

Synechococcus accessory genome (minus unique genes)

Synechococcus accessory genome (minus unique genes)						Synechococcus										Prochlorococcus		
						Subcluster 5.1A					Subcluster 5.1B		5.2	5.3	HL	LL		
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SS120
Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)													
1	6479		Conserved hypothetical membrane protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
2	6505		Conserved hypothetical membrane protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
3	6517		Conserved hypothetical membrane protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
4	6519		Conserved hypothetical membrane protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
5	2521		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
6	2533		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
7	2538		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
8	2544		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
9	2547		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
10	2550		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
11	2553		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
12	2561		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
13	2563		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
14	2564		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
15	2571		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
16	2572		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
17	2575		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
18	2577		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
19	2579		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
20	2580		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
21	2583		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
22	2588		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
23	2589		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
24	2590		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
25	2595		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
26	2597		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
27	2598		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
28	2599		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
29	2602		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
30	2603		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
31	2608		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
32	2609		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
33	2611		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
34	2613		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
35	2617		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
36	2621		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
37	2623		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
38	3107		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
39	3172		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
40	3179		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
41	3190		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
42	3193		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
43	3208		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
44	3227		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
45	3235		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
46	3237		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
47	3242		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
48	3250		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
49	3251		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
50	3261		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
51	3264		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
52	3265		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
53	3275		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
54	3279		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
55	3280		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
56	3284		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
57	3285		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
58	3293		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
59	3296		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
60	3298		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
61	3300		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
62	3310		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
63	3316		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
64	3317		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
65	3321		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
66	3322		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
67	3329		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
68	3331		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
69	3337		Conserved hypothetical protein	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
70	2559		Two component system sensor histidine kinase	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0
71	3150		AraC-type DNA-binding domain-containing proteins	2	2	1	0	0	0	1	0	0	0	0	0	0	0	0
72	2285		Conserved hypothetical protein	2	3	1	0	2	0	0	0	0	0	0	0	0	0	0
73	2524		Conserved hypothetical protein	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
74	2566		Conserved hypothetical protein	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
75	2620		Conserved hypothetical protein	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
76	3185		Conserved hypothetical protein	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
77	2531		conserved hypothetical protein distantly related to sialidases	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
78	2569		DNA breaking-rejoining enzymes, integrase/recombinase, C-terminal catalytic domain	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0
79	2568		DNA-directed RNA polymerase	2	2	1	0	1	0</									

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						Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	HL	LL
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SSL20	MIT9313
111	8010		truncated cation efflux transporter (CDF family)	2	5	0	1	4	0	0	0	0	0	0	0	0	0	0	
112	2093		Conserved hypothetical protein	2	5	0	1	0	4	0	0	0	0	0	0	0	0	0	
113	2094		Conserved hypothetical protein	2	5	0	1	0	4	0	0	0	0	0	0	0	0	0	
114	2480		Conserved hypothetical protein	2	9	0	1	0	8	0	0	0	0	0	0	0	0	0	
115	2882		Conserved hypothetical protein	2	2	0	1	0	1	0	0	0	0	0	0	0	0	0	
116	2916		Conserved hypothetical protein	2	2	0	1	0	1	0	0	0	0	0	0	0	0	0	
117	5183		Conserved hypothetical protein	2	2	0	1	0	1	0	0	0	0	0	0	0	0	0	
118	2881		Possible beta-glycosyltransferase, family 2	2	2	0	1	0	1	0	0	0	0	0	0	0	0	0	
119	6458		Conserved hypothetical membrane protein	2	2	0	1	0	0	1	0	0	0	0	0	0	0	0	
120	6498		Conserved hypothetical membrane protein	2	2	0	1	0	0	1	0	0	0	0	0	0	0	0	
121	2336		Conserved hypothetical protein	2	3	0	1	0	0	0	1	0	0	0	0	0	0	1	
122	2495		Conserved hypothetical protein	2	3	0	1	0	0	0	2	0	0	0	0	0	0	0	
123	2496		Conserved hypothetical protein	2	3	0	1	0	0	0	2	0	0	0	0	0	0	0	
124	2959		Conserved hypothetical protein	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
125	2961		Conserved hypothetical protein	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
126	2962		Conserved hypothetical protein	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
127	2967		Conserved hypothetical protein	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
128	5932		conserved hypothetical protein distantly related to glycosyltransferases	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
129	2966		conserved hypothetical protein distantly related to alpha-glycosyltransferases, family 4	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
130	5935		conserved hypothetical protein distantly related to glycosyltransferases, family 9	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
131	2965		Conserved hypothetical protein with tetratricopeptide repeat domains	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
132	2963		Possible beta-glycosyltransferase, family 41	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
133	2964		Possible beta-glycosyltransferase, family 41	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
134	2960		Possible Zn-dependent metalloprotease	2	3	0	1	0	0	0	1	0	0	0	0	0	0	1	
135	3002		Possible multicopper oxidase	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	
136	4695		Conserved hypothetical protein	2	2	0	1	0	0	0	0	1	0	0	0	0	0	0	
137	2838		N-acetylneuraminate synthase	2	2	0	1	0	0	0	0	0	1	0	0	0	0	0	
138	2337		Possible nucleoside-diphosphate sugar epimerase	2	3	0	1	0	0	0	0	0	1	0	0	0	0	1	
139	2241		Conserved hypothetical protein	2	4	0	0	0	2	2	0	0	0	0	0	0	0	0	
140	2885		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
141	2891		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
142	2894		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
143	2895		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
144	2896		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
145	2900		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
146	2902		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
147	2903		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
148	2904		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
149	2908		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
150	2912		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
151	2918		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
152	3055		Conserved hypothetical protein	2	3	0	0	0	2	1	0	0	0	0	0	0	0	0	
153	5272		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
154	6262		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
155	6273		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
156	6425		Conserved hypothetical protein	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
157	2327		Conserved hypothetical protein	2	3	0	0	0	1	1	0	0	0	0	0	1	0	0	
158	2097		Phage integrase family	2	5	0	0	0	3	2	0	0	0	0	0	0	0	0	
159	2890		Possible alpha-glycosyltransferase, family 60	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
160	2343		Possible-TPR Domain containing protein	2	3	0	0	0	1	1	0	0	0	0	0	0	0	1	
161	2911		Possible cytidine/deoxycytidine deaminase	2	2	0	0	0	1	1	0	0	0	0	0	0	0	0	
162	6180		Conserved hypothetical membrane protein	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	
163	6217		Conserved hypothetical membrane protein	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	
164	6324		Conserved hypothetical membrane protein	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	
165	6368		Conserved hypothetical membrane protein	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	
166	6403		Conserved hypothetical membrane protein	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	
167	2511		Conserved hypothetical protein	2	6	0	0	0	3	0	3	0	0	0	0	0	0	0	
168	3068		Alpha/beta superfamily hydrolase	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
169	3053		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
170	3066		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
171	3067		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
172	7397		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
173	8986		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	
174	8076		ABC-type multidrug transport system, ATPase and permease components	2	3	0	0	0	1	0	0	0	0	1	0	0	0	1	
175	6117		Conserved hypothetical membrane protein	2	3	0	0	0	2	0	0	0	0	1	0	0	0	0	
176	2382		Conserved hypothetical protein	2	3	0	0	0	2	0	0	0	0	1	0	0	0	0	
177	2741		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
178	2780		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
179	2781		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
180	4413		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
181	4649		Conserved hypothetical protein	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
182	2405		Conserved hypothetical protein	2	3	0	0	0	2	0	0	0	0	1	0	0	0	0	
183	2739		Glutathione S-transferase	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
184	2363		membrane-fusion protein	2	3	0	0	0	1	0	0	0	0	1	0	0	0	1	
185	2760		Peptidase family M23	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
186	2748		Possible aminoglycoside phosphotransferase	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
187	2770		Possible molybdopterin synthase sulfurylase	2	2	0	0	0	1	0	0	0	0	1	0	0	0	0	
188	2738		Sulfotransferase domain fused to a GAF domain	2	2	0													

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						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	ME4	SS120
222	6067		Conserved hypothetical membrane protein	2	2	0	0	0	0	1	1	0	0	0	0	0	0	0
223	8648		Conserved hypothetical protein	2	2	0	0	0	0	1	1	0	0	0	0	0	0	0
224	6040		Conserved hypothetical protein	2	5	0	0	0	0	4	1	0	0	0	0	0	0	0
225	6079		Possible transcriptional regulator	2	2	0	0	0	0	1	1	0	0	0	0	0	0	0
226	7348		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
227	7349		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
228	7383		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
229	7387		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
230	7479		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
231	7504		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
232	7506		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
233	7644		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
234	7703		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
235	7716		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
236	8210		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
237	8419		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
238	8440		Conserved hypothetical protein	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
239	7499		Possible urea transporter, UT family	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
240	7526		Response regulator receiver domain	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
241	7572		Sodium:solute symporter family	2	2	0	0	0	0	1	0	1	0	0	0	0	0	0
242	4518		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
243	4612		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
244	4620		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
245	4672		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
246	4688		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
247	4714		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
248	4751		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
249	4761		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
250	8127		Dehydrogenase (related to short-chain alcohol dehydrogenases)	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
251	4599		Possible FAD-dependent oxidoreductase	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
252	4454		Possible transporter of the major facilitator superfamily	2	2	0	0	0	0	1	0	0	1	0	0	0	0	0
253	4853		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	1	0	0	0	0
254	4913		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	1	0	0	0	0
255	5087		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	1	0	0	0	0
256	4837		Possible permease of the major facilitator superfamily	2	2	0	0	0	0	1	0	0	0	1	0	0	0	0
257	6683		Conserved hypothetical membrane protein	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
258	7075		Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
259	6566		Aldo/keto reductase family	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
260	2690		Conserved hypothetical protein	2	3	0	0	0	0	1	0	0	0	0	1	0	0	1
261	6930		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
262	6939		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
263	6948		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
264	7319		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
265	6743		Oxidoreductase alpha (molybdopterin) subunit	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
266	6622		RNA polymerase ECF-type (group 3) sigma factor	2	2	0	0	0	0	1	0	0	0	0	1	0	0	0
267	2699		Transaldolase	2	3	0	0	0	0	1	0	0	0	0	1	0	0	1
268	8138		Aldehyde dehydrogenase family protein	2	3	0	0	0	0	2	0	0	0	0	0	1	0	0
269	5642		Conserved hypothetical protein	2	2	0	0	0	0	1	0	0	0	0	0	1	0	0
270	5831		Gluconolactonase	2	2	0	0	0	0	1	0	0	0	0	0	1	0	0
271	2994		Alcohol dehydrogenase, class IV	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
272	2974		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
273	2980		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
274	2986		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
275	2996		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
276	3000		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
277	3019		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
278	3030		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
279	3038		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
280	3044		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
281	3045		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
282	2501		Conserved hypothetical protein	2	3	0	0	0	0	0	1	2	0	0	0	0	0	0
283	2972		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
284	2977		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
285	2982		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
286	2983		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
287	2987		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
288	2988		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
289	3001		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
290	3004		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
291	3011		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
292	3021		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
293	3022		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
294	3027		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
295	3032		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
296	3046		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
297	5938		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
298	5983		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0
299	7339		Conserved hypothetical protein	2	2	0	0	0	0	0	1	1	0	0	0	0	0	0</

						Synechococcus										Prochlorococcus			
						Subcluster 5.1A		Subcluster 5.1B		5.2	5.3	HL	LL						
						BLU07	CC9902	CC9605	WH4102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	PCC307	MED4	SS120	MIT9313
Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)														
333	2817		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
334	2823		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
335	2861		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
336	2453		Conserved hypothetical protein	2	3	0	0	0	0	0	2	0	0	1	0	0	0	0	0
337	2857		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
338	2858		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
339	2862		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
340	5007		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
341	2815		Conserved hypothetical secreted protein	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
342	2426		MFS family transporter	2	3	0	0	0	0	0	1	0	0	2	0	0	0	0	0
343	2444		Possible ABC transporter, substrate binding protein	2	3	0	0	0	0	0	2	0	0	1	0	0	0	0	0
344	2868		Possible thiurpin S-methyltransferase	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
345	2870		Possible ATPase	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
346	2844		Two-component system response regulator	2	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0
347	3015		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	1	0	0	0	1	0	0	0	0
348	3017		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	0	1	0	0	0	0
349	2676		Peptide deformylase	2	3	0	0	0	0	0	1	0	0	0	1	0	0	0	1
350	3016		Spermidine synthase	2	2	0	0	0	0	0	1	0	0	0	1	0	0	0	0
351	2947		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
352	2949		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
353	2950		Conserved hypothetical protein	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
354	5712		Possible glyoxalase	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
355	2951		Possible cyanophycin synthetase	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
356	2490		TPR-repeat-containing protein	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
357	2948		TPR-repeat-containing protein	2	2	0	0	0	0	0	1	0	0	0	0	1	0	0	0
358	2372		Conserved hypothetical membrane protein	2	3	0	0	0	0	0	0	1	2	0	0	0	0	0	0
359	2763		Monoamine oxidase	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
360	2411		Carbohydrate-selective porin, OprB family	2	3	0	0	0	0	0	0	1	2	0	0	0	0	0	0
361	2765		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
362	2381		Conserved hypothetical protein	2	3	0	0	0	0	0	2	1	0	0	0	0	0	0	0
363	2764		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
364	4452		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
365	4701		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
366	7451		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0
367	2854		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	0	1	0	0	0	0	0
368	2853		ArsR Possible transcriptional regulator	2	2	0	0	0	0	0	0	1	0	1	0	0	0	0	0
369	2034		Conserved hypothetical protein	2	5	0	0	0	0	0	0	1	0	1	0	0	0	0	3
370	2850		Conserved hypothetical protein	2	2	0	0	0	0	0	0	1	0	1	0	0	0		

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus			
						Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	HL	LL
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SSL20	MIT9313
444	2874		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
445	2875		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
446	2876		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
447	2878		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
448	2879		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
449	2880		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
450	9133		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
451	8856		D-lactate dehydrogenase	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
452	2221		FlaA DNA-directed RNA polymerase specialized sigma subunit	2	4	0	0	0	0	0	0	0	0	2	2	0	0	0	0
453	2848		integral membrane signal transducer protein	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
454	1981		MgtA Cation transport ATPase	2	6	0	0	0	0	0	0	0	0	2	4	0	0	0	0
455	2465		NAD(FAD)-dependent dehydrogenase	2	3	0	0	0	0	0	0	0	0	2	1	0	0	0	0
456	12	cpcC	Phycobilisome linker polypeptide CpcC, phycocyanin-associated	2	5	0	0	0	0	0	0	0	0	2	3	0	0	0	0
457	2828	cpcD	Phycobilisome linker polypeptide CpcD, phycocyanin-associated	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
458	2860		Possible ABC transporter, membrane component	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
459	2466		Possible DNA/RNA helicase	2	3	0	0	0	0	0	0	0	0	1	2	0	0	0	0
460	192		possible transposase	2	14	0	0	0	0	0	0	0	0	13	1	0	0	0	0
461	2091		Restriction endonuclease	2	5	0	0	0	0	0	0	0	0	1	4	0	0	0	0
462	2851		Sterol desaturase	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
463	7995	sodA	superoxide dismutase [Mn]	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
464	2434		Transposase	2	3	0	0	0	0	0	0	0	0	1	2	0	0	0	0
465	2835		Transposase	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
466	2429		XerC Integrase	2	3	0	0	0	0	0	0	0	0	1	2	0	0	0	0
467	2804		XerC Integrase	2	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0
468	2182		Acid phosphatase	2	4	0	0	0	0	0	0	0	0	1	0	1	0	0	2
469	2847		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0
470	5031		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0
471	2829		Kef-type K+ transport system, membrane component	2	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0
472	2827		Conserved hypothetical protein related to phosphatidylserine/phosphatidylglycerophosphate	2	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0
473	2845	clc4	Possible chloride channel	2	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0
474	2926		alpha-glycosyltransferase, family 4	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
475	2936		Bacterioferritin	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
476	2922		beta-glycosyltransferase, family 2	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
477	2921		Conserved hypothetical membrane protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
478	2023		Conserved hypothetical protein	2	5	0	0	0	0	0	0	0	0	0	1	1	1	1	1
479	2934		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
480	2937		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
481	2941		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
482	2944		Conserved hypothetical protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
483	7223		Conserved hypothetical secreted protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
484	8105		Cysteine synthase	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
485	2942		Glycerol-3-phosphate dehydrogenase [NAD(P)+]	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
486	2945		glycoside hydrolase family 19, distantly related to chitinases	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
487	2483		hydrolase, HAD superfamily	2	3	0	0	0	0	0	0	0	0	2	1	0	0	0	0
488	2955		Iron-sulfur cluster binding protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
489	2923	btpA	Photosystem I assembly protein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
490	2920		Possible alpha-glycosyltransferase, family 4	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
491	2935	cbtT	Precorrin-6Y C5,15-methyltransferase (Decarboxylating)	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
492	2943		Possible epimerase, PhzC/PhzF homolog	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
493	2927		Possible hydrolase (HAD superfamily)	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
494	2940		Possible periplasmic or secreted lipoprotein	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
495	9113	thrC	Threonine synthase	2	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0
496	2306		ABC-type polysaccharide/polyol phosphate transport system, ATPase component	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
497	2297		Beta-lactamase class C and other penicillin-binding proteins	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
498	2121		Conserved hypothetical protein	3	7	2	1	1	0	0	0	0	0	0	0	0	1	1	1
499	2273		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
500	2275		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
501	2296		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
502	2304		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
503	2305		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
504	2310		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
505	2311		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
506	2313		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
507	2315		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
508	2317		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
509	2322		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
510	2519		Conserved hypothetical protein	3	4	1	1	1	0	0	0	0	0	0	0	0	0	1	0
511	2545		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
512	2578		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
513	2591		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
514	3240		Conserved hypothetical protein	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
515	2151		two-domain glycosyltransferase, family 2	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0
516	2120		Conserved hypothetical protein	3	4	2	1	0	1	0	0	0	0	0					

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus		
						Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SSL120
554	2238		Possible phage integrase	3	4	0	1	2	1	0	0	0	0	0	0	0	0	0
555	2410		Conserved hypothetical protein	3	3	0	1	1	0	0	0	0	1	0	0	0	0	0
556	2236		Possible alpha-glycosyltransferase, family 4	3	4	0	1	0	1	0	0	2	0	0	0	0	0	0
557	2788		Conserved hypothetical membrane protein	3	3	0	1	0	0	1	0	0	0	1	0	0	0	0
558	2373		Conserved hypothetical protein with TPR repeat, possibly involved in cell envelope biogenesis	3	3	0	1	0	0	0	1	0	0	0	0	0	0	0
559	2349		Conserved hypothetical protein	3	4	0	0	1	1	0	0	0	0	1	0	0	0	1
560	2481		Conserved hypothetical protein	3	3	0	0	1	1	0	0	1	0	0	0	0	0	0
561	2939		Conserved hypothetical protein	3	3	0	0	1	1	0	0	0	0	0	0	0	0	0
562	3060		Conserved hypothetical protein	3	3	0	0	1	1	0	0	1	0	0	0	0	0	0
563	3642		Conserved hypothetical protein	3	4	0	0	1	1	0	0	0	1	0	0	0	0	1
564	4722		Conserved hypothetical protein	3	3	0	0	1	1	0	0	0	1	0	0	0	0	0
565	9027		Conserved hypothetical protein	3	3	0	0	1	1	0	0	0	1	0	0	0	0	0
566	2167		Conserved hypothetical protein	3	4	0	0	1	1	0	0	1	0	0	0	1	0	0
567	2402		Conserved hypothetical protein	3	3	0	0	1	1	0	0	0	1	0	0	0	0	0
568	2357		Conserved hypothetical membrane protein	3	4	0	0	1	0	1	0	0	0	0	1	0	0	1
569	2775		Conserved hypothetical protein	3	3	0	0	1	0	1	0	0	0	1	0	0	0	0
570	3947		Conserved hypothetical protein	3	4	0	0	1	0	1	0	0	0	0	0	0	1	0
571	7723		Conserved hypothetical protein	3	3	0	0	1	0	1	0	0	0	0	0	0	0	0
572	2487		Conserved hypothetical membrane protein	3	3	0	0	1	0	0	1	0	0	0	0	1	0	0
573	4449		Conserved hypothetical protein	3	3	0	0	1	0	0	0	0	1	0	0	1	0	0
574	5906		Conserved hypothetical protein	3	3	0	0	1	0	0	0	0	0	0	1	1	0	0
575	2028		beta-glycosyltransferase, family 2	3	5	0	0	1	0	0	0	0	0	0	1	1	1	0
576	2375		Possible ABC transporter, ATP binding and membrane components	3	3	0	0	0	1	0	0	1	0	0	0	0	0	0
577	2237		Conserved hypothetical protein	3	4	0	0	0	1	0	0	0	0	2	0	0	0	0
578	2482		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	0	0	0
579	2394		Conserved hypothetical protein	3	3	0	0	0	1	0	0	1	1	0	0	0	0	0
580	2260		Conserved hypothetical protein	3	4	0	0	0	1	0	0	0	1	0	0	2	0	0
581	2079		Possible ribosomal protein S6 modification protein	3	5	0	0	0	1	0	0	3	0	1	0	0	0	0
582	2184		Conserved hypothetical protein	3	4	0	0	0	1	0	0	0	0	1	1	0	0	1
583	1826		Conserved hypothetical protein with hemolysin-type calcium-binding regions	3	8	0	0	0	1	0	0	0	1	0	0	6	0	0
584	2228		Conserved hypothetical protein	3	4	0	0	0	1	0	0	0	0	0	1	2	0	0
585	2432		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
586	2433		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
587	2435		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
588	2436		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
589	2439		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
590	2440		Conserved hypothetical protein	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
591	2036		Possible nuclease	3	5	0	0	0	1	0	0	0	0	1	1	0	0	2
592	2826	chrA1	chromate transporter, CHR family	3	6	0	0	0	1	0	0	0	0	2	0	2	1	0
593	2478		UDP-N-acetylmuramyl pentapeptidase	3	3	0	0	0	1	0	0	0	0	0	1	1	0	0
594	3008		Conserved hypothetical membrane protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
595	2981		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
596	2984		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
597	2993		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
598	3007		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
599	3020		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
600	7965		Conserved hypothetical protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
601	3028		Conserved hypothetical secreted protein	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
602	2503		Possible ABC transporter, branched chain amino acid binding protein	3	5	0	0	0	0	2	1	2	0	0	0	0	0	0
603	2968		Possible alpha-glycosyltransferase, family 4	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
604	3012		Possible esterase related to lysophospholipase L1	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
605	2973		Sugar kinase, ribokinase family	3	3	0	0	0	0	1	1	1	0	0	0	0	0	0
606	2805		Conserved hypothetical protein	3	3	0	0	0	0	1	1	0	0	0	1	0	0	0
607	2856		Conserved hypothetical protein	3	3	0	0	0	0	1	1	0	0	0	1	0	0	0
608	2859		Conserved hypothetical protein related to glyoxalase/bleomycin resistance protein	3	3	0	0	0	0	1	1	0	0	0	1	0	0	0
609	2359		Possible transporter, MFS family	3	4	0	0	0	0	1	1	0	0	0	0	0	0	1
610	2933		Possible multicopper oxidase	3	3	0	0	0	0	1	1	0	0	0	0	1	0	0
611	2755		Conserved hypothetical protein	3	3	0	0	0	0	1	0	1	1	0	0	0	0	0
612	2767		Conserved hypothetical protein	3	3	0	0	0	0	1	0	1	1	0	0	0	0	0
613	2768		Conserved hypothetical protein	3	3	0	0	0	0	1	0	1	1	0	0	0	0	0
614	2747		PBPb, Bacterial periplasmic transport system protein	3	3	0	0	0	0	1	0	1	1	0	0	0	0	0
615	2813		Conserved hypothetical protein	3	3	0	0	0	0	1	0	1	0	0	0	1	0	0
616	3086		Conserved hypothetical protein	3	3	0	0	0	0	1	0	1	0	0	1	0	0	0
617	9124		Cation or drug efflux system protein	3	3	0	0	0	0	1	0	1	0	0	0	1	0	0
618	2946		Conserved hypothetical membrane protein	3	3	0	0	0	0	1	0	1	0	0	0	1	0	0
619	2930		Possible carboxyvinyl-carboxyphosphonate phosphorylmutase	3	3	0	0	0	0	1	0	1	0	0	0	1	0	0
620	2953		Possible secreted oxidoreductase	3	3	0	0	0	0	1	0	1	0	0	0	1	0	0
621	2789		Response regulator	3	3	0	0	0	0	1	0	0	1	1	0	0	0	0
622	2773		Conserved hypothetical protein	3	3	0	0	0	0	1	0	0	1	1	0	0	0	0
623	2759		LysR Transcriptional regulator	3	5	0	0	0	0	1	0	0	2	2	0	0	0	0
624	2790		two-component hybrid sensor histidine kinase	3	3	0	0	0	0	1	0	0	1	1	0	0	0	0
625	2347		Curli production assembly/transport component CsgG subfamily protein	3	4	0	0	0	0	1	0	0	0	1	0	0	0	1
626	8030		Two-component system response regulator	3	3	0	0	0	0	1	0	0	0	0	0	1	0	0
627	9107		Two-component system sensor histidine kinase	3	3	0	0	0	0	1	0	0	0	0	0	1	0	0
628	2361		Conserved hypothetical protein	3	4	0	0	0	0	1	0	0	0	0	1	1	0	0
629	2464	feoB	protein of the ferrous iron uptake family	3	4	0	0	0	0	1	0	0	0	2	1	0	0	0
630	2824		Uncharacterized protein involved in exopolysaccharide biosynthesis	3	3	0	0	0	0	1	0	0	0	1</				

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus	
						Subcluster 5.1A	Subcluster 5.1B	5.2	5.3	HL	LL	HL	LL	HL	LL	HL	LL
665	2412		Nucleoside deaminase	3	3	0	0	0	0	0	0	0	0	0	0	0	0
666	2371		Possible phosphoribosyltransferase	3	3	0	0	0	0	0	0	0	0	0	0	0	0
667	2467		Nucleotidyltransferase domain, NTP_transf_2 superfamily	3	3	0	0	0	0	0	0	0	0	0	0	0	0
668	2232		Conserved hypothetical protein	3	4	0	0	0	0	0	0	0	0	0	0	0	0
669	2489		Conserved hypothetical secreted protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
670	2486		Conserved hypothetical membrane protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
671	2180		Possible mechanosensitive ion channel	3	4	0	0	0	0	0	0	0	0	0	0	0	1
672	8021	mcsS3	small mechanosensitive ion channel, MscS family	3	4	0	0	0	0	0	0	0	0	0	0	0	1
673	2377		Conserved hypothetical secreted protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
674	2380		Conserved hypothetical protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
675	2417		Conserved hypothetical protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
676	2925		Peroxisomal protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0
677	1903		beta-glycosyltransferase, family 2	4	4	1	1	1	1	0	0	0	0	0	0	0	0
678	2138		Conserved hypothetical membrane protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
679	1906		Conserved hypothetical protein	4	6	1	2	2	1	0	0	0	0	0	0	0	0
680	1924		Conserved hypothetical protein	4	6	1	1	1	1	0	0	0	0	0	0	1	1
681	2008		Conserved hypothetical protein	4	5	1	1	1	2	0	0	0	0	0	0	0	0
682	2010		Conserved hypothetical protein	4	5	1	1	1	1	0	0	0	0	0	0	1	0
683	2020		Conserved hypothetical protein	4	5	1	1	1	2	0	0	0	0	0	0	0	0
684	2101		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
685	2107		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
686	2111		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
687	2118		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
688	2126		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
689	2134		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
690	2137		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
691	2140		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
692	2143		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
693	2148		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
694	2149		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
695	2156		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
696	2160		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
697	2161		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
698	2162		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
699	2283		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
700	2298		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
701	2307		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
702	3225		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
703	9077		Conserved hypothetical protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
704	2153		Possible ABC polysaccharide efflux transporter, membrane component	4	4	1	1	1	1	0	0	0	0	0	0	0	0
705	2157		Possible acyl carrier protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
706	2159		Possible acylneuraminate cytidyltransferase	4	4	1	1	1	1	0	0	0	0	0	0	0	0
707	2163		Possible integrase/recombinase	4	4	1	1	1	1	0	0	0	0	0	0	0	0
708	2102		Possible MTA/SAH nucleosidase	4	4	1	1	1	1	0	0	0	0	0	0	0	0
709	9017		Possible N-acetylneuraminic acid synthetase	4	4	1	1	1	1	0	0	0	0	0	0	0	0
710	2152		Possible polysaccharide efflux protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
711	2158		Possible polysaccharide export protein	4	4	1	1	1	1	0	0	0	0	0	0	0	0
712	1929		similar to capsule polysaccharide protein kpsS	4	6	2	1	2	1	0	0	0	0	0	0	0	0
713	2110		Conserved hypothetical protein	4	5	1	1	1	0	1	0	0	0	0	0	0	1
714	2280		Conserved hypothetical protein	4	4	1	1	1	0	1	0	0	0	0	0	0	0
715	8099		Ferredoxin	4	4	1	1	1	0	1	0	0	0	0	0	0	0
716	1833	isiB	Flavodoxin	4	8	1	1	2	0	1	0	0	0	0	0	1	1
717	9095	isiA	Iron stress-induced chlorophyll-binding protein (IsiA)	4	4	1	1	1	0	1	0	0	0	0	0	0	0
718	9073	cpcG3	phycobilisome rod-core linker polypeptide	4	4	1	1	1	0	1	0	0	0	0	0	0	0
719	2271		Possible hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	4	4	1	1	1	0	1	0	0	0	0	0	0	0
720	1904	trxB	Thioredoxin-disulfide reductase	4	7	1	1	1	0	1	0	0	0	0	0	1	1
721	2106		Transcriptional regulator, AraC family	4	4	1	1	1	0	0	0	0	0	0	0	0	0
722	2004		Conserved hypothetical protein	4	5	1	1	1	0	0	0	0	0	0	0	0	1
723	2108		Conserved hypothetical protein	4	4	1	1	1	0	0	0	0	0	0	0	0	0
724	2546		Possible transcriptional regulator, Crp/Fnr family	4	5	1	1	1	0	0	0	0	0	0	0	0	1
725	1920		Conserved hypothetical protein	4	6	1	1	1	0	0	0	0	0	0	0	1	1
726	1839		Conserved hypothetical membrane protein	4	8	1	1	1	0	0	0	0	0	0	0	1	2
727	2144		Conserved hypothetical protein	4	4	1	1	0	0	1	0	0	0	0	0	0	0
728	2309		Possible gluconolactonase	4	4	1	1	0	0	1	0	0	0	0	0	0	0
729	2277		Conserved hypothetical membrane protein	4	4	1	1	0	0	1	0	0	0	0	0	0	0
730	2308		Conserved hypothetical protein	4	4	1	1	0	0	1	0	0	0	0	0	0	0
731	2319		Conserved hypothetical protein	4	5	1	1	0	0	1	0	0	0	0	0	0	0
732	2555		Conserved hypothetical protein	4	5	2	1	0	0	1	0	0	0	0	0	0	0
733	1990		Conserved hypothetical protein	4	6	1	1	0	0	1	0	0	0	0	0	1	1
734	3192		Conserved hypothetical protein	4	4	1	1	0	0	1	0	0	0	0	0	0	0
735	1998		Short-chain dehydrogenase/reductase family enzyme	4	5	1	1	0	0	0	2	1	0	0	0	0	0
736	2523		Conserved hypothetical protein	4	4	1	1	0	0	0	0	0	0	0	0	0	0
737	1806		Autotransporter beta-domain-containing protein	4	8	3	2	0	0	0	0	0	0	0	0	0	0
738	2115	rpcG	Possible phycobilin:phycocyanin lyase-isomerase	4	4	1	0	1	1	0	0	0	0	0	0	0	0
739	1930		Conserved hypothetical protein	4	6	1	0	1	1	0	0	0	0	0	0	0	0
740	1763		Phage integrase family protein	4	8	1	0	2	4	0	0	0	0	0	0	0	0
741	2274		Conserved hypothetical protein	4	4	1	0	1	0	1	0	0	0	0	0	0	0
742	2122		Possible nuclease	4	5	1	0	1	0	1	0	0	0	0	0	1	1
743	2268		UDP-N-acetylglucosamine 2-epimerase	4	4	1	0	0	1	1	0	0	0	0	0	0	0
744	1748		Possible N-acetylneuraminic acid synthetase	4	5	1	0	0	1	1	0	0	0	0	0	0	1
745	7768		Conserved hypothetical protein	4	4	1	0	0	0	1	0	0	0	0	0	0	0
746	1999		Bacterial acid phosphatase	4	5	1	0	0	0	0	1	1	0	0	0	0	1
747	2001		Conserved hypothetical protein	4	5	1	0	0	0	0	0	0	0	0	0	0	0
748	2239		Conserved hypothetical protein	4	4	0	1	1	0	0	0	0	0	0	0	0	0
749	2224	mcsS5	Possible large-conductance mechanosensitive channel mscL	4	5	0	1	0	0	1	0	0	0	0	0	0	1
750	2512		ChaA Ca2+/H+ antiporter	4	4	0	1	0	0	1	0	0	0	0	0	0	0
751	2413		Conserved hypothetical protein	4	4	0	0	1	1	1	0	0	0	0	0	0	0
752	2406		Conserved hypothetical protein	4	4	0	0	1	1	1	0	0	0	0	0	0	0
753	2244		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
754	2245		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
755	1875		Fatty acid desaturase	4	7	0	0	1	1	0	0	0	0	0	0	1	1
756	2211		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
757	2252		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
758	2253		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
759	2254		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
760	2255		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
761	2257		Conserved hypothetical protein	4	4	0	0	1	1	0	0	0	0	0	0	0	0
762	2258		Possible flavoprotein involved in K+ transport (COG2072)	4	4	0</											

Synechococcus accessory genome (minus unique genes)

Line No.	Cluster No.	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus			
						Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	HL	LL
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	ME4	SS120	MIT9313
776	2404		Conserved hypothetical protein	4	4	0	0	1	0	1	0	0	1	0	0	1	0	0	0
777	4450		Conserved hypothetical protein	4	4	0	0	1	0	1	0	0	1	0	0	1	0	0	0
778	2415		Conserved hypothetical membrane protein	4	6	0	0	2	0	0	1	2	1	0	0	0	0	0	0
779	2217		Conserved hypothetical protein	4	4	0	0	1	0	0	1	1	1	0	0	0	0	0	0
780	4617		Conserved hypothetical protein	4	4	0	0	1	0	0	1	1	1	0	0	0	0	0	0
781	2078		Conserved hypothetical protein	4	5	0	0	2	0	0	1	1	0	1	0	0	0	0	0
782	2403		Conserved hypothetical protein	4	5	0	0	2	0	0	1	0	1	0	0	1	0	0	0
783	2391		Conserved hypothetical protein	4	4	0	0	0	1	1	0	0	1	1	0	0	0	0	0
784	2392		Conserved hypothetical protein	4	5	0	0	0	1	1	0	0	1	2	0	0	0	0	0
785	9011		Conserved hypothetical protein	4	4	0	0	0	1	1	0	0	0	1	1	0	0	0	0
786	2223		Conserved hypothetical protein	4	6	0	0	0	2	2	0	0	0	1	1	0	0	0	0
787	8026		ABC-type Mn2+/Zn2+ transport system permease component	4	4	0	0	0	1	1	0	0	0	1	0	1	0	0	0
788	8084		ABC-type Mn2+/Zn2+ transport systems, ATPase component	4	4	0	0	0	1	1	0	0	0	1	0	1	0	0	0
789	2462		Possible ABC zinc transport system substrate-binding protein	4	4	0	0	0	1	1	0	0	0	1	0	1	0	0	0
790	3025		Conserved hypothetical protein	4	4	0	0	0	1	0	1	1	1	0	1	0	0	0	0
791	1962		Conserved hypothetical protein	4	6	0	0	0	1	0	0	0	1	1	0	2	0	1	0
792	8025		ABC-type multidrug transport system, ATPase and permease components	4	6	0	0	0	1	0	0	0	1	1	0	1	1	1	0
793	2055		Conserved hypothetical protein	4	6	0	0	0	0	1	2	2	1	0	0	0	0	0	0
794	2185		Conserved hypothetical protein	4	5	0	0	0	0	1	1	1	1	0	0	0	0	1	0
795	2395		Possible carboxylesterase	4	4	0	0	0	0	1	1	1	1	0	0	0	0	0	0
796	2472		Conserved hypothetical protein	4	4	0	0	0	0	1	1	1	0	1	0	0	0	0	0
797	4833		Conserved hypothetical protein	4	5	0	0	0	0	1	1	1	0	2	0	0	0	0	0
798	2437		Indole-3-pyruvate decarboxylase	4	4	0	0	0	0	1	1	1	0	1	0	0	0	0	0
799	2033		Two-component system sensor histidine kinase	4	6	0	0	0	0	1	1	2	0	1	0	0	0	0	1
800	2499		Conserved hypothetical membrane protein	4	5	0	0	0	0	1	1	1	0	0	1	0	1	0	0
801	2505		Glutamine synthetase III	4	4	0	0	0	0	1	1	1	0	0	1	0	0	0	0
802	8125		Possible peptidase family protein with a signal peptide	4	4	0	0	0	0	1	1	1	0	0	1	0	0	0	0
803	2502		SAM-dependent methyltransferase	4	4	0	0	0	0	1	1	1	0	0	1	0	0	0	0
804	2488		Conserved hypothetical protein	4	4	0	0	0	0	1	1	1	0	0	0	1	0	0	0
805	2494		Conserved hypothetical secreted protein	4	4	0	0	0	0	1	1	1	0	0	0	1	0	0	0
806	4368		Conserved hypothetical protein	4	4	0	0	0	0	1	1	0	1	1	0	0	0	0	0
807	5089		Conserved hypothetical protein	4	4	0	0	0	0	1	1	0	1	1	0	0	0	0	0
808	2409		Gluconolactonase	4	4	0	0	0	0	1	1	0	1	1	0	0	0	0	0
809	2177		Conserved hypothetical membrane protein	4	5	0	0	0	0	1	1	0	1	0	0	1	0	0	1
810	2422		Possible esterase	4	4	0	0	0	0	1	1	0	0	1	1	0	0	0	0
811	2423		Probable alcohol dehydrogenase class III (Glutathione-dependent formaldehyde dehydrogenase)	4	4	0	0	0	0	1	1	0	0	1	0	1	0	0	0
812	2458		Conserved hypothetical membrane protein	4	4	0	0	0	0	1	1	0	0	1	0	1	0	0	0
813	8129		Glucose 1-dehydrogenase	4	4	0	0	0	0	1	1	0	0	1	0	1	0	0	0
814	4347		Conserved hypothetical protein	4	4	0	0	0	0	1	0	1	1	0	1	0	0	0	0
815	3740		Conserved hypothetical membrane protein	4	4	0	0	0	0	1	0	0	1	0	0	1	0	0	1
816	2365		Possible Tripartite transporter component (TRAP-T family)	4	4	0	0	0	0	1	0	0	1	0	0	1	0	0	1
817	2366		Possible Tripartite transporter component (TRAP-T family)	4	4	0	0	0	0	1	0	0	1	0	0	1	0	0	1
818	2364		Possible Tripartite transporter component (TRAP-T family), substrate binding protein	4	4	0	0	0	0	1	0	0	1	0	0	1	0	0	1
819	1933		Conserved hypothetical membrane protein	4	6	0	0	0	0	0	1	1	1	2	0	0	1	0	0
820	2215		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
821	2218		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
822	2219		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
823	2393		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
824	4862		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
825	3029		Conserved hypothetical secreted protein	4	4	0	0	0	0	0	1	1	1	1	0	0	0	0	0
826	2043		Conserved hypothetical protein	4	5	0	0	0	0	0	1	1	0	1	1	0	0	0	1
827	2227		Phosphoketolase	4	4	0	0	0	0	0	1	1	0	1	1	0	0	0	0
828	2452		Conserved hypothetical membrane protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
829	1819		Conserved hypothetical protein	4	8	0	0	0	0	0	4	1	0	1	0	1	0	0	1
830	2455		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
831	2457		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
832	2476		Conserved hypothetical secreted protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
833	2234		Drug/metabolite transporter (DMT) superfamily efflux protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
834	2456		Possible biopolymer transport protein	4	4	0	0	0	0	0	1	1	0	1	0	1	0	0	0
835	2262		Conserved hypothetical protein	4	4	0	0	0	0	0	1	1	0	0	1	1	0	0	0
836	1873	gltS	Possible Na+/glutamate symporter	4	7	0	0	0	0	0	1	1	0	0	1	1	1	1	1
837	2852		Conserved hypothetical membrane protein	4	4	0	0	0	0	0	1	0	0	1	1	1	0	0	0
838	2198		Conserved hypothetical membrane protein	4	4	0	0	0	0	0	0	1	1	1	1	0	0	0	0
839	2006		Conserved hypothetical protein	5	6	1	1	2	1	1	0	0	0	0	0	0	0	0	0
840	2007		Conserved hypothetical protein	5	6	1	1	1	2	1	0	0	0	0	0	0	0	0	0
841	2146		Conserved hypothetical protein	5	5	1	1	1	1	1	0	0	0	0	0	0			

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus			
						Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	HL	LL
						BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SSL20	MIT9313
887	2500	CRP	Conserved hypothetical secreted protein	5	9	0	0	2	0	1	2	2	0	0	2	0	0	0	
888	2049		Possible cAMP or cGMP receptor protein	5	6	0	0	1	0	1	0	1	1	0	0	0	0	1	
889	2181		Conserved hypothetical protein	5	5	0	0	1	0	1	0	1	0	0	1	0	0	1	
890	1959		Possible adenylate/guanylate cyclase	5	7	0	0	1	0	1	0	0	2	0	0	0	0	2	
891	2084		Deoxycytidine triphosphate deaminase	5	5	0	0	1	0	0	1	1	0	1	0	0	0	0	
892	2082		Conserved hypothetical protein	5	5	0	0	1	0	0	1	1	0	1	0	1	0	0	
893	2096		Conserved hypothetical protein	5	5	0	0	1	1	0	0	0	1	1	0	0	0	0	
894	2095		Conserved hypothetical membrane protein	5	5	0	0	1	1	0	1	1	0	0	0	1	0	0	
895	2213		Conserved hypothetical membrane protein	5	5	0	0	1	1	0	0	1	1	0	0	0	0	0	
896	2214		Possible Multisubunit Na ⁺ /H ⁺ antiporter subunit	5	5	0	0	1	0	0	1	0	1	1	1	0	0	0	
897	2076	Possible Multisubunit Na ⁺ /H ⁺ antiporter, MnhB subunit	5	5	0	0	1	0	0	1	0	1	1	1	0	0	0		
898	2074	Possible Multisubunit Na ⁺ /H ⁺ antiporter, MnhC subunit	5	5	0	0	1	0	0	1	0	1	1	1	0	0	0		
899	2212	Possible Multisubunit Na ⁺ /H ⁺ antiporter, MnhD subunit	5	5	0	0	1	0	0	1	0	1	1	1	0	0	0		
900	2075	Possible Multisubunit Na ⁺ /H ⁺ antiporter, MnhG subunit	5	5	0	0	1	0	0	1	0	1	1	1	0	0	0		
901	4316	Conserved hypothetical membrane protein	5	5	0	0	1	0	0	0	1	1	1	0	1	0	0		
902	9020	Conserved hypothetical protein	5	6	0	0	0	1	1	1	1	0	0	1	0	0	1		
903	2039	Permease	5	6	0	0	0	1	1	0	1	0	0	1	1	0	0		
904	2051	Nucleotide-diphosphate-sugar epimerase, membrane associated	5	6	0	0	0	1	1	0	0	0	1	1	1	0	0		
905	1943	proW	ABC glycine betaine/proline transporter, membrane component	5	6	0	0	0	1	0	1	1	1	1	0	0	0		
906	1944	proX	ABC glycine betaine/proline transporter, substrate binding component	5	6	0	0	0	1	0	1	1	1	1	0	0	0		
907	8061	proV	ABC-type proline/glycine betaine transport system, ATPase component	5	6	0	0	0	1	0	1	1	1	1	0	0	0		
908	1942	gbmt1	Glycine-sarcosine methyltransferase	5	6	0	0	0	1	0	1	1	1	1	0	0	0		
909	1941	gbmt2	Sarcosine-dimethylglycine methyltransferase	5	6	0	0	0	1	0	1	1	1	1	0	0	0		
910	2081	Acetate kinase	5	5	0	0	0	1	0	1	1	0	1	1	0	0	0		
911	2086	Conserved hypothetical protein	5	5	0	0	0	1	0	1	1	0	1	0	1	0	0		
912	2088	Conserved hypothetical secreted protein	5	5	0	0	0	1	0	1	1	0	1	0	1	0	0		
913	1985	Dienelactone hydrolase family protein	5	6	0	0	0	1	0	1	2	0	1	0	1	0	0		
914	2083	Possible low molecular weight phosphotyrosine protein phosphatase	5	5	0														

						Synechococcus										Prochlorococcus			
						Subcluster 5.1A			Subcluster 5.1B			5.2	5.3	HL	LL				
Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SS120	MIT9313
998	3013		Conserved hypothetical protein	6	6	0	0	1	1	0	1	1	0	1	1	0	0	0	0
999	1887		Possible phosphohydrolase	6	7	0	0	1	1	0	1	1	0	1	1	0	0	0	1
1000	1815	arsB	arsenate efflux pump	6	8	0	0	1	1	0	1	1	0	2	0	1	1	0	0
1001	1731		Conserved hypothetical protein	6	9	0	0	1	1	0	1	1	0	1	0	1	1	1	1
1002	2379		Conserved hypothetical protein	6	7	0	0	1	1	0	1	0	1	1	1	0	0	1	0
1003	4687		Conserved hypothetical protein	6	7	0	0	1	0	1	1	2	1	0	0	1	0	0	0
1004	1961		Possible transcriptional regulator protein	6	7	0	0	1	0	1	0	1	1	1	1	0	0	0	1
1005	1978	chrA2	chromate transporter, CHR family	6	6	0	0	1	0	0	1	1	1	1	0	1	0	0	0
1006	1742		Conserved hypothetical protein	6	10	0	0	0	1	1	1	0	1	1	5	0	0	0	0
1007	2751		Conserved hypothetical protein	6	7	0	0	0	1	1	1	0	1	1	2	0	0	0	0
1008	2063		Conserved hypothetical secreted protein	6	6	0	0	0	1	1	1	0	1	1	1	0	0	0	0
1009	2187		Conserved hypothetical protein	6	7	0	0	0	1	0	1	1	1	1	1	0	0	0	1
1010	2233		Conserved hypothetical protein	6	6	0	0	0	1	0	1	1	0	1	1	1	0	0	0
1011	3010		Conserved hypothetical membrane protein	6	7	0	0	0	0	1	1	1	1	1	1	0	0	1	0
1012	2056		Conserved hypothetical protein	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1013	2445		Conserved hypothetical protein	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1014	7830		Conserved hypothetical protein	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1015	2427		Conserved hypothetical secreted protein	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1016	2428		Conserved hypothetical secreted protein	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1017	9008		Possible membrane-fusion protein	6	8	0	0	0	0	2	1	1	1	1	1	0	0	0	1
1018	9121		Two-component system response regulator	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1019	2065		Two-component system sensor histidine kinase	6	6	0	0	0	0	1	1	1	1	1	1	0	0	0	0
1020	9019	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	6	6	0	0	0	0	1	1	1	1	1	0	1	0	0	0
1021	1934		Amino acid permease	6	7	0	0	0	0	1	1	1	1	1	0	1	0	0	1
1022	2196		Conserved hypothetical membrane protein	6	6	0	0	0	0	1	1	1	1	1	0	1	0	0	0
1023	1950		Conserved hypothetical protein	6	7	0	0	0	0	1	1	1	1	1	0	1	0	0	1
1024	2194		Conserved hypothetical protein	6	6	0	0	0	0	1	1	1	1	1	0	1	0	0	0
1025	2210																		

						Synechococcus										Prochlorococcus			
				No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Subcluster 5.1A	Subcluster 5.1B	5.2	5.3	HL	LL								
Line No.	Cluster No.	Gene Name	Product			BL107	CC9902	CC9605	WH4102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SS120	MIT9313
1109	1885		Conserved hypothetical membrane protein	7	8	0	0	0	0	1	1	1	1	1	1	1	0	0	1
1110	1947		Conserved hypothetical membrane protein	7	8	0	0	0	0	1	1	1	1	1	1	1	0	0	1
1111	1970		Conserved hypothetical membrane protein	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1112	1734		Conserved hypothetical protein	7	10	0	0	0	0	1	1	1	1	1	1	1	1	1	1
1113	1877		Conserved hypothetical protein	7	8	0	0	0	0	1	1	1	1	1	1	1	0	0	1
1114	1896		Conserved hypothetical protein	7	8	0	0	0	0	1	2	1	1	1	1	1	0	0	0
1115	1980		Conserved hypothetical protein	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1116	2723		Conserved hypothetical protein	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1117	7842		Conserved hypothetical protein	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1118	1971		Conserved hypothetical secreted protein	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1119	2032		Conserved hypothetical secreted protein	7	8	0	0	0	0	1	1	1	1	1	1	1	0	0	1
1120	2762		Conserved hypothetical secreted protein	7	8	0	0	0	0	2	1	1	1	1	1	1	0	0	0
1121	1733		Possible enzyme of the cupin superfamily	7	10	0	0	0	0	1	1	1	1	1	1	1	1	1	1
1122	9125		Possible RND family multidrug efflux transporter	7	9	0	0	0	0	2	1	1	1	1	1	1	0	0	1
1123	1889	DpsA	potential DpsA	7	8	0	0	0	0	1	1	1	1	1	1	1	0	0	1
1124	1976	mscS4	small mechanosensitive ion channel, MscS family	7	7	0	0	0	0	1	1	1	1	1	1	1	0	0	0
1125	1841		Conserved hypothetical membrane protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1126	1398	unk3	Conserved hypothetical protein	8	12	1	1	1	1	1	1	1	1	0	0	0	1	1	2
1127	1728		Conserved hypothetical protein	8	11	1	1	1	1	1	1	1	1	0	0	0	1	1	1
1128	1774		Conserved hypothetical protein	8	9	1	1	1	1	1	2	1	1	0	0	0	0	0	0
1129	1793		Conserved hypothetical protein	8	9	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1130	1846		Conserved hypothetical protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1131	1848		Conserved hypothetical protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1132	1854		Conserved hypothetical protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1133	1856		Conserved hypothetical protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1134	1860		Conserved hypothetical protein	8	13	1	1	1	2	1	1	1	1	0	0	0	1	1	2
1135	1864		Conserved hypothetical protein	8	8	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1136	1869		Conserved hypothetical protein	8															

Synechococcus accessory genome (minus unique genes)

				Synechococcus										Prochlorococcus					
				Subcluster 5.1A					Subcluster 5.1B					5.2	5.3	HL	LL		
Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	BL107	CC9902	CC9605	WH8102	CC9311	WH7803	WH7805	RS9916	RS9917	WH5701	RCC307	MED4	SSL20	MT19313
1220	1495		Conserved hypothetical protein	9	12	1	1	1	1	1	1	1	1	0	0	0	1	1	1
1221	1666		Conserved hypothetical protein	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1222	1804		Conserved hypothetical protein	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1223	1810		Conserved hypothetical protein	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1224	1953		Conserved hypothetical protein	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1225	2131		Conserved hypothetical protein	9	12	1	1	1	1	3	1	1	1	1	0	0	1	1	0
1226	2136		Conserved hypothetical protein	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1227	2560		Conserved hypothetical protein	9	10	1	1	1	1	1	1	1	1	0	0	0	1	1	0
1228	9063		Conserved hypothetical protein	9	12	1	1	1	1	1	1	1	1	0	0	1	1	1	1
1229	1543		Conserved hypothetical protein distantly related to glycosyltransferases, family 4	9	11	1	1	1	1	1	1	1	1	0	0	0	1	1	1
1230	1723		Conserved hypothetical secreted protein	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1231	1784		Conserved hypothetical secreted protein	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1232	1509		Cysteine synthase	9	12	1	1	1	1	1	1	1	1	0	0	1	1	1	1
1233	1286		FAD/FMN-containing dehydrogenase	9	13	1	1	1	1	1	2	1	1	0	0	0	1	1	1
1234	1508		Cystathionine beta-lyase/cystathionine gamma-synthase	9	12	1	1	1	1	1	1	1	1	0	0	1	1	1	1
1235	8120		peptidoglycan lytic transglycosylase	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1236	1753		Possible L-asparaginase	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1237	1775		Possible Na+/H+ antiporter, CPA2 family	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1238	1788		Possible peptidase (U32 family)	9	9	1	1	1	1	1	1	1	1	0	0	0	0	0	0
1239	1688		Ribonuclease PH	9	10	1	1	1	1	1	1	1	1	0	0	0	0	0	1
1240	1708		Beta-glycosyltransferase, family 2	9	10	1	1	1	1	1	1	1	1	0	1	0	0	0	1
1241	1558		Conserved hypothetical membrane protein	9	11	1	1	1	1	1	1	1	1	0	1	0	1	0	1
1242	1811		Conserved hypothetical protein	9	9	1	1	1	1	1	1	1	1	0	1	0	0	0	0
1243	2132		Conserved hypothetical protein with a signal peptide	9	9	1	1	1	1	1	1	1	1	0	1	0	0	0	0
1244	1556		Possible multidrug efflux ABC transporter	9	11	1	1	1	1	1	1	1	1	0	1	0	1	0	1
1245	1557		Possible multidrug efflux ABC transporter	9	11	1	1	1	1	1	1	1	1	0	1	0	1	0	1
1246	1395	pebA	15,16 dihydroxylverdin:ferredoxin oxidoreductase	9	12	1	1	1											

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus			
						Subcluster 5.1A	Subcluster 5.1B	5.2	5.3	HL	LL	HL	LL						
1331	1686	gmD	Pentapeptide and Tetrapeptide repeat-containing protein	9	10	1	0	0	1	1	1	1	1	1	0	0	1		
1332	2		Two-component system response regulator	9	11	0	1	1	1	2	1	1	1	1	0	1	0	1	
1333	1161		GDP-mannose 4,6-dehydratase	9	12	0	1	0	1	1	1	1	1	1	2	1	1	0	
1334	1898		Conserved hypothetical membrane protein	9	9	0	0	1	1	1	1	1	1	1	1	1	0	0	
1335	1899		Conserved hypothetical membrane protein	9	9	0	0	1	1	1	1	1	1	1	1	1	0	0	
1336	9126		Conserved hypothetical membrane protein	9	10	0	0	1	1	1	1	1	1	1	1	1	0	0	
1337	190		Conserved hypothetical protein	9	23	0	0	1	1	5	2	2	4	3	2	1	0	0	
1338	1738		Conserved hypothetical protein	9	10	0	0	1	1	1	1	1	1	1	1	1	0	0	
1339	2048		Conserved hypothetical protein	9	10	0	0	1	1	1	1	1	1	1	1	1	0	0	
1340	1163		Conserved hypothetical secreted protein	9	14	0	0	1	1	1	2	1	1	2	3	1	0	0	
1341	8118	envZ	Cytochrome c oxidase subunit I	9	11	0	0	1	1	1	1	1	1	1	2	2	0	0	
1342	1900		Cytochrome c oxidase subunit II	9	9	0	0	1	1	1	1	1	1	1	1	1	0	0	
1343	1827		Cytochrome c oxidase subunit III	9	9	0	0	1	1	1	1	1	1	1	1	1	0	0	
1344	1735		Fe-S oxidoreductase	9	10	0	0	1	1	1	1	1	1	1	1	1	0	0	
1345	1737		HKIII HAMP, chk91, Possible osmosensory histidine kinase	9	10	0	0	1	1	1	1	1	1	1	1	1	0	0	
1346	1536		Possible flavoprotein related to choline dehydrogenase	9	13	0	0	1	1	1	2	2	1	1	2	1	2	0	0
1347	1657		Possible membrane-bound transcriptional regulator	9	11	0	0	1	1	1	1	1	1	1	1	2	1	0	0
1348	1658		Possible phosphohistidine phosphatase	9	11	0	0	1	1	1	1	1	1	1	1	1	0	0	
1349	1732		Possible Pirin-related protein	9	10	0	0	1	1	1	1	1	1	1	1	1	1	0	0
1350	1828		Possible polysaccharide-forming beta-glycosyltransferase, family 2	9	9	0	0	1	1	1	1	1	1	1	1	1	0	0	
1351	8017	phoR	RRII, OmpR, crr72	9	10	0	0	1	1	1	1	1	1	1	1	0	0	1	
1352	1531		Two-component system sensor histidine kinase, phosphate sensing PhoR	9	12	0	0	1	1	1	0	1	1	1	1	1	1	0	3
1353	34	groL2	60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL protein 2)	10	13	1	1	1	1	1	1	1	1	1	1	0	1	1	
1354	8060		ABC transporter for amino acids, ATP binding component	10	12	1	1	1	1	1	1	1	1	1	1	0	0	1	
1355	1309		ABC transporter, substrate binding protein	10	13	1	1	1	2	1	2	1	1	1	1	0	0	0	
1356	1600		ABC transporter, substrate binding protein, possibly Mn	10	13	1	1	1	1	1	1	1	1	1	1	0	1	1	
1357	22		ABC-type Mn2+/Zn2+ transport system ATPase component	10	13	1	1	1	1	1	1	1	1	1	1	0	1	1	
1358	1244		ABC-type Mn2+/Zn2+ transport system permease component	10	13	1	1	1	1	1	1	1	1	1	1	0	1	1	
1359	1587		CbbX protein homolog	10	11	1	1	1	1	1	1								

Line No.	Cluster No. in cyanorak	Gene Name	Product	No. of Synechococcus strains per cluster	No. of sequ. per cluster (14 genomes)	Synechococcus										Prochlorococcus	
						Subcluster 5.1A	Subcluster 5.1B	5.2	5.3	HL	LL	HL	LL	HL	LL	HL	LL
1442	26		Cysteine synthase	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1443	1588	smr	DMT family multidrug efflux pump	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1444	1370	gpgP	Glucosyl-3-phosphoglycerate phosphatase	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1445	1368	gpgS	Glucosyl-3-phosphoglycerate synthase	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1446	1539		Glutamate dehydrogenase/leucine dehydrogenase	10	11	1	1	1	2	1	1	1	1	1	1	1	1
1447	1697		Histone deacetylase family protein	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1448	1285		Homoserine O-succinyltransferase	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1449	1344		Integral membrane protein possibly involved in chromosome condensation	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1450	1548		Integral membrane protein possibly involved in chromosome condensation	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1451	1234	mqaA	Malate:quinone oxidoreductase	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1452	1284		O-Acetyl homoserine sulphydrylase	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1453	1187		Possible flavoprotein	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1454	1663		Possible glycine betaine transporter, BCCT family	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1455	1690		Possible Pex protein (Period-extender gene product)	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1456	1224		Possible pterin-4-alpha-carbinolamine dehydratase	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1457	1503		Possible sodium-dependent transporter, NSS family	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1458	8100		RNA-binding protein, RRM domain	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1459	1424		RRII, LuxR	10	13	1	1	1	1	2	2	2	1	1	1	1	1
1460	1585		SAM-dependent methyltransferase	10	11	1	1	1	1	1	1	1	1	1	1	1	1
1461	1662		Sarcosine oxidase	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1462	1564		Secreted protein with pentapeptide repeats	10	11	1	1	1	1	1	1	1	1	1	1	1	1
1463	1511		S-isoprenylcysteine O-methyltransferase related enzyme	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1464	964	alsT	Sodium:alanine symporter family protein	10	14	1	1	1	1	1	2	2	2	1	1	1	1
1465	1369		sucrose phosphorylase	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1466	45	sulP2	sulfate ion transporter	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1467	1925		Conserved hypothetical membrane protein	10	11	1	1	2	1	1	1	1	1	1	1	1	1
1468	62		Conserved hypothetical protein	10	21	3	2	3	3	1	1	3	0	1	1	0	2
1469	94		Conserved hypothetical protein	10	16	1	2	1	2	1	1	1	0	2	2	0	0
1470	162		Conserved hypothetical protein	10	16	1	2	2	1	1	1	2	0	2	1	0	0
1471	1225		Conserved hypothetical protein	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1472	1674		Conserved hypothetical protein	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1473	1726		Conserved hypothetical protein	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1474	1291		Conserved hypothetical secreted protein	10	14	2	2	2	2	1	1	1	1	1	1	1	1
1475	1376		Hydroxyacid dehydrogenase/reductase family protein	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1476	1678		Molybdenum cofactor biosynthesis protein A	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1477	1670		Molybdenum cofactor biosynthesis protein B	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1478	1673		Molybdenum cofactor biosynthesis protein C	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1479	1672		Molybdopterin biosynthesis protein moeA	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1480	1749		Molybdopterin converting factor subunit 1	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1481	1671		Molybdopterin converting factor subunit 2	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1482	1677		Molybdopterin-guanine dinucleotide biosynthesis protein A	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1483	1675	narB	nitrate reductase	10	10	1	1	1	1	1	1	1	1	1	1	1	1
1484	1619		Possible cytochrome P450	10	11	1	1	1	1	1	1	1	1	1	1	1	1
1485	1171		Possible thioredoxin	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1486	1264		Short-chain dehydrogenase/reductase (SDR) superfamily	10	13	1	1	1	1	1	1	1	1	1	1	1	1
1487	8098		Ferredoxin	10	11	1	1	2	1	1	1	0	1	1	1	0	0
1488	1576		glycoside hydrolase, family 13	10	11	1	1	1	1	1	1	1	1	1	1	1	1
1489	8045	bicA	SulP-type bicarbonate transporter	10	10	1	1	1	1	1	1	0	1	1	1	1	1
1490	1367	urtD	ATP-binding subunit of urea ABC transporter UrtD	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1491	8074	urtE	ATP-binding subunit of urea ABC transporter UrtE	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1492	713		Conserved hypothetical protein	10	14	1	1	1	1	1	1	1	1	2	1	1	1
1493	1555		Conserved hypothetical protein	10	11	1	1	1	1	1	1	1	1	1	1	1	1
1494	1182		Transglutaminase-like enzyme	10	13	1	1	1	1	1	1	1	1	3	1	1	0
1495	1365	urtB	Urea ABC transporter, membrane component	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1496	1366	urtC	Urea ABC transporter, membrane component	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1497	1361	ureD	Urease accessory protein D	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1498	1362	ureE	Urease accessory protein E	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1499	1363	ureF	Urease accessory protein F	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1500	1364	ureG	Urease accessory protein G	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1501	1358	ureC	Urease alpha subunit	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1502	1359	ureB	Urease beta subunit	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1503	1360	ureC	Urease gamma subunit	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1504	1173		2-dehydro-3-deoxyphosphooctonate aldolase	10	12	1	1	2	1	0	1	1	1	1	1	0	0
1505	1172		3-deoxy-manno-octulosonate cytidyltransferase	10	12	1	1	2	1	0	1	1	1	1	1	0	0
1506	1323		Conserved hypothetical membrane protein	10	12	1	1	1	1	1	1	1	1	1	1	1	1
1507	41		Conserved hypothetical protein	10	13	1	1	1	2	0	1	2	1	2	1	0	0
1508	91		Conserved hypothetical protein	10	14	1	1	2	1	0	1	1	1	1	1	0	3
1509	215		Conserved hypothetical protein	10	13	1	1	1	1	0	1	1	1	1	1	1	1
1510	1094		Conserved hypothetical protein	10	13	1	1	1	1	0	1	1	1	1	1	1	1
1511	1951		Conserved hypothetical protein	10	13	1	1	1	1	0	1	1	2	1	1	1	0
1512	1305		dTDP-4-dehydroharnose 3,5-epimerase	10	12	1	1	1	1	1	0	1	1	1	2	1	0
1513	1515		dTDP-glucose-4,6-dehydratase	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1514	1513		glucose-1-phosphate thymidyltransferase	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1515	1333		Low specificity phosphatase (HAD superfamily)	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1516	1443		NUDIX hydrolase	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1517	1332		Polysialic acid capsule expression protein	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1518	1514		Possible dTDP-4-dehydroharnose reductase	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1519	1401		Possible enolase-phosphatase E-1	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1520	1324		Possible inverting glycosyltransferase family 83 utilizing lipid monophospho-sugar donors	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1521	1402		Sugar aldolase	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1522	1630		Conserved hypothetical membrane protein	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1523	1612		Conserved hypothetical protein	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1524	1627		Conserved hypothetical protein	10	12	1	1	1	1	0	1	1	1	1	1	1	0
1525	1709		Conserved hypothetical protein	10	12	1	1	1	1	0	1	1	1	1	1	1	0
1526	1807		Conserved hypothetical protein	10	10	1	1	1	1	0	1	1	1	1	1	1	0
1527	1945		Conserved hypothetical protein	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1528	1786		Possible group 3 RNA polymerase sigma factor	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1529	605		Possible metalloendopeptidase	10	11	1	1	1	1	0	1	1	1	1	1	1	0
1530	400		Possible small-conductance mechanosensitive channel	10	15	1	1	1	1	0	2	2	3	1	2	1	0
1531	2164		Conserved hypothetical membrane protein	10	10	1	1	1	1	1	0	1	1	1	1	1	0
1532	1375		Conserved hypothetical protein	10	12	1	1	1	1	1	0	1	1	1	1	1	0
1533	2171		Conserved hypothetical protein	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1534	2535		Conserved hypothetical protein	10	11	1	1	1	1	1	0	1	1	1	1	1	0
1535	1629		Phosphoglycerate mutase family protein	10	11	1	1	1	1	1</							