Table 4. Annotation of genes and protein coding regions in Monterey Bay BAC clone EBAC31A08

#	Nucleotide range	Dir.	Putative function	Closest BLASTP hit (E-value)	
1	59 - 583	+	Predicted glutathione peroxidase	NP_800761.1 (3e-38)	gamma
2	589 - 1227	-	Predicted ribose 5-phosphate isomerase	NP_747251.1 (1e-55)	gamma
3	1266 - 2807	+	Predicted threonine dehydratase	NP_249022.1 (1e-128)	gamma
4	2812 - 5097	-	Conserved hypothetical protein	ZP_00102669.1 (1e-44)	LGC
5	5126 - 5701	-	Predicted 5-formyltetrahydrofolate cyclo-ligase	NP_439018.1 (1e-14)	gamma
6	6433 - 7728	+	Predicted Xaa-Pro aminopeptidase	ZP_00067121.1 (1e-107)	gamma
7	7732 - 8892	+	Predicted 2-polyprenyl-6-methoxyphenol hydroxylase	ZP_00124991.1 (7e-38)	gamma
8	8900 - 9136	-	Ribosomal protein L28	NP_439112.1 (2e-25)	gamma
9	9182 - 9670	+	Predicted phosphohistidine phosphatase SixA	NP_660997.1 (5e-17)	BCF
10	9710 - 10129	+	Predicted dUTPase	NP_719777.1 (8e-48)	gamma
11	10443 - 12431	+	Predicted primosomal protein N' (replication factor Y)	AAO91308.1 (1e-135)	gamma
12	12428 - 13510	-	Predicted N-acetylmuramoyl-L-alanine amidase	ZP_00065013.1 (3e-50)	gamma
13	13670 - 14131	-	Predicted ATPase or kinase	NP_253635.1 (2e-17)	gamma
14	14128 - 14985	-	Predicted sugar kinase	ZP_00065015.1 (3e-46)	gamma
15	15024 - 16391	-	Conserved hypothetical protein	ZP_00095220.1 (3e-13)	alpha
16	16395 - 17288	-	Predicted hydrolase	NP_422102.1 (7e-29)	alpha
17	17321 - 18115	+	Predicted NTP pyrophosphohydrolase	ZP_00012706.1 (1e-33)	alpha
18	18121 - 18918	+	Predicted Zn-dependent hydrolase	ZP_00021230.1 (3e-57)	beta
19	18915 - 19298	-	Hypothetical protein	-	-
20	19295 - 21220	-	Predicted acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	ZP_00066690.1 (0.0)	gamma
21	21223 - 21888	-	Predicted deoxynucleoside kinase	ZP_00067328.1 (2e-71)	gamma
22	21915 - 23147	-	Predicted tRNA nucleotidyltransferase/poly(A) polymerase	ZP_00091219.1 (3e-89)	gamma
23	23180 - 23737	-	Predicted DnaK suppressor protein	NP_790808.1 (7e-41)	gamma
24	23793 - 24794	-	Predicted ribokinase	ZP_00067399.1 (4e-53)	gamma
25	24784 - 26034	-	Predicted glutamate-1-semialdehyde aminotransferase	NP_245399.1 (1e-131)	gamma
26	26143 - 26664	-	Predicted flavodoxins	NP_715667.1 (8e-54)	gamma
27	26742 - 27248	+	Conserved hypothetical protein	NP_719733.1 (4e-06)	gamma
28	27251 - 27580	+	Uncharacterized ACR	ZP_00092439.1 (4e-27)	gamma
29	27570 - 28664	-	Uncharacterized BCR	NP_716933.1 (1e-55)	gamma
30	28657 - 29910	-	Predicted metalloendopeptidase	ZP_00086772.1 (6e-76)	gamma
31	29910 - 32876	-	Predicted NAD-dependent aldehyde dehydrogenase	NP_719311.1 (0.0)	gamma
32	33031 - 34218	+	Predicted tyrosyl-tRNA synthetase	NP_716935.1 (1e-138)	gamma
33	34218 - 34682	+	Predicted FKBP-type peptidyl-prolyl cis-trans isomerase 1	ZP_00092021.1 (2e-23)	gamma
34	34679 - 36793	-	Predicted prolyl endopeptidase	NP_486573.1 (1e-171)	cyanobacteria
35	36889 - 37488	+	Hypothetical protein	-	-
36	37601 - 37678	+	tRNA Ile (GAT anticodon)		
37	37853 - 38530	-	Hypothetical protein	-	-
38	38789 - 39154	-	Hypothetical protein	-	-
39	39160 - 39567	-	Hypothetical protein	-	-
40	39580 - 40185	-	Hypothetical protein	-	-
41	40220 - 41566	-	Predicted Na+-driven multidrug efflux pump	ZP_00011269.1 (1e-82)	alpha
42	41820 - 43931	+	Predicted TonB-dependent receptor	NP_718299.1 (1e-131)	gamma
43	43921 - 44517	+	Predicted nicotinamide mononucleotide transporter	ZP_00067355.1 (2e-37)	gamma
44	44501 - 45328	+	Predicted LicA choline kinase	NP_561949.1 (6e-13)	LGC
45	45404 - 46600	+	Predicted NAD-dependent formate dehydrogenase	CAA73696.1 (1e-170)	gamma
46	46604 - 47572	-	Predicted 2-nitropropane dioxygenase	NP_769246.1 (1e-130)	alpha
47	47582 - 48370	-	Predicted dehydrogenase	ZP_00023929.1 (3e-49)	beta
48	48446 - 49234	+	Predicted dehydrogenase	ZP_00094214.1 (2e-48)	alpha
49	49283 - 50797	+	Predicted acyl-CoA synthetases (AMP-forming)/AMP-acid ligases	ZP_00010336.1 (1e-159)	alpha
50	50866 - 51615	-	Proteorhodopsin	-	-
51	51815 - 52402	+	Predicted phosphopantetheine adenylyltransferase	NP_747224.1 (2e-44)	gamma
52	52292 - 53104	-	Predicted formamidopyrimidine-DNA glycosylase	NP_418092.1 (5e-62)	gamma
53	53107 - 54435	-	Predicted outer membrane protein TolC	NP_253661.1 (1e-70)	gamma
54	54574 - 56469	+	Predicted DNA gyrase (topoisomerase II) B subunit	NP_747018.1 (0.0)	gamma
55	56472 - 58721	+	Predicted DNA gyrase (topoisomerase II) A subunit	ZP_00067679.1 (0.0)	gamma
56	58708 - 59985	-	Predicted PLP-dependent aminotransferase	ZP_00090273.1 (3e-92)	gamma
57	59922 - 60422	+	Hypothetical protein	-	-
58	60405 - 61655	-	Predicted 6-phosphofructokinase	ZP_00003577.1 (1e-137)	beta
59	61709 - 63019	+	Predicted UDP-N-acetylmuramate-alanine ligase	NP_796693.1 (1e-94)	gamma
60	63009 - 63599	+	Conserved hypothetical protein	ZP_00086879.1 (8e-18)	gamma
61	63727 - 64032	-	Hypothetical protein	-	-
62	64089 - 64397	-	Hypothetical protein	-	-
63	64462 - 64926	+	Uncharacterized ACR	NP_563516.1 (7e-24)	LGC
64	64923 - 66761	+	Predicted penicillin-binding protein 2	NP_716793.1 (1e-102)	gamma
65	66758 - 67315	+	Predicted rod shape-determining protein RodA	AAO90095.1 (5e-26)	gamma
66	67393 - 67857	+	Predicted rod shape-determining protein RodA	ZP_00090590.1 (1e-35)	gamma
67	67854 - 68741	+	Predicted membrane-bound lytic murein transglycosylase B	ZP_00067290.1 (1e-58)	gamma
68	68738 - 69895	+	Predicted D-alanyl-D-alanine carboxypeptidase	ZP_00126123.1 (2e-93)	gamma
69	69879 - 70709	+	Predicted D-alanine aminotransferase	NP_243677.1 (3e-36)	LGC
70	70702 - 71688	-	Predicted DNA polymerase III, delta subunit	NP_716797.1 (4e-12)	gamma
71	71672 - 72136	-	Hypothetical protein	-	-
72	72181 - 74595	-	Predicted Leucyl-tRNA synthetase	AAO90104.1 (0.0)	gamma
73	74592 - 75935	-	Predicted biotin carboxylase	ZP_00087052.1 (1e-147)	gamma
74	75937 - 76380	-	Predicted biotin carboxyl carrier protein	NP_246029.1 (4e-33)	gamma
75	76381 - 76821	-	Predicted 3-dehydroquinate dehydratase II	ZP_00123462.1 (6e-29)	gamma
76	76874 - 77290	-	Predicted thiol-disulfide isomerase/thioredoxin	NP_710001.1 (2e-12)	gamma
77	77362 - 78369	+	Predicted esterase/lipase	ZP_00011968.1 (5e-29)	alpha
78	78366 - 79964	+	Predicted ABC transporter, ATP-binding protein	NP_106147.1 (1e-155)	alpha
79	80043 - 81641	+	Predicted dihydroxyacid dehydratase	NP_713139.1 (1e-172)	spirochaetales
80	81644 - 82642	+	Predicted delta-aminolevulinic acid dehydratase	ZP_00065782.1 (4e-84)	gamma
81	82639 - 82965	+	Predicted thiol-disulfide isomerase/thioredoxin	ZP_00065824.1 (2e-28)	gamma
82	83095 - 84372	+	Predicted transcription termination factor Rho	NP_253926.1 (1e-178)	gamma
83	84365 - 85066	-	Hypothetical protein	-	-

84	85056	-	85967	-	Predicted porphobilinogen deaminase	O66621 (5e-51)	aquifecales
85	85964	-	86518	-	Predicted N6-adenine-specific methylase	NP_438926.1 (1e-29)	gamma
86	86628	-	87062	+	Potential flavoprotein oxygenase, DIM6/NTAB family	ZP_00067862.1 (2e-13)	gamma
87	87040	-	87531	+	Conserved hypothetical protein	ZP_00067936.1 (1e-16)	gamma
88	87524	-	88138	-	Predicted transcriptional regulator, AcrR family	ZP_00108788.1 (2e-19)	cyanobacteria
89	88237	-	89220	+	Predicted membrane-fusion protein, AcrA famly	NP_718832.1 (5e-26)	gamma
90	89222	-	92284	+	Predicted cation/multidrug efflux pump	NP_485696.1 (1e-121)	cyanobacteria
91	92499	-	93317	-	Predicted TPR-repeat-containing protein	NP_742784.1 (8e-50)	gamma
92	93398	-	94330	+	Predicted pseudouridylate synthase, 23S rRNA-specific	NP_796938.1 (2e-68)	gamma
93	94425	-	96137	+	Predicted thiamine pyrophosphate-requiring enzyme	ZP_00064897.1 (0.0)	gamma
94	96449	-	97492	+	Predicted ketol-acid reductoisomerase	ZP_00003033.1 (1e-119)	beta
95	97663		99189	+	16S rRNA		
96	99433		102194	+	23S rRNA		
97	102589	-	103182	+	Predicted dephospho-CoA kinase	O69082 (2e-39)	gamma
98	103342	-	106053	-	Predicted preprotein translocase subunit SecA	ZP_00067433.1 (0.0)	gamma
99	106096	-	107013	-	Predicted UDP-3-O-acyl-N-acetylglucosamine deacetylase	NP_253096.1 (1e-104)	gamma
100	107028	-	107750	-	Predicted rRNA methylase	NP_290810.1 (7e-26)	gamma
101	107747	-	109234	-	Predicted exoribonuclease	AAO90604.1 (5e-92)	gamma
102	109306	-	111915	-	Predicted TonB-dependent receptor	NP_421988.1 (4e-53)	alpha
103	111997	-	112398	-	Hypothetical protein	-	-
104	112464	-	114695	-	Predicted outer membrane receptor protein	NP_643138.1 (6e-48)	gamma
105	115018	-	116073	-	Predicted Zn-dependent alcohol dehydrogenase	AAG10028.1 (4e-65)	gamma
106	116152	-	117546	+	Predicted amidohydrolase	NP_420779.1 (1e-135)	alpha
107	117546	-	118811	+	Predicted amidohydrolase	NP_638718.1 (1e-29)	gamma
108	118817	-	118892	-	tRNA Thr (TGT anticodon)		
109	118915	-	119472	-	Predicted peptide methionine sulfoxide reductase	NP_439944.1 (1e-60)	cyanobacteria
110	119477	-	120226	-	Predicted biotin-(acetyl-CoA carboxylase) ligase	NP_252970.1 (2e-20)	gamma
111	120278	-	120361	+	tRNA Tyr (GTA anticodon)		
112	120482	-	120556	+	tRNA Thr (GGT anticodon)		
113	120594	-	121031	+	GTPases - translation elongation factor Tu (EF-Tu)	NP_799149.1 (3e-58)	gamma
114	121045	-	121782	+	GTPases - translation elongation factor Tu (EF-Tu)	AAO89781.1 (1e-106)	gamma
115	121853	-	121928	+	tRNA Trp (CCA anticodon)		
116	121959	-	122321	+	Predicted preprotein translocase subunit SecE	NP_252966.1 (5e-17)	gamma
117	122326	-	122853	+	Predicted transcription antiterminator NusG	NP_457922.1 (6e-60)	gamma
118	122853	-	123281	+	Ribosomal protein L11	NP_282996.1 (8e-51)	beta
119	123278	-	123970	+	Ribosomal protein L1	NP_252963.1 (7e-60)	gamma
120	124084	-	124662	+	Ribosomal protein L10	ZP_00067854.1 (2e-45)	gamma
121	124681	-	125061	+	Ribosomal protein L7/L12	ZP_00067853.1 (3e-28)	gamma
122	125101	-	128758	+	DNA-directed RNA polymerase beta subunit (RpoB)	ZP_00067852.1 (0.0)	gamma