uncharacterized protein, similar to the N-terminal	NO DATA	-	99.54	5way_CG_23_GENE_10	ATP-dependent Lon protease	NO DATA	-	-	
192	UBA_8049_GENE_79	Hypothetical	42.1	0	96.99	5way_CG_23_GENE_11	hypo unique	42.1		0	1.00
193	UBA_8049_GENE_80	Hypothetical	20.1	0	95.57	5way_CG_23_GENE_12	c hypo	19.2		0	1.05
194	UBA_8049_GENE_81	ATP-dependent DNA ligase	20.3	7	96.19	5way_CG_23_GENE_13	DNA ligase	11.9		0	1.71
195	UBA_8049_GENE_82	Hypothetical	NO DATA	-	92.41	5way_CG_23_GENE_14	hypo unique	NO DATA	-	-	
196	UBA_8049_GENE_83	Hypothetical	58.1	15	94.97	5way_CG_23_GENE_15	hypo unique	40.2		0	1.45
197	UBA_8049_GENE_84	Apolipoprotein N-acyltransferase	12.5	4	92.12	5way_CG_23_GENE_16	olipoprotein N-acetyltransferase	NO DATA	-		20.00
198	UBA_8049_GENE_85	Protein chain release factor B	60	15	98.38	5way_CG_23_GENE_17	peptide chain release factor	49.5		1	1.21
199	UBA_8049_GENE_86	Molecular chaperone (small heat shock protein)	63.9	0	100.00	5way_CG_23_GENE_18	heat shock protein	63.9		0	1.00
200	UBA_8049_GENE_87	ATP-dependent Lon protease, bacterial type	56.6	53	96.68	5way_CG_23_GENE_19	ATP-dependent protease La	37.8		0	1.50
201	UBA_8049_GENE_88	Predicted EndoIII-related endonuclease	NO DATA	-	89.63	5way_CG_23_GENE_20	endonuclease III	NO DATA	-	-	
202	UBA_8049_GENE_89	conserved hypothetical protein [Silicibacter pome	NO DATA	-	100.00	5way_CG_23_GENE_21	c hypo	NO DATA	-	-	
203	UBA_8049_GENE_90	Predicted oxidoreductases (related to aryl-alcoho	NO DATA	-	94.03	5way_CG_23_GENE_22	aldo/keto reductase	NO DATA	-	-	
204	UBA_8049_GENE_91	AraC-type DNA-binding domain-containing protei	NO DATA	-	91.40	5way_CG_23_GENE_23	transcriptional regulator	7		1	0.06
205	UBA_8049_GENE_92	Glucoamylase and related glycosyl hydrolases	5	0	96.64	5way_CG_23_GENE_24	glucoamylase	5		0	1.00
206	UBA_8049_GENE_93	Histidyl-tRNA synthetase	47.8	10	95.87	5way_CG_23_GENE_25	histidyl tRNA synthetase	29.1		0	1.64
207	UBA_8049_GENE_94	Glucoamylase and related glycosyl hydrolases	7.6	0	97.57	5way_CG_23_GENE_27	glucoamylase	7.6		0	1.00
208	UBA_8049_GENE_95	Hypothetical, probable tn	NO DATA	-				NO GENE	-	-	
209	UBA_8049_GENE_96	Hypothetical	NO DATA	-				NO GENE	-	-	
210	UBA_8049_GENE_97	Membrane GTPase LepA	25.6	18	99.18	5way_CG_23_GENE_28	GTP-binding protein, LepA	16.4		0	1.56
211	UBA_8049_GENE_98	Signal peptidase I	44.8	32	96.41	5way_CG_23_GENE_29	signal peptidase I	16.6		0	2.70
212	UBA_8049_GENE_99	ADP-heptose synthase, bifunctional sugar kinase/	59.9	16	98.30	5way_CG_23_GENE_30	ADP-heptose synthase	48.3		0	1.24
213	UBA_8049_GENE_100	CMP-2-keto-3-deoxyoctulosonic acid synthetase	35.7	6	98.19	5way_CG_23_GENE_31	octylosonate cytidylyltransferase	20.9		0	1.71
214	UBA_8049_GENE_101	CTP synthase (UTP-ammonia lyase)	50.8	11	98.17	5way_CG_23_GENE_32	CTP synthetase	36.3		0	1.40
215	UBA_8049_GENE_102	3-deoxy-D-manno-octulosonic acid (KDO) 8-phos	60.9	23	94.81	5way_CG_23_GENE_33	eoxyphosphooctonate aldolase	NO DATA	-		20.00
216	UBA_8049_GENE_103	Predicted sugar phosphate isomerase involved in	71.1	54	95.18	5way_CG_23_GENE_34	sugar isomerase	34.3		0	2.07
217	UBA_8049_GENE_104	Low specificity phosphatase (HAD superfamily)	70.9	14	97.25	5way_CG_23_GENE_35	hatase/phosphatidyl transferase	45.6		0	1.55
218	UBA_8049_GENE_105	Phosphatidylglycerophosphate synthase	NO DATA	-	98.94	5way_CG_23_GENE_36	sphate 3-phosphatidyltransferase	NO DATA	-	-	

219	UBA_8049_GENE_106	Predicted membrane protein	NO DATA	-		97.57	5way_CG_23_GENE_37	c hypo	NO DATA	-	-	
220	UBA_8049_GENE_107	**Membrane proteins related to metalloendopeptid**	55.7	7		96.64	5way_CG_23_GENE_39	**cell wall endopeptidase**	38.8		0	1.44
221	UBA_8049_GENE_108	**Signal transduction histidine kinase**	39.1	5		99.41	5way_CG_23_GENE_40	**omponent sensor histidine kinase**	32		0	1.22
222	UBA_8049_GENE_109	**Hypothetical**	46.6	0		99.43	5way_CG_23_GENE_41	**hypo unique**	46.6		0	1.00
223	UBA_8049_GENE_110	**Response regulator containing CheY-like receiver,**	27.5	6		95.85	5way_CG_23_GENE_42	**transcriptional regulator**	21.4		0	1.29
224	UBA_8049_GENE_111	Predicted permeases	NO DATA	-		96.09	5way_CG_23_GENE_43	c hypo	NO DATA	-	-	
225	UBA_8049_GENE_112	Hypothetical	NO DATA	-		81.27	5way_CG_23_GENE_44	c hypo	NO DATA	-	-	
226	UBA_8049_GENE_114	**Small-conductance mechanosensitive channel**	22.6	10		95.40	5way_CG_23_GENE_45	e mechanosensitive ion channel	NO DATA	-		20.00
227	UBA_8049_GENE_115	**Hypothetical**	62.7	14		97.06	5way_CG_23_GENE_46	**hypo unique**	NO DATA	-		20.00
228	UBA_8049_GENE_116	Membrane-associated phospholipid phosphatase	NO DATA	-		96.68	5way_CG_23_GENE_47	hosphatidylglycerophosphate B	NO DATA	-	-	
229	UBA_8049_GENE_117	Predicted Fe-S-cluster redox enzyme	NO DATA	-		95.25	5way_CG_23_GENE_48	l SAM enzyme/Fe-S redox protein	NO DATA	-	-	
230	UBA_8049_GENE_118	Hypothetical	NO DATA	-		100.00	5way_CG_23_GENE_49	hypo unique	NO DATA	-	-	
231	UBA_8049_GENE_119	**Catalytic LigB subunit of aromatic ring-opening di**	18.9	5		98.11	5way_CG_23_GENE_50	**oxidoreductase/dioxygenase**	9.5		0	1.99
232	UBA_8049_GENE_120	**hypothetical protein [Parachlamydia sp. UWE25]gi**	9.5	0		100.00	5way_CG_23_GENE_51	**c hypo**	9.5		0	1.00
233			NO GENE	-			5way_CG_23_GENE_52	hypo unique	NO DATA	-	-	
234	UBA_8049_GENE_121	**Cbb3-type cytochrome oxidase, subunit 1**	16.9	0		100.00	5way_CG_33_GENE_1	e c oxidase, cbb3 type, subunit I	16.9		0	1.00
235	UBA_8049_GENE_122	**Hypothetical**	35.6	0		100.00	5way_CG_33_GENE_4	**ent protein secretion component**	35.6		0	1.00
236	UBA_8049_GENE_123	**Hypothetical**	39.2	0		100.00	5way_CG_33_GENE_5	**c hypo**	39.2		0	1.00
237	UBA_8049_GENE_124	Predicted dehydrogenase	NO DATA	-		99.76	5way_CG_33_GENE_6	FAD-dependent oxidreductase	NO DATA	-	-	
238	UBA_8049_GENE_125	7 Permeases of the drug/metabolite transporter (D	NO DATA	-		100.00	5way_CG_33_GENE_7	transporter/permease	NO DATA	-	-	
239	UBA_8049_GENE_126	**NADH:flavin oxidoreductases, Old Yellow Enzyme**	45.5	0		100.00	5way_CG_33_GENE_8	**reductase/xenobiotic reductase**	45.5		0	1.00
240	UBA_8049_GENE_127	77 Permeases of the major facilitator superfamily	NO DATA	-		99.80	5way_CG_33_GENE_9	multidrug resistance transporter	NO DATA	-	-	
241	UBA_8049_GENE_127a		NO DATA	-		100.00	5way_CG_33_GENE_10	hypo unique	NO DATA	-	-	
242	UBA_8049_GENE_128	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_11	hypo unique	NO DATA	-	-	
243	UBA_8049_GENE_129	hypothetical protein [Wolinella succinogenes]gi | 3	NO DATA	-		100	5way_CG_33_GENE_12	c hypo	NO DATA	-	-	
244	UBA_8049_GENE_129		NO DATA	-		100	5way_CG_33_GENE_12a		NO DATA	-	-	
245	UBA_8049_GENE_130	**Hypothetical**	13.9	0		100.00	5way_CG_33_GENE_14	**hypo unique**	13.9		0	1.00
246	UBA_8049_GENE_131	PAS [Solibacter usitatus Ellin6076]gi | 67860453 | gb |	NO DATA	-		100.00	5way_CG_33_GENE_15	DEF domain/EAL domain protein	NO DATA	-	-	
247	UBA_8049_GENE_132	**FOG: GGDEF domain**	5.6	0		100.00	5way_CG_33_GENE_16	**GDEF domain/EAL domain protein**	5.6		0	1.00
248	UBA_8049_GENE_133	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_17	hypo unique	NO DATA	-	-	
249	UBA_8049_GENE_134	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_18	possible serine endoprotease	NO DATA	-	-	
250	UBA_8049_GENE_135	**Hypothetical**	52.2	0		100.00	5way_CG_33_GENE_19	**c hypo**	52.2		0	1.00
251	UBA_8049_GENE_136	**Hypothetical**	12.2	0		100.00	5way_CG_33_GENE_20	**hypo unique**	12.2		0	1.00
252	UBA_8049_GENE_137	Membrane-bound serine protease (ClpP class)	NO DATA	-		99.78	5way_CG_33_GENE_21	nodulation protein NfeD	NO DATA	-	-	
253	UBA_8049_GENE_138	**Membrane protease subunits, stomatin/prohibitin**	14.3	0		100.00	5way_CG_33_GENE_22	**Band 7 protein**	14.3		0	1.00
254	UBA_8049_GENE_139	**Hypothetical**	25.3	0		100.00	5way_CG_33_GENE_23	**ymuconolactone decarboxylase**	25.3		0	1.00
255	UBA_8049_GENE_140	**Hypothetical**	69.1	2		99.43	5way_CG_33_GENE_24	**hypo unique**	63.4		0	1.09
256	UBA_8049_GENE_141	**3-hydroxyisobutyrate dehydrogenase and related**	51.9	0		100.00	5way_CG_33_GENE_25	**oxidoreductase**	51.9		0	1.00
257	UBA_8049_GENE_141a		NO DATA	-		100.00	5way_CG_33_GENE_26		NO DATA	-	-	
258	UBA_8049_GENE_142	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_26	acyl transferase	NO DATA	-	-	
259	UBA_8049_GENE_143	**Hypothetical**	63.3	0		100.00	5way_CG_33_GENE_27	**hypo unique**	63.3		0	1.00
260	UBA_8049_GENE_144	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_28	hypo unique	NO DATA	-	-	
261	UBA_8049_GENE_145	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_29	hypo unique	NO DATA	-	-	
262	UBA_8049_GENE_146	**Response regulator containing CheY-like receiver,**	62.2	0		100.00	5way_CG_33_GENE_30	**DNA-binding response regulator**	62.2		0	1.00
263	UBA_8049_GENE_147	**Signal transduction histidine kinase**	59.8	0		100.00	5way_CG_33_GENE_31	**sensory box histidine kinase**	59.8		0	1.00
264	UBA_8049_GENE_148	**Uncharacterized protein conserved in bacteria**	54.6	0		100.00	5way_CG_33_GENE_32	**c hypo**	54.6		0	1.00
265	UBA_8049_GENE_149	NADH:ubiquinone oxidoreductase subunit 5 (chai	NO DATA	-		100.00	5way_CG_33_GENE_33	NADH dehydrogenase, subunit F	NO DATA	-	-	
266	UBA_8049_GENE_150	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_33a		NO DATA	-	-	
267	UBA_8049_GENE_151	**Dihydroxyacid dehydratase/phosphogluconate d**	64.9	0		100.00	5way_CG_33_GENE_36	**dihydroxyacid dehydratase**	64.9		0	1.00
268	UBA_8049_GENE_152	**Putative translation factor (SUA5)**	13.9	0		100.00	5way_CG_33_GENE_37	**translation factor sua5-like**	13.9		0	1.00
269	UBA_8049_GENE_153	**Dihydroxyacid dehydratase/phosphogluconate d**	21	0		100.00	5way_CG_33_GENE_38	**dihydroxyacid dehydratase**	21		0	1.00
270	UBA_8049_GENE_154	**glr2085[Gloeobacter violaceus PCC 7421]gi | 3752**	NO DATA	-		100.00	5way_CG_33_GENE_39	**c hypo**	NO DATA	-	-	
271	UBA_8049_GENE_155	**Uncharacterized protein conserved in bacteria**	59.9	0		99.88	5way_CG_33_GENE_41	**c hypo**	64.6		6	0.93
272	UBA_8049_GENE_157	NADH:ubiquinone oxidoreductase subunit 5 (chai	NO DATA	-		100.00	5way_CG_33_GENE_42	NADH dehydrogenase, subunit 5	NO DATA	-	-	
273	UBA_8049_GENE_159	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_42a		NO DATA	-	-	
274	UBA_8049_GENE_160	PIN (PilT N terminus) domain [Nitrosomonas europ	NO DATA	-		100.00	5way_CG_33_GENE_44	c hypo	NO DATA	-	-	
275	UBA_8049_GENE_161	Hypothetical	NO DATA	-		100.00	5way_CG_33_GENE_45	hypo unique	NO DATA	-	-	
276	UBA_8049_GENE_162	NAD-dependent aldehyde dehydrogenases	NO DATA	-		100.00	5way_CG_691_GENE_3		NO DATA	-	-	
277			NO GENE	-			5way_CG_691_GENE_4	transposase	NO DATA	-	-	
278			NO GENE	-			5way_CG_33_GENE_47	glycosyl transferase	NO DATA	-	-	
279			NO GENE	-			5way_CG_33_GENE_48	glycosyl transferase	NO DATA	-	-	
280			NO GENE	-			5way_CG_33_GENE_49	proline oxidase	NO DATA	-	-	
281			NO GENE	-			5way_CG_369_GENE_1	transposase-like	NO DATA	-	-	
282	UBA_8049_GENE_163	Hypothetical	NO DATA	-		100.00	5way_CG_369_GENE_2	hypo unique	NO DATA	-	-	
283			NO GENE	-			5way_CG_369_GENE_3	glycosyltransferase	NO DATA	-	-	
284	UBA_8049_GENE_164	Glycosyltransferase	NO DATA	-		69.52	5way_CG_369_GENE_5	glycosyltransferase	NO DATA	-	-	
285	UBA_8049_GENE_165	Glycosyltransferase	NO DATA	-		100.00	5way_CG_369_GENE_6	glycosyltransferase	NO DATA	-	-	
286	UBA_8049_GENE_166	Sugar transferases involved in lipopolysaccharide	4.2	0		99.18	5way_CG_369_GENE_7	glycosyltransferase	4.1		0	1.02
287			NO GENE	-			5way_CG_369_GENE_8	BC transporter permease protein	NO DATA	-	-	
288			NO GENE	-			5way_CG_369_GENE_9	C transporter ATP-binding protein	NO DATA	-	-	
289	UBA_8049_GENE_167	ABC-type polysaccharide/polyol phosphate expo	NO DATA	-					NO GENE	-	-	
290	UBA_8049_GENE_168	Hypothetical	NO DATA	-					NO GENE	-	-	

291	UBA_8049_GENE_169	unknown [B.halodurans] Transposase	NO DATA	-				NO GENE	-	-	
292	UBA_8049_GENE_169a		NO DATA	-	100.00	5way_CG_318_GENE_1	hypo unique	NO DATA	-	-	
293	UBA_8049_GENE_170	Uncharacterized protein conserved in bacteria	NO DATA	-	100.00	5way_CG_318_GENE_2	c hypo	NO DATA	-	-	
294	UBA_8049_GENE_171	**Helix-turn-helix protein, CopG family [Nitrosomonc**	20.3	-	100.00	5way_CG_318_GENE_3	**c hypo**	20.3	-	-	
295	UBA_8049_GENE_172	**Helix-turn-helix split gene with above?**	20.3	-	100.00	5way_CG_318_GENE_3	**c hypo**	20.3	-	-	
296	UBA_8049_GENE_173	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_318_GENE_4	transposase	1.7	-	-	
297	UBA_8049_GENE_174	Transposase split with 173?	4.1	-	100.00	5way_CG_318_GENE_4	transposase	1.7	-	-	
298	UBA_8049_GENE_175	Methylated DNA-protein cysteine methyltransfera:	NO DATA	-	100.00	5way_CG_318_GENE_5	tein-cysteine S-methyltransferase	NO DATA	-	-	
299	UBA_8049_GENE_176	3-methyladenine DNA glycosylase/8-oxoguanine I	NO DATA	-	100.00	5way_CG_318_GENE_6	tion and regulatory protein, Ada	NO DATA	-	-	
300	UBA_8049_GENE_177	**Hypothetical**	20.4	0	100.00	5way_CG_318_GENE_7	**hypo unique**	20.4	0	1.00	
301	UBA_8049_GENE_178	Hypothetical	NO DATA	-	100.00	5way_CG_318_GENE_8	hypo unique	NO DATA	-	-	
302	UBA_8049_GENE_179	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_318_GENE_9	transposase	NO DATA	-	-	
303	UBA_8049_GENE_180	salicylate hydroxylase [Sphingomonas xenophagc	NO DATA	-	99.76	5way_CG_191_GENE_2	FAD binding monooxygenase	NO DATA	-	-	
304	UBA_8049_GENE_181	**Hypothetical**	26.2	0	100.00	5way_CG_191_GENE_3	**hosphate 1-dehydrogenase 5 3 _**	26.2	0	1.00	
305	UBA_8049_GENE_184	**Glucose-6-phosphate 1-dehydrogenase**	47.9	0	100.00	5way_CG_191_GENE_4	**ose 6-phosphate dehydrogenase**	47.9	0	1.00	
306	UBA_8049_GENE_185	**Transaldolase**	63.1	0	100.00	5way_CG_191_GENE_5	**transaldolase**	63.1	0	1.00	
307	UBA_8049_GENE_186	**Transketolase**	55.8	-	100.00	5way_CG_191_GENE_6	**transketolase**	66.9	-	-	
308			NO GENE	-		5way_CG_191_GENE_7		73.3	0	0.03	
309			NO GENE	-		5way_CG_191_GENE_9		4.7	-	-	
310	UBA_8049_GENE_187	**6-phosphogluconolactonase/Glucosamine-6-pho**	56.3	-	100.00	5way_CG_511_GENE_9	hypo unique	NO DATA	-	-	
311	UBA_8049_GENE_188	Glucokinase	3.5	0	100.00	5way_CG_511_GENE_8	glucokinase	3.5	0	1.00	
312	UBA_8049_GENE_188a		NO DATA	-	100.00	5way_CG_511_GENE_7	hypo unique	NO DATA	-	-	
313	UBA_8049_GENE_189	Hypothetical	NO DATA	-	100.00	5way_CG_511_GENE_5a		NO DATA	-	-	
314	UBA_8049_GENE_190	**Hypothetical**	74.6	0	100.00	5way_CG_511_GENE_5	**hypo**	74.6	0	1.00	
315	UBA_8049_GENE_191	Hypothetical	10	0	100.00	5way_CG_511_GENE_4	**hypo unique**	10	0	1.00	
316	UBA_8049_GENE_192	**Hypothetical**	68.2	-	100.00	5way_CG_511_GENE_2	**hypo**	69.4	-	-	
317	UBA_8049_GENE_195	**Uncharacterized cons.protein not in CG**	27.6	-	100.00	5way_CG_736_GENE_4	above?? ..helicases, SNF2 family	30.4	-	-	
318	UBA_8049_GENE_196	**Superfamily II DNA/RNA helicases, SNF2 family**	4.3	-	99.52	5way_CG_736_GENE_2	above?? ..helicases, SNF2 family	NO DATA	-	-	
319	UBA_8049_GENE_199	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_412_GENE_6	transposase	NO DATA	-	-	
320	UBA_8049_GENE_200a		NO DATA	-	100.00	5way_CG_412_GENE_5	transposase (single)	NO DATA	-	-	
321	UBA_8049_GENE_200	**hypothetical protein [Wolinella succinogenes]gi|3**	27.3	0				NO GENE	-	35.00	
322	UBA_8049_GENE_201	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
323	UBA_8049_GENE_202	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
324	UBA_8049_GENE_203	Predicted signal transduction protein containing a	NO DATA	-	96.77	5way_CG_412_GENE_4	DEF domain/EAL domain protein	NO DATA	-	-	
325	UBA_8049_GENE_204	**c.hypothetical protein, tranposase?**	71.4	-	100.00	5way_CG_412_GENE_2	**probable transposase**	71.4	-	-	
326	UBA_8049_GENE_205	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_412_GENE_1	transposase	NO DATA	-	-	
327	UBA_8049_GENE_206	Hypothetical	NO DATA	-				NO GENE	-	-	
328			NO GENE	-		5way_CG_73_GENE_39	transposase	NO DATA	-	-	
329	UBA_8049_GENE_208	**c. hypothetical protein tranposase?**	71.4	-	100.00	5way_CG_73_GENE_38	**probable transposase**	71.4	-	-	
330	UBA_8049_GENE_209	**Hypothetical**	80.8	500				NO GENE	-	35.00	
331	UBA_8049_GENE_210	Hypothetical	NO DATA	-				NO GENE	-	-	
332	UBA_8049_GENE_211	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
333			NO GENE	-		5way_CG_73_GENE_37	protein detected on 165-11 etc)	NO DATA	-	-	
334			NO GENE	-		5way_CG_73_GENE_36	transposase	NO DATA	-	-	
335			NO GENE	-		5way_CG_73_GENE_35	**transposase**	73.3	-	-	
336	UBA_8049_GENE_212	**Retron-type reverse transcriptase**	8.9	4				NO GENE	-	35.00	
337	UBA_8049_GENE_213	Hypothetical	NO DATA	-				NO GENE	-	-	
338	UBA_8049_GENE_214	Hypothetical	NO DATA	-				NO GENE	-	-	
339	UBA_8049_GENE_215	Hypothetical	NO DATA	-				NO GENE	-	-	
340	UBA_8049_GENE_216	Hypothetical	NO DATA	-				NO GENE	-	-	
341	UBA_8049_GENE_217	FOG: GGDEF domain	NO DATA	-				NO GENE	-	-	
342	UBA_8049_GENE_218	Predicted oxidoreductases (related to aryl-alcoho	NO DATA	-				NO GENE	-	-	
343	UBA_8049_GENE_219	Hypothetical	NO DATA	-				NO GENE	-	-	
344	UBA_8049_GENE_220	Hypothetical	NO DATA	-				NO GENE	-	-	
345	UBA_8049_GENE_222	-PB, isoform B [Drosophila melanogaster]gi|45551	6.6	-				NO GENE	-	-	
346	UBA_8049_GENE_223	Hypothetical	NO DATA	-				NO GENE	-	-	
347	UBA_8049_GENE_224	hypothetical protein MlgDRAFT_2172 [Alkalilimnico	NO DATA	-				NO GENE	-	-	
348	UBA_8049_GENE_225	Transposase, IS4 [Magnetococcus sp. MC-1]gi|69	NO DATA	-				NO GENE	-	-	
349	UBA_8049_GENE_226	**Transposase and inactivated derivatives**	73.3	-				NO GENE	-	-	
350	UBA_8049_GENE_227	Retron-type reverse transcriptase	2.8	-	100.00	5way_CG_73_GENE_33	**reverse transcriptase**	3.7	-	-	
351	UBA_8049_GENE_228	conserved hypothetical protein [Alkalilimnicola	NO DATA	-				NO GENE	-	-	
352	UBA_8049_GENE_229	Predicted oxidoreductases (related to aryl-alcoho	NO DATA	-				NO GENE	-	-	
353	UBA_8049_GENE_230	Hypothetical	NO DATA	-				NO GENE	-	-	
354	UBA_8049_GENE_230a		NO DATA	-				NO GENE	-	-	
355	UBA_8049_GENE_231	-PB, isoform B [Drosophila melanogaster]gi|45551	6	0				NO GENE	-	35.00	
356	UBA_8049_GENE_232	Hypothetical	NO DATA	-				NO GENE	-	-	
357	UBA_8049_GENE_233	hypothetical protein MlgDRAFT_2172 [Alkalilimnico	NO DATA	-				NO GENE	-	-	
358	UBA_8049_GENE_234	conserved hypo as in 228, split by ins ertion?	NO DATA	-	100.00	5way_CG_73_GENE_31	hypo unique	NO DATA	-	-	
359	UBA_8049_GENE_234a		NO DATA	-	100.00	5way_CG_73_GENE_29a		NO DATA	-	-	
360	UBA_8049_GENE_235	**hypothetical protein [uncultured Acidobacteria**	46.4	0	100.00	5way_CG_73_GENE_29	**hypo - TPR domain**	46.4	0	1.00	
361	UBA_8049_GENE_236	**3-hydroxyisobutyrate dehydrogenase etc.**	50.5	0	100.00	5way_CG_73_GENE_27	**artronic semialdehyde reductase**	50.5	0	1.00	
362	UBA_8049_GENE_237	**[Bradyrhizobium japonicum USDA 110]gi**	50.4	0	100.00	5way_CG_73_GENE_26	**weak (possible hydrolase)**	50.4	0	1.00	

363	UBA_8049_GENE_238	**hypothetical protein [uncultured Acidobacteria**	37.6	0	100.00	5way_CG_73_GENE_25	**hypo**	37.6		0	1.00
364	UBA_8049_GENE_239	Hypothetical (prob a Tn)	NO DATA	-	100.00	5way_CG_73_GENE_23a		NO DATA	-	-	
365	UBA_8049_GENE_239a		NO DATA	-	100.00	5way_CG_73_GENE_23	hypo unique	NO DATA	-	-	
366	UBA_8049_GENE_240	Transposase and inactivated derivatives	NO DATA	-	99.66	5way_CG_73_GENE_22	transposase	NO DATA	-	-	
367	UBA_8049_GENE_241	Transposase IS3/IS911 [Moorella thermoa. 73-21	NO DATA	-	100.00	5way_CG_73_GENE_21	transposase	NO DATA	-	-	
368	UBA_8049_GENE_242	Hypothetical	NO DATA	-	100.00	5way_CG_73_GENE_19	hypo unique	NO DATA	-	-	
369	UBA_8049_GENE_243	PilT protein, N-terminal [Syntrophobacter fum.]	NO DATA	-	100.00	5way_CG_73_GENE_18	c hypo	NO DATA	-	-	
370	UBA_8049_GENE_244	Prevent-host-death protein [Syntrophobacter fum.	NO DATA	-	100.00	5way_CG_73_GENE_17	c hypo	NO DATA	-	-	
371	UBA_8049_GENE_245	Hypothetical	NO DATA	-	100.00	5way_CG_73_GENE_16	hypo unique	NO DATA	-	-	
372	UBA_8049_GENE_246	Plasmid maintenance system antidote protein	NO DATA	-	100.00	5way_CG_73_GENE_14	maintenance system killer protein	NO DATA	-	-	
373	UBA_8049_GENE_247a		36.6	0	100.00	5way_CG_73_GENE_13	**plasmid maintenance protein**	36.6		0	1.00
374	UBA_8049_GENE_248	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_73_GENE_12	transposase	NO DATA	-	-	
375	UBA_8049_GENE_248a	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_73_GENE_11	ely split with above transposase	NO DATA	-	-	
376	UBA_8049_GENE_249	similarto ATPase (AAA+ superfamily) [Chlorobium li	NO DATA	-	100.00	5way_CG_73_GENE_9	ATPase, AAA superfamily	NO DATA	-	-	
377	UBA_8049_GENE_250a		NO DATA	-	99.74	5way_CG_73_GENE_8	transposase	NO DATA	-	-	
378	UBA_8049_GENE_251a		NO DATA	-	100.00	5way_CG_73_GENE_7	ATPase, AAA superfamily	NO DATA	-	-	
379	UBA_8049_GENE_252a		NO DATA	-	86.05	5way_CG_73_GENE_6	hypo unique	NO DATA	-	-	
380	UBA_8049_GENE_252	**Uncharacterized conserved protein (same 239?)**	10.1	-	100.00	5way_CG_73_GENE_5	**transposase**	10.1	-	-	
381	UBA_8049_GENE_253	**Glycosyltransferase**	18.2	0	100.00	5way_CG_73_GENE_4	**glycosyltransferase**	18.2		0	1.00
382	UBA_8049_GENE_254	Glycosyltransferase	9.7	-	100.00	5way_CG_627_GENE_2	glycosyltransferase	9.1	-	-	
383	UBA_8049_GENE_255	Sugar transferases involved in lipopolysaccharide :	NO DATA	-	100.00	5way_CG_73_GENE_1		NO DATA	-	-	
384	UBA_8049_GENE_257	ABC-type polysaccharide/polyol phosphate expo	NO DATA	-	97.35	5way_CG_627_GENE_4	BC transporter permease protein	NO DATA	-	-	
385	UBA_8049_GENE_258	**ABC-type polysacc/polyol phosph. Trans**	15.5	-	97.16	5way_CG_955_GENE_4	lactosyl-1-phosphate transferase	NO DATA	-	-	
386	UBA_8049_GENE_260	Hypothetical	NO DATA	-				NO GENE	-	-	
387	UBA_8049_GENE_261	Glycosyltransferases involved in cell wall biogenes	NO DATA	-				NO GENE	-	-	
388	UBA_8049_GENE_262	Hypothetical	NO DATA	-				NO GENE	-	-	
389	UBA_8049_GENE_263	putative transposase [Klebsiella pneumoniae]	NO DATA	-	100.00	5way_CG_659_GENE_6		NO DATA	-	-	
390	UBA_8049_GENE_264	Hypothetical	NO DATA	-				NO GENE	-	-	
391	UBA_8049_GENE_265a		NO DATA	-				NO GENE	-	-	
392	UBA_8049_GENE_266a		NO DATA	-				NO GENE	-	-	
393	UBA_8049_GENE_266	Hypothetical no match in CG	NO DATA	-				NO GENE	-	-	
394	UBA_8049_GENE_267	Transposase and inactivated derivatives, IS5 famil	NO DATA	-				NO GENE	-	-	
395	UBA_8049_GENE_268	Glycosyltransferase	NO DATA	-				NO GENE	-	-	
396	UBA_8049_GENE_269	Sugar transf.inv. lipopolysaccharide syn 73-1, 369-7	NO DATA	-	100.00	5way_CG_73_GENE_1	lactosyl-1-phosphate transferase	NO DATA	-	-	
397	UBA_8049_GENE_270	ABC-type polysaccharide/polyol phosphate expo	NO DATA	-	97.35	5way_CG_627_GENE_4	BC transporter permease protein	NO DATA	-	-	
398			NO GENE	-		5way_CG_955_GENE_6		NO DATA	-	-	
399			NO GENE	-		5way_CG_955_GENE_4a		NO DATA	-	-	
400	UBA_8049_GENE_271	**ABC-type polysaccharide/polyol phosphate trans**	15.5	-	97.16	5way_CG_955_GENE_4	lactosyl-1-phosphate transferase	NO DATA	-	-	
401			NO GENE	-		5way_CG_659_GENE_7	???	NO DATA	-	-	
402			NO GENE	-		5way_CG_659_GENE_6	???	NO DATA	-	-	
403			NO GENE	-		5way_CG_659_GENE_5	transposase	NO DATA	-	-	
404			NO GENE	-		5way_CG_659_GENE_4	hypo unique	NO DATA	-	-	
405	UBA_8049_GENE_273	**conserved hypothetical protein [Nitrosomonas eur**	NO DATA	-				NO GENE	-	-	
406	UBA_8049_GENE_274	Hypothetical	NO DATA	-	96.28	5way_CG_659_GENE_3	**hypo unique**	NO DATA	-	-	
407	UBA_8049_GENE_275	Hypothetical	NO DATA	-	99.08	5way_CG_659_GENE_2	hypo unique	NO DATA	-	-	
408	UBA_8049_GENE_278	**Glycosyltransferases involved in cell wall biogene**	20.1	-	96.70	5way_CG_659_GENE_1	**glycosyltransferase**	31.2	-	-	
409	UBA_8049_GENE_279	Transaldolase	NO DATA	-				NO GENE	-	-	
410	UBA_8049_GENE_280	: Histidinol phosphatase and related phosphatase:	NO DATA	-				NO GENE	-	-	
411	UBA_8049_GENE_281	Phosphoheptose isomerase	NO DATA	-				NO GENE	-	-	
412	UBA_8049_GENE_282	Nucleoside-diphosphate-sugar pyrophosphorylase	NO DATA	-				NO GENE	-	-	
413	UBA_8049_GENE_283	Predicted kinase related to galactokinase and me	NO DATA	-				NO GENE	-	-	
414	UBA_8049_GENE_284	Predicted dehydrogenases and related proteins	NO DATA	-				NO GENE	-	-	
415	UBA_8049_GENE_285	8 Dehydrogenases with different specificities	NO DATA	-				NO GENE	-	-	
416	UBA_8049_GENE_286	Nucleoside-diphosphate-sugar epimerases	NO DATA	-				NO GENE	-	-	
417	UBA_8049_GENE_287	Hypothetical no match in CG by tbn	NO DATA	-				NO GENE	-	-	
418	UBA_8049_GENE_288	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
419	UBA_8049_GENE_289	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
420	UBA_8049_GENE_290	Methyltransferase FkbM [Jannaschia sp. CCS1] no	NO DATA	-				NO GENE	-	-	
421	UBA_8049_GENE_291	**Hypothetical weak to glycosyltransf. no match ir**	NO DATA	-				NO GENE	-	-	
422	UBA_8049_GENE_292	probable transposase [Rhodopirellula baltica SH 1	NO DATA	-				NO GENE	-	-	
423	UBA_8049_GENE_293	**Transposase and inactivated derivatives, IS5 famil**	10.7	-				NO GENE	-	-	
424	UBA_8049_GENE_294	**Transposase and inactivated derivatives, IS5 famil**	40.2	-				NO GENE	-	-	
425	UBA_8049_GENE_295	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
426	UBA_8049_GENE_297	hypothetical protein Cpha266DRAFT_1332 [Chloro	NO DATA	-				NO GENE	-	-	
427	UBA_8049_GENE_298a		NO DATA	-	100.00	5way_CG_955_GENE_2		NO DATA	-	-	
428			NO GENE	-		5way_CG_955_GENE_1		NO DATA	-	-	
429	UBA_8049_GENE_299	hypothetical protein Daro03000134 [Dechloromon	NO DATA	-	91.18	5way_CG_659_GENE_5	transposase	NO DATA	-	-	
430	UBA_8049_GENE_300	hypothetical protein Shewana3DRAFT_3857	NO DATA	-				NO GENE	-	-	
431	UBA_8049_GENE_301	**Hypothetical**	6.5	0				NO GENE	-		35.00
432	UBA_8049_GENE_302	**Transposase and inactivated derivatives**	27.6	-				NO GENE	-	-	
433	UBA_8049_GENE_303	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
434	UBA_8049_GENE_303a		NO DATA	-		5way_CG_985_GENE_1	hypo unique	NO DATA	-	-	

435	UBA_8049_GENE_304	ORF376 [Leptospirillum ferrooxidans]gi | 62195101	NO DATA	-		100.00	5way_CG_985_GENE_2	gene with above? hypo unique	NO DATA	-		-
436	UBA_8049_GENE_306	ORF376 [Leptospirillum ferrooxidans]gi | 62195101 |	NO DATA	-					NO GENE	-		-
437	UBA_8049_GENE_307	IS1595 transposase [Xanthomonas camp..]	NO DATA	-					NO GENE	-		-
438	UBA_8049_GENE_308	ORF264 [Leptospirillum ferrooxidans]gi | 62195098 |	NO DATA	-		98.39	5way_CG_985_GENE_3	rome c biogenesis protein, CcsA	NO DATA	-		-
439	UBA_8049_GENE_308a		NO DATA	-		100.00	5way_CG_985_GENE_4	hypo unique	NO DATA	-		-
440	UBA_8049_GENE_309	**Zn-dependent hydrolases, including glyoxylases**	15.6		0	99.59	5way_CG_178_GENE_1	**ydroxyacylglutathione hydrolase**	15.6		0	1.00
441	UBA_8049_GENE_310	**Predicted transcriptional regulators**	37		0	99.16	5way_CG_178_GENE_2	**transcriptional regulator**	37		0	1.00
442	UBA_8049_GENE_311	77 Permeases of the major facilitator superfamily	NO DATA	-		100.00	5way_CG_178_GENE_3	facilitator superfamily transporter	NO DATA	-		-
443	UBA_8049_GENE_312	Hypothetical	NO DATA	-		100.00	5way_CG_178_GENE_4	hypo unique	NO DATA	-		-
444	UBA_8049_GENE_313	Hypothetical no match in CG, nt insert before:	NO DATA	-		100.00	5way_CG_178_GENE_4a		NO DATA	-		-
445	UBA_8049_GENE_314	Hypothetical Transposase (repeat)	NO DATA	-					NO GENE	-		-
446	UBA_8049_GENE_315	Hypothetical repeat, probable transposase	NO DATA	-					NO GENE	-		-
447	UBA_8049_GENE_316	unknown [Bacillus halodurans] Transposase	NO DATA	-					NO GENE	-		-
448	UBA_8049_GENE_317	Hypothetical	NO DATA	-		98.03	5way_CG_178_GENE_5	hypo unique	NO DATA	-		-
449	UBA_8049_GENE_318	**Outer membrane protein**	41.6		0	100.00	5way_CG_178_GENE_6	**metal ion efflux protein, CzcC**	41.6		0	1.00
450	UBA_8049_GENE_319	**Membrane-fusion protein**	49.4		0	100.00	5way_CG_178_GENE_7	**em transmembrane protein, CzrB**	49.4		0	1.00
451	UBA_8049_GENE_320	**Putative silver efflux pump**	25.8		0	100.00	5way_CG_178_GENE_8	**m transmembrane protein, CzcA**	25.8		0	1.00
452	UBA_8049_GENE_321	**Hypothetical**	38.8		0	100.00	5way_CG_178_GENE_9	**similarity to cation efflux pumps)**	38.8		0	1.00
453			NO GENE	-			5way_CG_178_GENE_10	transposase	NO DATA	-		-
454	UBA_8049_GENE_322	Hypothetical many copies, probably TN	NO DATA	-					NO GENE	-		-
455	UBA_8049_GENE_323	Hypothetical many identical copies, probably a T	NO DATA	-					NO GENE	-		-
456	UBA_8049_GENE_324	ABC-type polysaccharide/polyol phosphate trans	NO DATA	-					NO GENE	-		-
457	UBA_8049_GENE_325	Hypothetical no match in CG	NO DATA	-					NO GENE	-		-
458	UBA_8049_GENE_326	DNA replication protein I	NO DATA	-		100.00	5way_CG_321_GENE_1	DNA replication protein	NO DATA	-		-
459	UBA_8049_GENE_327	Transposase and inactivated derivatives	NO DATA	-		100.00	5way_CG_321_GENE_2	Hypothetical	NO DATA	-		-
460	UBA_8049_GENE_328	Transposase and inactivated derivatives	NO DATA	-		100.00	5way_CG_321_GENE_3	Transposase	NO DATA	-		-
461	UBA_8049_GENE_329	Transposase and inactivated derivatives	NO DATA	-		100.00	5way_CG_321_GENE_4	Transposase	NO DATA	-		-
462	UBA_8049_GENE_330	Transposase and inactivated derivatives	NO DATA	-		100.00	5way_CG_321_GENE_5	Transposase Hypothetical	NO DATA	-		-
463	UBA_8049_GENE_331	DNA replication protein	NO DATA	-		100.00	5way_CG_321_GENE_6	DNA replication protein	NO DATA	-		-
464	UBA_8049_GENE_331a		NO DATA	-		100.00	5way_CG_321_GENE_7	Hypothetical	NO DATA	-		-
465	UBA_8049_GENE_332	Transposase and inactivated derivatives	NO DATA	-		100.00	5way_CG_321_GENE_8	protein - E.coli plasmid R68.45 ins	NO DATA	-		-
466	UBA_8049_GENE_333a		NO DATA	-		100.00	5way_CG_581_GENE_8	DNA replication protein	NO DATA	-		-
467	UBA_8049_GENE_334	Transposase, IS4 [Magnetococcus sp. MC-1]gi | 69%	NO DATA	-					NO GENE	-		-
468	UBA_8049_GENE_335	unknown [Bacillus halodurans]	NO DATA	-					NO GENE	-		-
469	UBA_8049_GENE_336	Hypothetical	NO DATA	-					NO GENE	-		-
470			NO GENE	-			5way_CG_45_GENE_48	transposase	NO DATA	-		-
471	UBA_8049_GENE_337	**: ABC-type molybdate transport system, periplasm**	16.1		0	99.72	5way_CG_45_GENE_46	**c hypo**	15.8		0	1.02
472	UBA_8049_GENE_338	**Hypothetical no match in CG**	65.8	-			5way_CG_45_GENE_45a		NO DATA	-		-
473	UBA_8049_GENE_339	Transcriptional regulator	NO DATA	-		98.95	5way_CG_45_GENE_45	transcriptional regulator	NO DATA	-		-
474	UBA_8049_GENE_341	Hypothetical	NO DATA	-		100.00	5way_CG_45_GENE_43	c hypo	NO DATA	-		-
475	UBA_8049_GENE_342	unknown[Bacillus halodurans] likely transposase (r	NO DATA	-					NO GENE	-		-
476	UBA_8049_GENE_343	**Response regulator containing a CheY-like receiv**	40.6		0	99.61	5way_CG_45_GENE_41	**HD-GYP domain/GGDEF domain)**	40.6		0	1.00
477	UBA_8049_GENE_344	**Uncharacterized protein conserved in cyanobacte**	56.4		0	100.00	5way_CG_45_GENE_40	**c hypo**	56.4		0	1.00
478	UBA_8049_GENE_344a		NO DATA	-		100.00	5way_CG_45_GENE_39	hypo unique	NO DATA	-		-
479	UBA_8049_GENE_345a	**transposase**	NO DATA	-		100.00	5way_CG_45_GENE_38	transposase (single)	NO DATA	-		-
480	UBA_8049_GENE_346	putative transposase [Mycobacterium ulcerans]gi	NO DATA	-		100.00	5way_CG_45_GENE_37	transposase (single)	NO DATA	-		-
481	UBA_8049_GENE_346a		NO DATA	-		100.00	5way_CG_45_GENE_36	c hypo	NO DATA	-		-
482	UBA_8049_GENE_347	**Predicted nucleic acid-binding protein, contains P**	26.4		0	100.00	5way_CG_45_GENE_35	**plasmid stabilization, StbB**	26.4		0	1.00
483	UBA_8049_GENE_348	Plasmid stability protein	NO DATA	-		100.00	5way_CG_45_GENE_34	plasmid stabilization protein, StbC	NO DATA	-		-
484	UBA_8049_GENE_349	**Uncharacterized protein cons. in cyanobacteria**	18.2		0	100.00	5way_CG_45_GENE_33	**c hypo**	18.2		0	1.00
485	UBA_8049_GENE_350	[Leptospirillum ferrooxidans]gi | 62195088 | ref | YP_2	NO DATA	-		100.00	5way_CG_45_GENE_32	c hypo	NO DATA	-		-
486	UBA_8049_GENE_351	Uncharacterized protein conserved in bacteria	NO DATA	-		100.00	5way_CG_45_GENE_31	c hypo	NO DATA	-		-
487	UBA_8049_GENE_352	**Hypothetical**	38.3		0	100.00	5way_CG_45_GENE_30	**c hypo**	38.3		0	1.00
488	UBA_8049_GENE_353	Hypothetical	NO DATA	-		100.00	5way_CG_45_GENE_29	hypo unique	NO DATA	-		-
489	UBA_8049_GENE_354	Uncharacterized protein conserved in bacteria	NO DATA	-		100.00	5way_CG_45_GENE_28	c hypo	NO DATA	-		-
490	UBA_8049_GENE_355a		NO DATA	-		100.00	5way_CG_45_GENE_27	hypo unique	NO DATA	-		-
491	UBA_8049_GENE_355	Hypothetical	NO DATA	-		100.00	5way_CG_45_GENE_26	hypo unique	NO DATA	-		-
492	UBA_8049_GENE_356	Hypothetical	NO DATA	-		100.00	5way_CG_45_GENE_25	transcriptional regulator	NO DATA	-		-
493	UBA_8049_GENE_357	[Leptospirillum ferrooxidans]gi | 62195101 | ref | YP_2	NO DATA	-		99.53	5way_CG_45_GENE_24	algenate regulatory protein	NO DATA	-		-
494	UBA_8049_GENE_358	Ni,Fe-hydrogenase III small subunit	NO DATA	-		100.00	5way_CG_45_GENE_23	hydrogenase 3, subunit G	NO DATA	-		-
495	UBA_8049_GENE_359	Ni,Fe-hydrogenase III large subunit	NO DATA	-		90.78	5way_CG_45_GENE_22	3, subunit E / Ni,Fe, hydrogenase	NO DATA	-		-
496	UBA_8049_GENE_360	Formate hydrogenlyase subunit 3/Multisubunit Na-	NO DATA	-		90.52	5way_CG_45_GENE_21	drogenase 4, membrane subunit	NO DATA	-		-
497	UBA_8049_GENE_361	Hydrogenase 4 membrane component (E)	NO DATA	-		98.18	5way_CG_45_GENE_20	hydrogenase, membrane subunit	NO DATA	-		-
498	UBA_8049_GENE_362	Formate hydrogenlyase subunit 4	NO DATA	-		87.86	5way_CG_45_GENE_19	ormate hydrogenlyase subunit IV	NO DATA	-		-
499	UBA_8049_GENE_363	Formate hydrogenlyase subunit 3/Multisubunit Na-	NO DATA	-		85.20	5way_CG_45_GENE_18	formate hydrogenlyase subunit III	NO DATA	-		-
500	UBA_8049_GENE_364	Plasmid maintenance system antidote protein	NO DATA	-		85.34	5way_CG_45_GENE_17	DNA binding protein	NO DATA	-		-
501	UBA_8049_GENE_365	Hypothetical	NO DATA	-		72.73	5way_CG_45_GENE_16	hypo unique	NO DATA	-		-
502	UBA_8049_GENE_366	**Uncharacterized conserved protein**	75.1		177	86.70	5way_CG_45_GENE_15	**c hypo**	47.2		7	1.59
503	UBA_8049_GENE_368	**Uncharacterized conserved protein**	37.9		11	94.41	5way_CG_45_GENE_13	**c hypo**	10.4		0	3.64
504	UBA_8049_GENE_369	Uncharacterized protein conserved in bacteria	NO DATA	-		90.78	5way_CG_45_GENE_12	c hypo	NO DATA	-		-
505	UBA_8049_GENE_370	**Predicted proteasome-type protease**	18.7		2	94.42	5way_CG_45_GENE_11	c hypo	NO DATA	-		20.00
506	UBA_8049_GENE_371	3-methyladenine DNA glycosylase	NO DATA	-		83.96	5way_CG_45_GENE_10	-methyladenine DNA glycosylase	NO DATA	-		-

507	UBA_8049_GENE_372	Hypothetical	NO DATA	-		85.40	5way_CG_45_GENE_9	hypo unique	NO DATA	-		-
508	UBA_8049_GENE_373	Predicted nucleic acid-binding protein, contains F	NO DATA	-					NO GENE	-		-
509	UBA_8049_GENE_374	Lfe123p4 [Leptospirillum ferrooxidans]	NO DATA	-		90.38	5way_CG_45_GENE_8	hypo unique	NO DATA	-		-
510	UBA_8049_GENE_375	**Lfe123p3 [Leptospirillum ferrooxidans]**	23.1		0	97.69	5way_CG_45_GENE_7	**c hypo**	23.1		0	1.00
511	UBA_8049_GENE_376	Lfe123p2 [Leptospirillum ferrooxidans]	NO DATA	-		95.26	5way_CG_45_GENE_6	hypo unique	NO DATA	-		-
512	UBA_8049_GENE_377	Methylated DNA-protein cysteine methyltransfera:	NO DATA	-		65.85	5way_CG_45_GENE_5	protein cystein methyltransferase	NO DATA	-		-
513	UBA_8049_GENE_378	3-methyladenine DNA glycosylase/8-oxoguanine I	3.3		1	82.77	5way_CG_45_GENE_4	-methyladenine DNA glycosylase	NO DATA	-		20.00
514	UBA_8049_GENE_380	**Predicted oxidoreductases (related to aryl-alcoho**	50.1		33	95.07	5way_CG_45_GENE_3	oxidoreductase	NO DATA	-		20.00
515			NO GENE	-			5way_CG_45_GENE_2	hypo unique	NO DATA	-		-
516			NO GENE	-			5way_CG_45_GENE_1	hypo unique	NO DATA	-		-
517			NO GENE	-			5way_CG_454_GENE_1	hypo unique	NO DATA	-		-
518			NO GENE	-			5way_CG_454_GENE_2	transposase	NO DATA	-		-
519	UBA_8049_GENE_381	hypothetical protein Shewana3DRAFT_3857 [Shew	NO DATA	-		98.20	5way_CG_454_GENE_3	c hypo	NO DATA	-		-
520	UBA_8049_GENE_382	Hypothetical	NO DATA	-		84.09	5way_CG_454_GENE_4	hypo unique	NO DATA	-		-
521	UBA_8049_GENE_383	Hypothetical	NO DATA	-		98.11	5way_CG_454_GENE_5	hypo unique	NO DATA	-		-
522			NO GENE	-			5way_CG_454_GENE_6	**yl-accepting chemotaxis protein**	41.5	-		-
523			NO GENE	-			5way_CG_454_GENE_8	transposase	NO DATA	-		-
524	UBA_8049_GENE_384	**FOG: PAS/PAC domain**	69.8		55				NO GENE	-		35.00
525	UBA_8049_GENE_385	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
526	UBA_8049_GENE_387	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
527	UBA_8049_GENE_388	DNA replication protein	NO DATA	-					NO GENE	-		-
528	UBA_8049_GENE_389	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
529	UBA_8049_GENE_390	Hypothetical, likely transposase	NO DATA	-					NO GENE	-		-
530	UBA_8049_GENE_391	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
531	UBA_8049_GENE_392	Hypothetical	NO DATA	-					NO GENE	-		-
532	UBA_8049_GENE_393	Hypothetical	NO DATA	-					NO GENE	-		-
533	UBA_8049_GENE_394	**Hypothetical**	47.2		0				NO GENE	-		35.00
534	UBA_8049_GENE_395	**[Nostoc sp. PCC 7120]gi|17231131|ref|NP_487679**	28.8		10				NO GENE	-		35.00
535	UBA_8049_GENE_396	**Integrase**	13.1	-		91.94	5way_CG_75_GENE_31	**integrase fragment**	NO DATA	-		-
536	UBA_8049_GENE_397	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_30	hypo unique	NO DATA	-		-
537	UBA_8049_GENE_398	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_28a		NO DATA	-		-
538	UBA_8049_GENE_399	Bacteriophage protein gp37	NO DATA	-		100.00	5way_CG_75_GENE_28	C transporter, ATP-binding protein	NO DATA	-		-
539	UBA_8049_GENE_400	[Gloeobacter violaceus PCC 7421]gi|37522523|re	NO DATA	-		100.00	5way_CG_75_GENE_27	c hypo	NO DATA	-		-
540	UBA_8049_GENE_401	Predicted membrane protein	NO DATA	-		100.00	5way_CG_75_GENE_26	integral membrane protein?	NO DATA	-		-
541	UBA_8049_GENE_402	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_25	hypo unique	NO DATA	-		-
542	UBA_8049_GENE_403	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_24	hypo unique	NO DATA	-		-
543	UBA_8049_GENE_404	Predicted O-methyltransferase	NO DATA	-		100.00	5way_CG_75_GENE_23	affeoyl-CoA O-methyltransferase	NO DATA	-		-
544	UBA_8049_GENE_405	hypothetical protein [Photobacterium profundum	NO DATA	-		100.00	5way_CG_75_GENE_22	c hypo	NO DATA	-		-
545			NO GENE	-			5way_CG_75_GENE_21	glycoprotein	NO DATA	-		-
546	UBA_8049_GENE_406	Uncharacterized flavoproteins	NO DATA	-		99.61	5way_CG_75_GENE_20	n/metallo-beta-lactamase family	NO DATA	-		-
547	UBA_8049_GENE_407	Predicted signal transduction protein containing a	NO DATA	-		99.86	5way_CG_75_GENE_19	DEF domain/EAL domain protein	NO DATA	-		-
548	UBA_8049_GENE_408	Methyl-accepting chemotaxis protein	NO DATA	-		100.00	5way_CG_75_GENE_18	yl-accepting chemotaxis protein	NO DATA	-		-
549	UBA_8049_GENE_409a		NO DATA	-		100.00	5way_CG_75_GENE_17	yl-accepting chemotaxis protein	NO DATA	-		-
550	UBA_8049_GENE_410	Uncharacterized flavoprotein	NO DATA	-		96.36	5way_CG_75_GENE_16	n/metallo-beta-lactamase family	NO DATA	-		-
551	UBA_8049_GENE_411	**Methyl-accepting chemotaxis protein**	14.4		29	93.06	5way_CG_75_GENE_15	**yl-accepting chemotaxis protein**	9.1		0	1.58
552	UBA_8049_GENE_411a		NO DATA	-		100.00	5way_CG_75_GENE_13	c hypo	NO DATA	-		-
553	UBA_8049_GENE_412a		NO DATA	-		100.00	5way_CG_75_GENE_12	transposase	NO DATA	-		-
554	UBA_8049_GENE_412	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_11	hypo unique	NO DATA	-		-
555	UBA_8049_GENE_413	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_10	hypo unique	NO DATA	-		-
556	UBA_8049_GENE_414	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_9	transposase	NO DATA	-		-
557	UBA_8049_GENE_415	Predicted O-methyltransferase	NO DATA	-		100.00	5way_CG_75_GENE_8	affeoyl-CoA O-methyltransferase	NO DATA	-		-
558	UBA_8049_GENE_416	SAM-dependent methyltransferases	NO DATA	-		100.00	5way_CG_75_GENE_7	M-dependent methyltransferase	NO DATA	-		-
559	UBA_8049_GENE_417	Hypothetical	NO DATA	-		100.00	5way_CG_75_GENE_6	pectin degradation protein	NO DATA	-		-
560	UBA_8049_GENE_418	**Transposase and inactivated derivatives**	25.6	-					NO GENE	-		-
561	UBA_8049_GENE_419	Hypothetical no match in CG	NO DATA	-					NO GENE	-		-
562			NO GENE	-			5way_CG_75_GENE_5	hypo unique	NO DATA	-		-
563			NO GENE	-			5way_CG_75_GENE_4	**DNA helicase**	2.2		6	0.03
564			NO GENE	-			5way_CG_75_GENE_3	hypo unique	NO DATA	-		-
565	UBA_8049_GENE_420	Predicted transcriptional regulator	NO DATA	-		67.86	5way_CG_75_GENE_2	nscriptional regulator, LexA family	NO DATA	-		-
566	UBA_8049_GENE_421	Hypothetical	NO DATA	-		52.86	5way_CG_75_GENE_1	phage protein homology?	NO DATA	-		-
567	UBA_8049_GENE_422	Hypothetical no match in CG	NO DATA	-					NO GENE	-		-
568	UBA_8049_GENE_423	Hypothetical no match in CG by tbn	NO DATA	-					NO GENE	-		-
569	UBA_8049_GENE_424	Hypothetical tiny match all over, not to 376	NO DATA	-					NO GENE	-		-
570	UBA_8049_GENE_425	Hypothetical	NO DATA	-					NO GENE	-		-
571	UBA_8049_GENE_426	Hypothetical no sig match	NO DATA	-					NO GENE	-		-
572		TRNA Ser CGA 397456..397546 (+)		-			**missing tRNA???**			-		
573			NO GENE	-			5way_CG_376_GENE_1	hypo unique	NO DATA	-		-
574	UBA_8049_GENE_427	Hypothetical - no match in CG	NO DATA	-		100.00	5way_CG_376_GENE_1a		NO DATA	-		-
575	UBA_8049_GENE_428	Hypothetical)	NO DATA	-		100.00	5way_CG_376_GENE_3	c hypo	NO DATA	-		-
576			NO GENE	-			5way_CG_376_GENE_4	hypo unique	NO DATA	-		-
577	UBA_8049_GENE_429	Hypothetical	NO DATA	-		80.39	5way_CG_376_GENE_5	hypo unique	NO DATA	-		-
578	UBA_8049_GENE_429a		NO DATA	-		78.38	5way_CG_376_GENE_6	hypo unique	NO DATA	-		-

579	UBA_8049_GENE_431	Hypothetical	NO DATA	-	89.13	5way_CG_376_GENE_7	hypo unique	NO DATA	-	-	
580	UBA_8049_GENE_432	Hypothetical	NO DATA	-	80.33	5way_CG_376_GENE_8	hypo unique	NO DATA	-	-	
581	UBA_8049_GENE_432a		NO DATA	-	67.11	5way_CG_376_GENE_9	hypo unique	NO DATA	-	-	
582	UBA_8049_GENE_434	Hypothetical	NO DATA	-	96.67	5way_CG_376_GENE_10	hypo unique	NO DATA	-	-	
583	UBA_8049_GENE_435	Hypothetical protein [Clostridium acetobutylicum	NO DATA	-	100.00	5way_CG_376_GENE_11	?phage-related c hypo	NO DATA	-	-	
584	UBA_8049_GENE_436	Hypothetical	NO DATA	-	100.00	5way_CG_376_GENE_12	hypo unique	NO DATA	-	-	
585	UBA_8049_GENE_437	Hypothetical in different ORF from CG!!	NO DATA	-	95.16	5way_CG_376_GENE_12a		NO DATA	-	-	
586	UBA_8049_GENE_438	Hypothetical	NO DATA	-	97.57	5way_CG_376_GENE_14	hypo unique	NO DATA	-	-	
587	UBA_8049_GENE_439	Hypothetical	NO DATA	-	89.36	5way_CG_376_GENE_15	hypo unique	NO DATA	-	-	
588	UBA_8049_GENE_440	Hypothetical no match in CG by tbn	NO DATA	-				NO GENE	-	-	
589	UBA_8049_GENE_441	Hypothetical no match in CG tbn	NO DATA	-				NO GENE	-	-	
590	UBA_8049_GENE_442	Hypothetical no match in CG tbn	NO DATA	-				NO GENE	-	-	

	8692										
1	UBA_8692_GENE_1	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
2	UBA_8692_GENE_2	Histidinol-phosphate/aromatic aminotransferase c	NO DATA	-	85.64	5way_CG_94_GENE_1	osphate aminotransferase, CobC	NO DATA	-	-	
3	UBA_8692_GENE_3	Cobalamin biosynthesis protein CobD/CbiB	NO DATA	-	89.94	5way_CG_94_GENE_2	alamin biosynthesis protein, CobD	NO DATA	-	-	
4	UBA_8692_GENE_4	**Cobyric acid synthase**	19	7	93.20	5way_CG_94_GENE_3	cobyric acid synthase, CobQ	NO DATA	-		20.00
5			NO GENE	-		5way_CG_94_GENE_4	hypo unique	NO DATA	-	-	
6	UBA_8692_GENE_5	**Hypothetical**	32.2	23	85.79	5way_CG_94_GENE_5	**hypo unique**	4.9	0	6.57	
7	UBA_8692_GENE_6	**Dihydroxyacid dehydratase/phosphogluconate d**	46.5	25	97.67	5way_CG_94_GENE_6	**dihydroxy acid dehydratase**	33.4	0	1.39	
8	UBA_8692_GENE_7	**Uncharacterized protein conserved in bacteria**	47.6	19	93.71	5way_CG_94_GENE_7	**NA recombination protein RmuC**	20.5	0	2.32	
9	UBA_8692_GENE_8	Membrane protein of unknown function [Pelodict	NO DATA	-	98.21	5way_CG_94_GENE_8	c hypo	NO DATA	-	-	
10	UBA_8692_GENE_9	Predicted Co/Zn/Cd cation transporters	NO DATA	-	92.38	5way_CG_94_GENE_9	ein/magnetosome protein MamB	NO DATA	-	-	
11	UBA_8692_GENE_10	Fe-S oxidoreductase	NO DATA	-	93.91	5way_CG_94_GENE_10	nomethyl ester oxidative cyclase	NO DATA	-	-	
12	UBA_8692_GENE_11	**Hypothetical**	58.4	34	93.21	5way_CG_94_GENE_11	**hypo unique**	23.5	0	2.49	
13	UBA_8692_GENE_12	**Hypothetical**	57	48	93.30	5way_CG_94_GENE_12	**hypo unique**	44.7	0	1.28	
14	UBA_8692_GENE_13	**Precorrin-4 methylase**	62.6	18	98.56	5way_CG_94_GENE_13	**esis precorrin-3 methylase, CobM**	42.7	0	1.47	
15	UBA_8692_GENE_14	Hypothetical	NO DATA	-	95.53	5way_CG_94_GENE_14	hypo unique	NO DATA	-	-	
16	UBA_8692_GENE_15	**Precorrin-2 methylase**	56.2	14	93.63	5way_CG_94_GENE_15	**in-2 C20-methyltransferase, CobI**	14.7	0	3.82	
17	UBA_8692_GENE_16	Hypothetical	NO DATA	-	93.44	5way_CG_94_GENE_16	c hypo	NO DATA	-	-	
18	UBA_8692_GENE_17	**Riboflavin synthase alpha chain**	35.7	3	91.90	5way_CG_94_GENE_17	**riboflavin synthase, alpha chain**	13.8	0	2.59	
19	UBA_8692_GENE_18	**Pyrimidine reductase, riboflavin biosynthesis**	20.4	2	96.13	5way_CG_94_GENE_18	**oflavin biosynthesis protein RibD**	11.9	0	1.71	
20	UBA_8692_GENE_19	**Glycyl-tRNA synthetase, beta subunit**	58.7	71	94.05	5way_CG_94_GENE_19	**cyl-tRNA synthetase, beta subunit**	26	0	2.26	
21	UBA_8692_GENE_20	**Glycyl-tRNA synthetase, alpha subunit**	19.7	5	95.32	5way_CG_94_GENE_20	yl-tRNA synthetase, alpha subunit	NO DATA	-		20.00
22			NO GENE	-		5way_CG_94_GENE_21	transposase	NO DATA	-	-	
23	UBA_8692_GENE_21	Hypothetical, likely transposase	NO DATA	-				NO GENE	-	-	
24	UBA_8692_GENE_22	Transposase, IS4 [Thermoanaerobacter ethanolicu	NO DATA	-				NO GENE	-	-	
25	UBA_8692_GENE_23	**FOG: GGDEF domain**	9.5	1	97.82	5way_CG_317_GENE_3	DEF domain/EAL domain protein	NO DATA	-		20.00
26	UBA_8692_GENE_24	**Biotin synthase and related enzymes**	31.8	1	97.98	5way_CG_317_GENE_4	**biotin synthetase**	26.6	0	1.20	
27	UBA_8692_GENE_24a		48.3	11	83.67	5way_CG_317_GENE_5	**6-carboxyhexanoate-CoA ligase**	19.1	1	2.53	
28	UBA_8692_GENE_25	**7-keto-8-aminopelargonate synthetase and relate**	27.4	5	92.11	5way_CG_317_GENE_6	**amino-7-oxononanoate synthase**	12.9	0	2.12	
29	UBA_8692_GENE_26	**FOG: CBS domain**	96.3	0	100.00	5way_CG_317_GENE_7	**e dehydrogenase (purine biosyn)**	96.3	0	1.00	
30	UBA_8692_GENE_27	**Cell division protein FtsI/penicillin-binding protei**	12	-	98.73	5way_CG_30_GENE_46	**cell division protein FtsI**	7.2	-	-	
31	UBA_8692_GENE_28	Glycogen debranching enzyme	NO DATA	-	95.86	5way_CG_30_GENE_45	glycogen debranching enzyme	NO DATA	-	-	
32	UBA_8692_GENE_29	**Uncharacterized stress-induced protein**	44	27	92.15	5way_CG_30_GENE_44	**c hypo**	18.4	0	2.39	
33	UBA_8692_GENE_30	**Uncharacterized protein conserved in bacteria**	24.5	0	100.00	5way_CG_30_GENE_43	**c hypo**	24.5	0	1.00	
34	UBA_8692_GENE_31	**Guanylate kinase**	35	1	97.94	5way_CG_30_GENE_42	**guanylate kinase**	29.6	0	1.18	
35	UBA_8692_GENE_32	**Hypothetical**	82.1	4	94.78	5way_CG_30_GENE_41	**c hypo**	45.5	0	1.80	
36	UBA_8692_GENE_33	**Phosphopantothenoylcysteine synthetase/decarb**	37.6	26	90.12	5way_CG_30_GENE_40	**A and pantothenate metabolism**	10.4	0	3.62	
37	UBA_8692_GENE_34	**hypothetical protein Pcar_2131 [Pelobacter carbin**	61.5	91	88.60	5way_CG_30_GENE_39	**c hypo**	24.4	1	2.52	
38	UBA_8692_GENE_35	**3-dehydroquinate dehydratase II**	68.5	17	93.96	5way_CG_30_GENE_38	**hypo unique**	28.9	0	2.37	
39	UBA_8692_GENE_36	**Translation elongation factor P (EF-P)/translation i**	64.4	0	99.48	5way_CG_30_GENE_37	**translation elongation factor**	61.8	0	1.04	
40	UBA_8692_GENE_37	**Biotin carboxyl carrier protein**	62.2	15	95.54	5way_CG_30_GENE_36	**se/biotin carboxyl carrier protein**	33.1	0	1.88	
41	UBA_8692_GENE_38	**Biotin carboxylase**	47.8	9	97.59	5way_CG_30_GENE_35	**biotin carboxylase**	44.7	1	1.07	
42	UBA_8692_GENE_39	**Thiamine monophosphate synthase**	46.7	13	91.04	5way_CG_30_GENE_34	ynthase (pyrophosphorylase) ThiE	NO DATA	-		20.00
43	UBA_8692_GENE_40	**Hypothetical**	30.4	13	94.05	5way_CG_30_GENE_33	**box/EAL domain/GGDEF domain**	18.4	0	1.65	
44	UBA_8692_GENE_41	**FOG: CheY-like receiver**	42.6	2	98.65	5way_CG_30_GENE_32	**nponent response regulator CheY**	33.8	0	1.26	
45	UBA_8692_GENE_42	**Signal transduction histidine kinase**	13.9	7	91.61	5way_CG_30_GENE_31	**sory transduction histidine kinase**	NO DATA	-		20.00
46	UBA_8692_GENE_43	**Hypothetical**	100	0	100.00	5way_CG_30_GENE_30	**hypo unique**	100	0	1.00	
47	UBA_8692_GENE_44	**Hypothetical**	50	17	99.14	5way_CG_30_GENE_29	**hypo unique**	41.4	0	1.21	
48	UBA_8692_GENE_45	**Hypothetical**	76.8	35	99.30	5way_CG_30_GENE_28	**hypo unique**	66.5	0	1.15	
49	UBA_8692_GENE_45a		50	3	98.53	5way_CG_30_GENE_27	**hypo unique**	13.2	0	3.79	
50	UBA_8692_GENE_46	**Hypothetical**	78.2	30	98.18	5way_CG_30_GENE_26	**hypo unique**	50.9	0	1.54	
51	UBA_8692_GENE_46a		NO DATA	-	91.14	5way_CG_30_GENE_25	dethiobiotin synthetase	NO DATA	-	-	
52	UBA_8692_GENE_47	**Predicted redox protein, regulator of disulfide bon**	75.7	82	97.69	5way_CG_30_GENE_24	**c hypo**	40.5	0	1.87	
53	UBA_8692_GENE_48	**Predicted pyridoxal phosphate-dependent enzym**	53.2	22	94.12	5way_CG_30_GENE_23	**pleiotropic regulatory protein**	21.5	0	2.47	
54	UBA_8692_GENE_49	**FOG: TPR repeat**	69.6	174	97.26	5way_CG_30_GENE_22	**c hypo**	44.2	0	1.57	
55	UBA_8692_GENE_50a		NO DATA	-	97.84	5way_CG_30_GENE_21	hypo unique	NO DATA	-	-	
56	UBA_8692_GENE_51	Hypothetical, split gene with below	NO DATA	-	89.29	5way_CG_30_GENE_20	hypo unique	NO DATA	-	-	

57	UBA_8692_GENE_52	Hypothetical	NO DATA	-	89.77	5way_CG_30_GENE_20	hypo unique	NO DATA	-	-	
58	UBA_8692_GENE_53	3-hydroxyacyl-CoA dehydrogenase	NO DATA	-	94.44	5way_CG_30_GENE_19	droxybutyryl-coA dehydrogenase	NO DATA	-	-	
59	UBA_8692_GENE_54	**Hypothetical**	37	9	97.11	5way_CG_30_GENE_18	**hypo unique**	13.3		0	2.78
60	UBA_8692_GENE_55	**Hypothetical**	54.5	10	93.39	5way_CG_30_GENE_17	**phenol hydroxylase**	21		0	2.60
61	UBA_8692_GENE_56	ABC-type multidrug transport system, permease c	NO DATA	-	96.49	5way_CG_30_GENE_16	BC transporter permease protein	NO DATA	-	-	
62	UBA_8692_GENE_57	ABC-type multidrug transport system, ATPase com	NO DATA	-	95.31	5way_CG_30_GENE_15	C transporter ATP-binding protein	NO DATA	-	-	
63	UBA_8692_GENE_58	**Hypothetical**	31.9	18	97.10	5way_CG_30_GENE_14	**hypo unique**	13.5		0	2.36
64	UBA_8692_GENE_60	Hypothetical	NO DATA	-	95.06	5way_CG_30_GENE_13	hypo unique	NO DATA	-	-	
65	UBA_8692_GENE_61	**Outer membrane protein**	46.4	38	96.62	5way_CG_30_GENE_12	**outer membrane efflux protein**	34		1	1.36
66	UBA_8692_GENE_62	**Transcriptional regulator**	43.2	8	96.45	5way_CG_30_GENE_11	**transcriptional regulator**	25.5		0	1.69
67	UBA_8692_GENE_63	**Cation/multidrug efflux pump split**	22.2	19	98.60	5way_CG_30_GENE_10	**cation efflux protein**	14		1	1.59
68	UBA_8692_GENE_66	**Membrane-fusion protein**	70.2	88	97.34	5way_CG_30_GENE_9	**efflux transporter**	32.4		0	2.17
69	UBA_8692_GENE_67	**Outer membrane protein**	42.9	55	96.73	5way_CG_30_GENE_8	**outer membrane efflux protein**	31.4		1	1.37
70	UBA_8692_GENE_68	**Hypothetical**	8	2	95.36	5way_CG_30_GENE_7	transcriptional regulator	NO DATA	-		20.00
71	UBA_8692_GENE_69	**Hypothetical**	50.8	18	94.12	5way_CG_30_GENE_6	**hypo unique**	41.2		0	1.23
72	UBA_8692_GENE_70	Uncharacterized protein conserved in bacteria	NO DATA	-	93.77	5way_CG_30_GENE_5	c hypo	NO DATA	-	-	
73	UBA_8692_GENE_71	**Phosphoribosylformylglycinamidine (FGAM) synth**	63.1	32	91.76	5way_CG_30_GENE_4	**mylglycinamidine synthase PurM**	19.6		0	3.22
74	UBA_8692_GENE_72	**Phosphoribosylformylglycinamidine (FGAM) synth**	41	22	95.12	5way_CG_88_GENE_1	**rmylglycinamidine synthase, PurL**	28.2		0	1.45
75	UBA_8692_GENE_73	**Glutamine phosphoribosylpyrophosphate amidotr**	38.7	13	97.62	5way_CG_88_GENE_2	**ophosphoribosyltransferase PurF**	25.2		0	1.54
76	UBA_8692_GENE_75	**Lfe208p1 [Leptospirillum ferrooxidans]**	63.3	94	95.74	5way_CG_88_GENE_3	**hypo unique**	47.4		0	1.34
77	UBA_8692_GENE_76	**Nucleoside-diphosphate-sugar epimerases**	64	1	99.01	5way_CG_88_GENE_4	**-D-manno-heptose-6-epimerase**	53.1		0	1.21
78	UBA_8692_GENE_77	77 Permeases of the major facilitator superfamily	NO DATA	-	97.67	5way_CG_88_GENE_5	macrolide efflux protein	NO DATA	-	-	
79	UBA_8692_GENE_78	77 Permeases of the major facilitator superfamily	NO DATA	-	98.60	5way_CG_88_GENE_6	macrolide efflux protein	NO DATA	-	-	
80	UBA_8692_GENE_79	Glycosyltransferase	NO DATA	-	98.61	5way_CG_88_GENE_7	glycosyltransferase	NO DATA	-	-	
81	UBA_8692_GENE_80	Trehalose-6-phosphate synthase	NO DATA	-	96.20	5way_CG_88_GENE_8	trehalose-phosphate synthase	NO DATA	-	-	
82	UBA_8692_GENE_81	**Trehalose-6-phosphatase**	47.8	16	84.29	5way_CG_88_GENE_10	hypo unique	10.2		1	4.69
83	UBA_8692_GENE_82	**dTDP-4-dehydrorhamnose reductase**	14.9	3	89.51	5way_CG_88_GENE_11	P-4-dehydrorhamnose reductase	NO DATA	-		20.00
84	UBA_8692_GENE_83	**Hypothetical**	50.3	9	97.20	5way_CG_88_GENE_12	**hypo unique**	24.5		0	2.05
85	UBA_8692_GENE_84	**Ribosomal protein L17**	69.5	0	100.00	5way_CG_88_GENE_13	**ribosomal protein L17**	69.5		0	1.00
86	UBA_8692_GENE_85	**DNA-directed RNA polymerase, alpha subunit/40**	87	41	99.38	5way_CG_88_GENE_14	**RNA polymerase**	76.2		0	1.14
87	UBA_8692_GENE_86	**Ribosomal protein S4 and related proteins**	57.9	0	100.00	5way_CG_88_GENE_15	**ribosomal protein S4P**	57.9		0	1.00
88	UBA_8692_GENE_87	**Ribosomal protein S11**	53.9	-	100.00	5way_CG_88_GENE_15a		59	-	-	
89	UBA_8692_GENE_88	**Ribosomal protein S13**	55.6	86				NO GENE	-		35.00
90	UBA_8692_GENE_89	**Translation initiation factor 1 (IF-1)**	75	0	100.00	5way_CG_88_GENE_16a		75		0	1.00
91	UBA_8692_GENE_90	**Methionine aminopeptidase**	47.6	10	98.41	5way_CG_88_GENE_16	**methionine aminopeptidase**	38.5		0	1.24
92	UBA_8692_GENE_91	**Adenylate kinase and related kinases**	92.2	18	98.63	5way_CG_88_GENE_17	**adenylate kinase**	71.2		0	1.29
93	UBA_8692_GENE_92	Preprotein translocase subunit SecY	4.8	0	99.31	5way_CG_88_GENE_18	protein translocase, SecY subunit	4.8		0	1.00
94	UBA_8692_GENE_93	**Ribosomal protein L15**	90.6	26	98.66	5way_CG_88_GENE_19	**ribosomal protein L15**	69.1		0	1.31
95	UBA_8692_GENE_94	**Hypothetical**	92.1	-	97.67	5way_CG_88_GENE_20	**hypo unique**	79.1	-	-	
96	UBA_8692_GENE_95	**Ribosomal protein S5**	83.9	42	98.76	5way_CG_349_GENE_1	**ribosomal protein S5**	62.1		0	1.35
97	UBA_8692_GENE_96	**Ribosomal protein L18**	70.9	46	94.02	5way_CG_349_GENE_2	**ribosomal protein L18**	57.3		0	1.24
98	UBA_8692_GENE_97	**Ribosomal protein L6P/L9E**	89.4	44	98.32	5way_CG_349_GENE_3	**ribosomal protein L6**	59.2		0	1.51
99	UBA_8692_GENE_98	**Ribosomal protein S8**	41.7	0	100.00	5way_CG_349_GENE_4	ribosomal protein S8	41.7		0	1.00
100	UBA_8692_GENE_98a		37.7	-		5way_CG_349_GENE_4a		NO DATA	-	-	
101	UBA_8692_GENE_99	**Ribosomal protein L5**	83.2	108	93.81	5way_CG_349_GENE_5	**ribosomal protein L5**	57.1		0	1.46
102	UBA_8692_GENE_100	**Ribosomal protein L24**	87.2	-		5way_CG_349_GENE_5a		NO DATA	-	-	
103	UBA_8692_GENE_101	**Ribosomal protein L14**	79.5	0	100.00	5way_CG_349_GENE_6	**ribosomal protein L14**	79.5		0	1.00
104	UBA_8692_GENE_102	**Ribosomal protein S17**	62.1	30	94.74	5way_CG_349_GENE_7	**ribosomal protein S17**	60		0	1.04
105	UBA_8692_GENE_103	**Hypothetical**	69.7	-		5way_CG_349_GENE_7a		NO DATA	-	-	
106	UBA_8692_GENE_104	**Ribosomal protein L16/L10E**	75.6	0	100.00	5way_CG_349_GENE_8	**ribosomal protein L16**	75.6		0	1.00
107	UBA_8692_GENE_105	**Ribosomal protein S3**	87.2	48	99.56	5way_CG_349_GENE_9	**ribosomal protein S3**	77		0	1.13
108	UBA_8692_GENE_106	**Ribosomal protein L22**	54.5	0	100.00	5way_CG_349_GENE_10	**ribosomal protein L22**	54.5		0	1.00
109	UBA_8692_GENE_107	**Ribosomal protein S19**	60.6	0	98.94	5way_CG_349_GENE_11	**ribosomal protein S19**	60.6		0	1.00
110	UBA_8692_GENE_108	**Ribosomal protein L2**	75.1	18	99.27	5way_CG_349_GENE_12	**ribosomal protein L2**	72.2		0	1.04
111	UBA_8692_GENE_109	**Ribosomal protein L23**	93.7	-				NO GENE	-	-	
112	UBA_8692_GENE_110	**Ribosomal protein L4**	85.3	95	94.04	5way_CG_349_GENE_13	**ribosomal protein L4**	53.2		0	1.60
113	UBA_8692_GENE_111	**Ribosomal protein L3**	86.5	58	100.00	5way_CG_349_GENE_14	**ribosomal protein L3**	83.9		0	1.03
114	UBA_8692_GENE_112	**Ribosomal protein S10**	81.2	134				NO GENE	-		35.00
115	UBA_8692_GENE_113	**GTPases - translation elongation factors**	90.7	0	100.00	5way_CG_713_GENE_1	**n elongation factor (duplicated)**	90.7		0	1.00
116	UBA_8692_GENE_114	**Translation elongation factors (GTPases)**	88.3	88	98.55	5way_CG_713_GENE_2	**ngation factor EF-G FusA GTPase**	76.3		0	1.16
117	UBA_8692_GENE_115	**Ribosomal protein S7**	86.6	65	98.09	5way_CG_713_GENE_3	**ribosomal protein S7**	76.4		4	1.13
118	UBA_8692_GENE_116	**Ribosomal protein S12**	43.5	-	100.00	5way_CG_713_GENE_4	**ribosomal protein S12**	57.4	-	-	
119	UBA_8692_GENE_117	**DNA-directed RNA polymerase, beta' subunit/160**	69.5	-	98.04	5way_CG_137_GENE_8	**d RNA polymerase, beta' subunit**	62.2	-	-	
120	UBA_8692_GENE_119	**DNA-directed RNA polymerase, beta subunit/140**	83.7	173	98.54	5way_CG_137_GENE_7	**ed RNA polymerase, beta subunit**	67.8		0	1.23
121	UBA_8692_GENE_120	**Ribosomal protein L7/L12**	93.8	47	98.44	5way_CG_137_GENE_6	**ribosomal protein L7/L12**	93.8		1	1.00
122	UBA_8692_GENE_121	**Ribosomal protein L10**	87.4	96	95.40	5way_CG_137_GENE_5	**ribosomal protein L10**	74.1		0	1.18
123	UBA_8692_GENE_122	**Ribosomal protein L1**	81	31	99.14	5way_CG_137_GENE_4	**ribosomal protein L1**	75.9		0	1.07
124	UBA_8692_GENE_123	**Ribosomal protein L11**	73.8	2	99.29	5way_CG_137_GENE_3	**50S ribosomal protein L11**	68.1		0	1.08
125	UBA_8692_GENE_124	**Transcription antiterminator**	95.1	82	97.28	5way_CG_137_GENE_2	**ion antitermination protein, NusG**	60.3		0	1.58
126	UBA_8692_GENE_125	**Hypothetical**	18.8	9				NO GENE	-		35.00
127		TRNA Trp CCA 120718..120794 (-)		-					-		
128	UBA_8692_GENE_125a		75.5	0	100.00	5way_CG_137_GENE_1a		75.5		0	1.00

129	UBA_8692_GENE_126	GTPases - translation elongation factors	90.7	0	100.00	5way_CG_137_GENE_1	GTPase elongation factor Tu	90.7		0	1.00
130		TRNA Thr GGT 122293..122368 (-)	-						-		
131		TRNA Gly TCC 122392..122466 (-)	-						-		
132		TRNA Tyr GTA 122504..122589 (-)	-						-		
133	UBA_8692_GENE_128	Hypothetical	95	138	91.86	5way_CG_271_GENE_2	hypo unique	45.7		0	2.08
134	UBA_8692_GENE_129	Uncharacterized NAD(FAD)-dependent dehydrog	90.2	43	98.68	5way_CG_271_GENE_3	flavoprotein oxidoreductase	67.5		0	1.34
135		TRNA Leu TAG 124846..124931 (-)	-						-		
136	UBA_8692_GENE_131	Hypothetical	NO DATA	-	83.94	5way_CG_271_GENE_5	hypo unique	NO DATA	-	-	
137	UBA_8692_GENE_132	2-methylthioadenine synthetase	42.4	13	96.48	5way_CG_271_GENE_6	/2-methylthioadenine synthetase	22.6		0	1.88
138	UBA_8692_GENE_133	Hypothetical	59.6	13	95.36	5way_CG_271_GENE_7	hypo unique	43		0	1.39
139	UBA_8692_GENE_134	Hypothetical	NO DATA	-	96.43	5way_CG_271_GENE_8	hypo unique	NO DATA	-	-	
140	UBA_8692_GENE_135	Hypothetical	66.2	19	94.52	5way_CG_271_GENE_9	hypo unique	35.1		1	1.89
141	UBA_8692_GENE_136	Lipoproteins	31.6	7	93.16	5way_CG_271_GENE_10	rare lipoprotein A	20.5		0	1.54
142	UBA_8692_GENE_137	Hypothetical	NO DATA	-	97.23	5way_CG_271_GENE_11	c hypo	NO DATA	-	-	
143	UBA_8692_GENE_137a		61.8	0	100.00	5way_CG_271_GENE_12	ribosomal protein S18	61.8		0	1.00
144	UBA_8692_GENE_138	Single-stranded DNA-binding protein	69.3	1	97.86	5way_CG_271_GENE_13	ingle-strand DNA binding protein	47.9		0	1.45
145	UBA_8692_GENE_139	Hypothetical	64.8	55	97.54	5way_CG_271_GENE_14	k (possible ribosomal protein S6)	45.9		0	1.41
146	UBA_8692_GENE_140	Predicted GTPase, probable translation factor	74.5	22	97.80	5way_CG_53_GENE_4	GTP-binding protein	54.7		0	1.36
147	UBA_8692_GENE_141	Peptidyl-tRNA hydrolase	81.3	97	96.79	5way_CG_53_GENE_5	peptidyl tRNA hydrolase	32.6		0	2.49
148	UBA_8692_GENE_142	Ribosomal protein L25 (general stress protein Ctc)	88.9	86	97.58	5way_CG_53_GENE_6	ribosomal protein L25	60.4		0	1.47
149	UBA_8692_GENE_143	Phosphoribosylpyrophosphate synthetase	73.9	5	99.68	5way_CG_53_GENE_7	e-phosphate pyrophosphokinase	67.5		0	1.09
150		TRNA Gln TTG 134768..134842 (-)	-						-		
151	UBA_8692_GENE_144	Hypothetical	46.1	28	96.25	5way_CG_53_GENE_8	dyl-2c-methyl-D-erythritol kinase	9.6		0	4.80
152	UBA_8692_GENE_145	Fe-S oxidoreductase, related to NifB/MoaA family	7.1	2	96.32	5way_CG_53_GENE_9	Fe-S oxidoreductase	NO DATA	-		20.00
153	UBA_8692_GENE_146	Phosphatidylglycerophosphate synthase	NO DATA	-	98.91	5way_CG_53_GENE_10	alcohol phosphatidyl transferase	NO DATA	-	-	
154	UBA_8692_GENE_147	Hypothetical	57.7	98	93.44	5way_CG_53_GENE_11	hypo unique	29.6		0	1.95
155	UBA_8692_GENE_148	Hypothetical	16.6	0	98.16	5way_CG_53_GENE_12	hypo unique	16.6		0	1.00
156	UBA_8692_GENE_149	ATP-dependent protease Clp, ATPase subunit	52.6	4	99.77	5way_CG_53_GENE_13	rotease ATP-binding subunit ClpX	49.1		0	1.07
157	UBA_8692_GENE_150	Protease subunit of ATP-dependent Clp proteases	43.3	12	99.51	5way_CG_53_GENE_14	protease	39.9		0	1.09
158	UBA_8692_GENE_151	Hypothetical	73	78	97.22	5way_CG_53_GENE_15	ptidyl-prolyl cis-trans isomerase)	41.3		0	1.77
159	UBA_8692_GENE_152	2-polyprenyl-6-methoxyphenol hydroxylase and r	22	3	90.58	5way_CG_53_GENE_16	FAD-binding monooxygenase	8.9		1	2.47
160	UBA_8692_GENE_152a		49	80	82.13	5way_CG_53_GENE_17	c hypo	8.9		1	5.51
161	UBA_8692_GENE_153	Glucose-6-phosphate 1-dehydrogenase	76.5	15	98.04	5way_CG_53_GENE_18	cose 6-phosphate deydrogenase	69.6		0	1.10
162	UBA_8692_GENE_154	Transaldolase	75.2	286	93.45	5way_CG_53_GENE_19	transaldolase	31		7	2.43
163	UBA_8692_GENE_155	Transketolase	62.6	106	94.09	5way_CG_53_GENE_20	transketolase	30.1		0	2.08
164	UBA_8692_GENE_156	6-phosphogluconolactonase/Glucosamine-6-pho	70.8	47	92.34	5way_CG_53_GENE_21	cose 6-phosphate deydrogenase	12		0	5.90
165	UBA_8692_GENE_157	Glucokinase	68.3	75	88.66	5way_CG_53_GENE_22	glucokinase	8.1		0	8.43
166	UBA_8692_GENE_158	Transposase and inactivated derivatives, IS5 famil	41.6	-				NO GENE	-	-	
167		QUESTIONALBE LINK THOUGH STILL ON Sc_53	-						-		
168	UBA_8692_GENE_159	Hypothetical	48.1	13	93.51	5way_CG_53_GENE_23	c hypo	10.3		0	4.67
169	UBA_8692_GENE_160	Hypothetical	NO DATA	-	93.51	5way_CG_53_GENE_24	kely split with below hypo unique	NO DATA	-	-	
170	UBA_8692_GENE_160	Hypothetical	NO DATA	-	95.71	5way_CG_53_GENE_25	c hypo	NO DATA	-	-	
171	UBA_8692_GENE_161	Hypothetical	15.3	21	87.32	5way_CG_53_GENE_26	dextran sucrase	6.6		1	2.32
172	UBA_8692_GENE_163	Hypothetical, likley tn	NO DATA	-				NO GENE	-	-	
173	UBA_8692_GENE_164	unknown [Bacillus halodurans], likley tn	NO DATA	-				NO GENE	-	-	
174		QUESTIONALBE LINK	-						-		
175	UBA_8692_GENE_165	Predicted signal transduction protein	NO DATA	-	93.50	5way_CG_53_GENE_27	c hypo (contains HD domain)	NO DATA	-	-	
176	UBA_8692_GENE_166	Hypothetical	NO DATA	-	89.81	5way_CG_53_GENE_28	hypo unique	NO DATA	-	-	
177	UBA_8692_GENE_167	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
178			NO GENE	-		5way_CG_682_GENE_2	transposase	NO DATA	-	-	
179	UBA_8692_GENE_168	Hypothetical	22.4	2				NO GENE	-		35.00
180	UBA_8692_GENE_169	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
181			NO GENE	-		5way_CG_682_GENE_3	ator/mercury resistance regulator	NO DATA	-	-	
182			NO GENE	-		5way_CG_682_GENE_4	mercuric reductase	NO DATA	-	-	
183	UBA_8692_GENE_170	Hypothetical	NO DATA	-				NO GENE	-	-	
184	UBA_8692_GENE_171	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
185			NO GENE	-		5way_CG_283_GENE_1		NO DATA	-	-	
186	UBA_8692_GENE_173	Predicted Fe-S oxidoreductases	21.9	4	98.83	5way_CG_283_GENE_2	eme d1 biosynthesis protein NirJ	17.5		0	1.25
187	UBA_8692_GENE_174	NADPH:quinone reductase and related Zn-depend	69.4	20	94.29	5way_CG_283_GENE_3	quinone oxidoreductase	22.2		0	3.13
188	UBA_8692_GENE_175	Diadenosine tetraphosphatase and related serine	NO DATA	-	89.43	5way_CG_283_GENE_4	e/threonine protein phosphatase	NO DATA	-	-	
189	UBA_8692_GENE_176	Protoporphyrinogen oxidase	52.4	20	95.02	5way_CG_283_GENE_5	protoporphyrinogen oxidase	21		0	2.50
190	UBA_8692_GENE_177	Hypothetical	NO DATA	-	89.74	5way_CG_283_GENE_6	hypo unique	NO DATA	-	-	
191	UBA_8692_GENE_179	hypothetical protein AcidDRAFT_5042 [Solibacter u	NO DATA	-	97.22	5way_CG_283_GENE_7	c hypo	NO DATA	-	-	
192	UBA_8692_GENE_180	Chloride channel protein EriC	NO DATA	-	99.12	5way_CG_283_GENE_8	chloride channel protein	NO DATA	-	-	
193		TRNA Arg CCG 174560..174637 (+)	-						-		
194			NO GENE	-		5way_CG_784_GENE_1	integrase (fragment, no domain)	NO DATA	-	-	
195	UBA_8692_GENE_182	Integrase	NO DATA	-	92.12	5way_CG_784_GENE_2	integrase	NO DATA	-	-	
196	UBA_8692_GENE_183	Uncharacterized protein conserved in bacteria	NO DATA	-				NO GENE	-	-	
197	UBA_8692_GENE_184	Type II secretory pathway, component PulF	NO DATA	-	99.75	5way_CG_1145_GENE_1	pili biogenesis protein	NO DATA	-	-	
198	UBA_8692_GENE_185a		NO DATA	-	96.32	5way_CG_784_GENE_5	hypo	NO DATA	-	-	
199	UBA_8692_GENE_186	Lj965 prophage protein [Pelodictyon phaeoclathr	NO DATA	-	98.37	5way_CG_784_GENE_6	protein	NO DATA	-	-	
200	UBA_8692_GENE_187	Hypothetical no match in Leptoll CG	NO DATA	-				NO GENE	-	-	

201	UBA_8692_GENE_188	Hypothetical no match in LeptoII CG	NO DATA	-				NO GENE	-	-	
202	UBA_8692_GENE_189	**Type II secretory pathway, ATPase PulE/Tfp pilus as**	5.9	2				NO GENE	-		35.00
203	UBA_8692_GENE_190	Flp pilus assembly protein, secretin CpaC no sig m	NO DATA	-				NO GENE	-	-	
204	UBA_8692_GENE_191	Hypothetical	NO DATA	-	94.64	5way_CG_582_GENE_8	hypo unique	NO DATA	-	-	
205	UBA_8692_GENE_191a		NO DATA	-	88.32	5way_CG_582_GENE_7	hypo unique	NO DATA	-	-	
206	UBA_8692_GENE_192	Hypothetical	NO DATA	-	97.72	5way_CG_582_GENE_6	hypo unique	NO DATA	-	-	
207	UBA_8692_GENE_193	Tfp pilus assembly protein, pilus retraction ATPase	NO DATA	-	97.40	5way_CG_582_GENE_4	protein/twitching motility protein	NO DATA	-	-	
208	UBA_8692_GENE_194	Hypothetical	NO DATA	-	94.33	5way_CG_582_GENE_3	hypo unique	NO DATA	-	-	
209			NO GENE	-		5way_CG_582_GENE_2	hypo unique	NO DATA	-	-	
210	UBA_8692_GENE_195	Hypothetical	NO DATA	-				NO GENE	-	-	
211	UBA_8692_GENE_196	sim antirepressor of bacteriophage P22 [Bacteriop	NO DATA	-				NO GENE	-	-	
212	UBA_8692_GENE_197	Hypothetical	NO DATA	-	86.34	5way_CG_582_GENE_1	hypo unique	NO DATA	-	-	
213	UBA_8692_GENE_198	Type IV secretory pathway, VirD4 comp	NO DATA	-	98.48	5way_CG_440_GENE_5	conjugal transfer protein TraG	NO DATA	-	-	
214	UBA_8692_GENE_199	Flp pilus assembly protein, ATPase CpaF	NO DATA	-	74.13	5way_CG_440_GENE_3	**conjugal transfer protein TrbB**	15		4	0.06
215	UBA_8692_GENE_200	Hypothetical low match to sc_44-15	NO DATA	-				NO GENE	-	-	
216	UBA_8692_GENE_201	Hypothetical	NO DATA	-	92.96	5way_CG_259_GENE_1	hypo unique	NO DATA	-	-	
217	UBA_8692_GENE_202	Type IV secretory pathway, VirB4 components	NO DATA	-	98.99	5way_CG_259_GENE_2	conjugal transfer protein TrbE	NO DATA	-	-	
218	UBA_8692_GENE_202	Type IV secretory pathway, VirB4 components	NO DATA	-	91.21	5way_CG_259_GENE_3	conjugal transfer protein TrbE	NO DATA	-	-	
219	UBA_8692_GENE_203	Hypothetical	NO DATA	-	98.26	5way_CG_259_GENE_4	conjugal transfer protein TrbJ	NO DATA	-	-	
220	UBA_8692_GENE_204	Type IV secretory pathway, TrbL components	NO DATA	-	95.55	5way_CG_259_GENE_5	conjugal transfer protein TrbL	NO DATA	-	-	
221	UBA_8692_GENE_205	Type IV secretory pathway, TrbF components	NO DATA	-	100.00	5way_CG_259_GENE_6	conjugal transfer protein TrbF	NO DATA	-	-	
222	UBA_8692_GENE_207	Type IV secretory pathway, VirB9 components	NO DATA	-	99.68	5way_CG_259_GENE_7	conjugal transfer protein TrbG	NO DATA	-	-	
223	UBA_8692_GENE_208	Type IV secretory pathway, VirB10 components	NO DATA	-	94.59	5way_CG_259_GENE_8	conjugal transfer protein TrbI	NO DATA	-	-	
224	UBA_8692_GENE_209	Hypothetical	NO DATA	-	96.10	5way_CG_259_GENE_9	hypo unique	NO DATA	-	-	
225			NO GENE	-		5way_CG_259_GENE_10	hypo unique	NO DATA	-	-	
226			NO GENE	-		5way_CG_259_GENE_11	hypo unique	NO DATA	-	-	
227			NO GENE	-		5way_CG_259_GENE_12	omain protein/response regulator	NO DATA	-	-	
228	UBA_8692_GENE_210	Uncharacterized conserved protein	NO DATA	-				NO GENE	-	-	
229	UBA_8692_GENE_211	Hypothetical	NO DATA	-				NO GENE	-	-	
230			NO GENE	-		5way_CG_751_GENE_6	c hypo	NO DATA	-	-	
231			NO GENE	-		5way_CG_751_GENE_5	c hypo	NO DATA	-	-	
232	UBA_8692_GENE_212	Type IV secretory pathway, VirD2 components (rel	NO DATA	-	92.57	5way_CG_751_GENE_4	relaxase/mobilization protein	NO DATA	-	-	
233	UBA_8692_GENE_213	DNA repair proteins	NO DATA	-	80.63	5way_CG_751_GENE_3	DNA repair protein RadC	NO DATA	-	-	
234	UBA_8692_GENE_214	Hypothetical	NO DATA	-	90.79	5way_CG_751_GENE_2	hypo unique	NO DATA	-	-	
235	UBA_8692_GENE_215	Hypothetical	NO DATA	-				NO GENE	-	-	
236			NO GENE	-		5way_CG_751_GENE_1	ssDNA binding protein	NO DATA	-	-	
237	UBA_8692_GENE_216	Single-stranded DNA-binding protein	NO DATA	-				NO GENE	-	-	
238	UBA_8692_GENE_217	Hypothetical	NO DATA	-	100.00	5way_CG_1147_GENE_1	hypo unique	NO DATA	-	-	
239	UBA_8692_GENE_218	Hypothetical	NO DATA	-	100.00	5way_CG_1147_GENE_2	ssDNA binding protein	NO DATA	-	-	
240	UBA_8692_GENE_219	**Topoisomerase IA**	5.4	0	100.00	5way_CG_1147_GENE_3	**topoisomerase TraE**	5.4		0	1.00
241	UBA_8692_GENE_220	Hypothetical	NO DATA	-	100.00	5way_CG_1147_GENE_3a		NO DATA	-	-	
242	UBA_8692_GENE_221	FOG: EAL domain	NO DATA	-	90.99	5way_CG_245_GENE_1	DEF domain/EAL domain protein	NO DATA	-	-	
243	UBA_8692_GENE_222	Type IV secretory pathway, protease TraF	NO DATA	-	89.07	5way_CG_245_GENE_2	below plasmid tran protein TraF	NO DATA	-	-	
244	UBA_8692_GENE_223	probable conjugal trans split? See 222	NO DATA	-	92.23	5way_CG_245_GENE_3	conjugal transfer protein TraB	NO DATA	-	-	
245	UBA_8692_GENE_224	1-acyl-sn-glycerol-3-phosphate acyltransferase	NO DATA	-	97.46	5way_CG_245_GENE_4	hoethanolamine acyltransferase	NO DATA	-	-	
246			NO GENE	-		5way_CG_245_GENE_5	short-chain dehydrogenase	NO DATA	-	-	
247			NO GENE	-		5way_CG_245_GENE_6	hypo unique	NO DATA	-	-	
248			NO GENE	-		5way_CG_245_GENE_7	isonitrile hydratase	NO DATA	-	-	
249			NO GENE	-		5way_CG_245_GENE_8	type II restriction endonuclease	NO DATA	-	-	
250			NO GENE	-		5way_CG_245_GENE_9	DNA methyltransferase	NO DATA	-	-	
251	UBA_8692_GENE_225	hypothetical protein MhunDRAFT_1604 [Methanos	NO DATA	-				NO GENE	-	-	
252	UBA_8692_GENE_226	unnamed protein product [Photorhabdus lumines	NO DATA	-				NO GENE	-	-	
253	UBA_8692_GENE_227	Type II restriction enzyme, methylase subunits	NO DATA	-				NO GENE	-	-	
254	UBA_8692_GENE_228	Hypothetical	NO DATA	-	62.75	5way_CG_245_GENE_10	hypo unique	NO DATA	-	-	
255	UBA_8692_GENE_229	Hypothetical	NO DATA	-				NO GENE	-	-	
256	UBA_8692_GENE_229a		NO DATA	-	97.06	5way_CG_245_GENE_11	hypo unique	NO DATA	-	-	
257	UBA_8692_GENE_230	NADPH:quinone reductase and related Zn-depen	NO DATA	-	99.70	5way_CG_245_GENE_12	alcohol dehydrogenase	NO DATA	-	-	
258	UBA_8692_GENE_231	Predicted transcriptional regulators	NO DATA	-	98.20	5way_CG_245_GENE_14	transcriptional regulator	NO DATA	-	-	
259	UBA_8692_GENE_232	Predicted transcriptional regulators	NO DATA	-	99.68	5way_CG_245_GENE_15	mosome partitioning protein ParB	NO DATA	-	-	
260	UBA_8692_GENE_233	ATPases involved in chromosome partitioning	NO DATA	-	100.00	5way_CG_245_GENE_16	plasmid replication protein, ParA	NO DATA	-	-	
261	UBA_8692_GENE_234	Hypothetical	NO DATA	-				NO GENE	-	-	
262	UBA_8692_GENE_235	Hypothetical	NO DATA	-				NO GENE	-	-	
263	UBA_8692_GENE_236	Hypothetical	NO DATA	-				NO GENE	-	-	
264	UBA_8692_GENE_237	Hypothetical	NO DATA	-				NO GENE	-	-	
265	UBA_8692_GENE_238	Hypothetical	NO DATA	-				NO GENE	-	-	

	7931										
1	UBA_7931_GENE_1	**Membrane proteins related to metalloendopeptid**	21.4	0	100.00	5way_CG_274_GENE_10	hypo - lipoprotein	21.4		0	1.00
2	UBA_7931_GENE_2	Hypothetical	NO DATA	-	100.00	5way_CG_274_GENE_9	hypo unique	NO DATA	-	-	
3	UBA_7931_GENE_3	Hypothetical	NO DATA	-	100.00	5way_CG_274_GENE_8	ribonuclease HII	NO DATA	-	-	

4	UBA_7931_GENE_4	Ribosomal protein L19	74.6	0	100.00	5way_CG_274_GENE_7	ribosomal protein L19	74.6		0	1.00
5	UBA_7931_GENE_5	tRNA-(guanine-N1)-methyltransferase	33.6	0	100.00	5way_CG_274_GENE_6	tRNA methytransferase	33.6		0	1.00
6	UBA_7931_GENE_6	Hypothetical	NO DATA	-	100.00	5way_CG_274_GENE_5a		NO DATA	-	-	
7	UBA_7931_GENE_7	Predicted RNA-binding protein (contains KH doma	48.7	0	100.00	5way_CG_274_GENE_5	RNA-binding protein	48.7		0	1.00
8	UBA_7931_GENE_8	Ribosomal protein S16	55.6	0	100.00	5way_CG_274_GENE_4	Ribosomal protein S16	55.6		0	1.00
9	UBA_7931_GENE_9	Signal recognition particle GTPase	69.8	0	100.00	5way_CG_274_GENE_3	ignal recognition particle protein	69.8		0	1.00
10	UBA_7931_GENE_9a		62.2	0	100.00	5way_CG_274_GENE_2a		62.2		0	1.00
11	UBA_7931_GENE_10	Periplasmic serine proteases (ClpP class)	49.5	0	100.00	5way_CG_274_GENE_2	signal peptidase	49.5		0	1.00
12	UBA_7931_GENE_11	Ribosomal protein S1	70.5	-	99.79	5way_CG_274_GENE_1	ribosomal protein S1	70.9	-	-	
13	UBA_7931_GENE_12	Hypothetical	NO DATA	-	95.29	5way_CG_428_GENE_1	hypo unique	NO DATA	-	-	
14	UBA_7931_GENE_13	Uncharacterized conserved protein	38.7	0	100.00	5way_CG_428_GENE_2	c hypo	38.7		0	1.00
15	UBA_7931_GENE_14	Hypothetical	43.5	0	100.00	5way_CG_428_GENE_3	hypo unique	43.5		0	1.00
16	UBA_7931_GENE_15	Fe2+/Zn2+ uptake regulation proteins	NO DATA	-	100.00	5way_CG_428_GENE_5	ferric uptake regulation protein	NO DATA	-	-	
17	UBA_7931_GENE_16	Hypothetical	77.7	0	100.00	5way_CG_428_GENE_6	hypo unique	77.7		0	1.00
18	UBA_7931_GENE_17	Cation/multidrug efflux pump	26.5	-	97.57	5way_CG_428_GENE_7	acriflavin resistance protein	18.7	-	-	
19	UBA_7931_GENE_19	Hypothetical	53.6	0	98.19	5way_CG_71_GENE_2	c hypo	53.6		0	1.00
20	UBA_7931_GENE_20	tRNA nucleotidyltransferase/poly(A) polymerase	NO DATA	-	85.06	5way_CG_71_GENE_3	polyA polymerase	NO DATA	-	-	
21	UBA_7931_GENE_21	Sulfotransferase:TPR repeat [Trichodesmium erythr	18.1	8	96.25	5way_CG_71_GENE_4	N-acetylglucosamine transferase	5.5		0	3.29
22	UBA_7931_GENE_22	Exopolyphosphatase	40.6	20	98.41	5way_CG_71_GENE_5	exopolyphosphatase	30.2		0	1.34
23	UBA_7931_GENE_23	Hypothetical	21	0	93.22	5way_CG_71_GENE_6	hypo unique	21		0	1.00
24	UBA_7931_GENE_24	RecG-like helicase	3.4	1	95.79	5way_CG_71_GENE_7	DNA helicase	NO DATA	-		20.00
25	UBA_7931_GENE_25a		42.9	0	100.00	5way_CG_71_GENE_7a		42.9		0	1.00
26	UBA_7931_GENE_26	Putative translation initiation inhibitor, yjgF fami	72.7	27	88.28	5way_CG_71_GENE_8	translational inhibitor	14.8		0	4.91
27	UBA_7931_GENE_27	Hypothetical	NO DATA	-	100.00	5way_CG_71_GENE_8a		NO DATA	-	-	
28	UBA_7931_GENE_28	Thiol-disulfide isomerase and thioredoxins	89.2	0	98.80	5way_CG_71_GENE_10	thioredoxin	89.2		0	1.00
29	UBA_7931_GENE_29	Cytochrome b subunit of the bc complex	4.4	3	97.60	5way_CG_71_GENE_11	chrome b subunit of bc complex	2.6		0	1.69
30	UBA_7931_GENE_30	Rieske Fe-S protein	34	6	97.73	5way_CG_71_GENE_12	e cyt b/b6 complex, Fe-S subunit	21.4		0	1.59
31	UBA_7931_GENE_31	Enoyl-[acyl-carrier-protein] reductase (NADH)	81.1	48	95.47	5way_CG_71_GENE_13	enoyl acyl carrier protein	49.1		1	1.65
32	UBA_7931_GENE_32	Hypothetical	38.5	12	84.87	5way_CG_71_GENE_14	hypo unique	4.9		0	7.86
33	UBA_7931_GENE_33	Hypothetical	30.4	2	93.96	5way_CG_71_GENE_15	hypo unique	18.6		0	1.63
34	UBA_7931_GENE_34	Mismatch repair ATPase (MutS family)	12.1	6	93.71	5way_CG_71_GENE_16	DNA mismatch repair protein	4.3		0	2.81
35	UBA_7931_GENE_35	Hypothetical	NO DATA	-	100.00	5way_CG_71_GENE_17	hypo unique	NO DATA	-	-	
36	UBA_7931_GENE_36	Uracil-DNA glycosylase	17.3	4	88.16	5way_CG_71_GENE_18	NA glycosylase/DNA polymerase	3.7		0	4.68
37	UBA_7931_GENE_37	Predicted sugar kinase	47.1	30	91.31	5way_CG_71_GENE_19	c hypo	14.5		0	3.25
38	UBA_7931_GENE_38	Phosphopantetheinyl transferase (holo-ACP synth	56.4	4	92.48	5way_CG_71_GENE_20	acyl-carrier protein synthase	48.9		1	1.15
39	UBA_7931_GENE_39	Pyridoxal phosphate biosynthesis protein	66.7	25	96.08	5way_CG_71_GENE_21	l phosphate biosynthetic protein	30.2		0	2.21
40	UBA_7931_GENE_40	Predicted Zn-dependent peptidases	53.8	26	96.11	5way_CG_71_GENE_22	zinc protease	28.2		0	1.91
41	UBA_7931_GENE_41	Hypothetical	NO DATA	-	100.00	5way_CG_71_GENE_23	hypo unique	NO DATA	-	-	
42	UBA_7931_GENE_42	Polyribonucleotide nucleotidyltransferase (polynu	69.3	33	98.74	5way_CG_71_GENE_24	nucleotidyltransferase	63.3		0	1.09
43	UBA_7931_GENE_43	Ribosomal protein S15P/S13E	70.8	0	100.00	5way_CG_71_GENE_25	ribsomal protein S15	70.8		0	1.00
44	UBA_7931_GENE_44	Pseudouridine synthase	28.3	8	94.15	5way_CG_467_GENE_1	tRNA-pseudouridine synthase B	9.5		0	2.98
45	UBA_7931_GENE_45	Hypothetical	68.7	18	94.66	5way_CG_467_GENE_2	ribosome binding factor A	35.9		0	1.91
46	UBA_7931_GENE_46	Hypothetical	NO DATA	-	95.96	5way_CG_467_GENE_3	c hypo	NO DATA	-	-	
47	UBA_7931_GENE_47	Translation initiation factor 2 (IF-2; GTPase)	60	81	94.74	5way_CG_467_GENE_4	translation initiation factor	34.7		0	1.73
48	UBA_7931_GENE_48	Transcription elongation factor	69.7	40	98.45	5way_CG_467_GENE_5	en utilization substance protein A	56.4		0	1.24
49	UBA_7931_GENE_49	Uncharacterized protein conserved in bacteria	88	-	97.58	5way_CG_467_GENE_5a		82.4	-	-	
50	UBA_7931_GENE_50	Hypothetical -likelly transposase	NO DATA	-				NO GENE	-	-	
51	UBA_7931_GENE_51	Hypothetical	55.4	4	87.84	5way_CG_410_GENE_8	hypo unique	28.4		0	1.95
52	UBA_7931_GENE_52	PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia so	29	2	96.50	5way_CG_410_GENE_7	c hypo	21.5		0	1.35
53	UBA_7931_GENE_54	Chemotaxis signal transduction protein	59.8	31	97.24	5way_CG_410_GENE_6	chemotaxis protein CheV	49.4		0	1.21
54		TRNA Thr TGT 50180..50255 (-)	-						-		
55	UBA_7931_GENE_55	: Protein-disulfide isomerase [Nostoc punctiforme I	91.3	18	98.82	5way_CG_410_GENE_5	protein disulfide isomerase	76.8		1	1.19
56	UBA_7931_GENE_56	Uncharacterized conserved protein	47.8	12	97.05	5way_CG_410_GENE_4	galactose-lipid carrier transferase	24.7		0	1.94
57	UBA_7931_GENE_57	Hypothetical	82.9	32	96.15	5way_CG_410_GENE_3	hypo unique	40		0	2.07
58	UBA_7931_GENE_59	Hypothetical split with above??	NO DATA	-	94.30	5way_CG_410_GENE_2	prepilin peptidase	NO DATA	-	-	
59			NO GENE	-		5way_CG_410_GENE_1	probable transposase	NO DATA	-	-	
60	UBA_7931_GENE_60	universal stress protein UspA-like protein [Thermus	64.6	31	93.26	5way_CG_134_GENE_11	universal stress protein	15.2		0	4.25
61	UBA_7931_GENE_61	Phosphate starvation-inducible protein PhoH, pred	30.2	0	99.70	5way_CG_134_GENE_10	starvation inducible protein phoB	30.2		0	1.00
62	UBA_7931_GENE_62	Predicted membrane-associated HD superfamily h	NO DATA	-	92.43	5way_CG_134_GENE_9	al dependant phosphohydrolase	NO DATA	-	-	
63	UBA_7931_GENE_63	Predicted metal-dependent hydrolase	50.9	12	89.35	5way_CG_134_GENE_8	c hypo	NO DATA	-		20.00
64	UBA_7931_GENE_64	Signal recognition particle GTPase (many copies)	69.6	13	97.40	5way_CG_134_GENE_7	cell division protein FtsY	48.9		0	1.42
65	UBA_7931_GENE_65	Shikimate 5-dehydrogenase	34.5	5	88.15	5way_CG_134_GENE_6	shikimate 5-dehydrogenase	NO DATA	-		20.00
66	UBA_7931_GENE_66	Hypothetical	NO DATA	-	94.05	5way_CG_134_GENE_5	hypo unique	NO DATA	-	-	
67	UBA_7931_GENE_67	Nuclease subunit of the excinuclease complex	NO DATA	-	95.06	5way_CG_134_GENE_4	exonuclease ABC subunit C	NO DATA	-	-	
68	UBA_7931_GENE_68	ATPases with chaperone activity, ATP-binding subu	4.7	0	96.00	5way_CG_134_GENE_3	Clp protease ATP-binding subunit	4.7		0	1.00
69	UBA_7931_GENE_69	Thiamine biosynthesis protein ThiC	59.2	9	99.36	5way_CG_134_GENE_2	ynthesis protein ThiC (66-1, 134-2)	51.3		0	1.15
70	UBA_7931_GENE_70	Lfe176p1 [Leptospirillum ferrooxidans]	46.1	12	96.45	5way_CG_66_GENE_3	c hypo	33.3		0	1.38
71	UBA_7931_GENE_71	Methionine synthase I, cobalamin-binding domair	55.7	23	98.16	5way_CG_66_GENE_4	ase I, cobalamin binding domain	43.6		0	1.28
72	UBA_7931_GENE_72	Metal-dependent hydrolases of the beta-lactama	43.9	4	96.95	5way_CG_66_GENE_5	metal-dependant hydrolase PhnP	37		0	1.19
73	UBA_7931_GENE_73	Peptidyl-prolyl cis-trans isomerase (rotamase) - cy	32.6	0	98.62	5way_CG_66_GENE_6	eptidyl-prolyl cis-trans isomerase	32.6		0	1.00
74	UBA_7931_GENE_74	Predicted membrane GTPase involved in stress res	57.5	0	100.00	5way_CG_66_GENE_7	GTP-binding protein	57.5		0	1.00
75	UBA_7931_GENE_75	Predicted SAM-dependent methyltransferases	17.6	7	95.14	5way_CG_66_GENE_8	methyltransferase	5.1		0	3.45

76	UBA_7931_GENE_76	hypothetical protein TC0668 [Chlamydia muridaru	12	0	94.58	5way_CG_66_GENE_9	c hypo	12		0	1.00
77	UBA_7931_GENE_77	Hypothetical	NO DATA	-	94.24	5way_CG_66_GENE_10	hypo unique	NO DATA	-	-	
78	UBA_7931_GENE_78	Hypothetical	NO DATA	-	89.84	5way_CG_66_GENE_11	DNA repair protein, RecO	NO DATA	-	-	
79	UBA_7931_GENE_79	GTPase	16.7	1	97.44	5way_CG_66_GENE_12	GTP-binding protein, ERA	8		0	2.09
80	UBA_7931_GENE_80	8 Dehydrogenases with different specificities (relat	NO DATA	-	92.78	5way_CG_66_GENE_13	tase/short chain dehydrogenase	NO DATA	-	-	
81	UBA_7931_GENE_81	Hypothetical	12.2	2	92.65	5way_CG_66_GENE_14	hypo unique	NO DATA	-		20.00
82	UBA_7931_GENE_82	Hypothetical	NO DATA	-	90.00	5way_CG_66_GENE_15	hypo unique	NO DATA	-	-	
83	UBA_7931_GENE_83	Mannose-1-phosphate guanylyltransferase	26.7	12	96.73	5way_CG_66_GENE_17	DP-mannose pyrophosphorylase	9.6		0	2.78
84	UBA_7931_GENE_84	Phosphomannomutase	49.5	44	95.72	5way_CG_66_GENE_18	phosphomannomutase	21.6		0	2.29
85	UBA_7931_GENE_85	Hemoglobin-like flavoprotein	27.1	0	100.00	5way_CG_66_GENE_19	flavohemoglobin	27.1		0	1.00
86	UBA_7931_GENE_86	Hypothetical	54.7	0	100.00	5way_CG_66_GENE_20	c hypo	54.7		0	1.00
87	UBA_7931_GENE_87	Hypothetical	46.7	0	100.00	5way_CG_66_GENE_21	Fe/Pb permease, cytochrome c)	46.7		0	1.00
88	UBA_7931_GENE_88	Flavodoxin reductases (ferredoxin-NADPH reductc	21	0	100.00	5way_CG_66_GENE_22	lene-1.2-dioxygenase reductase	21		0	1.00
89	UBA_7931_GENE_88a		25	0	100.00	5way_CG_66_GENE_23	c hypo	25		0	1.00
90	UBA_7931_GENE_89	Predicted transcriptional regulator	17.8	0	100.00	5way_CG_66_GENE_24	transcriptional regulator	17.8		0	1.00
91	UBA_7931_GENE_91	Hypothetical	NO DATA	-	100.00	5way_CG_66_GENE_26	hypo unique	NO DATA	-	-	
92	UBA_7931_GENE_92	Long-chain acyl-CoA synthetases (AMP-forming)	8.4	0	100.00	5way_CG_66_GENE_27	long chain fatty-acid CoA ligase	8.4		0	1.00
93	UBA_7931_GENE_93	Predicted exonuclease of the beta-lactamase folc	5.8	0	100.00	5way_CG_66_GENE_28	olyadenylation specificity factor	5.8		0	1.00
94	UBA_7931_GENE_94	High-affinity Fe2+/Pb2+ permease	NO DATA	-	100.00	5way_CG_297_GENE_8	high affinity Fe permease	NO DATA	-	-	
95	UBA_7931_GENE_95	hypothetical protein Rick02000674 [Rickettsia ricke	NO DATA	-	100.00	5way_CG_297_GENE_7	hypo	NO DATA	-	-	
96	UBA_7931_GENE_96	: Uncharacterized protein conserved in bacteria [B	58.7	0	100.00	5way_CG_297_GENE_6	hypo - kelch-like protein	58.7		0	1.00
97	UBA_7931_GENE_97	Hypothetical	67.5	0	100.00	5way_CG_297_GENE_5	hypo unique	67.5		0	1.00
98	UBA_7931_GENE_98	Hypothetical	34.5	0	100.00	5way_CG_297_GENE_4	hypo unique	34.5		0	1.00
99		[redacted]	NO GENE	-		5way_CG_297_GENE_3	transposase	NO DATA	-	-	
100	UBA_7931_GENE_99	Protein-tyrosine-phosphatase - or arsenate reduct	73.2	0	100.00	5way_CG_46_GENE_2	arsenate reductase	73.2		0	1.00
101	UBA_7931_GENE_100	Na+/H+ antiporter NhaD and related arsenite perr	NO DATA	-	100.00	5way_CG_46_GENE_3	arsenite efflux pump, ArsB	NO DATA	-	-	
102	UBA_7931_GENE_101	Hypothetical	67	0	100.00	5way_CG_46_GENE_4	hypo unique	67		0	1.00
103	UBA_7931_GENE_102	Hypothetical	52	0	100.00	5way_CG_46_GENE_5	c hypo	52		0	1.00
104	UBA_7931_GENE_103	Hypothetical	51.7	0	100.00	5way_CG_46_GENE_6	c hypo	51.7		0	1.00
105	UBA_7931_GENE_104	Cation/multidrug efflux pump	26.3	-	100.00	5way_CG_46_GENE_7	cation efflux protein	26.5	-	-	
106	UBA_7931_GENE_104a		NO DATA	-	100.00	5way_CG_46_GENE_7a		NO DATA	-	-	
107	UBA_7931_GENE_105	: Predicted hydrolase (HAD superfamily) [Burkhold	37	0	100.00	5way_CG_46_GENE_10	c hypo	37		0	1.00
108	UBA_7931_GENE_106	Glucose-6-phosphate isomerase	46.7	0	100.00	5way_CG_46_GENE_11	glucose-6-phosphate isomerase	46.7		0	1.00
109	UBA_7931_GENE_107	SOS-response transcriptional repressors (RecA-me	28.8	0	100.00	5way_CG_46_GENE_12	LexA transcriptional repressor	28.8		0	1.00
110	UBA_7931_GENE_108	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_13	hypo unique	NO DATA	-	-	
111	UBA_7931_GENE_109	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_14	hypo unique	NO DATA	-	-	
112	UBA_7931_GENE_110	DNA polymerase elongation subunit (family B)	NO DATA	-	100.00	5way_CG_46_GENE_15	DNA polymerase B2	NO DATA	-	-	
113	UBA_7931_GENE_111	Cytochrome c	65.1	0	100.00	5way_CG_46_GENE_16	cytochrome c	65.1		0	1.00
114	UBA_7931_GENE_112	Cytochrome c553	57.4	0	100.00	5way_CG_46_GENE_17	ytochrome cB/cytochrome c553	57.4		0	1.00
115	UBA_7931_GENE_113	Glycosyltransferases, probably involved in cell wal	NO DATA	-	100.00	5way_CG_46_GENE_18	cellulose synthase, subunit A	NO DATA	-	-	
116	UBA_7931_GENE_114	Cellulose synthase, subunit B [Ralstonia metallidurc	NO DATA	-	100.00	5way_CG_46_GENE_19	cellulose synthase, subunit B	NO DATA	-	-	
117	UBA_7931_GENE_115	putative cellulose synthase operon protein C [Xan	NO DATA	-	100.00	5way_CG_46_GENE_20	cellulose synthase, subunit C	NO DATA	-	-	
118	UBA_7931_GENE_116	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_21	hypo unique	NO DATA	-	-	
119	UBA_7931_GENE_117	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_22	c hypo	NO DATA	-	-	
120	UBA_7931_GENE_118	Phytoene dehydrogenase and related proteins	6.2	0	100.00	5way_CG_46_GENE_23	erase/phytoene dehydrogenase	6.2		0	1.00
121	UBA_7931_GENE_119a		19.1	0	100.00	5way_CG_46_GENE_24	c hypo	19.1		0	1.00
122	UBA_7931_GENE_120	Predicted signal transduction protein containing a	NO DATA	-	100.00	5way_CG_46_GENE_25	DEF domain/EAL domain protein	NO DATA	-	-	
123	UBA_7931_GENE_121	Cytochrome c553	NO DATA	-	100.00	5way_CG_46_GENE_26	cytochrome c	NO DATA	-	-	
124	UBA_7931_GENE_122	Cytochrome c	4.8	0	100.00	5way_CG_46_GENE_27	cytochrome c	4.8		0	1.00
125	UBA_7931_GENE_123	Cytochrome c	26.4	0	100.00	5way_CG_46_GENE_28	cytochrome c	26.4		0	1.00
126	UBA_7931_GENE_124	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_29	hypo unique	NO DATA	-	-	
127	UBA_7931_GENE_125	Hypothetical	NO DATA	-	100.00	5way_CG_46_GENE_30	hypo unique	NO DATA	-	-	
128		TRNA Gly CCC 131845..131919 (-)	-						-		
129	UBA_7931_GENE_126	Sulfur transfer protein involved in thiamine biosynt	58.6	0	100.00	5way_CG_186_GENE_2	thiamine biosynthesis, ThiS	58.6		0	1.00
130	UBA_7931_GENE_127	secretion pathway protein C [Bdellovibrio bacteric	6.5	0	100.00	5way_CG_186_GENE_3	general secretion pathway GspC	6.5		0	1.00
131	UBA_7931_GENE_128	Type II secretory pathway, component PulD	41.3	0	100.00	5way_CG_186_GENE_4	general secretion pathway GspD	41.3		0	1.00
132	UBA_7931_GENE_129	Type II secretory pathway, ATPase PulE/Tfp pilus as	16.1	0	100.00	5way_CG_186_GENE_5	general secretion pathway, GspE	16.1		0	1.00
133	UBA_7931_GENE_130	Type II secretory pathway, component PulF	24	0	100.00	5way_CG_186_GENE_6	general secretion pathway GspF	24		0	1.00
134	UBA_7931_GENE_131	Type II secretory pathway, pseudopilin PulG	60.4	0	100.00	5way_CG_186_GENE_7	eneral secretion pathway, GspG	60.4		0	1.00
135	UBA_7931_GENE_133	Hypothetical	37.6	0	100.00	5way_CG_186_GENE_8	c hypo	37.6		0	1.00
136	UBA_7931_GENE_134	Hypothetical	7.7	0	100.00	5way_CG_186_GENE_9	GspL-like	7.7		0	1.00
137	UBA_7931_GENE_135	Hypothetical	NO DATA	-	100.00	5way_CG_186_GENE_10	hypo unique	NO DATA	-	-	
138	UBA_7931_GENE_136	Type II secretory pathway, component PulK	NO DATA	-	100.00	5way_CG_186_GENE_11	general secretion pathway, GspK	NO DATA	-	-	
139	UBA_7931_GENE_137	FOG: TPR repeat	48	0	100.00	5way_CG_186_GENE_13	N-acetylglucosamine transferase	48		0	1.00
140	UBA_7931_GENE_138	FOG: GGDEF domain	12.5	-	97.20	5way_CG_2_GENE_1	hypo unique	NO DATA	-	-	
141	UBA_7931_GENE_139	Hypothetical	51.2	0	100.00	5way_CG_2_GENE_2	c hypo	51.2		0	1.00
142	UBA_7931_GENE_140	Hypothetical	NO DATA	-	99.00	5way_CG_2_GENE_3	c hypo	NO DATA	-	-	
143	UBA_7931_GENE_141	Hypothetical	67	38	91.63	5way_CG_2_GENE_4	hypo unique	NO DATA	-		20.00
144	UBA_7931_GENE_142	Hypothetical	79.7	25	90.75	5way_CG_2_GENE_5	ak (possible chemotaxis protein)	38.4		1	2.08
145	UBA_7931_GENE_143	Predicted signal transduction protein containing a	11.9	5	93.24	5way_CG_2_GENE_6	DEF domain/EAL domain protein	3.2		0	3.72
146	UBA_7931_GENE_144	Hypothetical	NO DATA	-	100.00	5way_CG_2_GENE_7	hypo unique	NO DATA	-	-	
147		[redacted]	NO GENE	-		5way_CG_2_GENE_8	transposase (one of two copies)	1.7	-	-	

148	UBA_7931_GENE_145	Fe-S cluster protector protein	66.2	0	100.00	5way_CG_2_GENE_9	c hypo	66.2		0	1.00
149	UBA_7931_GENE_146	Proline dehydrogenase	25.6	0	100.00	5way_CG_2_GENE_10	proline dehydrogenase	25.6		0	1.00
150	UBA_7931_GENE_147	Superfamily II DNA/RNA helicases, SNF2 family	NO DATA	-	94.38	5way_CG_2_GENE_11	DNA/RNA helicase, Snf2	NO DATA	-	-	
151	UBA_7931_GENE_148	Nitrogen regulatory protein PII	70.5	8	98.21	5way_CG_2_GENE_12	nitrogen regulator protein PII	58		0	1.22
152	UBA_7931_GENE_149	Ammonia permease	7.3	8	96.04	5way_CG_2_GENE_13	ammonia transporter	NO DATA	-		20.00
153	UBA_7931_GENE_150	Hypothetical	11.5	0	97.44	5way_CG_2_GENE_14	hypo unique	11.5		0	1.00
154	UBA_7931_GENE_151	SOS-response transcriptional repressors (RecA-mec	NO DATA	-	96.85	5way_CG_2_GENE_15	Lex A transcriptional repressor	NO DATA	-	-	
155	UBA_7931_GENE_152	NADH:ubiquinone oxidoreductase subunit 2 (chair	NO DATA	-	99.79	5way_CG_2_GENE_16	NADH dehydrogenase, subunit N	NO DATA	-	-	
156	UBA_7931_GENE_153	NADH:ubiquinone oxidoreductase subunit 4 (chair	NO DATA	-	99.40	5way_CG_2_GENE_17	NADH dehydrogenase, subunit M	NO DATA	-	-	
157	UBA_7931_GENE_154	NADH:ubiquinone oxidoreductase subunit 5 (chair	4.1	0	98.75	5way_CG_2_GENE_18	NADH dehydrogenase, subunit L	4.1		0	1.00
158	UBA_7931_GENE_155a		NO DATA	-	98.00	5way_CG_2_GENE_19	NADH degydrogenase, subunit K	NO DATA	-	-	
159	UBA_7931_GENE_156	NADH:ubiquinone oxidoreductase subunit 6 (chair	NO DATA	-	98.22	5way_CG_2_GENE_20	NADH dehydrogenase, subunit J	NO DATA	-	-	
160	UBA_7931_GENE_157	Formate hydrogenlyase subunit 6/NADH:ubiquinor	68.3	40	98.39	5way_CG_2_GENE_21	NADH dehydrogenase, subunit I	49.5		0	1.38
161	UBA_7931_GENE_158	NADH:ubiquinone oxidoreductase subunit 1 (chair	17.5	0	100.00	5way_CG_2_GENE_22	NADH dehydrogenase, subunit H	17.5		0	1.00
162	UBA_7931_GENE_159	Anaerobic dehydrogenases, typically selenocyste	65.3	92	96.23	5way_CG_2_GENE_23	NADH dehydrogenase, subunit G	45.4		0	1.44
163	UBA_7931_GENE_161	NADH:ubiquinone oxidoreductase, NADH-binding	60.9	24	98.87	5way_CG_2_GENE_24	NADH dehydrogenase, subunit F	41.3		0	1.47
164	UBA_7931_GENE_162	NADH:ubiquinone oxidoreductase 24 kD subunit	93.5	16	98.81	5way_CG_2_GENE_25	NADH dehydrogenase, subunit E	76.2		0	1.23
165	UBA_7931_GENE_163	NADH:ubiquinone oxidoreductase 49 kD subunit 7	53	20	98.58	5way_CG_2_GENE_26	NADH dehydrogenase, subunit D	36.4		0	1.46
166	UBA_7931_GENE_164	NADH:ubiquinone oxidoreductase 27 kD subunit	86.4	29	97.28	5way_CG_2_GENE_27	NADH dehydrogenase, subunit C	64.7		0	1.34
167	UBA_7931_GENE_165	NADH:ubiquinone oxidoreductase 20 kD subunit a	59	21	99.44	5way_CG_2_GENE_28	NADH dehydrogenase, subunit B	58.4		1	1.01
168	UBA_7931_GENE_166	NADH:ubiquinone oxidoreductase subunit 3 (chair	NO DATA	-	100.00	5way_CG_2_GENE_29	NADH dehydrogenase, subunit A	NO DATA	-	-	
169	UBA_7931_GENE_167	Preprotein translocase subunit SecA (ATPase, RNA	61.7	64	96.59	5way_CG_2_GENE_30	preprotein translocase	49.6		0	1.24
170	UBA_7931_GENE_168	Membrane proteins related to metalloendopeptid	49.4	16	91.14	5way_CG_2_GENE_31	mbrane-bound metallopeptidase	26.6		0	1.86
171	UBA_7931_GENE_168a		25.7	3	92.04	5way_CG_2_GENE_32	cation tolerance protein, chain A	NO DATA	-		20.00
172	UBA_7931_GENE_169	Nucleoside-diphosphate-sugar epimerases	50.8	15	94.25	5way_CG_2_GENE_33	UDP-glucose 4-epimerase	27.8		0	1.83
173	UBA_7931_GENE_170	Predicted rRNA methylase	NO DATA	-	92.80	5way_CG_2_GENE_34	hemolysin/rRNA methylase	NO DATA	-	-	
174	UBA_7931_GENE_171	Deoxyxylulose-5-phosphate synthase	69.8	72	97.62	5way_CG_2_GENE_35	xyxylulose-5-phosphate synthase	43.5		0	1.60
175	UBA_7931_GENE_172	Geranylgeranyl pyrophosphate synthase	49.2	56	95.05	5way_CG_2_GENE_36	ranylgeranyl phosphate synthase	26.4		0	1.86
176	UBA_7931_GENE_173	Hypothetical	82.5	6	93.75	5way_CG_2_GENE_37	weak (possible exonuclease VII)	48.5		0	1.70
177	UBA_7931_GENE_174	Hypothetical	4.6	2	92.64	5way_CG_2_GENE_38	oxyribonuclease VII large subunit	NO DATA	-		20.00
178	UBA_7931_GENE_175	Uncharacterized protein conserved in bacteria	39.1	9	93.66	5way_CG_2_GENE_39	c hypo	14.8		0	2.64
179	UBA_7931_GENE_176	Predicted HD superfamily hydrolase	52.4	20	97.89	5way_CG_2_GENE_40	hydrolase (HAD superfamily)	45.3		2	1.16
180	UBA_7931_GENE_177	ATPase related to the helicase subunit of the Hollid	6.8	2	93.47	5way_CG_2_GENE_41	ATPase related to helicase subunit	NO DATA	-		20.00
181	UBA_7931_GENE_179	Hypothetical	38.7	0	96.40	5way_CG_2_GENE_42	hypo unique	38.7		0	1.00
182	UBA_7931_GENE_180	Hypothetical	NO DATA	-	95.60	5way_CG_2_GENE_43	hypo unique	26.4		7	0.06
183	UBA_7931_GENE_181	Soluble lytic murein transglycosylase and related	59.3	78	90.41	5way_CG_2_GENE_44	soluble lytic transglycosylase	24.2		0	2.45
184	UBA_7931_GENE_182	Periplasmic protein TonB, links inner and outer mer	35.4	2	97.82	5way_CG_2_GENE_45	weak (TonB-like protein)	32.4		0	1.09
185	UBA_7931_GENE_183	Dimethyladenosine transferase (rRNA methylation)	9	4	91.41	5way_CG_2_GENE_46	dimethyladenosine transferase	NO DATA	-		20.00
186	UBA_7931_GENE_184	Predicted hydrolase of the metallo-beta-lactamas	50.4	7	98.75	5way_CG_2_GENE_47	Zn-dependent hydrolase	38.6		0	1.31
187	UBA_7931_GENE_185	DNA segregation ATPase FtsK/SpoIIIE and related	33	8	93.03	5way_CG_2_GENE_48	(DNA translocation) protein, FtsK	12		0	2.75
188	UBA_7931_GENE_186	Hypothetical	39.9	0	94.54	5way_CG_2_GENE_49	c hypo	39.9		0	1.00
189	UBA_7931_GENE_187	Excinuclease ATPase subunit	25.8	4	98.07	5way_CG_2_GENE_50	excinuclease ABC, subunit A	23.5		0	1.10
190	UBA_7931_GENE_188	Predicted Co/Zn/Cd cation transporters	NO DATA	-	98.01	5way_CG_2_GENE_51	cation efflux system protein	NO DATA	-	-	
191	UBA_7931_GENE_189	Pyridoxal phosphate biosynthesis protein	85.8	0	100.00	5way_CG_2_GENE_52	pyridoxal phosphate biosynthesis	85.8		0	1.00
192	UBA_7931_GENE_190	FOG: GGDEF domain	12.9	14	89.20	5way_CG_2_GENE_53	GDEF domain/EAL domain protein	NO DATA	-		20.00
193	UBA_7931_GENE_191	Hypothetical	27.4	11	93.81	5way_CG_2_GENE_54	hypo unique	17.7		0	1.55
194	UBA_7931_GENE_192	Predicted phosphohydrolases	10.4	1	94.55	5way_CG_2_GENE_55	DNA repair exonuclease	NO DATA	-		20.00
195	UBA_7931_GENE_193	ABC-type transport system involved in resistance t	72.3	12	99.38	5way_CG_2_GENE_56	nsporter, periplasmic component	63.4		0	1.14
196	UBA_7931_GENE_194	ABC-type transport system involved in resistance t	52.5	8	98.33	5way_CG_2_GENE_57	C transporter, ATP-binding protein	37.1		0	1.42
197	UBA_7931_GENE_195	ABC-type transport system involved in resistance t	NO DATA	-	99.60	5way_CG_2_GENE_58	BC transporter, permease protein	NO DATA	-	-	
198	UBA_7931_GENE_196	Endonuclease IV	NO DATA	-	90.19	5way_CG_2_GENE_59	Endonuclease IV	NO DATA	-	-	
199	UBA_7931_GENE_197	UDP-glucose 4-epimerase	62.5	3	98.76	5way_CG_2_GENE_60	UDP-glucose-4-epimerase	56.7		0	1.10
200	UBA_7931_GENE_198	Signal transduction histidine kinase	35	9	96.04	5way_CG_2_GENE_61	gnal transduction histidine kinase	20.1		0	1.74
201	UBA_7931_GENE_199	Response regulators consisting of a CheY-like rece	51.9	21	98.70	5way_CG_2_GENE_62	ulon transcription regulator, PhoB	33.8		0	1.54
202	UBA_7931_GENE_200	Lfe139p2 [Leptospirillum ferrooxidans]	89.4	22	94.37	5way_CG_2_GENE_63	se of the PAD1/JAB1 superfamily	58.5		0	1.53
203	UBA_7931_GENE_201	Dinucleotide-utilizing enzymes involved in molybd	28.8	9	95.51	5way_CG_2_GENE_64	pterin biosynthesis protein MoeB	6.4		0	4.50
204	UBA_7931_GENE_202	Hypothetical	68.8	3	98.75	5way_CG_2_GENE_65	ferredoxin	61.2		0	1.12
205	UBA_7931_GENE_203	Molybdopterin converting factor, small subunit	50.5	12	95.70	5way_CG_2_GENE_66	molybdopterin converting factor	28		0	1.80
206	UBA_7931_GENE_204	Threonine synthase	84.5	0	99.75	5way_CG_2_GENE_67	threonine synthase	84.5		0	1.00
207	UBA_7931_GENE_205	Dinucleotide-utilizing enzymes involved in molybd	23.7	3	97.78	5way_CG_2_GENE_68	thiamine biosynthesis protein ThiF	18.5		0	1.28
208	UBA_7931_GENE_206	Cysteine synthase	73.1	36	96.79	5way_CG_2_GENE_69	cysteine synthase	45.2		1	1.62
209	UBA_7931_GENE_207	thiamine biosynthesis protein ThiS [Pelobacter carb	18.4	0	94.59	5way_CG_2_GENE_70	c hypo (ThiS-like)	34.2		1	0.54
210	UBA_7931_GENE_208	S-adenosylhomocysteine hydrolase	64.4	37	99.04	5way_CG_2_GENE_71	adenosylhomocyteine hydrolase	62		0	1.04
211	UBA_7931_GENE_209	S-adenosylmethionine synthetase	68.1	2	99.74	5way_CG_2_GENE_72	S-adenosinemethionine synthase	63.9		0	1.07
212		TRNA Ala GGC 225668..225743 (-)		-					-		
213	UBA_7931_GENE_211	Hypothetical	76.2	21	96.83	5way_CG_2_GENE_74	hypo unique	60.3		0	1.26
214	UBA_7931_GENE_212	Coproporphyrinogen III oxidase and related Fe-S	52.7	23	97.82	5way_CG_2_GENE_75	independent coporphyrinogen II	35.7		0	1.48
215	UBA_7931_GENE_213	Uroporphyrinogen-III decarboxylase	37.6	9	98.03	5way_CG_2_GENE_76	roporphyrinogen decarboxylase	29.2		0	1.29
216	UBA_7931_GENE_214	c hypothetical	56.5	6	96.73	5way_CG_2_GENE_77	cobalt chetalase, cbiX	31.5		0	1.79
217	UBA_7931_GENE_215	membrane protein, putative [Syntrophobacter fur	NO DATA	-	91.02	5way_CG_2_GENE_78	c hypo	NO DATA	-	-	
218	UBA_7931_GENE_215a		NO DATA	-	100.00	5way_CG_2_GENE_79	c hypo	NO DATA	-	-	
219	UBA_7931_GENE_216	Glycosyltransferases, probably involved in cell wa	9.2	0	95.15	5way_CG_2_GENE_80	ceramide glycosyltransferase	9.2		0	1.00

220	UBA_7931_GENE_217	Fe-S oxidoreductase	56.8	3	99.79	5way_CG_2_GENE_81	Fe-S oxidoreductase	54.1		0	1.05
221	UBA_7931_GENE_218	Penicillin tolerance protein	47.7	13	98.34	5way_CG_2_GENE_82	penicillin tolerance protein, LytB	38.1		0	1.25
222	UBA_7931_GENE_219	Nucleoside-diphosphate-sugar epimerases	37.2	5	98.81	5way_CG_2_GENE_83	dihydroflavonol 4-reductase	23.2		0	1.60
223	UBA_7931_GENE_220	Hypothetical	45.7	20	91.38	5way_CG_2_GENE_84	hypo unique	10.8		0	4.23
224	UBA_7931_GENE_221	lipoprotein, putative [Geobacter sulfurreducens PC	24.2	0	98.43	5way_CG_2_GENE_85	c hypo	24.2		0	1.00
225	UBA_7931_GENE_222	Hypothetical	40.5	5	85.88	5way_CG_2_GENE_86	hypo unique	16.8		1	2.41
226	UBA_7931_GENE_223	Squalene cyclase	13.8	7	97.66	5way_CG_2_GENE_87	squalene-hopene cyclase	5.7		0	2.42
227			NO GENE	-		5way_CG_2_GENE_88	transposase (single)	NO DATA	-	-	
228			NO GENE	-		5way_CG_717_GENE_1	hypo unique	NO DATA	-	-	
229	UBA_7931_GENE_224	Hypothetical	NO DATA	-	100.00	5way_CG_717_GENE_2	transposase	NO DATA	-	-	
230	UBA_7931_GENE_225	Hypothetical	42.7	0	99.50	5way_CG_2_GENE_89	ribosomal protein S12	42.7		0	1.00
231	UBA_7931_GENE_225a		NO DATA	-	84.16	5way_CG_2_GENE_90	hypo unique	NO DATA	-	-	
232	UBA_7931_GENE_226	Hypothetical	81.7	51	95.43	5way_CG_2_GENE_91	cell division initiation protein	40		0	2.04
233	UBA_7931_GENE_226a		20.8	0	97.22	5way_CG_2_GENE_92	ypo - suspect cell division related	20.8		0	1.00
234	UBA_7931_GENE_227	Pyrroline-5-carboxylate reductase	56.2	17	94.44	5way_CG_2_GENE_93	yrroline-5-carboxylate reductase	31.2		0	1.80
235	UBA_7931_GENE_228	Predicted enzyme with a TIM-barrel fold	12.6	4	88.55	5way_CG_2_GENE_94	potassium uptake protein	NO DATA	-		20.00
236	UBA_7931_GENE_229	Uncharacterized conserved protein	NO DATA	-	91.20	5way_CG_2_GENE_95	c hypo	NO DATA	-	-	
237	UBA_7931_GENE_230	Cell division GTPase	48.5	5	98.97	5way_CG_2_GENE_96	tubulin-like, FtsZ	43.6		0	1.11
238	UBA_7931_GENE_231	Actin-like ATPase involved in cell division	53.7	13	97.96	5way_CG_2_GENE_97	cell division protein, FtsA	41.4		0	1.30
239	UBA_7931_GENE_232	Hypothetical	25.5	12	89.16	5way_CG_2_GENE_98	hypo unique	NO DATA	-		20.00
240	UBA_7931_GENE_233	D-alanine-D-alanine ligase and related ATP-grasp	89.4	60	96.36	5way_CG_2_GENE_99	D-ala D-ala ligase	53.1		0	1.68
241	UBA_7931_GENE_234	UDP-N-acetylmuramate dehydrogenase	13.8	1	97.04	5way_CG_2_GENE_100	lpyruvoylglucosamine reductase	9.2		1	1.50
242	UBA_7931_GENE_235	UDP-N-acetylmuramate-alanine ligase	21.8	6	95.69	5way_CG_2_GENE_101	cetymuramate dehyddrogenase	6.9		0	3.16
243	UBA_7931_GENE_236	UDP-N-acetylglucosamine:LPS N-acetylglucosami	34	9	92.72	5way_CG_2_GENE_102	mine-N-acetylmuramyl-(penta...	13.5		4	2.52
244	UBA_7931_GENE_237	Bacterial cell division membrane protein	NO DATA	-	96.97	5way_CG_2_GENE_103	cell division protein FtsW	NO DATA	-	-	
245	UBA_7931_GENE_238	UDP-N-acetylmuramoylalanine-D-glutamate ligas	48	20	92.61	5way_CG_2_GENE_104	moylalanine-D-glutamate ligase	13.3		0	3.61
246	UBA_7931_GENE_239	UDP-N-acetylmuramyl pentapeptide phosphotran	NO DATA	-	99.16	5way_CG_2_GENE_105	amoyl-pentapeptide transferase	NO DATA	-	-	
247	UBA_7931_GENE_240	UDP-N-acetylmuramyl pentapeptide synthase	50.9	35	91.72	5way_CG_2_GENE_106	imelate-D-alanyl-D-alanyl ligase	NO DATA	-		20.00
248	UBA_7931_GENE_241	UDP-N-acetylmuramyl tripeptide synthase	64.4	70	94.11	5way_CG_2_GENE_107	anyl-D-glutamate-2,6-diamino...	18.7		0	3.44
249	UBA_7931_GENE_242	Cell division protein FtsI/penicillin-binding protei	9.5	1	98.10	5way_CG_2_GENE_108	cell division protein FtsI	4		0	2.38
250	UBA_7931_GENE_242a		NO DATA	-	98.90	5way_CG_2_GENE_109	hypo unique	NO DATA	-	-	
251	UBA_7931_GENE_243	Predicted S-adenosylmethionine-dependent meth	37.5	17	93.81	5way_CG_2_GENE_110	denosyl-methyltransferase MraW	NO DATA	-		20.00
252	UBA_7931_GENE_244	Uncharacterized protein conserved in bacteria	81.1	4	98.65	5way_CG_2_GENE_111	c hypo	73		0	1.11
253	UBA_7931_GENE_244a		NO DATA	-	100.00	5way_CG_2_GENE_111a		NO DATA	-	-	
254	UBA_7931_GENE_245	Hypothetical	30	4	96.11	5way_CG_2_GENE_113	hypo unique	24.4		0	1.23
255	UBA_7931_GENE_246	Peroxiredoxin	96.1	4	99.35	5way_CG_2_GENE_114	eroxiredoxin - antioxidant protein	93.5		0	1.03
256	UBA_7931_GENE_247	Succinyl-CoA synthetase, alpha subunit	52.8	15	99.02	5way_CG_2_GENE_115	succinyl-coA synthetase	46.9		0	1.13
257	UBA_7931_GENE_248	Succinyl-CoA synthetase, beta subunit	73.2	20	99.24	5way_CG_2_GENE_116	succinyl-coA synthetase	69.7		0	1.05
258	UBA_7931_GENE_249	Succinate dehydrogenase/fumarate reductase, fl	65	36	97.18	5way_CG_2_GENE_117	succinate dehydrogenase	48.4		6	1.34
259	UBA_7931_GENE_250	Ferredoxin:4Fe-4S ferredoxin, iron-sulfur binding [S	38.6	22	97.81	5way_CG_2_GENE_118	drogenase/acetyl-CoA synthase	7.9		0	4.89
260	UBA_7931_GENE_251	hypothetical protein GSU1100 [Geobacter sulfurre	NO DATA	-	96.00	5way_CG_2_GENE_119	c hypo	NO DATA	-	-	
261	UBA_7931_GENE_252	Citrate synthase	64.7	2	98.51	5way_CG_2_GENE_120	citrate synthase	63.2		0	1.02
262	UBA_7931_GENE_253	Aconitase A	90	42	99.22	5way_CG_2_GENE_121	aconitase	76.6		0	1.17
263	UBA_7931_GENE_254	Hypothetical	NO DATA	-	98.00	5way_CG_2_GENE_122	hypo unique	NO DATA	-	-	
264	UBA_7931_GENE_255	Succinyl-CoA synthetase, alpha subunit	90.2	31	99.09	5way_CG_2_GENE_123	inyl co-A ligase, AbMem protein	76.8		0	1.17
265	UBA_7931_GENE_256	Succinyl-CoA synthetase, beta subunit	75.5	-	99.09	5way_CG_2_GENE_124	succinyl-coA ligase	66.8	-	-	
266			NO GENE	-		5way_CG_2_GENE_125	transposase	35.6	-	-	
267	UBA_7931_GENE_256	Succinyl-CoA synthetase, beta subunit	75.5	-	100.00	5way_CG_2_GENE_126	succinyl-coA synthase	75.6	-	-	
268		TRNA Glu TTC 277801..277878 (+)		-					-		
269			NO GENE	-		5way_CG_2_GENE_127	integrase (partial)	NO DATA	-	-	
270				-					-		
271			NO GENE	-		5way_CG_2_GENE_128	transposase	NO DATA	-	-	
272	UBA_7931_GENE_257	Hypothetical	NO DATA	-	96.24	5way_CG_7_GENE_1	hypo unique	NO DATA	-	-	
273	UBA_7931_GENE_258	Predicted signal transduction protein containing a	NO DATA	-	90.21	5way_CG_7_GENE_2	x protein/GGDEF domain protein	NO DATA	-	-	
274	UBA_7931_GENE_259	Protein-tyrosine-phosphatase	NO DATA	-	96.26	5way_CG_7_GENE_3	cytoplasmic phosphatase	NO DATA	-	-	
275	UBA_7931_GENE_260	Transcriptional regulators containing an AAA-type	35.6	11	96.21	5way_CG_7_GENE_4	t DNA binding response regulator	12.6		0	2.83
276	UBA_7931_GENE_261	Nucleoside-diphosphate-sugar epimerases	73.1	8	98.42	5way_CG_7_GENE_5	UDP-glucose 4-epimerase	64.6		0	1.13
277	UBA_7931_GENE_262	Hypothetical	NO DATA	-	93.53	5way_CG_7_GENE_6	hypo unique	NO DATA	-	-	
278	UBA_7931_GENE_263	UDP-N-acetyl-D-mannosaminuronate dehydroger	70	12	98.85	5way_CG_7_GENE_7	nosaminuronate dehydrogenase	58.9		0	1.19
279	UBA_7931_GENE_264	Glucosamine 6-phosphate synthetase, contains a	12.8	3	96.91	5way_CG_7_GENE_8	e-6-phosphate aminotransferase	8.1		0	1.58
280	UBA_7931_GENE_265	Response regulator containing CheY-like receiver,	17	3	96.33	5way_CG_7_GENE_9	pendant transcriptional regulator	14.1		1	1.21
281	UBA_7931_GENE_266	Transposase and inactivated derivatives, IS5 famil	25.3	-				NO GENE	-	-	
282	UBA_7931_GENE_267	Predicted ATPase	4.2	2	81.03	5way_CG_7_GENE_10	? adenylate/guanylate cyclase	1.5		0	2.80
283	UBA_7931_GENE_268	Nucleoside-diphosphate-sugar epimerases	15.8	2	93.26	5way_CG_7_GENE_11	nucleotide sugar epimerase	8.2		0	1.93
284	UBA_7931_GENE_269	UDP-galactopyranose mutase	61.3	25	96.45	5way_CG_7_GENE_12	UDP-galactopyranose mutase	47.1		0	1.30
285	UBA_7931_GENE_270	Site-specific DNA methylase	2.5	1	95.10	5way_CG_7_GENE_13	e-specific DNA methyltransferase	NO DATA	-		20.00
286	UBA_7931_GENE_271	Hypothetical	NO DATA	-	95.37	5way_CG_7_GENE_14	hypo unique	NO DATA	-	-	
287	UBA_7931_GENE_272	FOG: GGDEF domain	NO DATA	-	95.15	5way_CG_7_GENE_15	x protein/GGDEF domain protein	NO DATA	-	-	
288	UBA_7931_GENE_274	Small-conductance mechanosensitive channel	NO DATA	-	94.79	5way_CG_7_GENE_16	e mechanosensitive ion channel	NO DATA	-	-	
289	UBA_7931_GENE_275	Predicted transcriptional regulators	28.4	2	91.79	5way_CG_7_GENE_17	transcriptional regulator	NO DATA	-		20.00
290	UBA_7931_GENE_276	Pyruvate/2-oxoglutarate dehydrogenase comple	NO DATA	-	93.73	5way_CG_7_GENE_18	mercuric iron reductase, MerA	NO DATA	-	-	
291	UBA_7931_GENE_277	Pyruvate/2-oxoglutarate dehydrogenase comple	NO DATA	-	84.52	5way_CG_7_GENE_18		NO DATA	-	-	

292	UBA_7931_GENE_278	Hypothetical	NO DATA	-		83.22	5way_CG_7_GENE_19	hypo unique	NO DATA	-		-
293		[redacted]	NO GENE	-			5way_CG_7_GENE_20	RNA polymerase sigma factor	NO DATA	-		-
294			NO GENE	-			5way_CG_7_GENE_21	c hypo	NO DATA	-		-
295			NO GENE	-			5way_CG_7_GENE_21a		NO DATA	-		-
296			NO GENE	-			5way_CG_7_GENE_23	hypo unique	NO DATA	-		-
297			NO GENE	-			5way_CG_7_GENE_24	c hypo	NO DATA	-		-
298			NO GENE	-			5way_CG_7_GENE_25	c hypo	NO DATA	-		-
299	UBA_7931_GENE_279	**ATPases involved in chromosome partitioning**	23		8	97.42	5way_CG_7_GENE_26	**ATPase**	15		0	1.53
300	UBA_7931_GENE_280	Sugar transferases involved in lipopolysaccharide	NO DATA	-		97.99	5way_CG_7_GENE_27	sugar transferase	NO DATA	-		-
301	UBA_7931_GENE_281	**Periplasmic protein involved in polysaccharide ex**	59.3		22	96.14	5way_CG_7_GENE_28	**polysaccharide transport**	49.5		0	1.20
302	UBA_7931_GENE_282	Hypothetical	NO DATA	-		84.39	5way_CG_7_GENE_29	MmcA-like	NO DATA	-		-
303	UBA_7931_GENE_283	Predicted xylanase/chitin deacetylase	NO DATA	-		91.60	5way_CG_7_GENE_30	polysaccharide deacetylase	NO DATA	-		-
304	UBA_7931_GENE_284	**glycosyltransferase [Vibrio fischeri ES114]gi|59482**	8.9		1	95.54	5way_CG_7_GENE_31	glycosyltransferase	NO DATA	-		20.00
305	UBA_7931_GENE_285	**Glycosyltransferase**	7.6		2	93.40	5way_CG_7_GENE_32	glycosyltransferase	NO DATA	-		20.00
306	UBA_7931_GENE_286	**Glycosyltransferase**	7.4		6	90.20	5way_CG_7_GENE_33	glycosyltransferase	NO DATA	-		20.00
307	UBA_7931_GENE_287	**Glycosyltransferase**	26.7		3	91.18	5way_CG_7_GENE_34	**glycosyltransferase**	8		0	3.34
308	UBA_7931_GENE_288	O-antigen polymerase [Geobacter metallireduce	NO DATA	-		95.02	5way_CG_7_GENE_35	eted polysaccharide polymerase	NO DATA	-		-
309	UBA_7931_GENE_289	Hypothetical	NO DATA	-		94.69	5way_CG_7_GENE_36	hypo unique	NO DATA	-		-
310	UBA_7931_GENE_290	Glycosyltransferases involved in cell wall biogenes	NO DATA	-		94.91	5way_CG_7_GENE_37	glycosyltransferase	NO DATA	-		-
311	UBA_7931_GENE_291	Predicted glycosyltransferases	NO DATA	-		91.19	5way_CG_7_GENE_38	rhamnosyl transferase	NO DATA	-		-
312	UBA_7931_GENE_292	Signal transduction histidine kinase	4	-		92.75	5way_CG_7_GENE_39	sensor histidine kinase	NO DATA	-		-
313	UBA_7931_GENE_293	**UDP-glucose pyrophosphorylase**	64.8		5	97.39	5way_CG_7_GENE_41	**e-1-phosphate uridylyltransferase**	51.8		0	1.25
314	UBA_7931_GENE_294	hypothetical protein RPEDRAFT_0901 [Rhodopseuc	NO DATA	-		94.20	5way_CG_7_GENE_42	c hypo	NO DATA	-		-
315	UBA_7931_GENE_295	hypothetical protein Gmet_1503 [Geobacter met	NO DATA	-		89.03	5way_CG_7_GENE_43	c hypo	NO DATA	-		-
316	UBA_7931_GENE_296	**Response regulator containing CheY-like receiver**	23.6		7	96.18	5way_CG_7_GENE_44	**t DNA binding response regulator**	5.7		0	4.14
317	UBA_7931_GENE_298	**Hypothetical**	18.9		10	93.54	5way_CG_7_GENE_45	c hypo	3.4		0	5.56
318	UBA_7931_GENE_299	Predicted glycosyltransferases	NO DATA	-		81.83	5way_CG_7_GENE_46	c hypo	NO DATA	-		-
319	UBA_7931_GENE_300	Glycosyltransferases involved in cell wall biogenes	NO DATA	-		89.37	5way_CG_7_GENE_47	glycosyltransferase	NO DATA	-		-
320	UBA_7931_GENE_301	Hypothetical	NO DATA	-				[redacted]	NO GENE	-		-
321	UBA_7931_GENE_302	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
322	UBA_7931_GENE_303	Transposase and inactivated derivatives	NO DATA	-					NO GENE	-		-
323	UBA_7931_GENE_305	**Hypothetical**	16.9	-		86.83	5way_CG_7_GENE_48	sugar transferase	NO DATA	-		-
324	UBA_7931_GENE_306	Glycosyltransferases involved in cell wall biogenes	NO DATA	-		83.52	5way_CG_7_GENE_49	glycosyltransferase	NO DATA	-		-
325	UBA_7931_GENE_307	Glycosyltransferase	NO DATA	-		81.96	5way_CG_7_GENE_50	glycosyltransferase	NO DATA	-		-
326		[redacted]	NO GENE	-			5way_CG_7_GENE_51	M-dependent methyltransferase	NO DATA	-		-
327	UBA_7931_GENE_308	Hypothetical	NO DATA	-		77.41	5way_CG_7_GENE_52	chitinase	NO DATA	-		-
328	UBA_7931_GENE_309	**ABC-type multidrug transport system, ATPase and**	10.3		6	94.09	5way_CG_7_GENE_53	C transporter, ATP binding protein	NO DATA	-		20.00
329	UBA_7931_GENE_310	SAM-dependent methyltransferases	NO DATA	-		85.38	5way_CG_7_GENE_54	c hypo	NO DATA	-		-
330	UBA_7931_GENE_311	**Hypothetical**	81.5		386	89.22	5way_CG_7_GENE_56	??	34.3		1	2.38
331	UBA_7931_GENE_312	Hypothetical	NO DATA	-		70.21	5way_CG_7_GENE_57	(faint similarity to glucoamylase I)	NO DATA	-		-
332	UBA_7931_GENE_313	Hypothetical	NO DATA	-		92.54	5way_CG_7_GENE_58	c hypo	NO DATA	-		-
333	UBA_7931_GENE_314	Hypothetical	NO DATA	-		83.26	5way_CG_7_GENE_59	hypo unique	NO DATA	-		-
334	UBA_7931_GENE_315	**Response regulator containing a CheY-like receiv**	32.4		7	93.88	5way_CG_7_GENE_61	**o component response regulator**	14.1		0	2.30
335	UBA_7931_GENE_316	**Signal transduction histidine kinase**	9	-		91.49	5way_CG_7_GENE_62	**gnal transduction histidine kinase**	5.5	-		-
336	UBA_7931_GENE_317	Enoyl-CoA hydratase/carnithine racemase	NO DATA	-		97.92	5way_CG_206_GENE_1	tor of pathogenicity factors, RpfF	NO DATA	-		-
337	UBA_7931_GENE_318	**FOG: GGDEF domain**	12.2		11	91.35	5way_CG_206_GENE_2	ensory box/GGDEF family protein	3.4		0	3.59
338	UBA_7931_GENE_319	Hypothetical	NO DATA	-		98.13	5way_CG_206_GENE_3	hypo unique	NO DATA	-		-
339	UBA_7931_GENE_320	**Zn-dependent alcohol dehydrogenases**	96.5		117	96.83	5way_CG_206_GENE_4	**alcohol dehydrogenase**	66.9		1	1.44
340	UBA_7931_GENE_321	**Uncharacterized protein, probably involved in treh**	52		94	90.86	5way_CG_206_GENE_5	**glycosidase**	9.2		0	5.65
341	UBA_7931_GENE_322	**Glycosidases**	39.2		46	95.78	5way_CG_206_GENE_6	**glycosidase**	27.3		0	1.44
342		[redacted]	NO GENE	-			5way_CG_206_GENE_7	hypo unique	NO DATA	-		-
343	UBA_7931_GENE_323	Hypothetical	NO DATA	-		95.06	5way_CG_206_GENE_8	hypo unique	NO DATA	-		-
344	UBA_7931_GENE_324	Hypothetical	NO DATA	-				[redacted]	NO GENE	-		-
345	UBA_7931_GENE_325	Hypothetical	NO DATA	-					NO GENE	-		-
346		[redacted]	NO GENE	-			5way_CG_213_GENE_1	hypo unique	NO DATA	-		-
347	UBA_7931_GENE_326	Response regulator containing a CheY-like receive	NO DATA	-		91.58	5way_CG_213_GENE_3	o component response regulator	NO DATA	-		-
348	UBA_7931_GENE_327	Hypothetical	NO DATA	-		80.78	5way_CG_213_GENE_4	hypo unique	NO DATA	-		-
349	UBA_7931_GENE_329	**FOG: GGDEF domain**	42.1		21	91.47	5way_CG_213_GENE_5	**ensory box/GGDEF family protein**	13		0	3.24
350	UBA_7931_GENE_330	Fatty acid desaturase family [Rhodopseudomona	NO DATA	-		93.49	5way_CG_213_GENE_6	fatty acid desaturase	NO DATA	-		-
351	UBA_7931_GENE_331	**Glycosidases**	22.4		2	98.93	5way_CG_213_GENE_7	**trehalose synthase**	16.6		0	1.35
352	UBA_7931_GENE_332	**Glycosidases**	31.1		3	98.92	5way_CG_213_GENE_8	**trehalose synthase**	22.7		0	1.37
353		[redacted]	NO GENE	-			5way_CG_86_GENE_1	hypo unique	NO DATA	-		-
354	UBA_7931_GENE_333	**Maltooligosyl trehalose synthase**	11.9		4	93.75	5way_CG_86_GENE_2	**maltoligosyltrehalose synthase**	8.8		0	1.35
355	UBA_7931_GENE_334	**1,4-alpha-glucan branching enzyme**	29.2		15	93.09	5way_CG_86_GENE_3	**alpha amylase**	11.1		0	2.63
356	UBA_7931_GENE_335	**Glutamate decarboxylase and related PLP-depen**	42.5		32	96.72	5way_CG_86_GENE_4	**tamate decarboxylase isozyme I**	13.3		0	3.20
357	UBA_7931_GENE_336	Phosphohistidine phosphatase SixA	NO DATA	-		91.03	5way_CG_86_GENE_5	phosphohistidine phosphatase	NO DATA	-		-
358	UBA_7931_GENE_337	Predicted signal transduction protein containing a	NO DATA	-		96.81	5way_CG_86_GENE_6	DEF domain/EAL domain protein	NO DATA	-		-
359	UBA_7931_GENE_338	**FOG: TPR repeat, SEL1 subfamily**	57.6		52	89.24	5way_CG_86_GENE_7	**c hypo**	26.6		0	2.17
360	UBA_7931_GENE_339	77 Permeases of the major facilitator superfamily	NO DATA	-		95.76	5way_CG_86_GENE_8	facilitator superfamily transporter	NO DATA	-		-
361	UBA_7931_GENE_340	**dTDP-4-dehydrorhamnose 3,5-epimerase and rela**	33.9		7	96.72	5way_CG_86_GENE_9	**dehydrorhamnose 3,5-epimerase**	5.5		0	6.16
362	UBA_7931_GENE_341	**dTDP-glucose pyrophosphorylase**	48.8		7	95.99	5way_CG_86_GENE_10	**1-phosphate thymidyltransferase**	27.8		0	1.76
363	UBA_7931_GENE_342	**dTDP-D-glucose 4,6-dehydratase**	23.5		6	93.56	5way_CG_86_GENE_11	**dTDP-glucose 4,6-dehydratase**	11.8		0	1.99

364	UBA_7931_GENE_343	3-isopropylmalate dehydratase large subunit	68.8	62	97.63	5way_CG_86_GENE_12	aconitase	45.6		0	1.51
365	UBA_7931_GENE_344	3-isopropylmalate dehydratase small subunit	72.1	20	97.12	5way_CG_86_GENE_13	isopropylmalate dehydrogenase	61.5		0	1.17
366	UBA_7931_GENE_345	Predicted permease	NO DATA	-	97.78	5way_CG_86_GENE_14	permease	NO DATA	-	-	
367		TRNA Lys TTT 400895..400970 (+)	-						-		
368	UBA_7931_GENE_346	Hypothetical	53.5	21	83.72	5way_CG_86_GENE_16	hypo unique	NO DATA	-		20.00
369	UBA_7931_GENE_347	Hypothetical	56.6	54	81.23	5way_CG_86_GENE_17	hypo unique	21.9		5	2.58
370	UBA_7931_GENE_348	conserved hypothetical protein [Nitrosospira multiti	NO DATA	-	96.77	5way_CG_86_GENE_18	c hypo	NO DATA	-	-	
371	UBA_7931_GENE_349	Hypothetical	NO DATA	-	95.15	5way_CG_86_GENE_19	hypo unique	NO DATA	-	-	
372	UBA_7931_GENE_350	Predicted signal transduction protein containing a	6.1	1	93.02	5way_CG_287_GENE_2	DEF domain/EAL domain protein	NO DATA	-		20.00
373	UBA_7931_GENE_351	Peptide methionine sulfoxide reductase	45.4	20	90.81	5way_CG_287_GENE_3	e methionine sulfoxide reductase	NO DATA	-		20.00
374	UBA_7931_GENE_352	hypothetical protein SfumDRAFT_0193 [Syntrophob	72.3	51	87.38	5way_CG_287_GENE_4	hypo unique	15.5		0	4.66
375	UBA_7931_GENE_353	Hypothetical	NO DATA	-	92.92	5way_CG_287_GENE_5	protoporphyrinogen oxidase	NO DATA	-	-	
376	UBA_7931_GENE_354	Hypothetical	19.3	6	95.56	5way_CG_287_GENE_6	hypo unique	8.2		0	2.35
377	UBA_7931_GENE_355	Glutaredoxin and related proteins [Thermoanaerol	42.2	0	93.02	5way_CG_287_GENE_7	e glutathione disulfide isomerase)	41.9		0	1.01
378	UBA_7931_GENE_356	Hypothetical	NO DATA	-	98.53	5way_CG_287_GENE_8	chloride channel protein	NO DATA	-	-	
379		TRNA Arg TCT 412236..412312 (+)	-						-		
380		TRNA Leu CAG 412446..412531 (+)	-						-		
381	UBA_7931_GENE_357	Predicted nucleoside-diphosphate-sugar epimera	76.3	39	93.29	5way_CG_41_GENE_36	NADH dehydrogenase	29.2		0	2.61
382	UBA_7931_GENE_358	Cysteine sulfinate desulfinase/cysteine desulfurase	47.7	22	97.18	5way_CG_41_GENE_35	cysteine desulfhydrase	27.9		0	1.71
383	UBA_7931_GENE_359	1 [LLfe161peptospirillum ferrooxidans]	80.7	15	96.45	5way_CG_41_GENE_34	c hypo	52.8		0	1.53
384	UBA_7931_GENE_360	Fe-S oxidoreductase	12.6	2	92.86	5way_CG_41_GENE_33	rol-3-phosphate dehydrogenase	NO DATA	-		20.00
385	UBA_7931_GENE_362	Predicted CoA-binding protein	65.5	8	93.24	5way_CG_41_GENE_31	synthetase/acyl-CoA synthetase	19.6		0	3.34
386	UBA_7931_GENE_362a		NO DATA	-	64.86	5way_CG_41_GENE_30	pendent peroxidase, tyrA protein	NO DATA	-	-	
387	UBA_7931_GENE_363	Peroxiredoxin	44.5	13	92.67	5way_CG_41_GENE_29	omigratory protein/peroxiredoxin	37.7		0	1.18
388	UBA_7931_GENE_364	3-hydroxyisobutyrate dehydrogenase and related	75.9	66	91.53	5way_CG_41_GENE_28	eta-hydroxyacid dehydrogenase	22.8		0	3.33
389	UBA_7931_GENE_365	Hypothetical	65.7	102	93.53	5way_CG_41_GENE_27	hypo unique	40.1		0	1.64
390	UBA_7931_GENE_366	Hypothetical	NO DATA	-	96.88	5way_CG_41_GENE_26	hypo unique	NO DATA	-	-	
391	UBA_7931_GENE_367	Osmosensitive K+ channel histidine kinase	5	1	95.41	5way_CG_41_GENE_25	e D chain/sensor histidine kinase	3.6		0	1.39
392	UBA_7931_GENE_368	Hypothetical	28	3	95.79	5way_CG_41_GENE_24	hypo unique	NO DATA	-		20.00
393	UBA_7931_GENE_370	Hypothetical	NO DATA	-	77.16	5way_CG_41_GENE_22	hypo unique	NO DATA	-	-	
394	UBA_7931_GENE_371	Hypothetical	NO DATA	-	77.62	5way_CG_41_GENE_21	hypo unique	NO DATA	-	-	
395	UBA_7931_GENE_372	Hypothetical	NO DATA	-	91.58	5way_CG_41_GENE_20	hypo unique	NO DATA	-	-	
396	UBA_7931_GENE_373	High-affinity K+ transport system, ATPase chain B	11.8	2	97.46	5way_CG_41_GENE_19	K+-transporting ATPase B chain	NO DATA	-		20.00
397	UBA_7931_GENE_374	K+-transporting ATPase, A chain	NO DATA	-	96.83	5way_CG_41_GENE_18	K+-transporting ATPase A chain	NO DATA	-	-	
398	UBA_7931_GENE_375	K+-transporting ATPase, c chain	NO DATA	-	93.66	5way_CG_41_GENE_17	K+-transporting ATPase C chain	NO DATA	-	-	
399	UBA_7931_GENE_377	Lfe107p1 [Leptospirillum ferrooxidans]	22.8	3	91.49	5way_CG_41_GENE_16	hypo	15.1		0	1.51
400	UBA_7931_GENE_378	Amino acid transporters	16.4	7	97.44	5way_CG_41_GENE_15	ic amino acid transporter (cat-1)	11.3		0	1.45
401	UBA_7931_GENE_379	Signal transduction histidine kinase	5.3	1	90.23	5way_CG_41_GENE_14	sensor histidine kinase	NO DATA	-		20.00
402	UBA_7931_GENE_380	Response regulator containing a CheY-like receiv	44.1	10	93.84	5way_CG_41_GENE_13	o-component response regulator	NO DATA	-		20.00
403	UBA_7931_GENE_381	ADP-heptose:LPS heptosyltransferase	7.8	1	86.76	5way_CG_41_GENE_12	-heptose-LPS heptosyltransferase	NO DATA	-		20.00
404	UBA_7931_GENE_382	Hypothetical	NO DATA	-	87.44	5way_CG_41_GENE_11	multidrug efflux permease	NO DATA	-	-	
405	UBA_7931_GENE_382a		NO DATA	-	100.00	5way_CG_41_GENE_10	hypo unique	NO DATA	-	-	
406	UBA_7931_GENE_383	[Leptospirillum ferrooxidans]gi|62195094|ref|YP_2	44.7	0	98.00	5way_CG_41_GENE_9	hypo unique	44.7		0	1.00
407	UBA_7931_GENE_384	DNA repair photolyase	12.8	2	91.78	5way_CG_41_GENE_8	transporter/DNA photolyase	NO DATA	-		20.00
408	UBA_7931_GENE_385	Uncharacterized NAD(FAD)-dependent dehydrog	32.8	1	98.82	5way_CG_41_GENE_7	sulfide:quinone reductase	32.8		0	1.00
409	UBA_7931_GENE_385a		NO DATA	-	93.02	5way_CG_41_GENE_6	hypo unique	NO DATA	-	-	
410	UBA_7931_GENE_386	Cytochrome bd-type quinol oxidase, subunit 2	NO DATA	-	92.61	5way_CG_41_GENE_5	ome bd quinol oxidase, subunit II	NO DATA	-	-	
411	UBA_7931_GENE_387	Cytochrome bd-type quinol oxidase, subunit 1	NO DATA	-	95.13	5way_CG_41_GENE_4	rome bd quinol oxidase, subunit I	NO DATA	-	-	
412	UBA_7931_GENE_389	Transcriptional regulator containing GAF, AAA-typ	5.7	1	96.06	5way_CG_41_GENE_2	chemotaxis protein CheY	11		2	0.52
413	UBA_7931_GENE_390	Hypothetical	46.6	19	94.12	5way_CG_41_GENE_1	hypo unique	18.1		0	2.57
414	UBA_7931_GENE_391	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
415	UBA_7931_GENE_392	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
416	UBA_7931_GENE_393	Hypothetical	6.3	2				NO GENE	-		35.00
417	UBA_7931_GENE_394	Hypothetical	NO DATA	-				NO GENE	-	-	
418	UBA_7931_GENE_395	Superfamily I DNA and RNA helicases and helicase	3.2	3				NO GENE	-		35.00
419	UBA_7931_GENE_396	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
420	UBA_7931_GENE_397	Transposase and inactivated derivatives	37	-				NO GENE	-	-	
421	UBA_7931_GENE_398	Superfamily I DNA and RNA helicases and helicase	NO DATA	-				NO GENE	-	-	
422	UBA_7931_GENE_399	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
423	UBA_7931_GENE_400	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
424	UBA_7931_GENE_401	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
425	UBA_7931_GENE_402	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
426	UBA_7931_GENE_404	Transposase IS3/IS911 [Moorella thermoacetica AT	NO DATA	-				NO GENE	-	-	
427	UBA_7931_GENE_405	Integrase	NO DATA	-				NO GENE	-	-	
428	UBA_7931_GENE_406	shufflon-specific recombinase [Xanthomonas carr	NO DATA	-				NO GENE	-	-	
429	UBA_7931_GENE_407	Hypothetical	NO DATA	-				NO GENE	-	-	
430	UBA_7931_GENE_408	Integrase	NO DATA	-				NO GENE	-	-	
431			NO GENE	-		5way_CG_798_GENE_7	c hypo	NO DATA	-	-	
432			NO GENE	-		5way_CG_798_GENE_6	integrase, P4-like, partial	NO DATA	-	-	
433	UBA_7931_GENE_409	Hypothetical	NO DATA	-	100.00	5way_CG_798_GENE_5	c hypo	NO DATA	-	-	
434	UBA_7931_GENE_410	Hypothetical	81.2	0	100.00	5way_CG_798_GENE_4	c hypo	81.2		0	1.00
435	UBA_7931_GENE_411	Hypothetical	NO DATA	-	100.00	5way_CG_798_GENE_3	hypo unique	NO DATA	-	-	

436	UBA_7931_GENE_411	Hypothetical	NO DATA	-	93.24	5way_CG_798_GENE_2	hypo unique	NO DATA	-	-	
437			NO GENE	-		5way_CG_706_GENE_5	integrase P4	NO DATA	-	-	
438			NO GENE	-		5way_CG_706_GENE_4	hypo unique	NO DATA	-	-	
439	UBA_7931_GENE_412	Hypothetical	NO DATA	-	96.88	5way_CG_51_GENE_2	c hypo	NO DATA	-	-	
440	UBA_7931_GENE_413	Uncharacterized protein conserved in bacteria	NO DATA	-	77.69	5way_CG_706_GENE_2	DNA primase	NO DATA	-	-	
441	UBA_7931_GENE_414	Hypothetical Membrane Spanning Protein [Brucell	NO DATA	-	93.55	5way_CG_706_GENE_1	c hypo	NO DATA	-	-	
442	UBA_7931_GENE_415	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
443	UBA_7931_GENE_416	Hypothetical	NO DATA	-				NO GENE	-	-	
444	UBA_7931_GENE_417	conserved hypothetical membrane spanning prot	NO DATA	-				NO GENE	-	-	
445	UBA_7931_GENE_418	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
446	UBA_7931_GENE_419	Hypothetical	NO DATA	-				NO GENE	-	-	
447	UBA_7931_GENE_420	Hypothetical	NO DATA	-				NO GENE	-	-	
448	UBA_7931_GENE_421		NO DATA	-				NO GENE	-	-	
449	UBA_7931_GENE_421a		NO DATA	-	100.00	5way_CG_27_GENE_45		NO DATA	-	-	
450	UBA_7931_GENE_422a		NO DATA	-	100.00	5way_CG_27_GENE_45a		NO DATA	-	-	
451	UBA_7931_GENE_422	Hypothetical	NO DATA	-	100.00	5way_CG_27_GENE_46	hypo unique	NO DATA	-	-	
452	UBA_7931_GENE_423	**Predicted helicase**	34.6	-	100.00	5way_CG_27_GENE_47	**methyltransferase/helicase**	35.1	-	-	
453	UBA_7931_GENE_424	**Predicted helicase**	26.1	-	95.90	5way_CG_27_GENE_47	**methyltransferase/helicase**	35.1	-	-	
454	UBA_7931_GENE_424a		NO DATA	-	100.00	5way_CG_27_GENE_48	hypo	NO DATA	-	-	
455	UBA_7931_GENE_425a		NO DATA	-	100.00	5way_CG_27_GENE_49	c hypo	NO DATA	-	-	
456	UBA_7931_GENE_426	Hypothetical	NO DATA	-	100.00	5way_CG_27_GENE_50	hypo unique	NO DATA	-	-	
457	UBA_7931_GENE_427	**Hypothetical**	77.8	0	100.00	5way_CG_27_GENE_51	**hypo unique**	91.7	0	0.85	
458	UBA_7931_GENE_428	Hypothetical	NO DATA	-	86.33	5way_CG_27_GENE_52	**hypo unique**	18.5	2	0.06	
459	UBA_7931_GENE_429	Transposase and inactivated derivatives, IS5 famil	NO DATA	-				NO GENE	-	-	
460	UBA_7931_GENE_430	**Transposase and inactivated derivatives, IS5 famil**	10.6	-				NO GENE	-	-	
461	UBA_7931_GENE_431	Predicted ATPase	NO DATA	-	92.68	5way_CG_539_GENE_2	c hypo	NO DATA	-	-	
462	UBA_7931_GENE_431	Predicted ATPase	NO DATA	-	93.93	5way_CG_539_GENE_3	DNA primase	NO DATA	-	-	
463	UBA_7931_GENE_432	Hypothetical	NO DATA	-	88.70	5way_CG_539_GENE_4	hypo unique	NO DATA	-	-	
464	UBA_7931_GENE_433	Hypothetical	NO DATA	-				NO GENE	-	-	
465	UBA_7931_GENE_434	**Transposase and inactivated derivatives**	73.3	-				NO GENE	-	-	
466	UBA_7931_GENE_435	Hypothetical	NO DATA	-				NO GENE	-	-	
467			NO GENE	-		5way_CG_539_GENE_6	hypo unique	NO DATA	-	-	
468	UBA_7931_GENE_436	Hypothetical	NO DATA	-	95.60	5way_CG_539_GENE_7	hypo unique	NO DATA	-	-	
469	UBA_7931_GENE_437	Hypothetical	NO DATA	-	97.32	5way_CG_539_GENE_8	hypo unique	NO DATA	-	-	
470		TRNA Met CAT 489424..489499 (-)	-						-		
471	UBA_7931_GENE_438	Hypothetical	NO DATA	-				NO GENE	-	-	
472	UBA_7931_GENE_439	Hypothetical	NO DATA	-	98.36	5way_CG_539_GENE_9	hypo unique	NO DATA	-	-	
473			NO GENE	-		5way_CG_303_GENE_10	transposase	NO DATA	-	-	
474		TRNA Met CAT 491019..491094 (-)	-						-		
475			NO GENE	-		5way_CG_303_GENE_9	hypo unique	NO DATA	-	-	
476	UBA_7931_GENE_440	77 Permeases of the major facilitator superfamily	NO DATA	-	93.87	5way_CG_303_GENE_7	drug resistance transporter	NO DATA	-	-	
477	UBA_7931_GENE_441	**Fe-S oxidoreductase**	30.1	6	98.20	5way_CG_303_GENE_6	**Fe-S oxidoreductase**	25.4	0	1.19	
478	UBA_7931_GENE_442	Hypothetical	NO DATA	-	98.44	5way_CG_303_GENE_5	hypo unique	NO DATA	-	-	
479	UBA_7931_GENE_443	**Hypothetical**	36.4	0	99.17	5way_CG_303_GENE_4	**transcriptional regulator**	36.4	0	1.00	
480	UBA_7931_GENE_444	**ATP sulfurylase (sulfate adenylyltransferase)**	47.3	0	99.24	5way_CG_303_GENE_3	**sulfate adenylyl transferase**	55.2	6	0.86	
481	UBA_7931_GENE_445	Ferredoxin	NO DATA	-	96.49	5way_CG_303_GENE_2	enylylsulfate reductase, subunit B	NO DATA	-	-	
482	UBA_7931_GENE_446	**Succinate dehydrogenase/fumarate reductase, fl**	29.4	0	96.56	5way_CG_303_GENE_1	**adenylylsulfate reductase A**	42	14	0.70	

		NO GENE	-		5way_CG_234_GENE_1	DNA binding protein	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_2	nthesis protein/methyltransferase	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_3	c hypo	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_4	etolactate synthase small subunit	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_5	**acetolactate synth, large s/unit**	12.4	4	0.03	
		NO GENE	-		5way_CG_234_GENE_6	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_7	transposase (single)	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_8	romophore precursor synthetase	NO DATA	-	-	
		NO GENE	-		5way_CG_234_GENE_9	transposase	NO DATA	-	-	
	Probably inserts as strain variant, above		-						-	
			-		short hits only, e.g., 6 kb o				-	
		NO GENE	-		5way_CG_443_GENE_11	transposase	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_10	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_9	transposase	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_8	transposase	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_7	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_6	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_5	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_4	hypo unique	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_3	integrase Rci fragment	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_2	transposition helper protein, IstB	NO DATA	-	-	
		NO GENE	-		5way_CG_443_GENE_1	transposase	NO DATA	-	-	

			-					443-1/0=tRNA Met		-	
	8524										
1	UBA_8524_GENE_1	Restriction endonuclease	NO DATA	-					NO GENE	-	-
2	UBA_8524_GENE_2	putative adhesin precursor [Cupriavidus necator]g	NO DATA	-					NO GENE	-	-
3	UBA_8524_GENE_3	Hypothetical	NO DATA	-					NO GENE	-	-
4	UBA_8524_GENE_4	Response regulator containing a CheY-like receive	NO DATA	-					NO GENE	-	-
5	UBA_8524_GENE_5	**Predicted signal transduction protein**	59.7	136					NO GENE	-	35.00
6	UBA_8524_GENE_6	**Transposase and inactivated derivatives, IS5 famil**	38.5	-					NO GENE	-	-
7	UBA_8524_GENE_7	**Transposase and inactivated derivatives, IS5 famil**	9.6	-					NO GENE	-	-
8	UBA_8524_GENE_8	Predicted nuclease (RecB family) no significant m	2.7	1					NO GENE	-	35.00
9	UBA_8524_GENE_9	Hypothetical no sign match in CG	NO DATA	-					NO GENE	-	-
10	UBA_8524_GENE_10	Hypothetical	NO DATA	-	100.00	5way_CG_684_GENE_1		hypo unique	NO DATA	-	-
11	UBA_8524_GENE_11	Hypothetical	NO DATA	-	73.86	5way_CG_684_GENE_2		c hypo	NO DATA	-	-
12			NO GENE	-		5way_CG_684_GENE_3		**c hypo**	22.7	4	0.03
13			NO GENE	-		5way_CG_684_GENE_4		c hypo	NO DATA	-	-
14			NO GENE	-		5way_CG_684_GENE_5		c hypo	NO DATA	-	-
15			NO GENE	-		5way_CG_684_GENE_6		**c hypo**	48.3	25	0.03
16	UBA_8524_GENE_12	Hypothetical	NO DATA	-					NO GENE	-	-
17	UBA_8524_GENE_13	Hypothetical no match in CG	NO DATA	-					NO GENE	-	-
18	UBA_8524_GENE_14	Hypothetical	NO DATA	-					NO GENE	-	-
19	UBA_8524_GENE_15	Hypothetical I	NO DATA	-					NO GENE	-	-
20	UBA_8524_GENE_16	Restriction endonuclease no sig match in CG	NO DATA	-					NO GENE	-	-
21	UBA_8524_GENE_17	Restriction endonuclease no sig match in CG	NO DATA	-					NO GENE	-	-
22	UBA_8524_GENE_18	Hypothetical no match in CG	NO DATA	-					NO GENE	-	-
23	UBA_8524_GENE_19	Hypothetical no sig. match in CG	NO DATA	-					NO GENE	-	-
24	UBA_8524_GENE_20	Hypothetical no sig match in CG	NO DATA	-					NO GENE	-	-
25	UBA_8524_GENE_21	Hypothetical	NO DATA	-					NO GENE	-	-
26	UBA_8524_GENE_22	Type II secretory pathway, component PulF	NO DATA	-					NO GENE	-	-
27	UBA_8524_GENE_24	Type II secretory pathway, ATPase PulE/Tfp pilus as	NO DATA	-					NO GENE	-	-
28	UBA_8524_GENE_25	Hypothetical	NO DATA	-					NO GENE	-	-
29	UBA_8524_GENE_26	Hypothetical	NO DATA	-					NO GENE	-	-
30	UBA_8524_GENE_27	type IV pilus biogenesis protein PilN, putative [Burk	NO DATA	-					NO GENE	-	-
31	UBA_8524_GENE_28	Hypothetical	NO DATA	-					NO GENE	-	-
32			NO GENE	-		5way_CG_958_GENE_1			NO DATA	-	-
33	UBA_8524_GENE_29	hypothetical protein Noc_0623 [Nitrosococcus oc	NO DATA	-	60.00	5way_CG_958_GENE_2			NO DATA	-	-
34	UBA_8524_GENE_30	Hypothetical	NO DATA	-	83.72	5way_CG_958_GENE_3			NO DATA	-	-
35	UBA_8524_GENE_31	Tfp pilus assembly protein, pilus retraction ATPase	NO DATA	-	79.33	5way_CG_958_GENE_4			NO DATA	-	-
36	UBA_8524_GENE_32	Hypothetical	NO DATA	-					NO GENE	-	-
37	UBA_8524_GENE_33	Hypothetical	NO DATA	-					NO GENE	-	-
38	UBA_8524_GENE_34	hypothetical protein MaquDRAFT_3643 [Marinoba	NO DATA	-	75.16	5way_CG_569_GENE_4			NO DATA	-	-
39	UBA_8524_GENE_35	Hypothetical	NO DATA	-					NO GENE	-	-
40	UBA_8524_GENE_36	FOG: EAL domain	NO DATA	-	54.05	5way_CG_569_GENE_3			NO DATA	-	-
41	UBA_8524_GENE_37	conserved hypothetical protein [Marinobacter aq	NO DATA	-					NO GENE	-	-
42	UBA_8524_GENE_38	conserved hypothetical protein [Marinobacter aq	NO DATA	-					NO GENE	-	-
43	UBA_8524_GENE_39	Hypothetical	NO DATA	-					NO GENE	-	-
44	UBA_8524_GENE_40	conserved hypothetical protein [Marinobacter aq	NO DATA	-					NO GENE	-	-
45	UBA_8524_GENE_41	Hypothetical	NO DATA	-					NO GENE	-	-
46	UBA_8524_GENE_42	Phage integrase [Burkholderia vietnamiensis G4]gi	NO DATA	-					NO GENE	-	-
47	UBA_8524_GENE_43	Hypothetical	NO DATA	-					NO GENE	-	-
48	UBA_8524_GENE_44	hypothetical protein Mbar_A1563 [Methanosarcin	NO DATA	-					NO GENE	-	-
49	UBA_8524_GENE_45	Phage integrase (or fragment)	NO DATA	-					NO GENE	-	-
50	UBA_8524_GENE_46	Phage integrase (or fragment)	NO DATA	-					NO GENE	-	-
51	UBA_8524_GENE_47	Reverse gyrase	NO DATA	-					NO GENE	-	-
52	UBA_8524_GENE_48	Phage integrase (or fragment)	NO DATA	-	72.61	5way_CG_569_GENE_2			53.2	15	0.06
53			NO GENE	-		5way_CG_569_GENE_1			NO DATA	-	-
54	UBA_8524_GENE_49	Phage integrase (or fragment)	NO DATA	-					NO GENE	-	-
55	UBA_8524_GENE_50	IcmO protein (secretion) [Coxiella burnetii RSA 493	NO DATA	-					NO GENE	-	-
56	UBA_8524_GENE_51	Phage integrase (or fragment)	NO DATA	-					NO GENE	-	-
57	UBA_8524_GENE_52	Predicted transcriptional regulator	NO DATA	-					NO GENE	-	-
58	UBA_8524_GENE_53	hypothetical protein MburDRAFT_1148 [Methanoc	NO DATA	-					NO GENE	-	-
59	UBA_8524_GENE_54	Integrase	NO DATA	-					NO GENE	-	-
60	UBA_8524_GENE_55	Integrase	NO DATA	-					NO GENE	-	-
61	UBA_8524_GENE_56	Hypothetical	NO DATA	-					NO GENE	-	-
62	UBA_8524_GENE_57	Hypothetical	NO DATA	-					NO GENE	-	-
63	UBA_8524_GENE_58	hypothetical protein Haso02002010 [Haemophilus	NO DATA	-					NO GENE	-	-
64	UBA_8524_GENE_59	Hypothetical	NO DATA	-					NO GENE	-	-
65	UBA_8524_GENE_60	Hypothetical	NO DATA	-					NO GENE	-	-
66	UBA_8524_GENE_61	Hypothetical	NO DATA	-	100.00	5way_CG_1068_GENE_3			NO DATA	-	-
67	UBA_8524_GENE_62	Hypothetical	NO DATA	-	100.00	5way_CG_1068_GENE_2			NO DATA	-	-
68	UBA_8524_GENE_63	Hypothetical	NO DATA	-					NO GENE	-	-

69	UBA_8524_GENE_64	Hypothetical	NO DATA	-				NO GENE	-	-	
70	UBA_8524_GENE_65	Hypothetical	NO DATA	-				NO GENE	-	-	
71	UBA_8524_GENE_66	Hypothetical	NO DATA	-	99.62	5way_CG_1068_GENE_1		NO DATA	-	-	
72	UBA_8524_GENE_67	Hypothetical	NO DATA	-				NO GENE	-	-	
73	UBA_8524_GENE_68	**Transposase and inactivated derivatives**	32.2	-				NO GENE	-	-	
74	UBA_8524_GENE_69	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
75	UBA_8524_GENE_70	Hypothetical	NO DATA	-				NO GENE	-	-	
76	UBA_8524_GENE_71	Hypothetical	NO DATA	-				NO GENE	-	-	
77	UBA_8524_GENE_72	Hypothetical	NO DATA	-				NO GENE	-	-	
78	UBA_8524_GENE_73	Transposase and inactivated derivatives	NO DATA	-	100.00	5way_CG_1153_GENE_1		NO DATA	-	-	
79			NO GENE	-		5way_CG_1153_GENE_2		37.3		0	0.03
80	UBA_8524_GENE_74	conserved hypothetical protein [Pelodictyon lutec	NO DATA	-	100.00	5way_CG_527_GENE_7		NO DATA	-	-	
81	UBA_8524_GENE_75	Uncharacterized protein conserved in bacteria	NO DATA	-	99.22	5way_CG_527_GENE_6	ed to be Lepto III hypo unique	NO DATA	-	-	
82	UBA_8524_GENE_76	Hypothetical	NO DATA	-	100.00	5way_CG_527_GENE_5a		NO DATA	-	-	
83	UBA_8524_GENE_77	Hypothetical	NO DATA	-	100.00	5way_CG_527_GENE_4a		NO DATA	-	-	
84	UBA_8524_GENE_78	**Integrase**	17.4	-	100.00	5way_CG_527_GENE_4	possiblle integrase	17.4	-	-	
85			NO GENE	-		5way_CG_527_GENE_3	transposase	NO DATA	-	-	
86			NO GENE	-		5way_CG_527_GENE_2	integrase fragment, INT 22C	NO DATA	-	-	
87			NO GENE	-		5way_CG_527_GENE_1	hypo unique	88.8	-	-	
88	UBA_8524_GENE_79	**Uncharacterized protein conserved in bacteria**	18	-	86.60	5way_CG_6_GENE_66		NO DATA	-	-	
89	UBA_8524_GENE_80	Hypothetical	NO DATA	-				NO GENE	-	-	
90			NO GENE	-		5way_CG_6_GENE_65	ATP-dependant Clp protease	NO DATA	-	-	
91	UBA_8524_GENE_81	Membrane proteins related to metalloendopeptic	NO DATA	-	90.96	5way_CG_6_GENE_64		NO DATA	-	-	
92	UBA_8524_GENE_82	**ATPases with chaperone activity, ATP-binding subu**	65.3	0	100.00	5way_CG_6_GENE_62	**sialoglycoprotein endopeptidase**	65.3		0	1.00
93	UBA_8524_GENE_83	**Metal-dependent proteases with possible chaperc**	31	12	95.35	5way_CG_6_GENE_61	**arginyl tRNA synthetase**	7.5		0	4.13
94	UBA_8524_GENE_84	Hypothetical, probably a Tn	NO DATA	-				NO GENE	-	-	
95	UBA_8524_GENE_85	Hypothetical, probably a Tn	NO DATA	-				NO GENE	-	-	
96	UBA_8524_GENE_86	unknown Bacillus halodurans] Transposase	NO DATA	-				NO GENE	-	-	
97	UBA_8524_GENE_87	**Arginyl-tRNA synthetase**	56.3	48	94.96	5way_CG_6_GENE_60	**queuine tRNA-ribosyltransferase**	25.7		1	2.19
98	UBA_8524_GENE_88	**Queuine/archaeosine tRNA-ribosyltransferase**	21.2	6	90.48	5way_CG_6_GENE_59	??	NO DATA	-		20.00
99	UBA_8524_GENE_89	**Preprotein translocase subunit YajC**	58.3	9	97.92	5way_CG_6_GENE_58	**protein translocase, YajC subunit**	27.1		0	2.15
100	UBA_8524_GENE_90	**Preprotein translocase subunit SecD**	39.5	69	98.09	5way_CG_6_GENE_57	**-export membrane protein, SecD**	26		0	1.52
101	UBA_8524_GENE_91	**Preprotein translocase subunit SecF**	27.7	8	98.75	5way_CG_6_GENE_56	**n export membrane protein, SecF**	22.7		0	1.22
102	UBA_8524_GENE_91a		NO DATA	-	100.00	5way_CG_6_GENE_55	hypo unique	NO DATA	-	-	
103	UBA_8524_GENE_92	**Single-stranded DNA-specific exonuclease**	16	2	98.18	5way_CG_6_GENE_54	**ssDNA exonuclease**	8.4		0	1.90
104	UBA_8524_GENE_93	**Guanosine polyphosphate pyrophosphohydrolase**	26.4	9	98.56	5way_CG_6_GENE_53	**GTP pyrophosphokinase**	18.4		0	1.43
105	UBA_8524_GENE_95	Hypothetical	36.1	0	99.01	5way_CG_6_GENE_52	**rogenase formation protein, FdhE**	36.1		0	1.00
106	UBA_8524_GENE_96	Hypothetical	NO DATA	-	96.39	5way_CG_6_GENE_51	hypo unique	NO DATA	-	-	
107	UBA_8524_GENE_97	Hypothetical	26	6	95.24	5way_CG_6_GENE_50	transcriptional regulator	NO DATA	-		20.00
108	UBA_8524_GENE_98	**similar to Uncharacterized conserved protein [Synl**	31.5	5	93.50	5way_CG_6_GENE_49	**ble cytochrome c-554 precursor)**	13.5		0	2.33
109	UBA_8524_GENE_99	**Multidrug resistance efflux pump**	67.5	78	96.53	5way_CG_6_GENE_48	**multi-drug resistance efflux pump**	40.7		0	1.66
110	UBA_8524_GENE_100	77 Permeases of the major facilitator superfamily	NO DATA	-	98.86	5way_CG_6_GENE_47	drug resistance transporter	NO DATA	-	-	
111	UBA_8524_GENE_101	**Outer membrane protein**	53.7	94	96.34	5way_CG_6_GENE_46	**efflux protein**	39.7		0	1.35
112	UBA_8524_GENE_102	**Multidrug resistance efflux pump**	62.1	27	96.83	5way_CG_6_GENE_45	**efflux transporter**	30		0	2.07
113	UBA_8524_GENE_103	unknown [Bacillus halodurans]	NO DATA	-				NO GENE	-	-	
114	UBA_8524_GENE_104	Hypothetical	NO DATA	-				NO GENE	-	-	
115	UBA_8524_GENE_105	77 Permeases of the major facilitator superfamily	NO DATA	-	95.93	5way_CG_6_GENE_44	drug resistance transporter	NO DATA	-	-	
116	UBA_8524_GENE_106	Transcriptional regulator of heat shock gene	NO DATA	-	98.58	5way_CG_6_GENE_43	cible transcription repressor, HrcA	NO DATA	-	-	
117	UBA_8524_GENE_107	**Molecular chaperone GrpE (heat shock protein)**	89.4	20	97.87	5way_CG_6_GENE_42	**chaperone grpE**	63		0	1.42
118	UBA_8524_GENE_108	**Molecular chaperone**	83.6	117	98.75	5way_CG_6_GENE_41	**haperone dnaK, AbMem protein**	76.6		65	1.09
119	UBA_8524_GENE_109	**DnaJ-class molecular chaperone with C-terminal**	48.9	31	98.12	5way_CG_6_GENE_40	**heat shock protein dnaJ**	29.8		0	1.64
120	UBA_8524_GENE_110	Hypothetical	25.5	3	86.43	5way_CG_6_GENE_39	**c hypo**	9.1		0	2.80
121	UBA_8524_GENE_111	**Hypothetical**	6.1	2	89.86	5way_CG_6_GENE_38	hypo unique	NO DATA	-		20.00
122	UBA_8524_GENE_112	**SAM-dependent methyltransferases**	56.2	6	97.98	5way_CG_6_GENE_37	**methyl chloride transferase**	50.2		0	1.12
123	UBA_8524_GENE_113	**Adenosyl cobinamide kinase/adenosyl cobinami**	44.1	30	88.83	5way_CG_6_GENE_36	cobinamide kinase	NO DATA	-		20.00
124	UBA_8524_GENE_114	**NaMN:DMB phosphoribosyltransferase**	34.2	10	97.80	5way_CG_6_GENE_35	**dazole phosphoribosyltransferase**	21.8		0	1.57
125	UBA_8524_GENE_115	Cobalamin-5-phosphate synthase CobS [Bradyrhi	NO DATA	-	89.62	5way_CG_6_GENE_34	cobalamin synthase	NO DATA	-	-	
126	UBA_8524_GENE_116	Hypothetical	NO DATA	-	94.85	5way_CG_6_GENE_33	c hypo	NO DATA	-	-	
127	UBA_8524_GENE_117	Hypothetical	NO DATA	-	94.05	5way_CG_6_GENE_32	hypo unique	NO DATA	-	-	
128	UBA_8524_GENE_118	**Hypothetical**	18.8	1	90.62	5way_CG_6_GENE_31	hypo unique	NO DATA	-		20.00
129	UBA_8524_GENE_119	Hypothetical	NO DATA	-	91.89	5way_CG_6_GENE_30	cobalamin synthase	NO DATA	-	-	
130	UBA_8524_GENE_120	Hypothetical	NO DATA	-	96.30	5way_CG_6_GENE_29	hypo unique	NO DATA	-	-	
131	UBA_8524_GENE_121	**Predicted oxidoreductases (related to aryl-alcoho**	87.2	32	97.03	5way_CG_6_GENE_27	**aldo/keto reductase**	70.6		1	1.24
132	UBA_8524_GENE_122	**Fructose-2,6-bisphosphatase**	19	4	88.99	5way_CG_6_GENE_26	phosphoglycerate mutase	NO DATA	-		20.00
133	UBA_8524_GENE_123	**Cobyrinic acid a,c-diamide synthase**	13.4	4	87.21	5way_CG_6_GENE_25	**cobyrinic acid**	5.3		1	2.53
134	UBA_8524_GENE_124	**Precorrin isomerase**	50	41	96.11	5way_CG_6_GENE_24	**precorrin isomerase**	29.3		1	1.71
135	UBA_8524_GENE_125	**Isocitrate/isopropylmalate dehydrogenase**	78.6	48	99.40	5way_CG_6_GENE_23	**isocitrate dehydrogenase**	71.1		0	1.11
136	UBA_8524_GENE_126	**Lfe195p 1 [Leptospirillum ferrooxidans]**	69.8	0	100.00	5way_CG_6_GENE_22	**isocitrate dehydrogenase**	69.8		0	1.00
137		TRNA Phe GAA 114387..114462 (-)	-						-		
138	UBA_8524_GENE_127	**Outer membrane protein/protective antigen OMA**	43.5	7	98.98	5way_CG_6_GENE_20	**c hypo**	42.8		1	1.02
139	UBA_8524_GENE_128	**Hypothetical**	70.5	40	96.50	5way_CG_6_GENE_19	**c hypo**	59.5		0	1.18
140	UBA_8524_GENE_129	**UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acy**	78	23	96.00	5way_CG_6_GENE_18	**N-acetyltransferase**	45.4		0	1.72

141	UBA_8524_GENE_130	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl car	48	7	98.27	5way_CG_6_GENE_17	yl N-acetylglucosamine deac...	41.6		0	1.15
142	UBA_8524_GENE_131	Acyl-[acyl carrier protein]--UDP-N-acetylglucosar	78	44	95.47	5way_CG_6_GENE_16	acetyl transferase	35.2		0	2.22
143	UBA_8524_GENE_132	Uncharacterized protein conserved in bacteria	NO DATA	-	95.61	5way_CG_6_GENE_15	c hypo	10.5		1	0.06
144	UBA_8524_GENE_133	Predicted dehydrogenases and related proteins	41.1	7	97.20	5way_CG_6_GENE_14	oxidoreductase	26.5		0	1.55
145	UBA_8524_GENE_134	Lipid A disaccharide synthetase	21.3	3	88.72	5way_CG_6_GENE_13	lipid A disaccharide synthase	7.9		0	2.70
146	UBA_8524_GENE_135	Hypothetical	NO DATA	-				NO GENE	-	-	
147	UBA_8524_GENE_136	Glycosyltransferases involved in cell wall biogene	15.6	7				NO GENE	-		35.00
148			NO GENE	-		5way_CG_6_GENE_12	glycosyltransferase	NO DATA	-	-	
149	UBA_8524_GENE_137	Transposase and inactivated derivatives, IS5 famil	28.6	-				NO GENE	-	-	
150	UBA_8524_GENE_138	Transposase, IS4 [Moorella thermoacetica ATCC 3	NO DATA	-				NO GENE	-	-	
151	UBA_8524_GENE_139	Glycosyltransferases involved in cell wall biogenes	NO DATA	-				NO GENE	-	-	
152	UBA_8524_GENE_140	Hypothetical	NO DATA	-				NO GENE	-	-	
153	UBA_8524_GENE_141	Transposase and inactivated derivatives	73.3	-				NO GENE	-	-	
154	UBA_8524_GENE_142	Glycosyltransferase	NO DATA	-				NO GENE	-	-	
155	UBA_8524_GENE_143	Hypothetical	NO DATA	-				NO GENE	-	-	
156	UBA_8524_GENE_144	ABC-type multidrug transport system, ATPase and	27.8	22	95.00	5way_CG_6_GENE_11	ATP-binding protein, MsbA family	5.8		0	4.79
157	UBA_8524_GENE_145	3-deoxy-D-manno-octulosonic-acid transferase	19.3	5	80.96	5way_CG_6_GENE_10	nno-octulosonic acid transferase	NO DATA	-		20.00
158	UBA_8524_GENE_146	Tetraacyldisaccharide-1-P 4'-kinase	10.3	2	74.58	5way_CG_6_GENE_9	tetraacyldisaccharide 4'-kinase	NO DATA	-		20.00
159	UBA_8524_GENE_147	Lauroyl/myristoyl acyltransferase	NO DATA	-	87.33	5way_CG_6_GENE_8	osynthesis lauroyl acyltransferase	NO DATA	-	-	
160	UBA_8524_GENE_148	Glycosyltransferases involved in cell wall biogenes	NO DATA	-				NO GENE	-	-	
161	UBA_8524_GENE_149	Hypothetical	9.2	2				NO GENE	-		35.00
162	UBA_8524_GENE_150	: Glycosyltransferases involved in cell wall biogen	32.3	6				NO GENE	-		35.00
163			NO GENE	-		5way_CG_6_GENE_7	hypo unique	NO DATA	-	-	
164	UBA_8524_GENE_151	ADP-heptose:LPS heptosyltransferase	8.5	1	88.77	5way_CG_6_GENE_6	lysaccharide heptosyltransferase	NO DATA	-		20.00
165	UBA_8524_GENE_152	ADP-heptose:LPS heptosyltransferase	28.8	3	84.91	5way_CG_6_GENE_5	lysaccharide heptosyltransferase	NO DATA	-		20.00
166			NO GENE	-		5way_CG_6_GENE_4	glycosyltransferase	NO DATA	-	-	
167	UBA_8524_GENE_153	: Glycosyltransferases involved in cell wall biogen	24.4	10	76.68	5way_CG_6_GENE_3	c hypo	NO DATA	-		20.00
168			NO GENE	-		5way_CG_68_GENE_28	transposase	NO DATA	-	-	
169			NO GENE	-		5way_CG_68_GENE_27	c hypo	NO DATA	-	-	
170	UBA_8524_GENE_154	Glycosyltransferases involved in cell wall biogene	18.8	8	55.19	5way_CG_68_GENE_26	glycosyltransferase	NO DATA	-		20.00
171	UBA_8524_GENE_155	ADP-heptose:LPS heptosyltransferase	32.8	11	76.90	5way_CG_68_GENE_25	heptosyltransferase	NO DATA	-		20.00
172	UBA_8524_GENE_156	Histidinol phosphatase and related phosphatases	75.4	44	80.40	5way_CG_68_GENE_24	histidinol phosphatase	NO DATA	-		20.00
173	UBA_8524_GENE_157	conserved hypothetical protein [Desulfovibrio vulg	72.1	2	86.89	5way_CG_68_GENE_23	raacyldisaccharide-1-P 4'-kinase	NO DATA	-		20.00
174	UBA_8524_GENE_158	ADP-heptose:LPS heptosyltransferase	9	2	86.92	5way_CG_68_GENE_22		NO DATA	-		20.00
175	UBA_8524_GENE_159	ADP-heptose:LPS heptosyltransferase	16.3	4	78.12	5way_CG_68_GENE_21	-heptose:LPS heptosyltransferase	NO DATA	-		20.00
176	UBA_8524_GENE_160	Predicted xylanase/chitin deacetylase	11.7	2	88.75	5way_CG_68_GENE_20	polysaccharide deacetylase	NO DATA	-		20.00
177	UBA_8524_GENE_161	Glycosyltransferase	20.3	5	87.37	5way_CG_68_GENE_19	glycosyltransferase	12.3		1	1.65
178	UBA_8524_GENE_162	Hypothetical	78.9	4	92.55	5way_CG_68_GENE_18	c hypo	34.7		0	2.27
179	UBA_8524_GENE_163	Hypothetical	NO DATA	-	81.74	5way_CG_68_GENE_17	diacylglycerol kinase	NO DATA	-	-	
180	UBA_8524_GENE_165	Hypothetical	74	32	93.77	5way_CG_68_GENE_16	hypo unique	59.9		0	1.24
181	UBA_8524_GENE_166	Adenosylmethionine-8-amino-7-oxononanoate a	22.3	4	91.87	5way_CG_68_GENE_15	oxononanoate aminotransferase	8.6		0	2.59
182	UBA_8524_GENE_167	Predicted esterase of the alpha-beta hydrolase su	NO DATA	-	92.54	5way_CG_68_GENE_14	serine protease	NO DATA	-	-	
183	UBA_8524_GENE_168	Hypothetical	NO DATA	-	81.68	5way_CG_68_GENE_12	c hypo	NO DATA	-	-	
184	UBA_8524_GENE_169	Integral membrane protein (PIN domain superfam	30.2	3	99.72	5way_CG_68_GENE_11	pili retraction protein PilT	27.6		0	1.09
185	UBA_8524_GENE_170	2C-methyl-D-erythritol 2,4-cyclodiphosphate synt	48.9	41	91.31	5way_CG_68_GENE_10	IspD/IspF bifunctional enzyme	13.6		0	3.60
186	UBA_8524_GENE_171	Serine acetyltransferase	26.1	0	97.01	5way_CG_68_GENE_9	serine acetyltransferase	26.1		0	1.00
187	UBA_8524_GENE_172	Membrane-associated phospholipid phosphatase	NO DATA	-	92.90	5way_CG_68_GENE_8	p2 superfamily protein/permease	NO DATA	-	-	
188	UBA_8524_GENE_173	4-amino-4-deoxy-L-arabinose transferase and rel	6.4	2	88.46	5way_CG_68_GENE_7	glycosyltransferase	NO DATA	-		20.00
189	UBA_8524_GENE_174	ADP-heptose:LPS heptosyltransferase	50.7	18	94.54	5way_CG_68_GENE_6	eptose-LPS heptosyltransferase II	28.5		0	1.78
190	UBA_8524_GENE_175	Glycosyltransferases involved in cell wall biogene	58.5	31	93.33	5way_CG_68_GENE_5	glycosyltransferase	7.4		0	7.91
191	UBA_8524_GENE_176	4-amino-4-deoxy-L-arabinose transferase and rel	9.1	14	90.87	5way_CG_68_GENE_4	c hypo	1.8		0	5.06
192	UBA_8524_GENE_177	AICAR transformylase/IMP cyclohydrolase PurH (o	72.4	76	94.83	5way_CG_68_GENE_3	ecarboxamide formyltransferase	48.5		1	1.49
193	UBA_8524_GENE_178	Phosphoribosylamine-glycine ligase	72.5	91	87.76	5way_CG_68_GENE_2	sphoribosylamine-glycine ligase	18.6		1	3.90
194	UBA_8524_GENE_179	Putative translation factor (SUA5)	NO DATA	-	90.12	5way_CG_68_GENE_1	translation factor sua5-like	NO DATA	-	-	
195	UBA_8524_GENE_180	Hypothetical	78.3	-	100.00	5way_CG_8_GENE_1	e/peptidoglycan binding protein	78.3	-	-	
196	UBA_8524_GENE_181	N6-adenine-specific methylase	36	5	92.59	5way_CG_8_GENE_2	methyltransferase	NO DATA	-		20.00
197	UBA_8524_GENE_182	Phosphopantetheine adenylyltransferase	62	0	100.00	5way_CG_8_GENE_3	e-phosphate adenylyltransferase	62		0	1.00
198	UBA_8524_GENE_183	Aspartate/tyrosine/aromatic aminotransferase	65.8	3	99.26	5way_CG_8_GENE_4	aspartate aminotransferase	62		0	1.06
199	UBA_8524_GENE_184a		77.7	10	91.96	5way_CG_8_GENE_6	c hypo	37.5		0	2.07
200	UBA_8524_GENE_185	ABC-type antimicrobial peptide transport system,	62.1	20	95.83	5way_CG_8_GENE_7	C transporter, ATP-binding protein	30.4		0	2.04
201	UBA_8524_GENE_186	ABC-type transport system, involved in lipoprotein	6.3	1	98.79	5way_CG_8_GENE_8	BC transporter, permease protein	NO DATA	-		20.00
202	UBA_8524_GENE_187	Lysyl-tRNA synthetase (class II)	54.4	36	96.65	5way_CG_8_GENE_9	lysyl tRNA synthetase	37.5		0	1.45
203	UBA_8524_GENE_188	Predicted translation initiation factor 2B subunit,	79.7	19	99.43	5way_CG_8_GENE_10	translation initiation factor	66.6		0	1.20
204	UBA_8524_GENE_189	Glycogen debranching enzyme	6.3	4	84.07	5way_CG_8_GENE_11	glycogen debranching enzyme	NO DATA	-		20.00
205	UBA_8524_GENE_190	Protoheme ferro-lyase (ferrochelatase)	37.6	39	94.10	5way_CG_8_GENE_12	ferrochelatase	NO DATA	-		20.00
206	UBA_8524_GENE_191	Predicted permeases	NO DATA	-	98.07	5way_CG_8_GENE_13	permease-like	NO DATA	-	-	
207	UBA_8524_GENE_192	Predicted permeases	NO DATA	-	96.56	5way_CG_8_GENE_14	permease-like	NO DATA	-	-	
208	UBA_8524_GENE_193	2-methylthioadenine synthetase	NO DATA	-	93.80	5way_CG_8_GENE_15	2-methylthioadenine synthetase	NO DATA	-	-	
209	UBA_8524_GENE_194	Hypothetical	41.4	1	91.67	5way_CG_8_GENE_16	hypo unique	NO DATA	-		20.00
210	UBA_8524_GENE_195	SAM-dependent methyltransferases	62.8	17	97.38	5way_CG_8_GENE_17	M-dependant methyl transferase	51.8		0	1.21
211	UBA_8524_GENE_196	Hypothetical	52.9	15	94.23	5way_CG_8_GENE_18	hypo unique	13.9		0	3.81
212	UBA_8524_GENE_197	cytochrome c-552 Ks_3357 [Candidatus Kuenenia	43.6	8	87.88	5way_CG_8_GENE_20	hypo unique	28.6		0	1.52

213	UBA_8524_GENE_198	unknown [Bacillus halodurans], prob Tn	NO DATA	-				NO GENE	-	-	
214	UBA_8524_GENE_199	Hypothetical, prob Tn	NO DATA	-				NO GENE	-	-	
215			NO GENE	-		5way_CG_8_GENE_21	transposase	NO DATA	-	-	
216	UBA_8524_GENE_200	**Aspartate/tyrosine/aromatic aminotransferase**	51.1	3	99.25	5way_CG_8_GENE_22	**aminotransferase**	51.1		1	1.00
217	UBA_8524_GENE_201	**Hypothetical**	77.2	46	97.21	5way_CG_8_GENE_23	**hypo unique**	53		0	1.46
218	UBA_8524_GENE_202	**Homoserine dehydrogenase**	56.4	14	97.52	5way_CG_8_GENE_24	**homoserine dehydrogenase**	40		0	1.41
219	UBA_8524_GENE_203	**Threonine synthase**	57.2	2	99.15	5way_CG_8_GENE_25	**threonine synthase**	56.7		2	1.01
220	UBA_8524_GENE_205	Predicted phosphoglycerate mutase, AP superfan	6.5	2	88.22	5way_CG_8_GENE_26	osphonopyruvate decarboxylase	NO DATA	-		20.00
221	UBA_8524_GENE_206	**Aspartokinases**	51	18	99.03	5way_CG_8_GENE_27	**aspartate kinase**	36.4		0	1.40
222	UBA_8524_GENE_207	**Isopropylmalate/homocitrate/citramalate synthas**	39	20	92.46	5way_CG_8_GENE_28	**2-isopropylmalate synthase**	11.9		0	3.28
223	UBA_8524_GENE_208	Acyl-[acyl carrier protein]--UDP-N-acetylglucosam	NO DATA	-	95.56	5way_CG_8_GENE_29	etylglucosamine acyltransferase	NO DATA	-	-	
224	UBA_8524_GENE_209	**Bacterial nucleoid DNA-binding protein**	85.7	0	100.00	5way_CG_8_GENE_30	**ion host factor HimA/histone-like**	85.7		0	1.00
225	UBA_8524_GENE_211	**Hypothetical**	61.9	4	97.35	5way_CG_8_GENE_31	**hypo unique**	41.6		0	1.49
226		TRNA Pro GGG 196837..196913 (+)	-						-		
227	UBA_8524_GENE_212	**Predicted acid phosphatase**	38.7	4	96.99	5way_CG_8_GENE_32	**acid phosphatase**	25.6		0	1.51
228	UBA_8524_GENE_213	**Hypothetical**	39.2	7	89.42	5way_CG_8_GENE_33	**hypo unique**	9.5		1	4.13
229	UBA_8524_GENE_214	**Cysteinyl-tRNA synthetase**	48.2	50	93.27	5way_CG_8_GENE_34	**cytsteinyl tRNA synthetase**	16.3		0	2.96
230	UBA_8524_GENE_215	**rRNA methylases**	64.1	5	95.83	5way_CG_8_GENE_35	**tRNA/rRNA methyltransferase**	13.5		0	4.75
231	UBA_8524_GENE_216	**Thiol-disulfide isomerase and thioredoxins**	55.6	49	85.98	5way_CG_8_GENE_36	**thiol disulfide isomerae**	25.2		1	2.21
232	UBA_8524_GENE_217	**NAD synthase**	37.7	8	98.14	5way_CG_8_GENE_37	**l(3)-dependent NAD+ synthetase**	30.9		1	1.22
233	UBA_8524_GENE_218	**GTP cyclohydrolase II**	44.8	0	100.00	5way_CG_8_GENE_38	**GTP cyclohydrolase II**	44.8		0	1.00
234	UBA_8524_GENE_219	**Riboflavin synthase beta-chain**	63.4	21	97.52	5way_CG_8_GENE_39	**riboflavin synthase**	37.9		0	1.67
235	UBA_8524_GENE_220	**Transcription termination factor**	43.5	11	88.10	5way_CG_8_GENE_40	N utilization substance protein B	NO DATA	-		20.00
236	UBA_8524_GENE_221	Hypothetical	39.2	10	86.75	5way_CG_8_GENE_41	hypo unique	NO DATA	-		20.00
237	UBA_8524_GENE_222	**Adenylosuccinate lyase**	48.5	29	95.88	5way_CG_8_GENE_42	**adenylosuccinate lyase**	20.8		0	2.33
238	UBA_8524_GENE_223	**Phosphoribosylaminoimidazolesuccinocarboxami**	65.3	40	94.98	5way_CG_8_GENE_43	**e succinocarboxamide synthase**	40.6		0	1.61
239	UBA_8524_GENE_224	**Phosphoribosylformylglycinamidine (FGAM) synth**	87.8	44	92.86	5way_CG_8_GENE_44	rmylglycinamidine synthase, PurS	NO DATA	-		20.00
240	UBA_8524_GENE_225	**Hypothetical**	39.2	34	90.36	5way_CG_8_GENE_45	**hypo unique**	21.5		0	1.82
241	UBA_8524_GENE_226	**Asparaginase**	37.7	27	87.99	5way_CG_8_GENE_46	L-aspariginase	NO DATA	-		20.00
242	UBA_8524_GENE_227	**Acetate kinase**	25	7	88.50	5way_CG_8_GENE_47	**acetate kinase**	7.5		0	3.33
243	UBA_8524_GENE_228	SAM-dependent methyltransferases	NO DATA	-	88.39	5way_CG_8_GENE_48	ne biosynthesis methyltransferase	NO DATA	-	-	
244	UBA_8524_GENE_229	Hypothetical	NO DATA	-	94.59	5way_CG_8_GENE_49	ferrichrome-iron receptor	NO DATA	-	-	
245			NO GENE	-		5way_CG_8_GENE_50	TonB protein	NO DATA	-	-	
246			NO GENE	-		5way_CG_8_GENE_51	nB system transport protein, ExbD	NO DATA	-	-	
247			NO GENE	-		5way_CG_8_GENE_52	iopolymer transport protein, ExbB	NO DATA	-	-	
248	UBA_8524_GENE_230	ABC-type multidrug transport system, permease c	NO DATA	-	96.51	5way_CG_8_GENE_53	BC transporter, permease protein	NO DATA	-	-	
249	UBA_8524_GENE_231	ABC-type multidrug transport system, permease c	NO DATA	-	97.10	5way_CG_8_GENE_54	C transporter, ATP binding protein	NO DATA	-	-	
250	UBA_8524_GENE_232	ABC-type multidrug transport system, ATPase com	NO DATA	-	93.07	5way_CG_8_GENE_55	sporter, ATP binding protein, YbhF	NO DATA	-	-	
251	UBA_8524_GENE_233	**Membrane-fusion protein**	40.9	6	98.01	5way_CG_8_GENE_56	**HlyD family secretion protein**	28.2		0	1.45
252	UBA_8524_GENE_234	**Outer membrane protein**	47.4	47	91.93	5way_CG_8_GENE_57	**outer membrane efflux protein**	30.4		0	1.56
253	UBA_8524_GENE_235	**Cytochrome c551/c552**	73.6	31	93.64	5way_CG_8_GENE_58	**cytochrome c-551**	42.7		1	1.72
254	UBA_8524_GENE_236	**Phosphoketolase**	40	38	96.70	5way_CG_8_GENE_59	**phosphoketolase**	21.3		0	1.88
255	UBA_8524_GENE_237	**DhnA-type fructose-1,6-bisphosphate aldolase an**	83.9	64	94.75	5way_CG_8_GENE_60	**fructose bisphophate aldolase**	58		0	1.45
256	UBA_8524_GENE_238	**Pyruvate/2-oxoglutarate dehydrogenase comple**	54.8	75	91.50	5way_CG_8_GENE_61	**ihydrolipoamide dehydrogenase**	18		0	3.04
257	UBA_8524_GENE_239	**Hypothetical**	78.9	65	88.78	5way_CG_8_GENE_62	e diphosphate sugar epimerase)	4.6		0	17.15
258	UBA_8524_GENE_240	**Glucan phosphorylase**	22.5	15	92.69	5way_CG_8_GENE_63	maltodextrin phosphorylase	3.5		0	6.43
259	UBA_8524_GENE_241	**Phosphoglucomutase**	49.2	59	90.66	5way_CG_8_GENE_64	**phosphoglucomutase**	19.4		1	2.54
260	UBA_8524_GENE_242	Transposase and inactivated derivatives	NO DATA	-	69.94	5way_CG_8_GENE_65	transposase	NO DATA	-	-	
261	UBA_8524_GENE_244	**Cbb3-type cytochrome oxidase, subunit 1**	11.3	0	99.35	5way_CG_8_GENE_66	**chrome oxidase, subunit I/CcoN**	11.3		0	1.00
262	UBA_8524_GENE_245	77 Permeases of the major facilitator superfamily	NO DATA	-	88.28	5way_CG_8_GENE_67	drug resistance transporter	NO DATA	-	-	
263			NO GENE	-		5way_CG_8_GENE_68	hypo unique	NO DATA	-	-	
264	UBA_8524_GENE_246	**ATPase components of ABC transporters with dupli**	64.5	46	97.12	5way_CG_8_GENE_69	**C transporter, ATP binding subunit**	38.2		1	1.69
265	UBA_8524_GENE_247	**conserved hypothetical protein [Dechloromonas c**	86.3	37	94.74	5way_CG_8_GENE_70	**c hypo**	89.5		0	0.96
266	UBA_8524_GENE_248	**conserved hypothetical protein [Nitrosococcus oc**	64.4	112	90.84	5way_CG_141_GENE_2	**c hypo**	33.3		1	1.93
267	UBA_8524_GENE_249	**Outer membrane protein and related peptidoglyc**	87.9	66	97.36	5way_CG_141_GENE_3	**outer membrane protein OmpA)**	77.4		0	1.14
268	UBA_8524_GENE_250	SAM-dependent methyltransferases	NO DATA	-	90.75	5way_CG_141_GENE_5	c hypo	NO DATA	-	-	
269	UBA_8524_GENE_251	**predicted calcineurin-like phosphoesterase [Azoa**	40.2	5	92.43	5way_CG_141_GENE_6	c hypo	NO DATA	-		20.00
270	UBA_8524_GENE_252	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
271	UBA_8524_GENE_252a		NO DATA	-				NO GENE	-	-	
272			NO GENE	-		5way_CG_141_GENE_7	c hypo	NO DATA	-	-	
273			NO GENE	-		5way_CG_141_GENE_8	DNA repair exonuclease	NO DATA	-	-	
274			NO GENE	-		5way_CG_141_GENE_10	c hypo	NO DATA	-	-	
275			NO GENE	-		5way_CG_141_GENE_11	c hypo	NO DATA	-	-	
276			NO GENE	-		5way_CG_141_GENE_12	c hypo	NO DATA	-	-	
277			NO GENE	-		5way_CG_141_GENE_13	c hypo	NO DATA	-	-	
278			NO GENE	-		5way_CG_141_GENE_14	serine protease	NO DATA	-	-	
279			NO GENE	-		5way_CG_141_GENE_15	hypo unique	NO DATA	-	-	
280	UBA_8524_GENE_253	hypothetical protein [Bacillus sp. JF8]	NO DATA	-				NO GENE	-	-	
281	UBA_8524_GENE_254	Hypothetical	NO DATA	-				NO GENE	-	-	
282	UBA_8524_GENE_255	Hypothetical	NO DATA	-				NO GENE	-	-	
283			NO GENE	-		5way_CG_69_GENE_29	hypo unique	NO DATA	-	-	
284			NO GENE	-		5way_CG_69_GENE_28	hypo unique	NO DATA	-	-	

285			NO GENE	-		5way_CG_69_GENE_27	transposase	NO DATA	-	-	
286			NO GENE	-		5way_CG_69_GENE_26	hypo unique	NO DATA	-	-	
287	UBA_8524_GENE_256	Hypothetical	NO DATA	-	93.57	5way_CG_69_GENE_25	hypo unique	NO DATA	-	-	
288			NO GENE	-		5way_CG_69_GENE_24	c hypo	NO DATA	-	-	
289			NO GENE	-		5way_CG_69_GENE_21	c hypo	NO DATA	-	-	
290			NO GENE	-		5way_CG_69_GENE_20	transposase	NO DATA	-	-	
291			NO GENE	-		5way_CG_69_GENE_19	transposase	NO DATA	-	-	
292	UBA_8524_GENE_257	hypothetical protein [Nitrosomonas europaea ATC	NO DATA	-	87.67	5way_CG_69_GENE_18	c hypo	NO DATA	-	-	
293			NO GENE	-		5way_CG_69_GENE_17	hypo unique	NO DATA	-	-	
294			NO GENE	-		5way_CG_69_GENE_15	c hypo	NO DATA	-	-	
295			NO GENE	-		5way_CG_69_GENE_14	c hypo	NO DATA	-	-	
296			NO GENE	-		5way_CG_69_GENE_13	universal stress protein	NO DATA	-	-	
297			NO GENE	-		5way_CG_69_GENE_12	sulfate permease	NO DATA	-	-	
298			NO GENE	-		5way_CG_69_GENE_11	hypo unique	NO DATA	-	-	
299			NO GENE	-		5way_CG_69_GENE_10	c hypo	NO DATA	-	-	
300			NO GENE	-		5way_CG_69_GENE_9	transposase	NO DATA	-	-	
301			NO GENE	-		5way_CG_69_GENE_8	restriction endonuclease	NO DATA	-	-	
302			NO GENE	-		5way_CG_69_GENE_7	RNA helicase	NO DATA	-	-	
303			NO GENE	-		5way_CG_69_GENE_6	DeaD/DeaH box helicase	NO DATA	-	-	
304			NO GENE	-		5way_CG_69_GENE_5	hypo unique	NO DATA	-	-	
305			NO GENE	-		5way_CG_69_GENE_4	transposase	NO DATA	-	-	
306			NO GENE	-		5way_CG_69_GENE_3	hypo unique	NO DATA	-	-	
307			NO GENE	-		5way_CG_69_GENE_2	c hypo	NO DATA	-	-	
308			NO GENE	-		5way_CG_69_GENE_1	Superfamily II DNA/RNA helicases	NO DATA	-	-	
309			NO GENE	-		Unass_bact_scaffold_449	ction enzyme, methylase subunit	NO DATA	-	-	
310	UBA_8524_GENE_258	**Integrase**	43.1	-				NO GENE	-	-	
311	UBA_8524_GENE_258a		20.2	2				NO GENE	-		35.00
312	UBA_8524_GENE_259	Hypothetical	NO DATA	-				NO GENE	-	-	
313	UBA_8524_GENE_260	3-oxoacyl-(acyl carrier protein) synthase [Vibrio sp	NO DATA	-				NO GENE	-	-	
314	UBA_8524_GENE_261	Hypothetical	NO DATA	-				NO GENE	-	-	
315			NO GENE	-		5way_CG_869_GENE_5	hypo unique	NO DATA	-	-	
316			NO GENE	-		5way_CG_869_GENE_4	hypo unique	NO DATA	-	-	
317	UBA_8524_GENE_262	Hypothetical	NO DATA	-	92.78	5way_CG_869_GENE_2	hypo unique	NO DATA	-	-	
318			NO GENE	-		5way_CG_869_GENE_1	c hypo	NO DATA	-	-	
319	UBA_8524_GENE_263	**Transposase and inactivated derivatives**	9.1	-				NO GENE	-	-	
320	UBA_8524_GENE_264	Hypothetical	NO DATA	-				NO GENE	-	-	
321	UBA_8524_GENE_265	Putative secretion activating protein	NO DATA	-				NO GENE	-	-	
322	UBA_8524_GENE_266	Hypothetical	NO DATA	-				NO DATA	-	-	
323		TRNA Arg CCT 252819..252895 (-)		-					-		
324	UBA_8524_GENE_267	Hypothetical	NO DATA	-	96.43	5way_CG_167_GENE_11	hypo unique	NO DATA	-	-	
325	UBA_8524_GENE_268	**N-acetylmuramoyl-L-alanine amidase**	11.5	-	97.13	5way_CG_167_GENE_10	N-acetyl amidase	10.1	-	-	
326	UBA_8524_GENE_269	**Hypothetical**	46.8	-	90.06	5way_CG_167_GENE_10	**N-acetyl amidase**	10.1	-	-	
327	UBA_8524_GENE_270	**Uncharacterized conserved protein**	28	9	86.36	5way_CG_167_GENE_8	c hypo	NO DATA	-		20.00
328	UBA_8524_GENE_271	**Hypothetical**	67.3	97	91.46	5way_CG_167_GENE_7	**ain amino acid transport protein**	20.3		0	3.32
329	UBA_8524_GENE_272	Zn-dependent proteases	NO DATA	-	99.59	5way_CG_167_GENE_6	Zn-dependant protease	NO DATA	-	-	
330	UBA_8524_GENE_273	**Tryptophanyl-tRNA synthetase**	27.9	6	94.93	5way_CG_167_GENE_5	**tryptophanyl tRNA synthetase**	18		0	1.55
331	UBA_8524_GENE_274	**Acetyl-CoA carboxylase alpha subunit**	46.3	15	96.62	5way_CG_167_GENE_4	**arboxyl transferase alpha subunit**	20.3		0	2.28
332	UBA_8524_GENE_275	**DNA polymerase III, alpha subunit**	11.1	5	97.17	5way_CG_167_GENE_3	DNA polymerase III alpha subunit	3.4		0	3.26
333	UBA_8524_GENE_276	**Superfamily I DNA and RNA helicases**	19.4	4	96.92	5way_CG_167_GENE_2	**DNA helicase**	14.8		0	1.31

	8062										
1	UBA_8062_GENE_1	Uncharacterized membrane protein	NO DATA	-	97.91	5way_CG_76_GENE_22	membrane protein	NO DATA	-	-	
2	UBA_8062_GENE_2	**Ferredoxin**	73.2	20	97.32	5way_CG_76_GENE_21	**ferredoxin**	42.9		0	1.71
3	UBA_8062_GENE_3	**Homoserine kinase**	48.9	35	92.15	5way_CG_76_GENE_20	**homoserine kinase**	23		1	2.13
4	UBA_8062_GENE_4	**Dihydroorotate dehydrogenase**	67.9	17	98.10	5way_CG_76_GENE_19	**dihydroorotase dehydrogenase**	45.7		0	1.49
5	UBA_8062_GENE_5	**hypothetical protein BlinB01000018 [Brevibacteri**	46.6	8	96.81	5way_CG_76_GENE_18	**suspect proteosome component**	35.5		0	1.31
6	UBA_8062_GENE_6	**Hypothetical**	74.1	37	92.03	5way_CG_76_GENE_17	**proteosome, alpha subunit**	27.5		0	2.69
7	UBA_8062_GENE_7	**20S proteasome, alpha and beta subunits**	37.7	3	95.47	5way_CG_76_GENE_16	**proteosome, beta subunit**	18.9		0	1.99
8	UBA_8062_GENE_8	Hypothetical	NO DATA	-	87.50	5way_CG_76_GENE_15	hypo unique	NO DATA	-	-	
9	UBA_8062_GENE_9	**putative proteasome component [Thermobifida fu**	36.6	17	94.72	5way_CG_76_GENE_14	**suspect proteosome component**	17		0	2.15
10	UBA_8062_GENE_10	**ATPases of the AAA+ class**	36.3	19	96.00	5way_CG_76_GENE_13	**AAA-type ATPase**	18.8		0	1.93
11	UBA_8062_GENE_11	**Deoxycytidine deaminase**	35	12	97.54	5way_CG_76_GENE_12	**cytidine triphosphate deaminase**	12		0	2.92
12	UBA_8062_GENE_12	**Nitroreductase**	47.4	6	98.39	5way_CG_76_GENE_11	**nitroreductase**	38.6		0	1.23
13	UBA_8062_GENE_13	**Lysine 2,3-aminomutase**	30	3	97.13	5way_CG_76_GENE_10	**lysine 2,3-aminomutase**	17		0	1.76
14	UBA_8062_GENE_14	Hypothetical	NO DATA	-	93.40	5way_CG_76_GENE_9	c hypo	NO DATA	-	-	
15	UBA_8062_GENE_15a		NO DATA	-	99.26	5way_CG_76_GENE_8	rotein/ABC-type transport system	NO DATA	-	-	
16	UBA_8062_GENE_16	**Glutamyl-tRNA reductase**	15.9	4	97.13	5way_CG_76_GENE_7	**glutamyl-tRNA reductase**	8.6		0	1.85
17	UBA_8062_GENE_17	**Porphobilinogen deaminase**	72	63	95.48	5way_CG_76_GENE_6	**porphobilinogen deaminase**	27.7		0	2.60
18	UBA_8062_GENE_18	**Uroporphyrinogen-III methylase**	58.1	54	92.25	5way_CG_76_GENE_5	**hyrinogen-III c-methyltransferase**	16		0	3.63
19	UBA_8062_GENE_19	**Delta-aminolevulinic acid dehydratase**	52.5	47	95.09	5way_CG_76_GENE_4	**aminolevulinic acid dehydratase**	24.8		1	2.12

20	UBA_8062_GENE_20	**FAD synthase**	54.5	19	95.30	5way_CG_76_GENE_3	**riboflavin kinase/FAD synthase**	26		0	2.10
21	UBA_8062_GENE_21a		5.4	2	87.10	5way_CG_76_GENE_2	ATPase, cell cycle protein MesJ	NO DATA	-		20.00
22	UBA_8062_GENE_22	**Hypoxanthine-guanine phosphoribosyltrans**	75.6	6	97.73	5way_CG_76_GENE_1	**uanine phosphoribosyltransferase**	49.4		0	1.53
23	UBA_8062_GENE_23	**ATP-dependent Zn proteases**	75.1	12	99.50	5way_CG_98_GENE_1	**division protein/metalloprotease**	71.3		0	1.05
24	UBA_8062_GENE_24	**Dihydropteroate synthase and related enz**	57.6	14	90.11	5way_CG_98_GENE_2	dihydropteroate synthase	NO DATA	-		20.00
25	UBA_8062_GENE_25	**Uncharacterized conserved protein**	8.9	1	98.29	5way_CG_98_GENE_3	**c hypo**	8.9		1	1.00
26	UBA_8062_GENE_26	**Hypothetical**	32.3	4	94.47	5way_CG_98_GENE_4	**hypo**	20.4		0	1.58
27		TRNA Asn GTT 28401..28476 (+)	-						-		
28	UBA_8062_GENE_27	Putative ammonia monooxygenase	NO DATA	-	92.19	5way_CG_98_GENE_6	ty to ammonia monooxygenase)	NO DATA	-	-	
29	UBA_8062_GENE_28	**Amidases related to nicotinamidase**	35.1	7	91.49	5way_CG_98_GENE_7	isochorismatase	NO DATA	-		20.00
30	UBA_8062_GENE_29	Transcriptional regulator	NO DATA	-	88.13	5way_CG_98_GENE_8	transcriptional regulator	NO DATA	-	-	
31	UBA_8062_GENE_30	NhaP-type Na+/H+ and K+/H+ antiporters	NO DATA	-	93.83	5way_CG_98_GENE_9	Na+/H+ antiporter	NO DATA	-	-	
32	UBA_8062_GENE_31	**Hypothetical**	50	47	94.86	5way_CG_98_GENE_10	**hypo unique**	32.7		0	1.53
33	UBA_8062_GENE_32	**Hypothetical**	57.8	71	93.52	5way_CG_98_GENE_11	**hypo unique**	32.9		0	1.76
34	UBA_8062_GENE_34	**Hypothetical**	67.1	96	98.75	5way_CG_98_GENE_12	**hypo unique**	48.3		0	1.39
35	UBA_8062_GENE_35	**Predicted membrane protein**	11.1	3	91.35	5way_CG_98_GENE_13	**c hypo**	5.3		0	2.09
36	UBA_8062_GENE_36	Hypothetical	NO DATA	-	91.18	5way_CG_98_GENE_14	c hypo	NO DATA	-	-	
37	UBA_8062_GENE_37	**Multidrug resistance efflux pump**	22.4	3	93.65	5way_CG_98_GENE_15	**HlyD family secretion protein**	11		0	2.04
38	UBA_8062_GENE_38	**Hypothetical, LLNL: in complex 200 kda+, poss with**	49.3	67	93.21	5way_CG_98_GENE_16	**hypo unique**	25		0	1.97
39	UBA_8062_GENE_40	Deoxyribodipyrimidine photolyase	NO DATA	-	83.21	5way_CG_98_GENE_17	eoxyribodipyrimidine photolyase	NO DATA	-	-	
40	UBA_8062_GENE_41	Kef-type K+ transport systems, check ORF??	11.7	-	95.00	5way_CG_98_GENE_18	ith above?? K+ channel protein	NO DATA	-	-	
41	UBA_8062_GENE_43	**Pirin-related protein**	41.7	10	91.33	5way_CG_98_GENE_19	**pirin-related protein**	15.6		0	2.67
42	UBA_8062_GENE_44	**Hypothetical**	57	-	85.29	5way_CG_219_GENE_6		12.7	-	-	
43		TRNA Gly GCC 45239..45313 (+)	-						-		
44			NO GENE	-		5way_CG_219_GENE_7	integrase	NO DATA	-	-	
45			NO GENE	-		5way_CG_219_GENE_8	hypo unique	NO DATA	-	-	
46			NO GENE	-		5way_CG_219_GENE_9	hypo unique	NO DATA	-	-	
47			NO GENE	-		5way_CG_219_GENE_10	hypo unique	NO DATA	-	-	
48			NO GENE	-		5way_CG_219_GENE_12	hypo unique	NO DATA	-	-	
49			NO GENE	-		5way_CG_219_GENE_13	**hypo unique**	16		2	0.03
50			NO GENE	-		5way_CG_219_GENE_14	c hypo	NO DATA	-	-	
51			NO GENE	-		5way_CG_219_GENE_15	mobilization protein, MobD	NO DATA	-	-	
52			NO GENE	-		5way_CG_219_GENE_16	mobilization protein, MobE	NO DATA	-	-	
53			NO GENE	-		5way_CG_219_GENE_17	hypo unique	NO DATA	-	-	
54			NO GENE	-		5way_CG_219_GENE_18	mobilization protein, TraA	NO DATA	-	-	
55	UBA_8062_GENE_45	**Hypothetical**	10.8	2				NO GENE	-		35.00
56	UBA_8062_GENE_46	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
57	UBA_8062_GENE_47	**Transposase and inactivated derivatives**	25.5	-				NO GENE	-	-	
58	UBA_8062_GENE_48	Predicted transcriptional regulators	NO DATA	-				NO GENE	-	-	
59	UBA_8062_GENE_49	Co/Zn/Cd efflux system component	NO DATA	-				NO GENE	-	-	
60	UBA_8062_GENE_49a		NO DATA	-				NO GENE	-	-	
61	UBA_8062_GENE_50	Hypothetical	NO DATA	-				NO GENE	-	-	
62	UBA_8062_GENE_51	**Hypothetical**	50.3	44				NO GENE	-		35.00
63	UBA_8062_GENE_53	**Hypothetical**	46.5	98				NO GENE	-		35.00
64	UBA_8062_GENE_54	conserved hypothetical protein [Bradyrhizobium s	NO DATA	-				NO GENE	-	-	
65	UBA_8062_GENE_55	Hypothetical	NO DATA	-				NO GENE	-	-	
66	UBA_8062_GENE_56	Cation transport ATPase	NO DATA	-	100.00	5way_CG_768_GENE_1	Cation transport ATPases	NO DATA	-	-	
67	UBA_8062_GENE_57	HD-GYP domain	NO DATA	-	100.00	5way_CG_768_GENE_3	Response regulator containing a	NO DATA	-	-	
68	UBA_8062_GENE_58	**Hypothetical**	69.1	0	100.00	5way_CG_768_GENE_4	Hypothetical	69.1		0	1.00
69	UBA_8062_GENE_59	Uncharacterized conserved protein	NO DATA	-	100.00	5way_CG_768_GENE_5	Uncharacterized BCR	NO DATA	-	-	
70	UBA_8062_GENE_60	**Transposase and inactivated derivatives**	36.5	-	100.00	5way_CG_6_GENE_1		34.7	-	-	
71	UBA_8062_GENE_61	Transposase and inactivated derivatives	NO DATA	-		2.78		NO GENE	-	-	
72	UBA_8062_GENE_62	**conserved hypothetical protein [Chlorobium phae**	78	26	93.00	5way_CG_219_GENE_3	**hypo**	24		0	3.25
73	UBA_8062_GENE_63	**Hypothetical**	72.6	61	90.41	5way_CG_219_GENE_4	c hypo	NO DATA	-		20.00
74	UBA_8062_GENE_64	Integrase	NO DATA	-	91.86	5way_CG_219_GENE_5	integrase frag.(Rci type)	NO DATA	-	-	
75	UBA_8062_GENE_65	**Integrase**	37.1	-				NO GENE	-	-	
76	UBA_8062_GENE_66	Uncharacterized conserved protein	NO DATA	-				NO GENE	-	-	
77			NO GENE	-		5way_CG_637_GENE_4	hypo unique	NO DATA	-	-	
78			NO GENE	-		5way_CG_637_GENE_3	conjugal transfer protein TraA	NO DATA	-	-	
79			NO GENE	-		5way_CG_637_GENE_2	hypo unique	NO DATA	-	-	
80			NO GENE	-		5way_CG_637_GENE_1	hypo unique	NO DATA	-	-	
81			NO GENE	-		5way_CG_81_GENE_25		NO DATA	-	-	
82			NO GENE	-		5way_CG_81_GENE_26		NO DATA	-	-	
83			NO GENE	-		5way_CG_81_GENE_27		8.2		0	0.03
84	UBA_8062_GENE_67	ATP-dependent exoDNAse (exonuclease V),	NO DATA	-	100.00	5way_CG_829_GENE_6	TraC	NO DATA	-	-	
85	UBA_8062_GENE_68	**Type IV secretory pathway, VirD4 compone**	31.4	-	100.00	5way_CG_829_GENE_4	gene with above hypo unique	NO DATA	-	-	
86	UBA_8062_GENE_69	Hypothetical	NO DATA	-	100.00	5way_CG_829_GENE_3	hypo unique	NO DATA	-	-	
87	UBA_8062_GENE_70	Hypothetical	NO DATA	-	100.00	5way_CG_232_GENE_14	hypo unique	NO DATA	-	-	
88	UBA_8062_GENE_71	**Hypothetical**	13	0	100.00	5way_CG_232_GENE_13	**mobilization protein MobE**	13		0	1.00
89			NO GENE	-		5way_CG_232_GENE_12	c hypo	NO DATA	-	-	
90			NO GENE	-		5way_CG_232_GENE_11	transposase	NO DATA	-	-	
91	UBA_8062_GENE_72	**MobD mobilisation protein [Pseudomonas aerugin**	85.6	189				NO GENE	-		35.00

92	UBA_8062_GENE_73	Hypothetical	NO DATA	-				NO GENE	-		-
93	UBA_8062_GENE_74	Hypothetical	NO DATA	-				NO GENE	-		-
94	UBA_8062_GENE_75	Hypothetical	NO DATA	-				NO GENE	-		-
95	UBA_8062_GENE_76	**Uncharacterized protein conserved in bac**	21.4	7	94.90	5way_CG_232_GENE_9	**c hypo**	32.7		2	0.65
96	UBA_8062_GENE_77	Predicted transcriptional regulator	NO DATA	-	100.00	5way_CG_232_GENE_8	c hypo	NO DATA	-		-
97	UBA_8062_GENE_78	**Hypothetical**	53.1	28				NO GENE	-		35.00
98	UBA_8062_GENE_79	**Hypothetical**	16.2	4				NO GENE	-		35.00
99			NO GENE	-		5way_CG_232_GENE_6a		NO DATA	-		-
100			NO GENE	-		5way_CG_232_GENE_6	hypo unique	NO DATA	-		-
101			NO GENE	-		5way_CG_232_GENE_5	hypo unique	NO DATA	-		-
102			NO GENE	-		5way_CG_232_GENE_4	**ABC transporter ATP-binding**	12.1		4	0.03
103			NO GENE	-		5way_CG_232_GENE_3	hypo unique	NO DATA	-		-
104			NO GENE	-		5way_CG_232_GENE_2	c hypo	NO DATA	-		-
105			NO GENE	-		5way_CG_232_GENE_1	C transporter ATP-binding protein	NO DATA	-		-
106	UBA_8062_GENE_81	Transposase and inactivated derivatives,	NO DATA	-				NO GENE	-		-
107	UBA_8062_GENE_82	**Transposase and inactivated derivatives,**	34.2	-				NO GENE	-		-
108	UBA_8062_GENE_83	Predicted P-loop ATPase and inactivated	NO DATA	-				NO GENE	-		-
109	UBA_8062_GENE_84	**Hypothetical**	17.5	4				NO GENE	-		35.00
110	UBA_8062_GENE_85	hypothetical protein [Bacteroides fragilis]	NO DATA	-				NO GENE	-		-
111	UBA_8062_GENE_86	transposase [Klebsiella pneumoniae]	NO DATA	-				NO GENE	-		-
112	UBA_8062_GENE_87	Transposase, IS4 [Thermoanaerobacter ethanolicu	NO DATA	-				NO GENE	-		-
113	UBA_8062_GENE_88	Transposase, IS4 [Thermoanaerobacter ethanolicu	NO DATA	-				NO GENE	-		-
114	UBA_8062_GENE_89	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-		-
115	UBA_8062_GENE_90	**Transposase**	25	-				NO GENE	-		-
116	UBA_8062_GENE_91	**Outer membrane protein [Hahella chejuensis KCT(**	10.2	4				NO GENE	-		35.00
117	UBA_8062_GENE_92	Membrane-fusion protein	NO DATA	-				NO GENE	-		-
118	UBA_8062_GENE_93	**Putative silver efflux pump**	4.5	0				NO GENE	-		35.00
119	UBA_8062_GENE_94	**hypothetical protein BproDRAFT_0958 [Polaromonc**	22.2	4				NO GENE	-		35.00
120	UBA_8062_GENE_95	Hypothetical	NO DATA	-				NO GENE	-		-
121	UBA_8062_GENE_96	Hypothetical	NO DATA	-				NO GENE	-		-
122	UBA_8062_GENE_97	Cation transport ATPase	NO DATA	-				NO GENE	-		-
123	UBA_8062_GENE_98	Hypothetical	NO DATA	-				NO GENE	-		-
124	UBA_8062_GENE_99	Predicted transcriptional regulators	NO DATA	-				NO GENE	-		-
125	UBA_8062_GENE_100	Cation transport ATPase	NO DATA	-				NO GENE	-		-
126	UBA_8062_GENE_101	Tetrahydromethanopterin S-methyltransfer	NO DATA	-				NO GENE	-		-
127	UBA_8062_GENE_101a		NO DATA	-				NO GENE	-		-
128	UBA_8062_GENE_102	Rhodopirellula transposase [Chlorobium phaeoba	NO DATA	-				NO GENE	-		-
129	UBA_8062_GENE_103a		NO DATA	-				NO GENE	-		-
130	UBA_8062_GENE_104	Hypothetical	NO DATA	-				NO GENE	-		-
131	UBA_8062_GENE_105	Zn-dependent hydrolases, including glyox	NO DATA	-				NO GENE	-		-
132	UBA_8062_GENE_106a		NO DATA	-				NO GENE	-		-
133	UBA_8062_GENE_107	77 Permeases of the major facilitator su	NO DATA	-				NO GENE	-		-
134	UBA_8062_GENE_108	Hypothetical	NO DATA	-				NO GENE	-		-
135	UBA_8062_GENE_109	Phage integrase [Pelobacter propionicus DSM 237	NO DATA	-				NO GENE	-		-
136	UBA_8062_GENE_110	Uncharacterized conserved protein	NO DATA	-				NO GENE	-		-
137	UBA_8062_GENE_111	DNA-damage-inducible protein J	NO DATA	-				NO GENE	-		-
138	UBA_8062_GENE_112	Uncharacterized protein conserved in bac	NO DATA	-				NO GENE	-		-
139			NO GENE	-		5way_CG_51_GENE_27	hypo unique	NO DATA	-		-
140	UBA_8062_GENE_113	**hypothetical protein [Magnetospirillum magneticu**	68.1	78	76.89	5way_CG_51_GENE_26	c hypo	NO DATA	-		20.00
141	UBA_8062_GENE_114	**Outer membrane receptor for Fe3+-dicitra**	12	5	98.25	5way_CG_51_GENE_24	**ron(III) dicitrate transport protein)**	3		0	4.00
142	UBA_8062_GENE_115	Biopolymer transport proteins	NO DATA	-	97.86	5way_CG_51_GENE_23	biopolymer export protein, ExbB	NO DATA	-		-
143	UBA_8062_GENE_116	Biopolymer transport protein	NO DATA	-	97.84	5way_CG_51_GENE_22	nB system transport protein, ExbD	NO DATA	-		-
144	UBA_8062_GENE_117	Hypothetical	NO DATA	-	92.59	5way_CG_51_GENE_21	TonB	NO DATA	-		-
145	UBA_8062_GENE_118	Hypothetical	NO DATA	-	86.13	5way_CG_51_GENE_20	hypo unique	NO DATA	-		-
146	UBA_8062_GENE_119	Response regulators consisting of a Che	NO DATA	-	100.00	5way_CG_51_GENE_19	egulator/transcriptional regulator	NO DATA	-		-
147	UBA_8062_GENE_120	Uncharacterized conserved protein	NO DATA	-	100.00	5way_CG_51_GENE_18	c hypo	NO DATA	-		-
148	UBA_8062_GENE_121	**ATP-dependent exoDNAse (exonuclease V),**	6.6	2	99.65	5way_CG_51_GENE_17	oxyribonuclease V, alpha subunit	4.7		0	1.40
149	UBA_8062_GENE_122	**ATP-dependent exoDNAse (exonuclease V) b**	NO DATA	-	99.91	5way_CG_51_GENE_16	**eoxyribonuclease V, beta subunit**	NO DATA	-		-
150	UBA_8062_GENE_123	**Exonuclease V gamma subunit**	6.5	0	100.00	5way_CG_51_GENE_15	**uclease V, gamma subunit/RecC**	6.5		0	1.00
151	UBA_8062_GENE_124	**Zn-dependent alcohol dehydrogenases**	37.7	0	100.00	5way_CG_51_GENE_14	**pendent alcohol dehydrogenase**	37.7		0	1.00
152	UBA_8062_GENE_125	**Transcriptional regulators**	72.9	0	100.00	5way_CG_51_GENE_13	**tibiotic resistance MarR regulator**	72.9		0	1.00
153	UBA_8062_GENE_125a		NO DATA	-	100.00	5way_CG_51_GENE_12	hypo unique	NO DATA	-		-
154	UBA_8062_GENE_126	Outer membrane protein	NO DATA	-	100.00	5way_CG_51_GENE_11	outer membrane efflux protein	NO DATA	-		-
155	UBA_8062_GENE_127	**Cation/multidrug efflux pump**	NO DATA	-	99.23	5way_CG_51_GENE_10	multidrug efflux transporter	NO DATA	-		-
156	UBA_8062_GENE_128	**Membrane-fusion protein**	8.6	2	91.95	5way_CG_51_GENE_9	multidrug efflux transporter	NO DATA	-		20.00
157	UBA_8062_GENE_129	**Hypothetical**	12.4	4	85.09	5way_CG_51_GENE_8	hypo unique	NO DATA	-		20.00
158	UBA_8062_GENE_130	Uncharacterized membrane-anchored protei	NO DATA	-	86.26	5way_CG_51_GENE_7	c hypo	NO DATA	-		-
159	UBA_8062_GENE_131	FOG: GAF domain	31.4	7	93.48	5way_CG_14_GENE_2	**GDEF domain/EAL domain protein**	7.1		0	4.42
160		TRNA Lys CTT 136136..136211 (-)	-						-		
161	UBA_8062_GENE_132	NADH:ubiquinone oxidoreductase, NADH-bin	52	17	96.01	5way_CG_14_GENE_3	subunit C/NADH dehydrogenase	35.5		0	1.46
162			NO GENE	-		5way_CG_51_GENE_4	transposase	NO DATA	-		-
163			NO GENE	-		5way_CG_51_GENE_2	c hypo	NO DATA	-		-

164			NO GENE	-		5way_CG_51_GENE_1		hypo unique	NO DATA	-	-	
165	UBA_8062_GENE_133	**Hypothetical**	40.1	2	90.82	5way_CG_14_GENE_4		**hypo unique**	30		0	1.34
166	UBA_8062_GENE_134	Hypothetical	NO DATA	-	89.13	5way_CG_14_GENE_5		hypo unique	NO DATA	-	-	
167	UBA_8062_GENE_135	Adenine specific DNA methylase Mod	NO DATA	-	94.01	5way_CG_14_GENE_6		n modification system methylase	NO DATA	-	-	
168	UBA_8062_GENE_136	Predicted membrane metal-binding protein	NO DATA	-	88.38	5way_CG_14_GENE_7		competence factor ComA	NO DATA	-	-	
169	UBA_8062_GENE_137	**Phosphomannomutase CHECK ORFS**	46.8	10	98.68	5way_CG_14_GENE_8		**phosphoglucosamine mutase**	38.9		1	1.20
170	UBA_8062_GENE_137a		36.5	0	98.74	5way_CG_14_GENE_10		and 2 up transcriptional regulator	36.5		0	1.00
171	UBA_8062_GENE_138	**NADH:flavin oxidoreductases, Old Yellow**	85.8	59	98.09	5way_CG_14_GENE_11		**NADH:flavin oxidoreductase**	57.5		1	1.49
172	UBA_8062_GENE_139	Hypothetical	NO DATA	-	94.86	5way_CG_14_GENE_12		hypo unique	NO DATA	-	-	
173	UBA_8062_GENE_140	Outer membrane protein and related pepti	NO DATA	-	94.63	5way_CG_14_GENE_13		idoglycan associated lipoprotein	NO DATA	-	-	
174	UBA_8062_GENE_141	conserved hypothetical protein [Pelobacter propi	NO DATA	-	95.20	5way_CG_14_GENE_14		c hypo	NO DATA	-	-	
175	UBA_8062_GENE_142	Hypothetical	NO DATA	-	83.33	5way_CG_14_GENE_15		c hypo	NO DATA	-	-	
176	UBA_8062_GENE_143	Predicted double-glycine peptidase	NO DATA	-	92.47	5way_CG_14_GENE_16		C transporter ATP-binding protein	NO DATA	-	-	
177	UBA_8062_GENE_144	Hypothetical	NO DATA	-	91.74	5way_CG_14_GENE_17		hypo unique	NO DATA	-	-	
178	UBA_8062_GENE_145	Hypothetical	NO DATA	-	97.62	5way_CG_14_GENE_18		c hypo	NO DATA	-	-	
179	UBA_8062_GENE_146	Response regulator containing CheY-like	NO DATA	-	93.30	5way_CG_14_GENE_19		**o component response regulator**	3.9		1	0.06
180	UBA_8062_GENE_147	**Cytochrome c, class I [Ralstonia metallidurans C**	100	0	98.92	5way_CG_14_GENE_20		**ermeases, cytochrome c) cty579**	87.7		2	1.14
181	UBA_8062_GENE_148	**Hypothetical**	59.6	0	100.00	5way_CG_14_GENE_22		**hypo unique**	59.6		0	1.00
182	UBA_8062_GENE_148a		NO DATA	-	92.92	5way_CG_14_GENE_23		hypo unique	NO DATA	-	-	
183	UBA_8062_GENE_149	**Enolase**	74.7	40	98.83	5way_CG_14_GENE_24		**enolase**	48.9		0	1.53
184	UBA_8062_GENE_150	cytochrome c, NapC/NirT family [Carboxydothern	NO DATA	-	96.99	5way_CG_14_GENE_25		cytochrome c nitrite reductase	NO DATA	-	-	
185	UBA_8062_GENE_151	**Hypothetical**	63.9	18	95.96	5way_CG_14_GENE_26		**hypo unique**	52		0	1.23
186	UBA_8062_GENE_152	**Asp-tRNAAsn/Glu-tRNAGln amidotransferase**	61.4	26	97.55	5way_CG_14_GENE_27		**myl tRNA (Gln) amidotransferase**	38.6		0	1.59
187	UBA_8062_GENE_153	**Asp-tRNAAsn/Glu-tRNAGln amidotransferase**	47.6	2	98.37	5way_CG_14_GENE_28		**glutamyl tRNA amidotransferase**	37.8		0	1.26
188	UBA_8062_GENE_154	**Aspartate 1-decarboxylase**	60.3	0	100.00	5way_CG_14_GENE_29		**aspartate decarboxylase**	60.3		0	1.00
189	UBA_8062_GENE_155	**Asp-tRNAAsn/Glu-tRNAGln amidotransferase**	30.3	0	94.95	5way_CG_14_GENE_30		**glutamyl-tRNA amidotransferase**	30.3		0	1.00
190	UBA_8062_GENE_156	**Superfamily I DNA and RNA helicases**	9.9	2	93.30	5way_CG_14_GENE_31		**ATP-dependent DNA helicase**	5.9		0	1.68
191	UBA_8062_GENE_157	**Hypothetical**	83.1	18	98.86	5way_CG_14_GENE_32		**hypo unique**	69.5		0	1.20
192	UBA_8062_GENE_158	**Glucosamine 6-phosphate synthetase, cont**	60.8	12	97.36	5way_CG_14_GENE_33		**e-6-phosphate aminotransferase**	38.7		0	1.57
193	UBA_8062_GENE_159	**N-acetylglucosamine-1-phosphate uridyltr**	47.3	15	97.44	5way_CG_14_GENE_34		**glucosamine pyrophosphorylase**	29.9		0	1.58
194	UBA_8062_GENE_160	**Uncharacterized conserved protein**	41	13	97.75	5way_CG_14_GENE_35		**transporter**	21.6		0	1.90
195	UBA_8062_GENE_161	Hypothetical	NO DATA	-	92.63	5way_CG_14_GENE_36		hypo unique	NO DATA	-	-	
196	UBA_8062_GENE_162	**Lactoylglutathione lyase and related lya**	82.2	49	91.78	5way_CG_14_GENE_37		**lactoylglutathione lyase**	15.8		1	5.20
197	UBA_8062_GENE_162a		90.5	34	91.07	5way_CG_14_GENE_38		**ator in arsenic resistance operon**	51.3		11	1.76
198	UBA_8062_GENE_163	Hypothetical	NO DATA	-	92.80	5way_CG_14_GENE_39		hypo unique	NO DATA	-	-	
199	UBA_8062_GENE_164	NAD-dependent protein deacetylases, SIR2	NO DATA	-	92.47	5way_CG_14_GENE_41		transcriptional regulator	NO DATA	-	-	
200	UBA_8062_GENE_165	**Lfe142p3 [Leptospirillum ferrooxidans]**	69.7	4	98.68	5way_CG_14_GENE_42		**similarity to glutamate synthase)**	55.3		0	1.26
201	UBA_8062_GENE_166	Predicted membrane protein	NO DATA	-	97.33	5way_CG_14_GENE_43		c hypo	NO DATA	-	-	
202	UBA_8062_GENE_167	Transcriptional regulators	NO DATA	-	92.95	5way_CG_14_GENE_44		transcriptional regulator MarR	NO DATA	-	-	
203	UBA_8062_GENE_168	Ribulose-5-phosphate 4-epimerase and rel	NO DATA	-	89.90	5way_CG_14_GENE_45		fuculose-1-phosphate aldolase	NO DATA	-	-	
204	UBA_8062_GENE_169	**Uncharacterized conserved protein, possi**	32.4	7	91.20	5way_CG_14_GENE_46		**methylthioribose phosphatase**	7.9		0	4.10
205	UBA_8062_GENE_170	**Ribulose 1,5-bisphosphate carboxylase, l**	28	13	90.98	5way_CG_14_GENE_47		RuBisCO	NO DATA	-		20.00
206	UBA_8062_GENE_171	**Uncharacterized conserved protein, conta**	45.2	6	94.62	5way_CG_14_GENE_48		**oxidase**	13.4		0	3.37
207	UBA_8062_GENE_172	**Peroxiredoxin**	54	16	99.00	5way_CG_14_GENE_49		**peroxiredoxin**	40.5		0	1.33
208	UBA_8062_GENE_173	**Cytochrome c peroxidase**	51.5	116	94.67	5way_CG_14_GENE_50		**cytochrome c peroxidase**	33.7		0	1.53
209	UBA_8062_GENE_174	Fe2+/Zn2+ uptake regulation proteins	NO DATA	-	92.26	5way_CG_14_GENE_51		transcriptional regulator	NO DATA	-	-	
210	UBA_8062_GENE_175	Hypothetical	NO DATA	-	100.00	5way_CG_14_GENE_52		hypo unique	NO DATA	-	-	
211	UBA_8062_GENE_176	**Thymidylate kinase**	62.3	62	88.18	5way_CG_14_GENE_53		**thymidylate kinase**	18.6		1	3.35
212	UBA_8062_GENE_177	**DNA polymerase III, gamma/tau subunits**	12	1	90.09	5way_CG_14_GENE_54		**DNA polymerase III**	9		0	1.33
213	UBA_8062_GENE_178	**Uncharacterized homolog of PSP1**	30	0	98.33	5way_CG_14_GENE_55		**signal peptidase II**	30		0	1.00
214	UBA_8062_GENE_179	**Methionyl-tRNA synthetase**	54.5	43	95.84	5way_CG_14_GENE_56		**methionyl tRNA synthetase**	35.2		1	1.55
215	UBA_8062_GENE_180	**Mg-dependent DNase**	20.9	10	91.25	5way_CG_14_GENE_57		DNase TatD	NO DATA	-		20.00
216	UBA_8062_GENE_181	**Hypothetical**	19.5	5	89.63	5way_CG_14_GENE_58		c hypo	NO DATA	-		20.00
217	UBA_8062_GENE_182	Hypothetical	NO DATA	-	94.38	5way_CG_14_GENE_59		c hypo	NO DATA	-	-	
218	UBA_8062_GENE_183	Amino acid transporters	NO DATA	-	97.90	5way_CG_14_GENE_60		amino acid permease	NO DATA	-	-	
219	UBA_8062_GENE_184	Hypothetical	NO DATA	-	60.93	5way_CG_14_GENE_61		glycoprotein	NO DATA	-	-	
220			NO GENE	-		5way_CG_14_GENE_62		hypo unique	NO DATA	-	-	
221			NO GENE	-		5way_CG_14_GENE_63		hypo unique	NO DATA	-	-	
222	UBA_8062_GENE_186	Hypothetical	NO DATA	-	89.14	5way_CG_14_GENE_64		hypo unique	NO DATA	-	-	
223	UBA_8062_GENE_187	Hypothetical	NO DATA	-	90.58	5way_CG_14_GENE_65		pili-associated adhesion protein	NO DATA	-	-	
224	UBA_8062_GENE_188	**Amino acid transporters**	12.5	7	99.07	5way_CG_14_GENE_66		**amino acid transporter**	8.1		0	1.54
225	UBA_8062_GENE_189	**NADH dehydrogenase, FAD-containing subun**	7.6	0	95.13	5way_CG_14_GENE_67		**ADH dehydrogenase FAD subunit**	7.5		0	1.01
226	UBA_8062_GENE_190	Purine-cytosine permease and related pro	NO DATA	-	89.52	5way_CG_14_GENE_68		cytosine permease	NO DATA	-	-	
227	UBA_8062_GENE_191	Hypothetical	NO DATA	-					NO GENE	-	-	
228	UBA_8062_GENE_192	**Hypothetical**	35.8	16	84.28	5way_CG_135_GENE_1		hypo unique	NO DATA	-		20.00
229	UBA_8062_GENE_193	**Predicted GTPases**	33	3	97.85	5way_CG_135_GENE_2		**GTP-binding protein**	30.5		0	1.08
230	UBA_8062_GENE_194	**Phosphoenolpyruvate synthase/pyruvate ph**	78.1	64	99.12	5way_CG_135_GENE_3		**phosphoenolpyruvate synthase**	70.7		0	1.10
231	UBA_8062_GENE_195	Transcriptional regulator containing PA	NO DATA	-	92.24	5way_CG_135_GENE_4		-type ATPase/response regulator	NO DATA	-	-	
232	UBA_8062_GENE_196	Hypothetical	NO DATA	-	84.54	5way_CG_135_GENE_5		hypo unique	NO DATA	-	-	
233	UBA_8062_GENE_197	**Acetylglutamate kinase**	29.7	8	94.20	5way_CG_135_GENE_6		**amino-acid acetyltransferase**	14.3		1	2.08
234	UBA_8062_GENE_198	**Methyl-accepting chemotaxis protein**	69.2	25	96.88	5way_CG_135_GENE_8		**yl-accepting chemotaxis protein**	51		0	1.36
235	UBA_8062_GENE_199	**SAM-dependent methyltransferases**	43.3	19	93.02	5way_CG_135_GENE_9		**eak (similar to methyltransferase)**	18.3		0	2.37

236	UBA_8062_GENE_200	**Short-chain alcohol dehydrogenase of unk**	19.4	6	93.03	5way_CG_135_GENE_10	**dehydrogenae/oxidoreductase**	10.5		0	1.85
237	UBA_8062_GENE_201	**Glucose-6-phosphate 1-dehydrogenase**	71.2	40	92.52	5way_CG_135_GENE_11	**se-6-phosphate dehydrogenase**	37		0	1.92
238	UBA_8062_GENE_202	**Predicted 6-phosphogluconate dehydrogena**	67	55	93.51	5way_CG_135_GENE_12	**osphogluconate dehydrogenase**	33.9		0	1.98
239	UBA_8062_GENE_203	Hypothetical	NO DATA	-				NO GENE	-	-	
240	UBA_8062_GENE_204	Hypothetical	NO DATA	-				NO GENE	-	-	
241	UBA_8062_GENE_205	Hypothetical	NO DATA	-				NO GENE	-	-	
242	UBA_8062_GENE_206	Hypothetical	NO DATA	-				NO GENE	-	-	
243	UBA_8062_GENE_207	Hypothetical	NO DATA	-				NO GENE	-	-	
244	UBA_8062_GENE_208	Hypothetical	NO DATA	-				NO GENE	-	-	
245	UBA_8062_GENE_209	Hypothetical	NO DATA	-				NO GENE	-	-	
246	UBA_8062_GENE_210	Predicted P-loop ATPase and inactivated	NO DATA	-				NO GENE	-	-	
247	UBA_8062_GENE_211	Hypothetical	NO DATA	-				NO GENE	-	-	
248	UBA_8062_GENE_212	Hypothetical	NO DATA	-				NO GENE	-	-	
249	UBA_8062_GENE_213	Hypothetical	NO DATA	-				NO GENE	-	-	
250	UBA_8062_GENE_214	Hypothetical	NO DATA	-				NO GENE	-	-	
251	UBA_8062_GENE_215	Predicted P-loop ATPase and inactivated	NO DATA	-				NO GENE	-	-	
252	UBA_8062_GENE_216	Hypothetical	NO DATA	-		ub scaffold 1114 : 3.18 kb		NO GENE	-	-	
253	UBA_8062_GENE_217	**Integrase**	41.8	-				NO GENE	-	-	
254			NO GENE	-		5way_CG_295_GENE_3	hypo unique	NO DATA	-	-	
255		TRNA Ala CGC 226925..227000 (-)	-						-		
256	UBA_8062_GENE_218	**Folate-dependent phosphoribosylglycinami**	60.4	0	93.69	5way_CG_295_GENE_4	**sylglycinamide formyltransferase**	18.4		0	3.28
257	UBA_8062_GENE_219	**Phosphoribosylaminoimidazole (AIR) synth**	47.7	7	94.29	5way_CG_295_GENE_5	**ormylglycinamidine cyclo-ligase**	18		0	2.65
258	UBA_8062_GENE_220	Hypothetical	NO DATA	-	77.97	5way_CG_295_GENE_6	cell wall surface anchor	NO DATA	-	-	
259	UBA_8062_GENE_221	hypothetical protein predicted by Glimmer/Critic	NO DATA	-	95.03	5way_CG_295_GENE_7	c hypo	NO DATA	-	-	
260	UBA_8062_GENE_222	**dsRNA-specific ribonuclease**	38.9	0	95.53	5way_CG_295_GENE_8	**ribonuclease III**	23.5		0	1.66
261	UBA_8062_GENE_223	**3-oxoacyl-(acyl-carrier-protein) syntha**	57.8	0	97.85	5way_CG_295_GENE_9	**cyl carrier protein synthase II fabF**	50.6		0	1.14
262	UBA_8062_GENE_224	**Acyl carrier protein**	47.4	0	100.00	5way_CG_295_GENE_10	**acyl-carrier protein**	47.4		0	1.00
263	UBA_8062_GENE_225	**8 Dehydrogenases with different specific**	64.5	0	96.81	5way_CG_27_GENE_1	**acyl carrier protein**	45		0	1.43
264	UBA_8062_GENE_226	**(acyl-carrier-protein) S-malonyltransfer**	72.3	0	95.22	5way_CG_27_GENE_2	**carrier proteintransacylase fabD**	41.1		0	1.76
265	UBA_8062_GENE_227	**3-oxoacyl-[acyl-carrier-protein] synthas**	58.1	0	92.96	5way_CG_27_GENE_3	**toacyl-[ACP] synthase III fabHA?**	5.3		0	10.96
266	UBA_8062_GENE_228	**Fatty acid/phospholipid biosynthesis enz**	55.9	0	95.77	5way_CG_27_GENE_4	**phosholipid synthesis protein PlsX**	30.8		1	1.81
267	UBA_8062_GENE_228a		50	0	100.00	5way_CG_27_GENE_5	**k (possible ribosomal protein L32)**	50		0	1.00
268	UBA_8062_GENE_229	Hypothetical	NO DATA	-	96.34	5way_CG_27_GENE_6	c hypo	NO DATA	-	-	
269	UBA_8062_GENE_230	**Prolyl-tRNA synthetase**	57.6	0	97.16	5way_CG_27_GENE_7	**prolyl tRNA synthetase**	27.3		4	2.11
270	UBA_8062_GENE_231	**Enzyme involved in the deoxyxylulose pat**	64.2	0	99.47	5way_CG_27_GENE_8	**peptidoglycan acylation**	61.8		1	1.04
271	UBA_8062_GENE_232	**Predicted membrane-associated Zn-depende**	31.6	0	98.02	5way_CG_27_GENE_9	**zinc metallopeptidase**	18.6		1	1.70
272	UBA_8062_GENE_233	**1-deoxy-D-xylulose 5-phosphate reductois**	38.2	0	95.67	5way_CG_27_GENE_10	**e 5-phosphate reductoisomerase**	16.8		0	2.27
273	UBA_8062_GENE_234	CDP-diglyceride synthetase	NO DATA	-	95.34	5way_CG_27_GENE_11	hosphatidate cytidylyltransferase	NO DATA	-	-	
274	UBA_8062_GENE_235	Undecaprenyl pyrophosphate synthase	NO DATA	-	95.83	5way_CG_27_GENE_12	aprenyl pyrophosphate synthase	NO DATA	-	-	
275	UBA_8062_GENE_236	**Hypothetical**	75.2	0	95.95	5way_CG_27_GENE_13	**hypo unique**	52.8		0	1.42
276	UBA_8062_GENE_237	**Formyltetrahydrofolate synthetase**	50.8	0	96.77	5way_CG_27_GENE_14	**formate-tetrahydrofolate ligase**	32.9		1	1.54
277	UBA_8062_GENE_238	Uncharacterized bacitracin resistance pr	NO DATA	-	94.74	5way_CG_27_GENE_15	undecaprenyl kinase	NO DATA	-	-	
278	UBA_8062_GENE_239	Sec-independent protein secretion pathwa	NO DATA	-	94.05	5way_CG_27_GENE_16	independent protein translocase	NO DATA	-	-	
279	UBA_8062_GENE_240	**Hypothetical**	32.3	0	92.93	5way_CG_27_GENE_17	hypo unique	NO DATA	-		20.00
280	UBA_8062_GENE_241	**Hypothetical**	76.9	0	97.44	5way_CG_27_GENE_18	**hypo unique**	35.9		0	2.14
281	UBA_8062_GENE_242	Acetyltransferases	NO DATA	-	89.71	5way_CG_27_GENE_19	protein-alanine acetyltransferase	NO DATA	-	-	
282	UBA_8062_GENE_243	**Inactive homolog of metal-dependent prot**	NO DATA	-	91.63	5way_CG_27_GENE_20	**glycoprotein endopeptidase**	NO DATA	-	-	
283	UBA_8062_GENE_244	**Predicted ATP-dependent serine protease**	25.4	0	95.44	5way_CG_27_GENE_21	**DNA repair protein RadA**	14.3		1	1.78
284	UBA_8062_GENE_245	**Hypothetical**	4.5	0	92.71	5way_CG_27_GENE_22	hypo unique	4.5		0	1.00
285	UBA_8062_GENE_246	**Predicted Rossmann fold nucleotide-bindi**	51.4	0	93.43	5way_CG_27_GENE_23	**lase/nucleotide binding protein)**	32.7		1	1.57
286	UBA_8062_GENE_247	**Predicted Zn-dependent proteases and the**	74.8	0	96.02	5way_CG_27_GENE_24	**protease/DNA gyrase modulator**	44		7	1.70
287	UBA_8062_GENE_248	**Predicted Zn-dependent proteases and the**	62.7	0	97.32	5way_CG_27_GENE_25	**protease/DNA gyrase modulator**	45.2		0	1.39
288	UBA_8062_GENE_249	Beta-lactamase class C and other penicil	NO DATA	-	91.19	5way_CG_27_GENE_26	beta-lactamase	NO DATA	-	-	
289	UBA_8062_GENE_250	Phytoene/squalene synthetase	NO DATA	-	91.17	5way_CG_27_GENE_27	phytoene synthase	NO DATA	-	-	
290	UBA_8062_GENE_251	**Predicted NAD/FAD-binding protein**	10	0	95.52	5way_CG_27_GENE_28	phytoene dehydrogenase	NO DATA	-		20.00
291	UBA_8062_GENE_252a		17.5	3	92.19	5way_CG_27_GENE_29	**phytoene synthetase**	10.9		1	1.61
292	UBA_8062_GENE_253	**Uncharacterized protein, putative amidas**	39	0	97.21	5way_CG_27_GENE_30	**creatinase**	31.9		0	1.22
293	UBA_8062_GENE_254	**ATPases involved in chromosome partition**	66.3	0	99.52	5way_CG_27_GENE_31	**chromosome partitioning ATPase**	61.5		0	1.08
294	UBA_8062_GENE_255	Hypothetical	NO DATA	-	94.38	5way_CG_27_GENE_32	hypo unique	NO DATA	-	-	
295	UBA_8062_GENE_256	Uncharacterized proteins, homologs of mi	NO DATA	-	94.34	5way_CG_27_GENE_33	**yltetrapeptide carboxypeptidase**	12.2		4	0.06
296	UBA_8062_GENE_257	**Hypothetical**	53	0	95.15	5way_CG_27_GENE_34	**hypo unique**	71.1		79	0.75
297	UBA_8062_GENE_258	Hypothetical check ORF with above	31.1	0	98.01	5way_CG_27_GENE_35	gene with above?? hypo unique	54.3		9	0.57
298	UBA_8062_GENE_259	Hypothetical	NO DATA	-	88.89	5way_CG_27_GENE_36	**hypo unique**	78.4		38	0.06
299		TRNA Glu CTC 267614..267689 (+)	-						-		
300	UBA_8062_GENE_260	Predicted phosphatases	NO DATA	-	90.43	5way_CG_27_GENE_37	phosphoglycolate phosphatase	NO DATA	-	-	
301	UBA_8062_GENE_261	**Hypothetical**	34.6	0	94.68	5way_CG_27_GENE_38	**ible outer membrane lipoprotein**	55.9		8	0.62
302	UBA_8062_GENE_262	**Hypothetical**	54.1	0	96.79	5way_CG_27_GENE_39	**ble phage-shock operon protein**	73.9		36	0.73
303	UBA_8062_GENE_263	**Phage shock protein A (IM30), suppresse**	56	0	96.44	5way_CG_27_GENE_40	**phage shock protein**	84.4		72	0.66
304	UBA_8062_GENE_264	**2 [Leptospirillum ferrooxidans]**	15	0	88.42	5way_CG_27_GENE_41	**ble phage-shock operon protein**	41.8		95	0.36
305	UBA_8062_GENE_265	Predicted glycosyl transferase	NO DATA	-	89.97	5way_CG_27_GENE_42	**ble phage-shock operon protein**	54		37	0.06
306	UBA_8062_GENE_266	**Hypothetical**	20.7	0	93.26	5way_CG_27_GENE_43	**ble phage-shock operon protein**	50.3		18	0.41
307		TRNA Leu TAA 273529..273615 (+)	-						-		

308			NO GENE	-		5way_CG_27_GENE_44	hypo unique	NO DATA	-	-	
309	UBA_8062_GENE_267	Integrase	NO DATA	-				NO GENE	-	-	
310	UBA_8062_GENE_268	**Hypothetical**	75.2	0				NO GENE	-		35.00
311	UBA_8062_GENE_269	Hypothetical	NO DATA	-				NO GENE	-	-	
312	UBA_8062_GENE_270	probable conjugal transfer protein TraB [Rhizobi	NO DATA	-				NO GENE	-	-	
313	UBA_8062_GENE_270a		NO DATA	-	100.00	5way_CG_170_GENE_1	c hypo	NO DATA	-	-	
314	UBA_8062_GENE_271	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_1a		NO DATA	-	-	
315	UBA_8062_GENE_272	Transposase and inactivated derivatives	NO DATA	-	99.40	5way_CG_170_GENE_2	transposase	NO DATA	-	-	
316	UBA_8062_GENE_273	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_4	hypo unique	NO DATA	-	-	
317	UBA_8062_GENE_274	**ATP-dependent exoDNAse (exonuclease V),**	3.3	0	100.00	5way_CG_170_GENE_5	VC plasmid protein/DNA helicase	3.3	0	1.00	
318	UBA_8062_GENE_274a		NO DATA	-	100.00	5way_CG_170_GENE_6	hypo unique	NO DATA	-	-	
319	UBA_8062_GENE_275	**Type IV secretory pathway, VirD4 compone**	6.4	0	100.00	5way_CG_170_GENE_7	**TrwB plasmid protein**	6.4	0	1.00	
320	UBA_8062_GENE_276	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_8	hypo unique	NO DATA	-	-	
321	UBA_8062_GENE_277	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_9	hypo unique	NO DATA	-	-	
322	UBA_8062_GENE_278	Hypothetical	11.3	0	100.00	5way_CG_170_GENE_10	hypo unique	11.3	0	1.00	
323	UBA_8062_GENE_280	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_12	hypo unique	NO DATA	-	-	
324	UBA_8062_GENE_281	Hypothetical	NO DATA	-	100.00	5way_CG_170_GENE_13	hypo unique	NO DATA	-	-	
325	UBA_8062_GENE_282	Predicted P-loop ATPase	NO DATA	-	100.00	5way_CG_170_GENE_14	phage protein?	NO DATA	-	-	
326	UBA_8062_GENE_283	tical protein CUPA0102 [Campylobacter ups	NO DATA	-	100.00	5way_CG_170_GENE_15	hypo unique	NO DATA	-	-	
327	UBA_8062_GENE_284	e DNA helicase [Nitrosomonas eutropha C71	NO DATA	-	100.00	5way_CG_294_GENE_6	replication protein A/helicase	NO DATA	-	-	
328	UBA_8062_GENE_285	Hypothetical	NO DATA	-	100.00	5way_CG_294_GENE_5	hypo unique	NO DATA	-	-	
329	UBA_8062_GENE_286	Hypothetical	NO DATA	-	100.00	5way_CG_294_GENE_4	hypo unique	NO DATA	-	-	
330	UBA_8062_GENE_287	**Hypothetical**	61.6	0	100.00	5way_CG_294_GENE_3	**hypo unique**	61.6	0	1.00	
331	UBA_8062_GENE_288	**to ATP-dependent endonuclease of the OLD**	54.6	0	100.00	5way_CG_294_GENE_2	**c hypo**	54.6	0	1.00	
332			NO GENE	-		5way_CG_294_GENE_1		NO DATA	-	-	
333	UBA_8062_GENE_289	Integrase	NO DATA	-				NO GENE	-	-	
334	UBA_8062_GENE_289a		NO DATA	-				NO GENE	-	-	
335	UBA_8062_GENE_290	Hypothetical	NO DATA	-				NO GENE	-	-	
336	UBA_8062_GENE_291	Hypothetical	NO DATA	-				NO GENE	-	-	
337	UBA_8062_GENE_293	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
338	UBA_8062_GENE_294	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
339	UBA_8062_GENE_295	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
340	UBA_8062_GENE_296	transposase [Vibrio splendidus 12B01]gi |	NO DATA	-				NO GENE	-	-	
341	UBA_8062_GENE_297	**Transposase and inactivated derivatives**	27.1	-				NO GENE	-	-	
342	UBA_8062_GENE_298	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
343	UBA_8062_GENE_299	Hypothetical	NO DATA	-				NO GENE	-	-	
344	UBA_8062_GENE_300	**Transposase and inactivated derivatives,**	39.6	-				NO GENE	-	-	
345	UBA_8062_GENE_301	Transposase and inactivated derivatives,	NO DATA	-				NO GENE	-	-	
346	UBA_8062_GENE_302	DNA-damage-inducible protein J	NO DATA	-				NO GENE	-	-	
347	UBA_8062_GENE_303	Uncharacterized protein conserved in bac	NO DATA	-				NO GENE	-	-	
348	UBA_8062_GENE_304	Type I restriction-modification system m	NO DATA	-				NO GENE	-	-	
349	UBA_8062_GENE_305	Uncharacterized conserved protein	NO DATA	-				NO GENE	-	-	
350	UBA_8062_GENE_306	Restriction endonuclease S subunits	NO DATA	-				NO GENE	-	-	
351	UBA_8062_GENE_307	Transposase and inactivated derivatives,	NO DATA	-				NO GENE	-	-	
352	UBA_8062_GENE_308	Hypothetical	NO DATA	-				NO GENE	-	-	
353	UBA_8062_GENE_309	**Transposase and inactivated derivatives,**	34	-				NO GENE	-	-	
354	UBA_8062_GENE_310	Hypothetical	NO DATA	-				NO GENE	-	-	
355	UBA_8062_GENE_311	Hypothetical	NO DATA	-				NO GENE	-	-	
356	UBA_8062_GENE_312	**Hypothetical**	79.8	0				NO GENE	-		35.00
357	UBA_8062_GENE_314	**Type I site-specific restriction-modific**	2.2	1				NO GENE	-		35.00
358	UBA_8062_GENE_315	Uncharacterized conserved protein	NO DATA	-				NO GENE	-	-	
359	UBA_8062_GENE_316	Restriction endonuclease S subunits	NO DATA	-				NO GENE	-	-	
360	UBA_8062_GENE_317	**Transposase and inactivated derivatives,**	41.7	-				NO GENE	-	-	
361	UBA_8062_GENE_318	Hypothetical	NO DATA	-				NO GENE	-	-	
362	UBA_8062_GENE_319	Transposase and inactivated derivatives,	NO DATA	-				NO GENE	-	-	
363	UBA_8062_GENE_320	Uncharacterized protein conserved in bac	NO DATA	-				NO GENE	-	-	
364	UBA_8062_GENE_321	Predicted transcriptional regulator	NO DATA	-				NO GENE	-	-	
365	UBA_8062_GENE_322	Hypothetical	NO DATA	-				NO GENE	-	-	
366			NO GENE	-		5way_CG_175_GENE_14		40.4	0	0.03	
367	UBA_8062_GENE_323	Hypothetical	NO DATA	-	77.81	5way_CG_175_GENE_13	**hypo unique**	40.2	38	0.06	
368	UBA_8062_GENE_324	Hypothetical	NO DATA	-				NO GENE	-	-	
369			NO GENE	-		5way_CG_175_GENE_12	hypo unique	NO DATA	-	-	
370	UBA_8062_GENE_326	Zn-dependent hydrolases, including glyox	NO DATA	-	81.66	5way_CG_175_GENE_11	etallo-beta-lactamase hydrolase	NO DATA	-	-	
371	UBA_8062_GENE_327	77 Permeases of the major facilitator su	NO DATA	-	97.14	5way_CG_175_GENE_10	facilitator superfamily transporter	NO DATA	-	-	
372	UBA_8062_GENE_328	**Hypothetical**	21	0	86.71	5way_CG_175_GENE_9	**hypo unique**	30.8	11	0.68	
373	UBA_8062_GENE_329	**Type II secretory pathway, pullulanase P**	7.1	0	96.91	5way_CG_175_GENE_8	**glycogen debranching enzyme**	7.1	0	1.00	
374	UBA_8062_GENE_331	HD-GYP domain	9.7	-	96.37	5way_CG_175_GENE_6	**omain protein/response regulator**	13.6	-	-	
375	UBA_8062_GENE_333	Lipoate synthase	NO DATA	-	93.35	5way_CG_175_GENE_5	lipoate synthase	NO DATA	-	-	
376	UBA_8062_GENE_334	**Phosphoglycerate mutase 1**	41.7	0	97.76	5way_CG_175_GENE_4	**phosphoglycerate mutase**	84.3	31	0.49	
377	UBA_8062_GENE_335	Hypothetical	NO DATA	-	92.45	5way_CG_175_GENE_3	hypo unique	NO DATA	-	-	
378	UBA_8062_GENE_336	**Predicted membrane protein**	29.7	0	100.00	5way_CG_175_GENE_2	**c hypo**	29.7	0	1.00	
379	UBA_8062_GENE_337	Hypothetical	NO DATA	-	100.00	5way_CG_175_GENE_1	hypo unique	NO DATA	-	-	

380	UBA_8062_GENE_338	3 Superfamily II DNA and RNA helicases	57.2	0	99.10	5way_CG_288_GENE_1	helicase	60.1		1	0.95
381	UBA_8062_GENE_339	Predicted glutamine amidotransferases	NO DATA	-	92.89	5way_CG_288_GENE_2	hranilate synthase, component II	30.1		5	0.06
382	UBA_8062_GENE_340	Glutamate racemase	22	0	94.59	5way_CG_288_GENE_3	glutamate racemase	53.8		19	0.41
383	UBA_8062_GENE_341	Beta-glucosidase-related glycosidases	22.5	0	93.84	5way_CG_288_GENE_4	beta-hexosaminidase	70.2		27	0.32
384	UBA_8062_GENE_342	Xanthosine triphosphate pyrophosphatase	8.6	0	96.46	5way_CG_288_GENE_5	e triphosphate pyrophosphatase	63.1		32	0.14
385	UBA_8062_GENE_343	RNase PH	45.7	0	98.78	5way_CG_288_GENE_6	ribonuclease	53.1		24	0.86
386	UBA_8062_GENE_344	Predicted phosphohydrolase (DHH superfam	23.4	0	95.90	5way_CG_288_GENE_7	phosphohydrolase-like	38.9		10	0.60
387	UBA_8062_GENE_345	ATPase components of ABC transporters wi	27.8	0	97.05	5way_CG_288_GENE_8	C transporter ATP-binding protein	45.3		23	0.61
388	UBA_8062_GENE_346	Molecular chaperone (small heat shock pr	59.9	-	99.34	5way_CG_288_GENE_9	heat shock protein	59.9	-	-	
389	UBA_8062_GENE_347	Hypothetical	NO DATA	-	84.21	5way_CG_224_GENE_10	16S rRNA pseudouridine synthase	10.2	-	-	
390	UBA_8062_GENE_347a		NO DATA	-	98.18	5way_CG_224_GENE_9	lytic transglycosylase	14.5		4	0.06
391	UBA_8062_GENE_348	Hypothetical	NO DATA	-	96.36	5way_CG_224_GENE_8	hypo unique	17.3		11	0.06
392	UBA_8062_GENE_349	HD superfamily phosphohydrolases	NO DATA	-	96.15	5way_CG_224_GENE_7	HD domain phosphohydrolase	13.5		4	0.06
393	UBA_8062_GENE_349a		26.9	0	97.01	5way_CG_224_GENE_6	RnaseH	76.1		22	0.35
394	UBA_8062_GENE_350	Zn-ribbon protein, possibly nucleic acid	52.7	1	96.56	5way_CG_224_GENE_5	c hypo	65.6		38	0.80
395		TRNA Met CAT 346472..346546 (-)		-					-		
396	UBA_8062_GENE_351	DNA-directed RNA polymerase, sigma subun	52.8	0	99.33	5way_CG_224_GENE_4	RNA polym. sigma factor rpoD	58.2		5	0.91
397	UBA_8062_GENE_352	DNA primase (bacterial type)	13.9	1	92.84	5way_CG_224_GENE_3	DNA primase	22.8		1	0.61
398	UBA_8062_GENE_355	Uncharacterized conserved protein	33.8	0	94.96	5way_CG_224_GENE_1	c hypo	48.9		45	0.69
399			NO GENE	-		5way_CG_174_GENE_17	transposase	NO DATA	-	-	
400	UBA_8062_GENE_356	Hypothetical	49.2	61				NO GENE	-		35.00
401	UBA_8062_GENE_357	Bacterial nucleoid DNA-binding protein	83.3	0	100.00	5way_CG_174_GENE_16	nucleoid DNA-binding protein	83.3		0	1.00
402	UBA_8062_GENE_357a		14.4	0	91.53	5way_CG_174_GENE_15	HIT family hydrolase	89		34	0.16
403	UBA_8062_GENE_358	Phosphoribosyl-AMP cyclohydrolase	NO DATA	-	91.38	5way_CG_174_GENE_14	ibosyl-AMP cyclohydrolase, HisIE	28.8		10	0.06
404	UBA_8062_GENE_359	Imidazoleglycerol-phosphate synthase	37.3	0	99.61	5way_CG_174_GENE_13	HisF cyclase	48.2		2	0.77
405	UBA_8062_GENE_360	Phosphoribosylformimino-5-aminoimidazole	51.8	0	97.57	5way_CG_174_GENE_12	ino-5-amidoimidazole isomerase	66.4		13	0.78
406	UBA_8062_GENE_361	Glutamine amidotransferase	10.4	0	92.38	5way_CG_174_GENE_11	amidotransferase HisH	36		25	0.29
407	UBA_8062_GENE_362	Imidazoleglycerol-phosphate dehydratase	49	0	96.67	5way_CG_174_GENE_10	cerol phosphate dehydrogenase	62.9		13	0.78
408	UBA_8062_GENE_363	Histidinol-phosphate/aromatic aminotrans	17.8	0	94.15	5way_CG_174_GENE_9	histidinol aminotransferase	46		21	0.39
409	UBA_8062_GENE_364	Histidinol dehydrogenase	14.4	1	92.57	5way_CG_174_GENE_8	histidinol dehydrogenase	30.8		13	0.47
410	UBA_8062_GENE_365a		62.9	0	99.51	5way_CG_174_GENE_7	ansferase (histidine biosynthesis)	67.8		1	0.93
411	UBA_8062_GENE_366	UDP-N-acetylglucosamine enolpyruvyl tran	23.3	0	96.15	5way_CG_174_GENE_6	amine 1-carboxyvinyltransferase	43.9		15	0.53
412	UBA_8062_GENE_367	Methylase of polypeptide chain release f	NO DATA	-	88.74	5way_CG_174_GENE_5	modification methylase, HemK	NO DATA	-	-	
413	UBA_8062_GENE_369	Protein chain release factor A	35.2	0	99.17	5way_CG_174_GENE_4	peptide chain release factor I	42.4		4	0.83
414	UBA_8062_GENE_370	Ribosomal protein L31	70.6	0	100.00	5way_CG_174_GENE_3	ribosomal protein L31	70.6		0	1.00
415	UBA_8062_GENE_371	Transcription termination factor	85.8	0	99.52	5way_CG_174_GENE_2	transcription termination factor	88.9		20	0.97
416	UBA_8062_GENE_372	Cytochrome c, class I [Ralstonia metallidurans C	100	162				NO GENE	-		35.00
417	UBA_8062_GENE_374a		NO DATA	-				NO GENE	-	-	

	8027										
1	UBA_8027_GENE_1	Thiol-disulfide isomerase and thioredoxins	86.4	0	100.00	5way_CG_222_GENE_9	thioredoxin;	86.4		0	1.00
2	UBA_8027_GENE_3	ATPase involved in DNA repair	38.7	17	95.74	5way_CG_222_GENE_7	DNA repair protein RecN	24.8		0	1.56
3	UBA_8027_GENE_4	Uncharacterized conserved protein	6.2	2	96.17	5way_CG_222_GENE_6	c hypo	2.2		0	2.82
4	UBA_8027_GENE_5	Arginine/lysine/ornithine decarboxylases	17	3	97.96	5way_CG_222_GENE_5	argenine/lysine decarboxylase	11.5		0	1.48
5	UBA_8027_GENE_6	Spermidine synthase	51.3	14	98.37	5way_CG_222_GENE_4	spermidine synthase	44.4		0	1.16
6	UBA_8027_GENE_7	S-adenosylmethionine decarboxylase	53.9	12	98.05	5way_CG_222_GENE_3	adenosylmethionine carboxylase	40.3		0	1.34
7	UBA_8027_GENE_8	FOG: GGDEF domain	12.4	11	88.24	5way_CG_222_GENE_2	ensory box/GGDEF family protein	NO DATA	-		20.00
8	UBA_8027_GENE_9	Hypothetical	46.1	-	96.30	5way_CG_222_GENE_1	hypo unique	45.4	-	-	
9	UBA_8027_GENE_11	Hypothetical	17	6	97.17	5way_CG_44_GENE_1	hypo unique	NO DATA	-		20.00
10	UBA_8027_GENE_12	Phosphatidylglycerophosphatase A and related p	NO DATA	-	93.30	5way_CG_44_GENE_2	osphatidylglycerophosphatase A	NO DATA	-	-	
11	UBA_8027_GENE_13	RecA/RadA recombinase	81.4	42	97.50	5way_CG_44_GENE_3	RecA	54.4		1	1.50
12	UBA_8027_GENE_14	Alanyl-tRNA synthetase	62.6	45	96.75	5way_CG_44_GENE_4	alanyl tRNA synthetase	43.7		0	1.43
13	UBA_8027_GENE_16	Hypothetical	73.4	29	91.49	5way_CG_44_GENE_5	hypo unique	51.1		1	1.44
14	UBA_8027_GENE_17	Predicted endonuclease involved in recombinatio	18.1	1	92.90	5way_CG_44_GENE_6	ntegration recombination protein	NO DATA	-		20.00
15	UBA_8027_GENE_18	Predicted periplasmic solute-binding protein	43.7	25	94.43	5way_CG_44_GENE_7	amino-4-deoxychorismate lyase	14.7		0	2.97
16	UBA_8027_GENE_19	Valyl-tRNA synthetase	42.4	-	95.69	5way_CG_44_GENE_8	valyl tRNA synthetase	27.1	-	-	
17	UBA_8027_GENE_21	Nicotinate-nucleotide pyrophosphorylase	25.3	2	93.84	5way_CG_44_GENE_9	e-nucleotide pyrophosphorylase	20.9		0	1.21
18	UBA_8027_GENE_22	Hypothetical	NO DATA	-	87.01	5way_CG_44_GENE_10	biotin operon repressor BirA	NO DATA	-	-	
19	UBA_8027_GENE_23	Putative transcriptional regulator, homolog of Bvg	10.4	1	93.82	5way_CG_44_GENE_11	c hypo	NO DATA	-		20.00
20	UBA_8027_GENE_24	Transposase and inactivated derivatives	NO DATA	-				NO GENE	-	-	
21	UBA_8027_GENE_25	Transposase and inactivated derivatives	36.7	-		Tranposase		NO GENE	-	-	
22	UBA_8027_GENE_26	Hypothetical	NO DATA	-	85.00	5way_CG_44_GENE_12	hypo unique	NO DATA	-	-	
23	UBA_8027_GENE_27	FOG: GGDEF domain	11.7	-	95.31	5way_CG_44_GENE_13	DEF domain/EAL domain protein	3.9	-	-	
24	UBA_8027_GENE_27a		NO DATA	-	71.12	5way_CG_44_GENE_13		3.9	-	-	
25			NO GENE	-		5way_CG_44_GENE_14	hypo unique	NO DATA	-	-	
26	UBA_8027_GENE_29	Multidrug resistance efflux pump	59	7	92.71	5way_CG_44_GENE_15	multi-drug resistance efflux pump	42.9		0	1.38
27	UBA_8027_GENE_30	Outer membrane protein	46.8	58	95.44	5way_CG_44_GENE_16	outer membrane protein TolC	19.2		0	2.44
28	UBA_8027_GENE_31	Malate/lactate dehydrogenases	61.2	22	99.06	5way_CG_44_GENE_17	malate dehydrogenase	53.1		0	1.15
29	UBA_8027_GENE_32	Hypothetical	33.3	6	97.42	5way_CG_44_GENE_18	hypo unique	17.9		0	1.86
30	UBA_8027_GENE_33	Hypothetical	10	0	91.39	5way_CG_44_GENE_19	c hypo	10		0	1.00

31	UBA_8027_GENE_34	**ABC-type (unclassified) transport system, ATPase c**	19	0	99.60	5way_CG_44_GENE_20	**ABC transporter**	19		0	1.00
32	UBA_8027_GENE_35	**DNA-directed RNA polymerase specialized sigma**	40.9	7	94.86	5way_CG_44_GENE_21	**RNA polymerase sigma-54 factor**	28		0	1.46
33	UBA_8027_GENE_36	**Ribosome-associated protein Y (PSrp-1)**	85.8	67	97.16	5way_CG_44_GENE_22	**ribosomal protein S30**	58		0	1.48
34	UBA_8027_GENE_37	Predicted P-loop-containing kinase	NO DATA	-	98.61	5way_CG_44_GENE_23	o (contains ATP-binding domain)	NO DATA	-	-	
35	UBA_8027_GENE_38	**Hypothetical**	37.9	45	95.38	5way_CG_44_GENE_24	**sine and tryptophan biosynthesis**	21.5		0	1.76
36	UBA_8027_GENE_39	**Chorismate synthase**	70.1	36	95.51	5way_CG_44_GENE_25	**chorismate synthase**	36.4		0	1.93
37	UBA_8027_GENE_40	**Shikimate kinase**	53	2	97.81	5way_CG_44_GENE_26	**shikimate kinase**	32.2		0	1.65
38	UBA_8027_GENE_41	**3-dehydroquinate synthetase**	52.2	13	94.49	5way_CG_44_GENE_27	**3-dehydroquinate synthetase**	27.7		0	1.88
39	UBA_8027_GENE_42	**FOG: GAF domain**	56.3	11	98.81	5way_CG_44_GENE_28	**sigma factor regulatory protein**	43.2		0	1.30
40	UBA_8027_GENE_43	Hypothetical	NO DATA	-	100.00	5way_CG_44_GENE_29	hypo unique	NO DATA	-	-	
41	UBA_8027_GENE_44	**Hypothetical**	5.8	2	92.31	5way_CG_44_GENE_30	c hypo	NO DATA	-		20.00
42			NO GENE	-		5way_CG_44_GENE_31	acetyl transferase	NO DATA	-	-	
43	UBA_8027_GENE_45	**Enzyme related to GTP cyclohydrolase I**	88.6	57	92.47	5way_CG_44_GENE_32	**GTP cyclohydrolase I**	48.3		0	1.83
44			NO GENE	-		5way_CG_44_GENE_33	transposase	NO DATA	-	-	
45		TRNA Val TAC 45544..45619 (-)	-						-		
46	UBA_8027_GENE_46	Predicted thioesterase	NO DATA	-	95.95	5way_CG_44_GENE_34	hydroxybenzoyl-coA-thioesterase	NO DATA	-	-	
47			NO GENE	-		5way_CG_44_GENE_35	transposase	NO DATA	-	-	
48			NO GENE	-		5way_CG_96_GENE_1	probable transposase	NO DATA	-	-	
49		TRNA Asp GTC 46216..46292 (+)	-						-		
50	UBA_8027_GENE_47	**Biopolymer transport proteins**	30	0	100.00	5way_CG_96_GENE_3	**iopolymer transport protein, ExbB**	30		0	1.00
51	UBA_8027_GENE_48	**Biopolymer transport protein**	34.5	0	99.32	5way_CG_96_GENE_4	**ymer transport protein TolR, ExbD**	34.5		0	1.00
52	UBA_8027_GENE_48a		42.4	16	92.81	5way_CG_96_GENE_5	**c hypo (faint similarity to TonB)**	22.3		0	1.90
53	UBA_8027_GENE_49	**Periplasmic component of the Tol biopolymer tran**	85	40	95.08	5way_CG_96_GENE_6	**periplasmic TolB protein**	71.1		5	1.20
54	UBA_8027_GENE_50	**Uncharacterized protein conserved in bacteria**	79.6	32	97.45	5way_CG_96_GENE_7	**c hypo**	59.5		0	1.34
55	UBA_8027_GENE_51	**DNA mismatch repair enzyme (predicted ATPase)**	22.4	8	91.64	5way_CG_96_GENE_8	**NA mismatch repair protein MutL**	5		1	4.48
56	UBA_8027_GENE_52	tRNA delta(2)-isopentenylpyrophosphate transferc	NO DATA	-	91.50	5way_CG_96_GENE_9	ntenylpyrophosphate transferase	NO DATA	-	-	
57	UBA_8027_GENE_53	**Purine nucleoside phosphorylase**	53.7	16	95.33	5way_CG_96_GENE_10	**thylthioadenosine phosphorylase**	32		0	1.68
58	UBA_8027_GENE_54	**Sugar kinases, ribokinase family**	30	15	95.85	5way_CG_96_GENE_11	carbohydrate kinase	NO DATA	-		20.00
59	UBA_8027_GENE_55	**FOG: TPR repeat**	56.7	9	96.85	5way_CG_96_GENE_12	**cell division cycle protein Cdc57**	58.3		1	0.97
60	UBA_8027_GENE_56	**Uncharacterized protein conserved in bacteria**	59.7	82	86.84	5way_CG_96_GENE_13	**c hypo**	28.4		0	2.10
61	UBA_8027_GENE_57	**Hypothetical**	74.3	31	97.91	5way_CG_96_GENE_14	**hypo unique**	58.8		0	1.26
62		TRNA Thr CGT 58596..58670 (+)	-						-		
63	UBA_8027_GENE_58	Hypothetical	NO DATA	-				NO GENE	-	-	
64	UBA_8027_GENE_59	Predicted hydrolases of HD superfamily	NO DATA	-				NO GENE	-	-	
65	UBA_8027_GENE_60	DNA modification methylase	NO DATA	-				NO GENE	-	-	
66			NO GENE	-		5way_CG_96_GENE_15	hypo unique	NO DATA	-	-	
67			NO GENE	-		5way_CG_96_GENE_16	sim. to Holliday jxn. resolvases	NO DATA	-	-	
68			NO GENE	-		5way_CG_96_GENE_17	hypo unique	NO DATA	-	-	
69			NO GENE	-		5way_CG_96_GENE_18	hypo unique	NO DATA	-	-	
70			NO GENE	-		5way_CG_96_GENE_19	mobilization protein, MobD	NO DATA	-	-	
71			NO GENE	-		5way_CG_96_GENE_20	hypo unique	NO DATA	-	-	
72			NO GENE	-		5way_CG_96_GENE_21	hypo unique	NO DATA	-	-	
73			NO GENE	-		5way_CG_96_GENE_22	hypo unique	NO DATA	-	-	
74			NO GENE	-		5way_CG_96_GENE_23	TrwC plasmid protein	NO DATA	-	-	

			NO GENE	-		Unass_bact_scaffold_1042	c hypo	80.9		#N/A	0.03
			NO GENE	-		Unass_bact_scaffold_1042	tiny hypo	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_1	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_2	mobilization protein, MobC	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_3	mobilization protein, MobD	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_4	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_5	mobilization protein MobE	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_6	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_898_GENE_7	DNA helicase/TrwC	NO DATA	-	-	
			-				**matches on multiple scaffolds**		-		
			-						-		
			NO GENE	-		5way_CG_429_GENE_1	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_429_GENE_2		NO DATA	-	-	
			NO GENE	-		5way_CG_429_GENE_4		NO DATA	-	-	
			NO GENE	-		5way_CG_429_GENE_5		9.3	-	-	
			NO GENE	-		5way_CG_429_GENE_6		NO DATA	-	-	
			NO GENE	-		5way_CG_429_GENE_7		NO DATA	-	-	
			NO GENE	-		5way_CG_429_GENE_8		NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_1	integrase	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_2	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_3	hypo unique	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_4	transcriptional activator	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_5	transposase	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_6	transcriptional activator	NO DATA	-	-	
			NO GENE	-		5way_CG_435_GENE_7	xl-type quorum sensing regulator	NO DATA	-	-	

		NO GENE	-		5way_CG_435_GENE_8	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_435_GENE_9	**NADH dehydrogenase I, F subunit**	34.1	-	-
		-			**UBA in over scaffold_73??**	**[redacted]n ends**		-	
		-			may link to end of 6 by m			-	
		NO GENE	-		5way_CG_888_GENE_6	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_888_GENE_5	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_888_GENE_4	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_888_GENE_3	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_888_GENE_2	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_888_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_865_GENE_4	permease	NO DATA	-	-
		NO GENE	-		5way_CG_865_GENE_3	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_865_GENE_2	**hypo unique**	49.7	-	-
		NO GENE	-		5way_CG_865_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_830_GENE_5	helicase	NO DATA	-	-
		NO GENE	-		5way_CG_830_GENE_4	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_830_GENE_3	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_830_GENE_2	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_830_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_824_GENE_4	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_824_GENE_2	**ccepting chemotaxis transducer**	12.5	7	0.03
		NO GENE	-		5way_CG_824_GENE_1	probable transposase	NO DATA	-	-
		NO GENE	-		5way_CG_759_GENE_5	RNA helicase	NO DATA	-	-
		NO GENE	-		5way_CG_759_GENE_4	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_759_GENE_2	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_759_GENE_1	ATP-dependent protease La	3.7	2	0.03
		NO GENE	-		5way_CG_728_GENE_7	se/restriction modification system	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_6	ulfide interchange protein, DsbG	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_5	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_4	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_3	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_2	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_728_GENE_1	c hypo	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_8		NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_7		58.6	0	0.03
		NO GENE	-		5way_CG_710_GENE_6	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_5	DNA helicase	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_4	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_3	replication protein A	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_2	replication protein C	NO DATA	-	-
		NO GENE	-		5way_CG_710_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_708_GENE_5	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_708_GENE_4	glycosyltransferase	NO DATA	-	-
		NO GENE	-		5way_CG_708_GENE_3	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_708_GENE_2	transposase	NO DATA	-	-
		NO GENE	-		5way_CG_708_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_645_GENE_4	cellulose synthase, subunit C	NO DATA	-	-
		NO GENE	-		5way_CG_645_GENE_3	cellulose synthase, subunit C	NO DATA	-	-
		NO GENE	-		5way_CG_645_GENE_2	cellulase	NO DATA	-	-
		NO GENE	-		5way_CG_645_GENE_1	cellulose synthase CelB	NO DATA	-	-
		NO GENE	-		5way_CG_569_GENE_5	DotB (type II secretion)	NO DATA	-	-
		NO GENE	-		5way_CG_569_GENE_4	TraI	NO DATA	-	-
		NO GENE	-		5way_CG_569_GENE_3	DEF domain/EAL domain protein	NO DATA	-	-
		NO GENE	-		5way_CG_569_GENE_2	**hypo unique**	53.2	15	0.03
		NO GENE	-		5way_CG_569_GENE_1	chemotaxis motB protein	NO DATA	-	-
		NO GENE	-		5way_CG_402_GENE_5	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_402_GENE_4	DNA primase	NO DATA	-	-
		NO GENE	-		5way_CG_402_GENE_2	**Pase involved in ABC transporters**	13.6	18	0.03
		NO GENE	-		5way_CG_402_GENE_1	hypo unique	NO DATA	-	-
		NO GENE	-		5way_CG_1153_GENE_2	**c hypo (possible helicase)**	37.3	0	0.03
		NO GENE	-		5way_CG_1153_GENE_1	transposase	NO DATA	-	-
		NO GENE	-		5way_CG_183_GENE_1		48.8	0	0.03