Phyre^2

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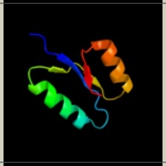
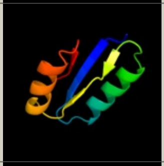
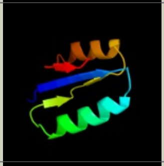
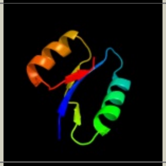
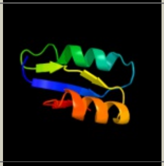
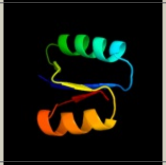
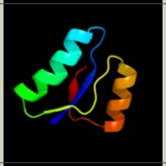
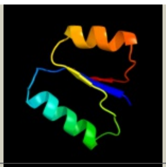
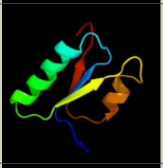
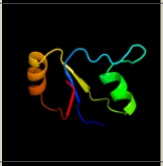
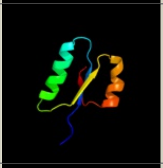
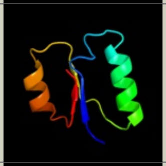
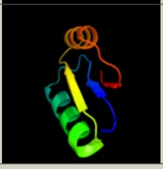
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cniA_	Alignment		99.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc type-2 transporter; **PDBTitle:** crystal structure of a domain of a putative abc type-2 transporter2 from thermotoga maritima msb8
2	d2p0sa1	Alignment		95.7	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**PG0945 N-terminal domain-like
3	c3eulB_	Alignment		86.3	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional **PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
4	d1a04a2	Alignment		79.2	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
5	c1rnlA_	Alignment		77.8	19	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
6	d1a2oa1	Alignment		73.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
7	c3cz5B_	Alignment		70.9	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two-component response regulator, luxr family; **PDBTitle:** crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
8	c1a2oB_	Alignment		70.7	17	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
9	d1dz3a_	Alignment		70.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
10	c3b2nA_	Alignment		66.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
11	c3t8yA_	Alignment		61.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb

12	c2qv0A_	Alignment		59.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
13	c3c3wB_	Alignment		55.2	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
14	c3cnbC_	Alignment		52.7	21	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna-binding response regulator, merr family; **PDBTitle:** crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
15	d1v95a_	Alignment		50.6	5	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
16	d1heya_	Alignment		46.0	4	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
17	c3fkqA_	Alignment		46.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntrc-like two-domain protein; **PDBTitle:** crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
18	c2gwrA_	Alignment		44.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
19	c3f6cB_	Alignment		40.9	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
20	c3cg4A_	Alignment		39.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-like); **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
21	c3kyiB_	Alignment	not modelled	39.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**chey6 protein; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
22	d1p6qa_	Alignment	not modelled	38.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	d1jbea_	Alignment	not modelled	37.8	5	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
24	c3r0jA_	Alignment	not modelled	33.5	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
25	d2ayxa1	Alignment	not modelled	32.5	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	c3k2dA_	Alignment	not modelled	29.5	4	**PDB header:**immune system **Chain:** A: **PDB Molecule:**abc-type metal ion transport system, periplasmic component; **PDBTitle:** crystal structure of immunogenic lipoprotein a from vibrio vulnificus
27	c1p99A_	Alignment	not modelled	28.8	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
28	d1p99a_	Alignment	not modelled	28.8	5	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like

29	d1xs5a_	Alignment	not modelled	28.8	4	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	d1dbwa_	Alignment	not modelled	26.6	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	d1s8na_	Alignment	not modelled	26.5	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	c1kgsA_	Alignment	not modelled	26.5	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
33	d1u0sy_	Alignment	not modelled	23.9	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
34	c3a0rB_	Alignment	not modelled	21.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
35	c3nhzA_	Alignment	not modelled	21.5	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
36	c3grcD_	Alignment	not modelled	20.1	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
37	d1zgza1	Alignment	not modelled	20.1	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
38	c3khtA_	Alignment	not modelled	17.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
39	c3t6kB_	Alignment	not modelled	17.8	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
40	c1zn2A_	Alignment	not modelled	17.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
41	d1ys7a2	Alignment	not modelled	17.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	c3chgB_	Alignment	not modelled	16.5	12	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
43	d1kgsa2	Alignment	not modelled	16.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	c1ys7B_	Alignment	not modelled	16.4	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
45	c3q9sA_	Alignment	not modelled	16.1	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
46	c2rejA_	Alignment	not modelled	16.1	3	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
47	d1mvoa_	Alignment	not modelled	16.0	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	d1xhfa1	Alignment	not modelled	15.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c2oqrA_	Alignment	not modelled	15.3	14	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
50	c3hdgE_	Alignment	not modelled	15.3	14	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
51	c2h9qC_	Alignment	not modelled	15.3	9	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** crystal structure of the effector binding domain of a catm2 variant (r156h)
52	c3nhmA_	Alignment	not modelled	15.3	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
53	c3ir1F_	Alignment	not modelled	15.1	4	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
54	c3breA_	Alignment	not modelled	14.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702

55	c3hv2B_	Alignment	not modelled	14.4	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator/hd domain protein; **PDBTitle:** crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
56	c3cg0A_	Alignment	not modelled	13.7	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
57	c3cu5B_	Alignment	not modelled	13.0	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
58	c3ho7A_	Alignment	not modelled	13.0	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
59	c2qzjC_	Alignment	not modelled	13.0	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
60	d1peya_	Alignment	not modelled	12.9	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3l6gA_	Alignment	not modelled	12.6	11	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
62	c3i42A_	Alignment	not modelled	12.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
63	c3lteH_	Alignment	not modelled	12.1	9	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
64	c2rjnA_	Alignment	not modelled	11.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
65	d1zesa1	Alignment	not modelled	11.3	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	d1ny5a1	Alignment	not modelled	11.1	6	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3hzhA_	Alignment	not modelled	10.2	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis response regulator (chey-3); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
68	d1yioa2	Alignment	not modelled	10.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	c2qxyB_	Alignment	not modelled	9.6	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
70	c2hqrA_	Alignment	not modelled	9.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
71	d1krwa_	Alignment	not modelled	9.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c3dzdA_	Alignment	not modelled	9.2	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
73	d1w25a1	Alignment	not modelled	8.8	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	c3c3mA_	Alignment	not modelled	8.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
75	c2qr3A_	Alignment	not modelled	8.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**two-component system response regulator; **PDBTitle:** crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
76	d2pl1a1	Alignment	not modelled	8.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d1zh2a1	Alignment	not modelled	8.4	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	c2ep5B_	Alignment	not modelled	8.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7

79	c2zwmA_	Alignment	not modelled	8.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
80	d2a9pa1	Alignment	not modelled	8.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	c2f7cA_	Alignment	not modelled	8.0	8	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
82	c3muqB_	Alignment	not modelled	7.9	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
83	d2czla1	Alignment	not modelled	7.8	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
84	c2jrlA_	Alignment	not modelled	7.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
85	c3c97A_	Alignment	not modelled	7.5	2	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
86	d1mb3a_	Alignment	not modelled	7.4	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c1ny5A_	Alignment	not modelled	7.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
88	c2nt3A_	Alignment	not modelled	7.2	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
89	c2zayA_	Alignment	not modelled	7.2	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
90	c3tmgA_	Alignment	not modelled	7.0	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
91	c3kn3C_	Alignment	not modelled	6.8	2	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
92	c2v25B_	Alignment	not modelled	6.6	5	**PDB header:**receptor **Chain:** B: **PDB Molecule:**major cell-binding factor; **PDBTitle:** structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
93	c1w25B_	Alignment	not modelled	6.4	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
94	c3gxaA_	Alignment	not modelled	6.4	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
95	d1k66a_	Alignment	not modelled	6.4	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	c2qsjB_	Alignment	not modelled	6.4	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
97	c3cfyA_	Alignment	not modelled	6.3	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
98	c3snkA_	Alignment	not modelled	6.2	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator chey-like protein; **PDBTitle:** crystal structure of a response regulator chey-like protein (mll6475)2 from mesorhizobium loti at 2.02 a resolution
99	c3ktoA_	Alignment	not modelled	6.1	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica