Transcription/Termination Factors

Top COG hit	2nd COG hit	RPA#	or#	Gene Name	Proteome positive	size # of aa	Protein domains from N-terminal to C-terminal (see explanation at the bottom) (in pairs of columns in black text - 1st column is the interpro domain name, 2nd column is the Pfam or Smart db domain name					
Sigma Factors												
COG0568 2e-97	COG1191 4e-29	RPA1288	or1917	rpoD	Y	699	NULL	P:sigma70_r1_1 sigma70_r2 sigma70_r3 sig	Sigma-70 factor family	P:sigma70_r1_2		
COG1508 e-130	none	RPA0050	or1000	rpoN	Y	549	Sigma-54 factor family	P:sigma54_AID	Sigma-54 factor, core	P:sigma54_CBD	NULL	P:sigma54_DBD
COG1544 5e-17	none	RPA0051	or1001	RPA0051	Y	202	Sigma 54 modulation protein/ribosomal protein S30EA	T:yfiA				
COG0568 8e-70	COG1191 2e-18	RPA0367	or5981	rpoH	Y	300	NULL	P:sigma70_r2 sigma70_r4				
COG1595 3e-15	COG4941 0.004	RPA4098	or0418	RPA4098	Y	233	NULL	P:sigma70_r2				
COG1595 2e-30	COG4941 0.001	RPA4225	or0511	RPA4225	Y	182	NULL	P:sigma70_r2				
COG1595 4e-26	COG4941 3e-06	RPA4792	or0933	RPA4792	N	204	NULL	P:sigma70_r2 sigma70_r4				
COG1595 6e-30	COG1191 1e-06	RPA0639	or1413	RPA0639	N	233	NULL	P:sigma70_r2 sigma70_r4				
COG1595 1e-22	COG4941 5e-04	RPA1116	or1776	RPA1116	N	302	NULL	P:sigma70_r2				
COG1595 1e-13	none	RPA1334	or1964	RPA1334	N	182	NULL (FecI)	P:sigma70_r2				
COG1595 6e-13		RPA1339	or1969	RPA1339	N	182	(FecI)					
COG1595 2e-14	none	RPA1347	or1979	RPA1347	N	184	NULL (FecI)	P:sigma70_r2				
COG1595 2e-21	COG4941 1e-06	RPA1635	or2211	RPA1635	N	183	NULL	P:sigma70_r2				
COG1595 2e-22	COG2197 4e-04	RPA1813	or2346	RPA1813	N	203	NULL	P:sigma70_r2				
COG1595 7e-29	COG4941 1e-05	RPA1819	or2352	RPA1819	Y	190	NULL (FecI)	P:sigma70_r2 sigma70_r4				
COG1595 4e-18	COG1191 3e-04	RPA2391	or2798	RPA2391	N	206	NULL (FecI)	P:sigma70_r2 sigma70_r4				
COG1595 7e-23	COG1191 6e-06	RPA3282	or3841	RPA3282	N	174	NULL (FecI)	P:sigma70_r2 sigma70_r4				
COG1595 1e-29	COG1191 1e-08	RPA0550	or5842	RPA0550	N	196	NULL	P:sigma70_r2 sigma70_r4				
COG1595 2e-23	COG4941 0.001	RPA4448	or6597	RPA4448	N	245	NULL	P:sigma70_r2				
COG4941 e-133	COG1595 2e-13	RPA1109	or1769	RPA1109	N	423	NULL	P:sigma70_r2				
Termination/Antitermination Factors												
COG1158 0.0	COG1157 1e-26	RPA0296	or6037	rho	Y	422	Cold-shock DNA-binding domain	S:CSP	SM:AAA ATPase	TF:Transcription termination factor Rho		
COG0195 3e-52		RPA0438	or5924	nusA	Y	537	PF:S1 RNA binding	PF:/SM:KH domain / RNA binding				
COG0781 1e-27		RPA2729	or3088	nusB	Y	177	Antitermination protein NusB					
COG0250 3e-51		RPA3274	or3849	nusG	Y	176	Bacterial transcription antitermination protein NusG					
Elongation Factors												
COG0782 4e-39		RPA4072	or0397	greA	Y	158	Prokaryotic transcription elongation factor GreA/GreB					
COG0782 3e-20		RPA0866	or5612	rnk	Y	134	Prokaryotic transcription elongation factor GreA/GreB					
COG0782 3e-19		RPA3829	or7082	RPA3829	Y	164	Prokaryotic transcription elongation factor GreA/GreB					
Transcription factors												
COG1278 8e-21	none	RPA1173	or5400	cspA1	Y	87	Cold-shock DNA-binding domain	P:CSD S:CSP				
COG1278 2e-17	none	RPA2525	or2911	cspA2	Y	236	Cold-shock DNA-binding domain	P:CSD CSD S:CSP CSP				
COG1278 1e-22	none	RPA3053	or4026	cspA3	Y	68	Cold-shock DNA-binding domain	P:CSD S:CSP				
COG1278 5e-22	none	RPA3399	or3569	cspA4	N	76	Cold-shock DNA-binding domain	P:CSD S:CSP				
COG1278 7e-24	none	RPA3672	or0121	cspA5	Y	85	Cold-shock DNA-binding domain	P:CSD S:CSP				
COG1420 2e-94	none	RPA0330	or1199	hrcA	N	363	Negative regulator of class I heat shock protein	P:HrcA T:hrcA				
COG0583 1e-20	none	RPA2322	or2753	RPA2322	N	298	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 1e-31	none	RPA1769	or4978	RPA1769	N	297	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 1e-39	none	RPA4076	or0401	RPA4076	Y	308	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 2e-28	none	RPA3738	or0171	RPA3738	N	297	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 2e-28	COG2005 9e-04	RPA4283	or6740	RPA4283	N	302	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 2e-31	none	RPA0430	or1269	oxyR	N	313	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 2e-32	COG2005 0.002	RPA1721	or2280	RPA1721	N	306	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 2e-33	none	RPA4695	or0852	ligR	N	301	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 3e-20	none	RPA3172	or3409	RPA3172	N	283	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 3e-24	none	RPA2994	or4065	RPA2994	Y	293	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 3e-28	none	RPA1562	or5120	RPA1562	N	325	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 3e-29	none	RPA1746	or4993	RPA1746	N	317	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 4e-29	COG1654 0.004	RPA4114	or0434	RPA4114	N	335	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 4e-32	none	RPA0809	or5650	RPA0809	N	288	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 4e-34	none	RPA0551	or5841	RPA0551	N	294	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 5e-25	none	RPA0130	or1058	RPA0130	N	293	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 5e-25	none	RPA2222	or2685	RPA2222	N	316	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 5e-29	none	RPA2642	or3016	RPA2642	N	297	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 5e-33	none	RPA0731	or1480	RPA0731	N	298	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 5e-35	none	RPA0911	or1619	RPA0911	N	308	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 6e-30	none	RPA2676	or4314	RPA2676	N	305	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 7e-24	COG2005 3e-05	RPA4151	or0460	RPA4151	N	291	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 7e-33	COG1321 0.003	RPA4747	or0896	RPA4747	N	305	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 7e-37	COG2005 7e-04	RPA1555	or5126	cbbR	N	323	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 8e-24	none	RPA1805	or2339	RPA1805	N	317	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 8e-30	none	RPA3387	or3562	RPA3387	Y	339	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0583 9e-25	none	RPA3796	or0205	RPA3796	N	277	Bacterial regulatory protein LysR, HTH motif	P:HTH_1	LysR substrate binding domain			
COG0703 9e-31	COG3620 7e-06	RPA4787	or0929	RPA4787	Y	306	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE	Shikimate kinase ?			
COG1396 0.002	none	RPA2481	or4448	RPA2481	N	279	Helix-turn-helix motif	S:HTH_XRE	unknown domain			
COG1396 0.008	none	RPA4134	or0444	RPA4134	N	93	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG1396 2e-07	COG1476 2e-06	RPA2607	or4370	RPA2607	Y	208	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE	CUPIN			
COG1396 2e-09	COG1476 5e-04	RPA0443	or5920	RPA0443	Y	140	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG1396 4e-06	COG1813 3e-05	RPA4129	or0441	RPA4129	Y	117	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG1396 7e-05	COG1395 1e-04	RPA3869	or7051	RPA3869	N	274	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE	unknown domain			
COG1813 4e-04	COG1476 0.001	RPA2243	or2692	RPA2243	N	82	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG2944 8e-13	COG1476 6e-06	RPA3162	or3946	RPA3162	N	122	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG3093 5e-20	none	RPA1290	or5314	RPA1290	N	108	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG3655 3e-21	none	RPA0927	or5555	RPA0927	N	70	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG3800 e-108	COG1396 1e-06	RPA4395	or0641	RPA4395	Y	481	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE	unknown domain			
COG5499 1e-21	none	RPA3130	or3972	RPA3130	N	127	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
COG5606 6e-08	COG1396 0.006	RPA3828	or0231	RPA3828	N	66	Helix-turn-helix motif	P:HTH_3 S:HTH_XRE				
none	none	RPA1926	or2443	RPA1926	N	284	Helix-turn-helix motif	S:HTH_XRE	unknown domain			
none	none	RPA3328	or3806	RPA3328	N	139	Helix-turn-helix motif	S:HTH_XRE	small unknown domain			
COG3620 1e-04	none	RPA4327	or6706	RPA4327	N	90	Helix-turn-helix motif	P:HTH_3				
COG0864 1e-30	none	RPA4756	or6341	RPA4756	N	149	Helix-turn-helix protein, CopG family	P:HTH_4				
none	none	RPA4131	or6857	RPA4131	N	155	Helix-turn-helix protein, CopG family	P:HTH_4				
COG0640 2e-07	none	RPA0997	or1678	RPA0997	N	143	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR				
COG0640 4e-11	COG4189 7e-07	RPA1019	or1695	RPA1019	N	114	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR				

COG0640 2e-06	COG2345 0.002	RPA1282	or5320	RPA1282	N	105	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG0640 6e-06	COG4189 7e-06	RPA2161	or2642	RPA2161	N	105	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG0640 2e-09	COG4189 7e-08	RPA2256	or2701	arsR1	N	111	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG4189 3e-08	COG0640 7e-08	RPA3556	or7299	arsR2	N	119	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG0640 4e-09	COG4189 3e-04	RPA3559	or7296	arsR3	N	100	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG0640 9e-09	COG4189 9e-06	RPA3561	or0036	RPA3561	N	119	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG0640 8e-08	none	RPA4474	or0700	RPA4474	N	125	Bacterial regulatory protein, ArsR family	P:HTH_5 S:HTH_ARSR		
COG1349 1e-60	COG2378 4e-04	RPA4411	or6631	glpR	N	266	Bacterial regulatory protein, DeoR family	P:deoR S:HTH_DEOR		
COG0789 2e-17	none	RPA4825	or0955	RPA4825	N	118	Bacterial regulatory protein, MerR family	P:merR S:HTH_MERR		
COG0789 2e-19	none	RPA3261	or3465	hmrR	N	134	Bacterial regulatory protein, MerR family	P:merR S:HTH_MERR		
COG0789 3e-13	none	RPA2743	or3101	RPA2743	N	251	Bacterial regulatory protein, MerR family	S:HTH_MERR	small unknown domain	
COG1309 7e-11	none	RPA0093	or1034	RPA0093	N	216	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-06	none	RPA0110	or1043	RPA0110	N	221	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-04	none	RPA0402	or1247	RPA0402	N	207	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-04	none	RPA0463	or1284	RPA0463	N	210	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 8e-05	none	RPA0903	or1613	RPA0903	N	200	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 5e-06	none	RPA0936	or1633	RPA0936	N	191	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-05	none	RPA1107	or1767	RPA1107	N	183	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-09	none	RPA1113	or1773	RPA1113	Y	235	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 0.0003		RPA1129	or1789	RPA1129	N					
COG1309 2e-10	none	RPA3544	or0019	RPA3544	N	217	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-09	none	RPA3769	or0190	RPA3769	N	227	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-09	none	RPA1704	or2266	RPA1704	N	236	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-04	none	RPA1854	or2377	RPA1854	N	212	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-08	none	RPA1954	or2462	RPA1954	N	229	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 6e-07	none	RPA2294	or2733	RPA2294	N	232	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 5e-04	none	RPA2441	or2845	RPA2441	N	231	Bacterial regulatory protein TetR, HTH motif	P:tetR	Tetracyclin repressor, C-terminal	
COG1309 3e-07	COG3226 0.002	RPA3905	or0285	RPA3905	N	188	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-08	none	RPA2968	or3262	RPA2968	N	250	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-09	none	RPA3021	or3300	RPA3021	Y	196	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 7e-07	COG3226 2e-05	RPA3290	or3483	RPA3290	N	221	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 8e-09	none	RPA3415	or3578	RPA3415	N	212	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-06	none	RPA3451	or3712	RPA3451	N	223	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-06	none	RPA3403	or3752	RPA3403	Y	211	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-12	COG3413 2e-04	RPA3300	or3821	RPA3300	N	249	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-08	COG3226 9e-07	RPA4085	or0408	RPA4085	Y	209	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-05	none	RPA4091	or0412	RPA4091	N	232	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-10	none	RPA4097	or0416	RPA4097	N	209	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-06	none	RPA2759	or4261	RPA2759	N	226	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 7e-09	none	RPA4108	or0428	RPA4108	N	223	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-05	none	RPA2189	or4689	RPA2189	N	219	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-08	none	RPA1966	or4840	RPA1966	N	211	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-12	COG3226 0.003	RPA1958	or4846	RPA1958	N	208	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-08	none	RPA0680	or5746	RPA0680	N	206	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-06	COG3226 6e-04	RPA0588	or5811	RPA0588	N	227	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 5e-07	none	RPA4413	or6629	RPA4413	N	205	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 5e-11	COG3226 3e-04	RPA4338	or6696	RPA4338	N	227	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 4e-08	none	RPA3894	or7031	RPA3894	N	208	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 1e-08	none	RPA3791	or7116	RPA3791	N	239	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 2e-06	none	RPA3777	or7127	RPA3777	N	234	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1309 3e-05	COG3226 0.004	RPA3696	or7189	RPA3696	N	209	Bacterial regulatory protein TetR, HTH motif	P:tetR	COG/small unknown domain	
COG1414 1e-31	none	RPA0685	or1447	RPA0685	N	292	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1414 1e-31	none	RPA3456	or3708	RPA3456	N	293	pseudogene Bacterial regulatory proteins, IclR famil	P:IclR S:HTH_ICLR	IclR	
COG1414 1e-33	none	RPA4560	or0761	RPA4560	N	244	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1414 1e-41	none	RPA1413	or5227	RPA1413	N	313	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1414 1e-46	COG4565 0.008	RPA0982	or5518	pcaR	N	264	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1414 1e-55	none	RPA4647	or6423	kdgR	N	252	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1414 2e-42	none	RPA3718	or0154	RPA3718	N	289	Bacterial regulatory proteins, IclR family	P:IclR S:HTH_ICLR	IclR	
COG1522 1e-29	none	RPA0006	or0970	RPA0006	N	160	Bacterial regulatory proteins, AsnC family	P:ASNC_trans_reg S:HTH_ASNC		
COG1522 2e-33	none	RPA0372	or1228	RPA0372	N	154	Bacterial regulatory proteins, AsnC family	P:ASNC_trans_reg S:HTH_ASNC		
COG1522 2e-33	COG1654 0.001	RPA2351	or4553	RPA2351	N	163	Bacterial regulatory proteins, AsnC family	P:ASNC_trans_reg S:HTH_ASNC		
COG1522 3e-33	COG1349 0.001	RPA4074	or6899	RPA4074	Y	161	Bacterial regulatory proteins, AsnC family	P:ASNC_trans_reg S:HTH_ASNC		
COG1522 8e-33	COG1654 5e-04	RPA0010	or6268	RPA0010	Y	170	Bacterial regulatory proteins, AsnC family	P:ASNC_trans_reg S:HTH_ASNC		
COG1167 1e-97	COG0436 7e-28	RPA0105	or1040	RPA0105	N	514	Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	aminotransferase domain (MocR family)	
COG1167 7e-99	COG0436 6e-34	RPA1394	or5241	RPA1394	N	501	Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	aminotransferase domain (MocR family)	
COG1167 e-102	COG0436 9e-37	RPA2797	or4237	RPA2797	N	484	Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	aminotransferase domain (MocR family)	
COG1802 1e-26	COG2186 4e-17	RPA2343	or2767	RPA2343	N	226		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 1e-31	COG2186 5e-18	RPA3444	or3602	RPA3444	N	237		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 2e-24	COG2186 6e-13	RPA3620	or0083	vanR	N	252		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 2e-28	COG2186 2e-17	RPA4169	or0474	RPA4169	N	244		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 3e-27	COG2186 5e-17	RPA1946	or4856	RPA1946		325	unknown domain	Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 3e-30	COG2186 1e-16	RPA2496	or4437	RPA2496	N	233		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 5e-23	COG2186 1e-17	RPA1443	or5204	RPA1443	Y	272		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1802 6e-32	COG2186 1e-24	RPA1467	or5189	RPA1467	Y	222		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG2186 9e-33	COG1802 2e-20	RPA2036	or2525	RPA2036	N	243		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG2188 1e-48	COG1725 3e-13	RPA0696	or1451	RPA0696	N	243		Bacterial regulatory protein, GntR family	P:gntR S:HTH_GNTR	COG/small unknown domain
COG1846 1e-08	none	RPA3757	or7141	RPA3757	N	180	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 1e-10	COG1339 0.003	RPA0655	or1427	badR	N	176	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 2e-09	none	RPA4676	or0835	RPA4676	N	166	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 2e-12	none	RPA0828	or1551	RPA0828	N	157	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 2e-12	none	RPA1870	or4902	RPA1870	N	172	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 2e-14	COG3682 0.003	RPA4102	or0422	RPA4102	N	154	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 3e-08	none	RPA0539	or1342	RPA0539	N	178	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 3e-12	none	RPA3264	or3466	RPA3264	N	154	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 3e-12	COG1339 5e-04	RPA4369	or6669	RPA4369	N	184	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 4e-07	none	RPA2715	or3075	RPA2715	Y	173	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 4e-07	none	RPA1601	or5089	RPA1601	N	175	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 5e-08	COG1339 1e-04	RPA0821	or1545	RPA0821	Y	189	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 5e-10	none	RPA3422	or3738	RPA3422	N	196	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 5e-11	COG3355 0.003	RPA1909	or2426	RPA1909	N	158	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 5e-12	none	RPA0516	or5863	RPA0516	N	162	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG1846 5e-14	COG1246 3e-04	RPA1031	or5486	RPA1031	N	336	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR	Acetyltransf	
COG1846 6e-13	none	RPA1794	or2332	RPA1794	N	184	Bacterial regulatory protein, MarR family	P:MarR S:HTH_MARR		
COG0350 5e-38	COG2207 9e-14		or6003			311	Helix-turn-helix, AraC type	P:HTH_AraC HTH_AraC S:HTH_ARAC		Methyltransf_1
2 other genes in this COG with just methyltransferase activity were deleted										
COG2207 1e-17	COG4977 8e-11	RPA2707	or4298	RPA2707	N	274	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC
COG2207 2e-12	COG4977 2e-08	RPA1935	or4867	RPA1935	N	341	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC S:HTH_ARAC
COG2207 2e-18	COG2169 5e-14	RPA1695	or5032	RPA1695	N	287	CUPIN		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC

COG2207 2e-19	COG4977 1e-12	RPA3839	or0241	pchR	N	280	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 3e-11	COG4977 1e-08	RPA2140	or2621	RPA2140	N	275	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 3e-12	COG4753 1e-06	RPA2301	or4589	RPA2301	N	331	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC S:HTH_ARAC								
COG2207 3e-21	COG4977 3e-17	RPA4664	or6410	RPA4664	N	249	CUPIN		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 4e-16	COG4753 3e-11	RPA1008	or5501	PA0248	N	297	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 4e-16	COG4977 3e-14	RPA4280	or6742	RPA4280	N	333	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 6e-16	COG4977 1e-15	RPA0567	or5828	RPA0567	N	326	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 6e-17	COG4977 1e-12	RPA3257	or3864	RPA3257	N	279	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 8e-21	COG4977 3e-17	RPA1321	or1949	RPA1321	N	280	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG2207 9e-17	COG4977 6e-12	RPA1058	or1729	RPA1058	N	312	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG3449 5e-25	COG4977 2e-17	RPA0878	or5603	RPA0878	N	302	Helix-turn-helix, AraC type	P:HTH_AraC HTH_AraC S:HTH_ARAC	DNA gyrase inhibitor									
COG4977 2e-15	COG2207 1e-14	RPA2404	or2814	RPA2404	N	335	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 3e-11	COG2207 6e-11	RPA1641	or2216	RPA1641	N	307	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 3e-19	COG2207 4e-18	RPA2110	or2591	RPA2110	N	203	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 3e-20	COG2207 1e-17	RPA2478	or4451	RPA2478	N	364	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 3e-23	COG2207 2e-22	RPA1078	or1740	RPA1078	N	301	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 4e-19	COG2207 1e-17	RPA1988	or4822	RPA1988	N	336	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 9e-23	COG2207 4e-22	RPA1326	or5289	RPA1326	N	328	unknown domain		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
COG4977 4e-68	COG2207 5e-17	RPA2423	or2834	RPA2423	N	313	Family of unknown function ThiJ/PfpI		Helix-turn-helix, AraC t	P:HTH_AraC HTH_AraC S:HTH_ARAC								
		RPA0917	or1622	RPA0917	N	169			Helix-turn-helix, AraC type									
COG0664 3E-11		RPA3419	or3739	RPA3419	N	255	unknown domain; COG - cNMP binding?		Bacterial regulatory pro	HTHCRP								
COG0664 4e-12	none	RPA0991	or1674	RPA0991	N	262	unknown domain; COG - cNMP binding?		Bacterial regulatory pro	S:HTH_CRP								
COG0664 3E-14		RPA3054	or3321	RPA3054	Y	258	unknown domain; COG - cNMP binding?			HTHCNTR								
COG0664 3e-17	none	RPA0992	or5514	RPA0992	Y	244	Cyclic nucleotide-binding domain	P:cNMP_binding	Bacterial regulatory pro	HTHCRP								
COG0664 3e-20	none	RPA2077	or4764	RPA2077	N	309	unknown domain; COG - cNMP binding?		Bacterial regulatory pro	S:HTH_CRP								
COG0664 4e-21	COG2390 0.004	RPA3318	or3811	RPA3318	N	243	Cyclic nucleotide-binding domain	P:cNMP_binding	Bacterial regulatory pro	S:HTH_CRP								
COG0664 1e-21	COG2905 1e-06	RPA1090	or1751	RPA1090	N	226	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 5e-24	COG2905 0.001	RPA0673	or5749	hbaR	N	242	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 1e-24	none	RPA3863	or7056	RPA3863	N	251	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 2e-26	none	RPA4422	or6620	RPA4422	N	238	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 1e-28	COG2905 2e-06	RPA3996	or6951	RPA3996	N	238	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 2e-29	COG2905 0.006	RPA4250	or0531	fixK2	N	231	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	P:crp S:HTH_CRP								
COG0664 6e-31	COG2905 3e-05	RPA0766	or1505	RPA0766	N	236	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	S:HTH_CRP								
COG0664 5e-31	none	RPA4234	or6782	aadR	Y	240	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	P:crp S:HTH_CRP								
COG0664 1e-38	COG2905 1e-05	RPA4143	or0453	nnrR	N	237	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	Bacterial regulatory pro	P:crp S:HTH_CRP								
none	none	RPA1713	or2274	RPA1713	N	225	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	hypothetical protein; no blast hits									
COG0492 9e-59	COG3634 2e-38	RPA4536	or6515	RPA4536	N	564	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	COG/FAD-dependent pyridine nucleotide-disulphide oxidoreductase									
									2 other genes in COG with just this domain									
COG0664 1e-13	COG2905 2e-06	RPA4233	or6783	RPA4233	N	413	Cation channel, non-ligand gated (IPR005820)		Cyclic nucleotide-bindi	P:cNMP_binding S:cNMP								
COG0664 2e-12	COG2905 1e-04	RPA0282	or6047	RPA0282	N	150	Cyclic nucleotide-binding domain	P:cNMP_binding S:cNMP	NO HTH domain									
COG0745 1e-29	COG3706 2e-20	RPA2369	or4540	RPA2369	N	138	Response regulator receiver	P:response_reg S:REC	possible pseudogene with 4541									
COG0745 4e-11	COG3710 6e-07	RPA2368	or4541	RPA2368	N	78	possible pseudogene with 4540		Transcriptional regulat	P:trans_reg_C								
COG0745 6e-57	COG3706 4e-21	RPA3570	or0042	RPA3570	N	241	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 6e-51	COG2204 2e-18	RPA4791	or0932	RPA4791	Y	247	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 5e-61	COG2204 2e-20	RPA1915	or2433	feuP	Y	225	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 4e-58	COG2204 3e-17	RPA1930	or2445	RPA1930	N	242	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 4e-54	COG2204 2e-27	RPA3000	or4062	kdpE	N	228	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 6e-55	COG2204 2e-19	RPA1632	or5068	ctrA	Y	234	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 9e-56	COG2204 2e-20	RPA0358	or5990	chvI	Y	234	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 7e-48	COG2197 1e-20	RPA0283	or6046	RPA0283	Y	229	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 4e-52	COG2204 1e-20	RPA4817	or6289	RPA4817	N	222	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 4e-62	COG3437 3e-23	RPA4775	or6325	phoB	N	238	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG0745 1e-48	COG3706 4e-21	RPA4368	or6670	RPA4368	Y	241	Response regulator receiver	P:response_reg S:REC	Transcriptional regulat	P:trans_reg_C								
COG2197 4e-13	COG2909 2e-08	RPA2299	or2738	RPA2299	N	249	unknown domain		Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG2197 6e-13	COG2771 1e-12	RPA0321	or6018	RPA0321	N	244	Autoinducer binding domain		Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG2771 6e-08	COG2197 2e-07	RPA2300	or2739	RPA2300	N	218	unknown domain		Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG2197 2e-44	COG4566 4e-22	RPA0852	or1572	RPA0852	Y	226	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG2197 2e-47	COG4753 8e-19	RPA3014	or3294	RPA3014	Y	236	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG2197 7e-51	COG4753 5e-22	RPA1489	or5170	RPA1489	N	224	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG4566 2e-61	COG2197 9e-27	RPA1315	or1944	RPA1315	N	229	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG4566 2e-62	COG2204 2e-26	RPA2109	or4743	RPA2109	N	212	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG4566 4e-49	COG2197 6e-31	RPA1682	or2248	RPA1682	Y	209	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG4566 6e-61	COG2204 1e-31	RPA4248	or0529	fixJ	Y	204	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG3706 6e-26	COG0745 1e-25	RPA1248	or5341	RPA1248	N	309	Response regulator receiver	P:response_reg S:REC	Bacterial regulatory pro	P:GerE S:HTH_LUXR								
COG0745 2e-13	COG0784 3e-13	RPA2433	or4486	RPA2433	Y	148	Response regulator receiver	P:response_reg S:REC										
COG2197 1e-10	COG0784 4e-09	RPA3017	or3297	rphyB	N	155	Response regulator receiver	P:response_reg S:REC										
COG4566 8e-25	COG2204 8e-23	RPA1314	or1943	RPA1314	N	144	Response regulator receiver	P:response_reg S:REC										
COG4566 2e-24	COG2204 3e-19	RPA2108	or4744	RPA2108	N	129	Response regulator receiver	P:response_reg S:REC										
COG4566 3e-22	COG2204 8e-18	RPA4249	or0530	RPA4249	Y	131	Response regulator receiver	P:response_reg S:REC										
COG0784 2e-09	COG2204 6e-07	RPA2839	or3175	RPA2839	N	125	Response regulator receiver	P:response_reg S:REC										
COG0784 2e-19	COG2204 1e-15	RPA3133	or3969	RPA3133	Y	122	Response regulator receiver	P:response_reg S:REC										
COG0784 9e-07	COG4753 4e-04	RPA2074	or4768	RPA2074	N	123	Response regulator receiver	S:REC										
COG2204 1e-10	COG0745 3e-07	RPA4322	or0586	RPA4322	N	153	Response regulator receiver	P:response_reg S:REC										
COG2204 2e-12	COG0784 8e-11	RPA1481	or2079	RPA1481	N	121	Response regulator receiver	P:response_reg S:REC										
COG2204 2e-14	COG0745 2e-13	RPA4523	or6527	RPA4523	N	130	Response regulator receiver	P:response_reg S:REC										
COG2204 3e-22	COG3706 6e-22	RPA0143	or6155	cheY1	Y	122	Response regulator receiver	P:response_reg S:REC	CheY									
COG2204 4e-11	COG4753 4e-10	RPA4010	or0351	RPA4010	N	126	Response regulator receiver	P:response_reg S:REC										
COG2204 4e-18	COG4753 2e-16	RPA4738	or0890	RPA4738	Y	127	Response regulator receiver	P:response_reg S:REC										
COG2204 5e-20	COG4753 2e-13	RPA0907	or1616	RPA0907	Y	120	Response regulator receiver	P:response_reg S:REC										
COG2204 9e-13	COG4567 3e-10	RPA1674	or2241	cheY3	N	168	Response regulator receiver	P:response_reg S:REC	CheY?									
COG3706 4e-20	COG0784 6e-19	RPA1629	or2206	cheY2	Y	122	Response regulator receiver	P:response_reg S:REC	CheY									
COG3706 3e-18	COG0745 2e-17	RPA1175	or1822	RPA1175	Y	132	Response regulator receiver	P:response_reg S:REC										
COG3706 9e-16	COG2204 4e-12	RPA1557	or2149	RPA1557	N	279	Response regulator receiver	P:response_reg response_reg S:REC REC										
COG4753 2e-19	COG3706 2e-18	RPA3380	or3555	RPA3380	N	182	Response regulator receiver	P:response_reg S:REC										
COG4753 0.003		RPA4512	or6538	RPA4512	N	104	Response regulator receiver	(PD only)										
COG3707 1e-12	COG0784 6e-04	RPA2409	or2820	RPA2409	N	222	Response regulator receiver (PS)		ANTAR domain	P:ANTAR								
COG3707 3e-44	COG2204 2e-04	RPA3706	or0144	nasT	N	195	Response regulator receiver	P:response_reg	ANTAR domain	P:ANTAR								
COG4567 5e-66	COG2204 2e-21	RPA0571	or5825	regR	Y	185	Response regulator receiver	P:response_reg S:REC			HTHFIS	(TIGRFAM, PS)						
COG2204 e-112	COG3829 1e-98	RPA0979	or1662	hoxA	Y	483	Response regulator receiver	P:response_reg S:REC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG2204 e-114	COG3829 8e-97	RPA1268	or1903	flbD	Y	460	Response regulator receiver	P:response_reg S:REC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG2204 e-137	COG3829 4e-98	RPA4187	or0489	RPA4187	Y	496	Response regulator receiver	P:response_reg S:REC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG2204 e-142	COG3829 9e-86	RPA2595	or2974	ntrX	Y	456	Response regulator receiver	P:response_reg S:REC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG2204 e-146	COG3829 6e-90	RPA2593	or2972	ntrC	Y	481	Response regulator receiver	P:response_reg S:REC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG3284 e-109	COG3829 5e-81	RPA1207	or1847	RPA1207	N	630	PAS domain-PAC motif	P:PAS_T:sensory_box S:PAS PAS: P:PAC	Sigma-54 factor interac	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG3829 3e-06	COG2204 6e-05	RPA1536	or2126	ppsR2	Y	465	unknown domain	PAS domain S:PAS PAS	small unknown domain		Helix-turn-helix, Fis-ty	P:HTH_8						

COG2204 9e-07	COG3829 1e-06	RPA1529	or2119	ppsR1	N	469	unknown domain	PAS domain S:PAS PAS	small unknown domain		Helix-turn-helix, Fis-ty	P:HTH_8						
COG3604 e-123	COG3829 e-110	RPA1439	or5208	anfA	N	543	GAF domain	P:GAF S:GAF	Sigma-54 factor intera	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG3604 e-128	COG2204 e-113	RPA1374	or2001	vnfA	N	545	GAF domain	P:GAF S:GAF	Sigma-54 factor intera	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG3604 e-156	COG3829 8e-98	RPA4632	or6436	nifA	Y	585	GAF domain	P:GAF S:GAF	Sigma-54 factor intera	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG3604 e-110	COG3829 e-102	RPA2111	or4742	RPA2111	Y	642	PAS domain	PAS domain-PAC motif	Sigma-54 factor intera	P:Sigma54_activat	Helix-turn-helix, Fis-ty	P:HTH_8						
COG0735 2E-26		RPA0517	or1324	RPA0517	N	165	Ferric-uptake regulator											
COG0735 7e-21		RPA2339	or2765	RPA2339	N	173	Ferric-uptake regulator											
COG0735 6e-31		RPA0450	or5913	RPA0450	Y	143	Ferric-uptake regulator											
COG0735 2e-21		RPA0424	or5937	RPA0424	Y	163	Ferric-uptake regulator											
COG1733 2E-22		RPA3632	or0092	RPA3632	N	160	DUF24 (trasncriptional regulator)											
COG1733 2e-30		RPA2702	or3062	RPA2702	N	170	DUF24 (trasncriptional regulator)											
COG1733 1e-31		RPA3222	or3897	RPA3222	N	158	DUF24 (trasncriptional regulator)											
COG1733 1e-26		RPA0326	or6013	RPA0326	Y	120	DUF24 (trasncriptional regulator)											
COG2005 2e-20		RPA1383	or2009	RPA1383	N	191												
COG2005 3e-22		RPA0147	or6151	RPA0147	Y	264	Helix-turn-helix, Fis-type	TOBE domain (Molybdenum-pterin binding domain)										
COG2005 2e-25		RPA4718	or6368	modE	Y	264	HTH_9 (ModE_repress)	TOBE domain (Molybdenum-pterin binding domain)										
		RPA0260	or1151	RPA0260	N	331	possible photosynthesis gene regulator, AppA/PpaA family											
COG4957 9e-52		RPA1852	or2376	mucR	Y	138												
COG1959 5e-19		RPA0663	or5756	badM	Y	156	Protein of unknown function UPF0074											
COG2002 5e-06		RPA3607	or0072	RPA3607	N	87	Transcriptional regulator AbrB											
COG1695 2e-15		RPA1015	or1690	RPA1015	N	196	Transcriptional regulator PadR-like family											
COG0704 4e-46		RPA4776	or6324	phoU	Y	238	PhoU											
COG1329 1e-46		RPA0488	or5885	RPA0488	Y	397	Transcription factor CarD											
COG1974 2e-51		RPA2903	or3220	lexA	N	275	LexA DNA-binding region	Peptidase S24, C-terminal										
Signal Transduction Proteins																		
Chemotaxis Signal Transduction Proteins																		
COG0840 6e-20	COG5000 9e-05	RPA3598	or0063	RPA3598	Y	604	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 4e-30	COG4564 1e-26	RPA4449	or0685	RPA4449	Y	564	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP H4	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 2e-27	none	RPA4684	or0843	RPA4684	Y	560	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 3e-26	COG5000 8e-04	RPA4691	or0848	RPA4691	Y	657	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 6e-27	none	RPA1822	or2355	RPA1822	Y	689	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 3e-28	none	RPA2479	or2872	RPA2479	Y	580	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 5e-22	COG5000 0.002	RPA3185	or3417	RPA3185	Y	673	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP H4	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 8e-24	COG5000 0.006	RPA1850	or4918	RPA1850	N	666	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 2e-25	COG5000 0.001	RPA1640	or5064	RPA1640	Y	564	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP H4	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 4e-23	COG4192 1e-06	RPA0856	or5618	RPA0856	Y	713	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 8e-25	COG5000 4e-04	RPA0234	or6085	RPA0234	N	564	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 1e-27	COG5000 1e-05	RPA0139	or6159	RPA0139	Y	734	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 0.002		RPA0136	or6162	RPA0136	Y	570					COG / blast / operon							
COG0840 5e-25	COG5000 6e-05	RPA4663	or6411	RPA4663	Y	681	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 6e-24	COG5000 7e-04	RPA4639	or6431	RPA4639	Y	565	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP H4	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 7e-25	none	RPA4638	or6432	RPA4638	Y	566	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 2e-28	COG4564 1e-09	RPA4307	or6724	RPA4307	Y	562	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 1e-27	COG4564 1e-11	RPA4306	or6725	RPA4306	Y	562	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 4e-37	COG5000 2e-07	RPA4302	or6729	RPA4302	Y	731	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 6e-24	COG5000 1e-05	RPA3750	or7148	RPA3750	Y	568	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 2e-30	COG5000 8e-06	RPA3546	or7307	RPA3546	Y	652	unknown domain, 1 TM domain		Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 9e-20	COG2202 5e-12	RPA1884	or2403	RPA1884	Y	560	unknown domain - no TM domains	PAS domain; PAC motif	unknown domain-HAMP?		Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 1e-31	none	RPA1931	or2446	RPA1931	Y	433	unknown domain - no TM domains	PAC			Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 2e-33	COG5000 5e-04	RPA1675	or2242	RPA1675	N	717	PAS domain	unknown domain, 1 TM domain	Histidine kinase, HAMP	P:HAMP S:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 1e-22	COG2202 4e-10	RPA0431	or5931	RPA0431	Y	561	PAS domain; PAC motif	unknown domain - no TM domains			Bacterial chemotaxis s	P:MCPsignal S:MA						
COG2202 1e-05	none	RPA4484	or6564	RPA4484	Y	178	PAS domain	T:sensory_box										
COG0840 2e-21	none	RPA4483	or6565	RPA4483	N	417			Histidine kinase, HAMP	P:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG2202 2e-05	none	RPA4482	or6566	RPA4482	N	179	PAS domain	T:sensory_box										
COG0840 4e-21	none	RPA4481	or6567	RPA4481	Y	441			unknown domain, 1 TM domain		Bacterial chemotaxis s	P:MCPsignal S:MA						
COG2202 0.006	none	RPA4312	or6719	RPA4312	N	175	PAS domain	T:sensory_box										
COG0840 2e-19	none	RPA4311	or6720	RPA4311	Y	435			Histidine kinase, HAMP	P:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG2202 9e-08	COG3829 5e-04	RPA4203	or6806	RPA4203	N	174	PAS domain	T:sensory_box S:PAS										
COG0840 6e-20	none	RPA4202	or6807	RPA4202	N	442			Histidine kinase, HAMP	P:HAMP	Bacterial chemotaxis s	P:MCPsignal S:MA						
COG0840 9e-26	none	RPA1096	or5445	RPA1096	N	584	Bacterial chemotaxis sensory transducer	P:MCPsignal S:MA	unknown domain - no TM domains									
COG0643 e-147	COG0784 1e-16	RPA1627	or2204	cheA2	Y	938	Hpt domain	P:Hpt S:HPT	unknown domain - no	Signal transducing hi	P:H-kinase_dim	CheW-like protein	P:CheW S:CheW	unknown domain	Response regulator (	P:response_reg S:REC		
COG0643 e-147	COG0784 1e-16	RPA1676	or2243	cheA3	Y	938	Hpt domain	P:Hpt S:HPT	unknown domain - no	Signal transducing hi	P:H-kinase_dim	CheW-like protein	P:CheW S:CheW	unknown domain	Response regulator (	P:response_reg S:REC		
COG0643 e-151	COG4191 2e-09	RPA0142	or6156	cheA1	Y	689	Hpt domain	P:Hpt S:HPT	unknown domain - no	Signal transducing hi	P:H-kinase_dim	CheW-like protein	P:CheW S:CheW					
COG0835 2e-24	COG0643 9e-05	RPA0141	or6157	cheW1-1	N	157	CheW-like protein	P:CheW S:CheW										
COG0835 3e-23	COG0643 9e-06	RPA1628	or2205	cheW2	Y	167	CheW-like protein	P:CheW S:CheW										
COG0835 3e-23	COG0643 9e-06	RPA1677	or2244	cheW3	Y	167	CheW-like protein	P:CheW S:CheW										
COG0835 7e-27	COG0643 0.003	RPA0140	or6158	cheW1-2	Y	163	CheW-like protein	P:CheW S:CheW										
COG1352 1e-61	none	RPA0138	or6160	cheR1	N	281			MCP methyltransferas	P:CheR S:MeTrc								
COG1352 1e-62	COG2201 8e-39	RPA3316	or3499	RPA3316	Y	1047	CheB methylesterase	P:CheB_methylest	MCP methyltransferas	P:CheR S:MeTrc	very large unknown domain							
COG1352 2e-71	none	RPA1631	or2208	cheR2	N	293			MCP methyltransferas	P:CheR S:MeTrc								
COG1352 3e-70	none	RPA1678	or2245	cheR3	Y	292			MCP methyltransferas	P:CheR S:MeTrc								
COG2201 1e-76	COG2197 1e-15	RPA1630	or2207	cheB2	Y	392	Response regulator receiver	P:response_reg S:REC	CheB methylesterase	P:CheB_methylest								
COG2201 3e-99	COG2197 2e-20	RPA0137	or6161	cheB1	Y	364	Response regulator receiver	P:response_reg S:REC	CheB methylesterase	P:CheB_methylest								
COG0659 e-110	COG2252 9e-08	RPA4326	or6707	sulP	N	584	Sulfate_transp	Sulfate transporter/antisigma-factor antagoni	P:STAS									
COG3113 5e-04	none	RPA0144	or6154	RPA0144	N	108		Sulfate transporter/antisigma-factor antagoni	P:STAS									
NON-Chemotaxis Signal Transduction																		
Signal Transduction Histidine Kinases (STHK)																		
COG0591 4e-57	COG0642 9e-34	RPA0853	or5621	RPA0853	Y	1170	Na+/solute symporter?						Histidine kinase A, N-	P:HisKA	Response regulator (	P:response_reg S:REC		
COG0642 4e-32	COG2205 2e-24	RPA3571	or0043	RPA3571	N	445	unknown domain, 1 TM domain				Histidine kinase, HAM	P:HAMP S:HAMP	Histidine kinase A, N-	P:HisKA				
COG0642 1e-42	COG5002 7e-36	RPA3933	or0299	RPA3933	Y	1022	unknown domain - no TM domains						Histidine kinase A, N-	P:HisKA	Response regulator (	P:response_reg S:R	PAS domain	PAS domain
COG0642 4e-36	COG4191 2e-34	RPA3934	or0300	RPA3934	Y	403				PAC?			Histidine kinase A, N-	P:HisKA	Response regulator (	P:response_reg S:REC		
COG0642 4e-25	COG2205 7e-19	RPA4140	or0450	RPA4140	Y	1193	PAS domain	large unknown domain, no TM domains		PAS domain	PAS domain: PAC?		Histidine kinase A, N-	P:HisKA				
COG0642 1e-32	COG3852 2e-30	RPA0494	or1309	RPA0494	N	1094	unknown domain, 1 TM domain	Histidine kinase, HAMP region	P:HAMP	PAS domain: PAC m	PAS domain		Histidine kinase A, N-	P:HisKA	Response regulator (	P:response_reg S:REC		

COG0642 4e-31	COG4191 1e-27	RPA0583	or1373	RPA0583	Y	914	unknown domain, 1 TM domain	Histidine kinase, HAMP region	P:HAMP	PAS domain?; PAC motif?		Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC		
COG0642 3e-25	COG3852 2e-24	RPA0635	or1412	RPA0635	N	493	unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 9e-39	COG5002 2e-35	RPA1558	or2150	RPA1558	N	904	small unknown domain, 2 TM domains	PAS domain: PAC motif	PAS domain: PAC motif				Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG0642 2e-46	COG2205 2e-40	RPA1858	or2380	RPA1858	N	611	unknown domain, 5 TM domains	PAS domain: PAC motif					Histidine kinase A, N-	P:HisKA			
COG0642 2e-27	COG2205 3e-12	RPA1916	or2434	feuQ	N	464	unknown domain, 1 TM domain				Histidine kinase, HAM	P:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 2e-33	COG2205 1e-25	RPA1932	or2447	RPA1932	N	483	unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP S:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 3e-29	COG4191 4e-28	RPA3216	or3441	RPA3216	Y	687	PAS domain: PAC?		PAS domain: PAC motif				Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG0642 4e-25	COG4191 6e-25	RPA3187	or3927	RPA3187	Y	918	unknown domain, 1 TM domain	Histidine kinase, HAMP region	P:HAMP S:HAMP		PAS domain: PAC motif		Histidine kinase A, N-	P:HisKA			
COG0642 9e-37	COG2205 1e-28	RPA2367	or4542	RPA2367	N	368	small unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP S:HAMP HA	Histidine kinase A, N-	P:HisKA			
COG0642 1e-30	COG4191 6e-29	RPA2135	or4727	RPA2135	N	708	large unknown domain, 2 TM domain						Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG0642 4e-39	COG2205 2e-31	RPA1972	or4833	RPA1972	N	533	unknown domain, 5 TM domains						Histidine kinase A, N-	P:HisKA			
COG0642 8e-42	COG2205 2e-37	RPA1938	or4864	RPA1938	N	780	unknown domain, 2 TM domains		PAS domain: PAC motif				Histidine kinase A, N-	P:HisKA			
COG0642 5e-40	COG2205 4e-29	RPA1681	or5038	RPA1681	N	864	unknown domain, 2 TM domains						Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:R	Hpt domain P:Hpt
COG0642 2e-46	COG2205 4e-36	RPA1249	or5340	RPA1249	N	1123	very large unknown domain, 10 TM domains						Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG0642 8e-24	COG2205 4e-17	RPA0572	or5824	regS	Y	441	unknown domain, 5 TM domains						Histidine kinase A, N-	P:HisKA			
COG0642 3e-35	COG2205 4e-33	RPA0357	or5991	exoS, chvG	N	582	unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP S:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 3e-41	COG2205 8e-32	RPA0317	or6023	RPA0317	N	637	small unknown domain, 2 TM domains						Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:R	Response regulator receiver
COG0642 3e-27	COG2205 1e-17	RPA4816	or6290	RPA4816	Y	459	unknown domain, 1 TM domain				Histidine kinase, HAM	P:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 5e-30	COG2205 2e-23	RPA4753	or6343	RPA4753	N	406	?						Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG0642 3e-40	COG2205 2e-33	RPA4417	or6625	RPA4417	N	874	unknown domain, 5 TM domains	PAS domain: PAC motif?					Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:R	Hpt domain P:Hpt
COG0642 2e-33	COG2205 2e-26	RPA4367	or6671	RPA4367	N	463	unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP	Histidine kinase A, N-	P:HisKA			
COG0642 2e-34	COG4191 5e-33	RPA3882	or7041	cckA	Y	883	small unknown domain, 2 TM domains	PAS domain	PAS domain	PAS domain			Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG2205 1e-39	COG0642 4e-34	RPA4790	or0931	RPA4790	Y	551	Response regulator receiver	unknown domain					Histidine kinase A, N-	P:HisKA			
COG2205 0.0	COG0642 9e-33	RPA3001	or4061	kdpD	N	908	Osmosensitive K+ channel His kinase sensor		K+ channel ? (4TM helixes)				Histidine kinase A, N-	P:HisKA			
COG2205 5e-37	COG0642 8e-36	RPA0079	or6208	RPA0079	N	849	unknown domain - no TM domains	PAS domain	PAS domain	PAS domain			Histidine kinase A, N-	P:HisKA			
COG3852 e-117	COG0642 2e-31	RPA2592	or2971	ntrB	N	391		PAS domain					Histidine kinase A, N-	P:HisKA			
COG4191 2e-43	COG5000 2e-32	RPA4247	or0528	fixL	Y	509	PAS domain: PAC motif	PAS domain: PAC motif					Histidine kinase A, N-	P:HisKA			
COG4191 2e-25	COG0642 2e-23	RPA4789	or0930	RPA4789	N	704	unknown domain, 2 TM domains				Histidine kinase, HAM	P:HAMP S:HAMP	Histidine kinase A, N-terminal				
COG4191 2e-40	COG0642 2e-30	RPA0980	or1663	RPA0980	N	451		PAS domain					Histidine kinase A, N-	P:HisKA			
COG4191 5e-31	COG0642 3e-29	RPA0981	or1664	RPA0981	Y	796	PAS domain: PAC motif	PAS domain: PAC motif	PAS domain: PAC motif				Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG4191 5e-35	COG4192 1e-27	RPA1313	or1942	RPA1313	N	633	small unknown domain, 3 TM domains	PAS domain: PAC motif	PAS domain: PAC motif				Histidine kinase A, N-	P:HisKA			
COG4191 4e-38	COG4192 6e-30	RPA2292	or4595	RPA2292	Y	475	unknown domain, 2 TM domains						Histidine kinase A, N-	P:HisKA			
COG4191 2e-22	COG0642 4e-20	RPA4524	or6526	RPA4524	N	519	unknown domain, 6 TM domains						Histidine kinase A, N-	P:HisKA			
COG5000 0.0	COG3852 2e-28	RPA2594	or2973	ntrY	N	764	unknown domain, 4 TM domains		Histidine kinase, HAM	P:HAMP S:HAMP	PAS domain: PAC motif?		Histidine kinase A, N-	P:HisKA			
COG5000 5e-32	COG3852 2e-31	RPA1767	or4980	RPA1767	N	770	unknown domain - no TM domains		Histidine kinase, HAM	P:HAMP	PAS domain?; PAC motif		Histidine kinase A, N-	P:HisKA	Response regulator	P:response_reg S:REC	
COG5002 8e-45	COG0642 2e-37	RPA4781	or6319	phoR	Y	450	unknown domain, 1 TM domain						Histidine kinase A, N-	P:HisKA			
none	none	RPA0259	or6061	RPA0259	Y	261					Histidine kinase, HAM	P:HAMP S:HAMP					
COG4251 e-158	COG0642 7e-29	RPA0122	or1053	phyB3	N	760	unknown domain - no TM domains		GAF domain (phytochrome)		phytochrome		Histidine kinase A, N-	P:HisKA			
COG4251 9e-15		RPA1537	or2127	RPA1537	N	165	unknown domain - no TM domains		possible pseudogene								
COG4251 6e-91	none	RPA1537	or2128	RPA1537		567	possible pseudogene		phytochrome		phytochrome	PAS domain: PAC motif					
COG4251 0.0	COG0642 3e-33	RPA3015	or3295	phyB1	Y	759	unknown domain - no TM domains		GAF domain (phytochrome)		phytochrome		Histidine kinase A, N-	P:HisKA			
COG4251 0.0	COG0642 1e-35	RPA3016	or3296	phyB2	N	776	unknown domain - no TM domains		GAF domain (phytochrome)		phytochrome		Histidine kinase A, N-	P:HisKA			
COG4251 4e-32	COG2205 1e-27	RPA2434	or4485	RPA2434	Y	511	unknown domain, 2 TM domains						Histidine kinase A, N-	P:HisKA			
COG4251 e-114	COG4585 2e-41	RPA1490	or5169	phyB4	N	771	unknown domain - no TM domains		GAF domain (phytochrome)		phytochrome		Histidine kinase A, N-terminal? COG; PS; HATPase				
COG4251 e-164	COG3920 4e-36	RPA0990	or5515	phyB5	N	846	unknown domain - no TM domains		GAF domain (phytochrome)		phytochrome		unknown domain - Histidine kinase? COG		Response regulator	P:response_reg S:REC	
COG4585 4e-38	COG4564 4e-32	RPA3018	or3298	RPA3018	N	379	Response regulator receiver	P:response_reg S:REC					Histidine kinase A, N-terminal? COG; PS; HATPase				
COG3920 2e-31	none	RPA4009	or0350	RPA4009	N	683	GAF domain	unknown domain - no TM domains	GAF domain	STHK - COG							
COG3920 5e-37		RPA1295	or1922	RPA1295	N	404	unknown domain - 4 TM domains			STHK - COG, PS: HATPase							
COG3920 9e-29		RPA1322	or1950	RPA1322	N	233				STHK - COG: HATPase							
COG3920 2e-38	COG4251 9e-07	RPA2787	or3133	RPA2787	N	353	PAS domain: PAC motif			STHK - COG							
COG3920 8e-29	COG0642 5e-08	RPA3106	or3985	RPA3106	Y	369	PAS domain: PAC motif?			STHK - COG: HATPase							
COG3920 1e-39	COG2204 5e-18	RPA2432	or4487	RPA2432	Y	364	Response regulator receiver	P:response_reg S:REC		STHK - COG, PS: HATPase							
COG3920 3e-27	COG2202 9e-11	RPA2075	or4767	RPA2075	Y	634	GAF domain	PAS domain: PAC motif	PAS domain: PAC mot	STHK - COG							
COG3920 1e-33	COG2202 9e-17	RPA0754	or5696	RPA0754	N	479	PAS domain: PAC motif	PAS domain: PAC motif		STHK - COG							
COG3920 2e-35	COG3290 0.009	RPA0007	or6271	RPA0007	Y	484	PAS domain: PAC motif?	PAS domain		STHK - COG							
COG3290 8e-19		RPA4226	or6789	RPA4226	N	589	unknown domain, 1 TM domain	CHASE	unknown domain, 1 TM	STHK - COG							
COG3920 6e-30		RPA4513	or6537	RPA4513	Y	334	unknown domain - no TM domains			STHK - COG							
COG3920 7e-22		RPA2076	or4765	RPA2076	N	228				STHK - COG							
COG3899 e-115	COG4191 1e-34	RPA2107	or4745	RPA2107	N	1713	Serine/Threonine protein kinase	S:S_TKc	very large unknown domain- no TM domains		GAF domain	P:GAF S:GAF	Histidine kinase A, N-	P:HisKA			
COG3899 1e-66	COG4191 5e-39	RPA1328	or1957	RPA1328	N	1381			very large unknown domain- no TM domains		GAF domain	P:GAF S:GAF	Histidine kinase A, N-	P:HisKA			
Cylclic Nucleotide Signal Transduction																	
COG3899 8e-55	COG2114 1e-24	RPA4000	or0339	RPA4000	Y	1106	Guanylate cyclase	P:guanylate_cyc S:CYCc	very large unknown domain- no TM domains								
COG2114 5e-26	none	RPA1202	or1843	RPA1202	N	400	unknown domain - no TM domains				Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG2114 1e-33	none	RPA1796	or2334	RPA1796	Y	525	unknown domain - 2 TM domains				Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG4252 2e-35	COG2114 1e-23	RPA2291	or2731	RPA2291	Y	765	large unknown domain - 2 TM domains				Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG2114 5e-29	COG3850 4e-09	RPA1965	or4842	RPA1965	N	663	unknown domain, 1 TM domain		Histidine kinase, HAM	P:HAMP S:HAMP	Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG2114 1e-23	COG0633 2e-14	RPA1582	or5105	cyaA	N	594	unknown domain - 6 TM domains		ferredoxin		Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG2114 5e-24	none	RPA0786	or5670	RPA0786	N	465	unknown domain - no TM domains				Guanylate cyclase	P:guanylate_cyc S:CYCc					
COG2200 1e-39	COG4943 6e-22	RPA4516	or0734	vieA	N	405	unknown domain - no TM domains				EAL domain	P:EAL S:DUF2					
COG2200 5e-74	COG4943 6e-57	RPA3184	or3930	RPA3184	N	450	unknown domain - 6 TM domains				EAL domain	P:EAL S:DUF2					
COG2200 6e-65	COG4943 3e-50	RPA1680	or2247	RPA1680	N	417	Response regulator receiver	P:response_reg S:REC			EAL domain	P:EAL S:DUF2					
COG2200 8e-27	COG4943 5e-12	RPA1180	or1827	RPA1180	N	522	unknown domain - 1 TM domains				EAL domain	P:EAL S:DUF2					
COG2200 9e-53	COG5001 2e-45	RPA0529	or1334	RPA0529	Y	581	unknown domain - no TM domains		GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2					
COG5001 e-104	COG2200 9e-81	RPA0390	or1242	RPA0390	N	746	PAS domain	PAS domain: PAC motif?		GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 2e-90	COG2200 4e-80	RPA0521	or1327	RPA0521	N	570	small unknown domain - no TM domains			GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 5e-93	COG2200 2e-72	RPA1121	or1781	RPA1121	N	777	unknown domain - 5 TM domains			GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 1e-85	COG2200 3e-76	RPA2152	or2633	RPA2152	N	710	unknown domain - 3 TM domains	PAS domain: PAC motif?		GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 e-100	COG2200 2e-80	RPA2957	or3254	RPA2957	N	883	large unknown domain - 1 TM domains			GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 8e-88	COG2200 1e-69	RPA3170	or3408	pdeA	N	874	PAS domain; PAC motif	PAS domain; PAC motif	GAF domain	GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 e-110	COG2200 7e-82	RPA3410	or3746	RPA3410	N	825	unknown domain - no TM domains	PAS domain	PAS domain; PAC mot	GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 9e-78	COG2200 2e-58	RPA3219	or3901	RPA3219	N	657	unknown domain - 5 TM domains			GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 3e-78	COG2200 5e-72	RPA0914	or5567	RPA0914	Y	960	unknown domain - no TM domains	unknown domain - 7 TM domains	PAS domain; PAC mot	GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 3e-78	COG2200 9e-55	RPA0783	or5672	RPA0783	N	606	small unknown domain - no TM domains			GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 e-100	COG2200 1e-82	RPA0777	or5677	RPA0777	N	905	unknown domain - 2 TM domains	PAS domain		GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 1e-89	COG2200 2e-74	RPA0370	or5978	RPA0370	N	839	PAS domain; PAC motif	PAS domain; PAC motif	PAS domain; PAC mot	GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG5001 e-100	COG2200 2e-82	RPA4167	or6832	RPA4167	N	913	PAS domain	PAS domain: PAC motif?	PAS domain: PAC mot	GGDEF	P:GGDEF T:GGDEF	EAL domain	P:EAL S:DUF2				
COG2199 3e-38	COG3706 2e-36	RPA0286	or1174	RPA0286	N	558	unknown domain - no TM domains	Histidine kinase, HAMP region	GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 4e-38	COG3706 3e-30	RPA0767	or1506	RPA0767	N	314		PAS domain; PAC motif	GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 1e-45	COG3706 6e-42	RPA0886	or1602	RPA0886	N	503	unknown domain - 2 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 7e-37	COG3706 9e-31	RPA1296	or1923	RPA1296	N	588	unknown domain - 2 TM domains	Histidine kinase, HAMP region	GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 7e-36	COG3706 2e-31	RPA1790	or2328	RPA1790	N	273	small unknown domain - 2 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 3e-32	COG5001 2e-30	RPA3022	or3301	RPA3022	N	389	unknown domain - 5 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 5e-46	COG3706 1e-33	RPA3076	or3338	RPA3076	N	450	unknown domain - 6 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 1e-39	COG3706 4e-39	RPA4112	or0432	RPA4112	N	298	small unknown domain - 3 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 6e-41	COG3706 7e-37	RPA1657	or5053	RPA1657	N	405	unknown domain - 7 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 1e-29	COG3706 1e-27	RPA4173	or6828	RPA4173	Y	251	small unknown domain - no TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG2199 1e-35	COG3706 3e-28	RPA4565	or0764	RPA4565	N	401	unknown domain - 5 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 7e-36	COG2199 6e-33	RPA1642	or2218	RPA1642	N	505	unknown domain - no TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1	unknown domain - no TM domains						
COG3706 2e-43	COG2199 4e-41	RPA1716	or2277	RPA1716	N	737	large unknown domain - 9 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 4e-39	COG2199 4e-38	RPA2769	or3120	RPA2769	N	412	unknown domain - 7 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 e-120	COG2199 1e-40	RPA3132	or3970	RPA3132	N	458	Response regulator receiver	Response regulator receiver	GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 1e-39	COG2199 8e-39	RPA2984	or4073	RPA2984	Y	384	unknown domain - 7 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 3e-44	COG2199 2e-40	RPA2476	or4453	RPA2476	N	356	unknown domain - no TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							

COG3706 3e-44	COG2199 2e-39	RPA1818	or4942	RPA1818	N	430	unknown domain - 6 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 6e-44	COG2199 4e-43	RPA3994	or6953	RPA3994	N	383	unknown domain - no TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 5e-41	COG2199 5e-37	RPA3832	or7079	RPA3832	N	357	PAS domain		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 1e-39	COG2199 2e-37	RPA3792	or7114	RPA3792	N	380	unknown domain - 6 TM domains		GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG3706 6e-36	COG2199 7e-36	RPA3616	or0078	RPA3616	N	645	unknown domain - 1 TM domains	PAS domain; PAC motif	GGDEF	P:GGDEF T:GGDEF S:DUF1							
COG0317 0.0	COG2357 5e-11	RPA2693	or3054	relA	N	761	Metal dependent phosphohydrolase, HD region	S:HDc	RelA_SpoT	TGS domain	unknown domain - no	Amino acid-binding ACT					
one gene or4192/RPA2855) with the		Metal depen	dent phosphohydrolase, HD region was deleted called dGTP triphosphohydrolase														
COG0317 8e-23	none	RPA3661	or7215	RPA3661	N	179	Metal dependent phosphohydrolase, HD region	S:HDc									
COG1896 2e-22	none	RPA0395	or5959	RPA0395	N	198	Metal dependent phosphohydrolase, HD region	S:HDc									
COG1896 2e-25		RPA1065	or5462	RPA1065	Y	206	Metal dependent phosphohydrolase, HD region	P:HD									
COG2844 0.0	COG0617 0.004	RPA0591	or5807	glnD	Y	950	NTP_transf_2	unknown domain - no TM domains	Metal dependent phos	S:HDc	Amino acid-binding A	Amino acid-binding ACT					
COG3437 6e-77	COG2206 6e-52	RPA0145	or1062	RPA0145	Y	389	Response regulator receiver	P:response_reg S:REC	Metal dependent phos	S:HDc							
COG2206 2e-29		RPA4830	or6280	RPA4830	Y	371	Response regulator receiver		Metal dependent phosphohydrolase, HD region								
COG0622 0.003		RPA1670	or2237	RPA1670	Y	246	Metallo-phosphoesterase										
		RPA3353	or3790	RPA3353	N	258	Metallo-phosphoesterase										
PTS NTR Regulator Proteins																	
COG3605 0.0	COG1080 e-124	RPA0605	or1392	ptsP	Y	801	GAF domain	P:GAF S:GAF	PTS I domain								
COG1493 9e-14		RPA0356	or5992	RPA0356	N	156	HPr Kinase (COG, operon with ref.)										
COG2893 3e-26		RPA0355	or5993	RPA0355	Y	134	EIIA-man										
COG1925 5e-24		RPA0354	or5994	RPA0354	Y	111	PTS-HPr										
COG1762 2e-29		RPA0052	or1003	ptsN1	N	154	PTS_EIIA_2										
COG1762 8e-23		RPA2999	or4063	ptsN2	N	149	PTS_EIIA_2										
Miscellaneous																	
COG3437 3e-15	COG2204 1e-14	RPA1556	or2148	RPA1556	N	230	Response regulator receiver	P:response_reg S:REC	Hpt domain	P:Hpt							
COG0643 0.009	none	RPA3381	or3556	RPA3381	N	197	Hpt domain	P:Hpt									
COG2198 1e-05	none	RPA3957	or6984	RPA3957	N	120	Hpt domain	P:Hpt									
COG4565 7e-09	COG4753 2e-08	RPA4223	or6790	RPA4223	Y	269	unknown domain - no TM domains		Response regulator re	P:response_reg S:REC							
COG0745 2e-13	COG0784 3e-13	RPA2433	or4486	RPA2433	Y	148	Response regulator receiver	P:response_reg S:REC									
COG2197 1e-10	COG0784 4e-09	RPA3017	or3297	rphyB	N	155	Response regulator receiver	P:response_reg S:REC									
COG4566 8e-25	COG2204 8e-23	RPA1314	or1943	RPA1314	N	144	Response regulator receiver	P:response_reg S:REC									
COG4566 2e-24	COG2204 3e-19	RPA2108	or4744	RPA2108	N	129	Response regulator receiver	P:response_reg S:REC									
COG4566 3e-22	COG2204 8e-18	RPA4249	or0530	RPA4249	Y	131	Response regulator receiver	P:response_reg S:REC									
COG0784 2e-09	COG2204 6e-07	RPA2839	or3175	RPA2839	N	125	Response regulator receiver	P:response_reg S:REC									
COG0784 2e-19	COG2204 1e-15	RPA3133	or3969	RPA3133	Y	122	Response regulator receiver	P:response_reg S:REC									
COG0784 9e-07	COG4753 4e-04	RPA2074	or4768	RPA2074	N	123	Response regulator receiver	S:REC									
COG2204 1e-10	COG0745 3e-07	RPA4322	or0586	RPA4322	N	153	Response regulator receiver	P:response_reg S:REC									
COG2204 2e-12	COG0784 8e-11	RPA1481	or2079	RPA1481	N	121	Response regulator receiver	P:response_reg S:REC									
COG2204 2e-14	COG0745 2e-13	RPA4523	or6527	RPA4523	N	130	Response regulator receiver	P:response_reg S:REC									
COG2204 3e-22	COG3706 6e-22	RPA0143	or6155	cheY1	Y	122	Response regulator receiver	P:response_reg S:REC									
COG2204 4e-11	COG4753 4e-10	RPA4010	or0351	RPA4010	N	126	Response regulator receiver	P:response_reg S:REC									
COG2204 4e-18	COG4753 2e-16	RPA4738	or0890	RPA4738	Y	127	Response regulator receiver	P:response_reg S:REC									
COG2204 5e-20	COG4753 2e-13	RPA0907	or1616	RPA0907	Y	120	Response regulator receiver	P:response_reg S:REC									
COG2204 9e-13	COG4567 3e-10	RPA1674	or2241	cheY3	N	168	Response regulator receiver	P:response_reg S:REC									
COG3706 4e-20	COG0784 6e-19	RPA1629	or2206	cheY2	Y	122	Response regulator receiver	P:response_reg S:REC									
COG3706 3e-18	COG0745 2e-17	RPA1175	or1822	RPA1175	Y	132	Response regulator receiver	P:response_reg S:REC									
COG3706 9e-16	COG2204 4e-12	RPA1557	or2149	RPA1557	N	279	Response regulator receiver	P:response_reg response_reg S:REC REC									
COG4753 2e-19	COG3706 2e-18	RPA3380	or3555	RPA3380	N	182	Response regulator receiver	P:response_reg S:REC									
COG4753 0.003		RPA4512	or6538	RPA4512	N	104	Response regulator receiver	(PD only)									
COG0515 3e-30	COG0631 2e-28	RPA3200	or3916	RPA3200	N	599	Protein phosphatase 2C-like	P:PP2C S:PP2C_SIG	Serine/Threonine prote	S:S_TKc							
COG0515 4e-16	none	RPA1327	or1956	RPA1327	N	319			Serine/Threonine prote	S:S_TKc							
COG0515 5e-31	COG0589 5e-07	RPA1671	or2238	RPA1671	N	480			Serine/Threonine prote	S:S_TKc	small unknown domain						
COG2453 6e-12		RPA4289	or0559	RPA4289	N	185	PS:TYR_PHOSPHATASE_2										
COG0347 2e-37	none	RPA0274	or1164	glnK2	N	113	Nitrogen regulatory protein P-II	P:P-II									
COG0347 4e-39	none	RPA0272	or1161	glnK1	Y	113	Nitrogen regulatory protein P-II	P:P-II									
COG0347 7e-39	none	RPA2966	or3260	glnB	Y	113	Nitrogen regulatory protein P-II	P:P-II									
COG3712		RPA1335	or1965	fecR1	N	328	FecR										
COG3712		RPA1340	or1970	fecR2	N	327	FecR										
COG3712		RPA1348	or1980	fecR3	N	322	FecR										
COG3712		RPA2381	or4529	fecR4	N	338	FecR										
COG3712		RPA3281	or3842	fecR5	Y	321	FecR										
COG3806		RPA0549	or5843	chrR	N	220	ChrR	next to FecI									
COG3476 4e-21		RPA1533	or2123	tspO	N	154	TspO and MBR related proteins										
		RPA4282	or0552	RPA4282	N	157	possible activator of photopigment and puc with BLUF domain										
		RPA3367	or3782	RPA3367	N	156	possible activator of photopigment and puc with BLUF domain										
		RPA0522	or1328	RPA0522	N	147	possible activator of photopigment and puc with BLUF domain										

The initial list was generated by searching all of the Interpro classifications for certain key words and then adding the defining Pfam and Smart db hits,
the top 2 COGs hits, the gene numbers, and arranging all of the domain hits in order from the N-terminal to the C-terminal.
The list was sorted by COG and then manually rearranged, analyzed, and expanded to generate this final table.
Only domains defined by Pfam and Smart hits were originally used since Prosite and some of the other dbs in Interpro gave too many false + hits.

The group of genes consisting of a single Response Regulator Receiver (RRR) domain are duplicated in the table. One group is in the miscellaneous
section, and the other is with the transcription factors that contain RRR domains since many of the these genes hit the same COGs and, therefore,
may provide some information about the evolution and/or origin of some of these genes.
The 3 genes named CheY1-3 have been left in this group despite being in operons with the rest of the Chemotaxis components.

COLOR KEY
all genes have all their domains included in order from N-terminus to C-terminus in pairs of columns in black text
- 1st column is the interpro domain name, 2nd column is the Pfam or Smart db domain name
Not all of the domains are in contiguous columns, some groups of genes have their defining domains (Histidine kinases) aligned to help with the manual analysis.
words in blue text were added manually (each domain is only a single column)
PD = ProDom hit, PS = Prosite hit
words in purple text are questionable additions
words in red text denote pseudogenes
gene names in green text with a sky blue background are genes in which I have changed the names based on this analysis
groups in light green background are uniform in their COGs and Interpro classifications
lines in red background describe genes that were deleted despite having the same COG or interpro hits as genes left in the table
color coded COGs boxes were used to help organize groups of genes from related COGs