Phyre^2

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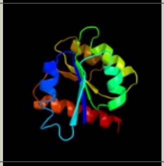
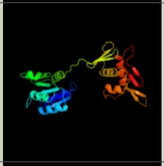
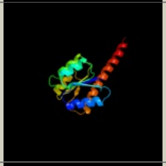
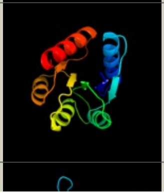
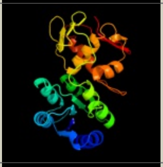
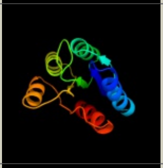
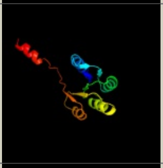
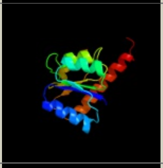
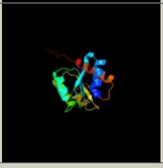
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv0A_	Alignment		100.0	93	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
2	c2ayxA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase protein rcsc; **PDBTitle:** solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
3	c3eq2A_	Alignment		100.0	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
4	c3breA_	Alignment		100.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
5	c3r0jA_	Alignment		99.9	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
6	c1w25B_	Alignment		99.9	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
7	d1ny5a1	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
8	c3i5aA_	Alignment		99.9	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
9	c3b2nA_	Alignment		99.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
10	c1ny5A_	Alignment		99.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
11	d1jbea_	Alignment		99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

12	c3cu5B_	Alignment		99.9	24	**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
13	d2ayxa1	Alignment		99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
14	c1ys7B_	Alignment		99.9	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
15	c1a2oB_	Alignment		99.9	27	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
16	d1kgsa2	Alignment		99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
17	c3eulB_	Alignment		99.9	20	**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
18	d1dz3a_	Alignment		99.9	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
19	d1s8na_	Alignment		99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
20	c3dzdA_	Alignment		99.9	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
21	c3cfyA_	Alignment	not modelled	99.9	19	**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
22	d1qkka_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	d1a04a2	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
24	d1ys7a2	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
25	d1w25a1	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	d1u0sy_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
27	c2rjnA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
28	d2a9pa1	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
29	d1mvoa_	Alignment	not modelled	99.9	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like

						Family: CheY-related
30	d2pl1a1	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	d1k66a_	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	d1yioa2	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	d1dbwa_	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
34	d1heya_	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	c3cz5B_	Alignment	not modelled	99.9	19	**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
36	c3cnbC_	Alignment	not modelled	99.9	16	**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
37	c3h1gA_	Alignment	not modelled	99.9	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
38	c3khtA_	Alignment	not modelled	99.9	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
39	c3hdgE_	Alignment	not modelled	99.9	27	**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
40	c2zwmA_	Alignment	not modelled	99.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
41	c3hebB_	Alignment	not modelled	99.9	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey); **PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
42	c3jteA_	Alignment	not modelled	99.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
43	c3gt7A_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
44	d1peya_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	c3hv2B_	Alignment	not modelled	99.9	18	**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
46	d1zh2a1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	d1krwa_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3t8yA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
49	d1p6qa_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
50	d2r25b1	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	c2jrlA_	Alignment	not modelled	99.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
52	c3nhzA_	Alignment	not modelled	99.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
53	c2qr3A_	Alignment	not modelled	99.9	22	**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
						Fold: Flavodoxin-like

54	d1a2oa1	Alignment	not modelled	99.9	24	**Superfamily:**CheY-like **Family:**CheY-related
55	c1kgsA_	Alignment	not modelled	99.9	18	**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
56	d1zesa1	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2qzjC_	Alignment	not modelled	99.9	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
58	c3rqiA_	Alignment	not modelled	99.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein; **PDBTitle:** crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
59	c3crnA_	Alignment	not modelled	99.9	15	**PDB header:**signaling protein **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
60	c2zayA_	Alignment	not modelled	99.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
61	d1zgza1	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c2qvgA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
63	c2gwrA_	Alignment	not modelled	99.9	18	**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
64	c3t6kB_	Alignment	not modelled	99.9	23	**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
65	d1i3ca_	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	c1p2fA_	Alignment	not modelled	99.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
67	d1p2fa2	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	c3kcnA_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
69	c2jk1A_	Alignment	not modelled	99.9	14	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
70	c2hqrA_	Alignment		99.9	13	**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	c3f6cB_	Alignment	not modelled	99.9	16	**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
72	c3ilhA_	Alignment	not modelled	99.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
73	c3cg0A_	Alignment	not modelled	99.9	26	**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
74	d1xhfa1	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
75	d1mb3a_	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c2oqrA_	Alignment	not modelled	99.9	16	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
77	c3hzhA_	Alignment	not modelled	99.9	20	**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
						PDB header:transferase

78	c3mmnA_	Alignment	not modelled	99.9	20	**Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
79	c3lteH_	Alignment	not modelled	99.9	19	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
80	c3m6mF_	Alignment	not modelled	99.9	19	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
81	c3q9sA_	Alignment	not modelled	99.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
82	c3cg4A_	Alignment	not modelled	99.9	21	**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
83	c3n0rA_	Alignment	not modelled	99.9	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
84	c3a0rB_	Alignment	not modelled	99.9	22	**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)
85	c2rdmB_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
86	d1k68a_	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c2qxyB_	Alignment	not modelled	99.9	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
88	c3grcD_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
89	c3i42A_	Alignment	not modelled	99.9	21	**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
90	c3hdvB_	Alignment	not modelled	99.9	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
91	c3c3mA_	Alignment	not modelled	99.9	20	**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
92	c3gl9B_	Alignment	not modelled	99.9	23	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
93	d2b4aa1	Alignment	not modelled	99.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	c3eqzB_	Alignment	not modelled	99.9	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from colwellia2 psychrerythraea
95	c3nhmA_	Alignment	not modelled	99.9	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
96	d1w25a2	Alignment	not modelled	99.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	c1zn2A_	Alignment	not modelled	99.9	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
98	c3snkA_	Alignment	not modelled	99.9	11	**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	c3c97A_	Alignment	not modelled	99.9	21	**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
100	c2hqoA_	Alignment	not modelled	99.9	18	**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
101	c3h5iA_	Alignment	not modelled	99.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator/sensory box protein/ggdef **PDBTitle:** crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydothermus hydrogenoformans
						PDB header:transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein;

102	c3luaA_	Alignment	not modelled	99.9	15	**PDBTitle:** crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
103	c3eodA_	Alignment	not modelled	99.8	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
104	c2j48A_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
105	d1dcfa_	Alignment	not modelled	99.8	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
106	c3ktoA_	Alignment	not modelled	99.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
107	c2nt3A_	Alignment	not modelled	99.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
108	c2qsjB_	Alignment	not modelled	99.8	24	**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
109	c3lufB_	Alignment	not modelled	99.8	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**two-component system response regulator/ggdef **PDBTitle:** structure of probable two-component system response2 regulator/ggdef domain protein
110	c3kyiB_	Alignment	not modelled	99.8	25	**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
111	d1qo0d_	Alignment	not modelled	99.8	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
112	c3c3wB_	Alignment	not modelled	99.8	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
113	c1rnlA_	Alignment	not modelled	99.7	21	**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
114	c3n53B_	Alignment	not modelled	99.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
115	c2yxbA_	Alignment	not modelled	99.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
116	c3d6wA_	Alignment	not modelled	99.7	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**methyl-accepting/dna response regulator; **PDBTitle:** lyttr dna-binding domain of putative methyl-accepting/dna response2 regulator from bacillus cereus.
117	c3cwoX_	Alignment	not modelled	99.7	19	**PDB header:**de novo protein **Chain:** X: **PDB Molecule:**beta/alpha-barrel protein based on 1thf and 1tmy; **PDBTitle:** a beta/alpha-barrel built by the combination of fragments2 from different folds
118	c3bs1A_	Alignment	not modelled	99.3	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**accessory gene regulator protein a; **PDBTitle:** structure of the staphylococcus aureus agra lyttr domain2 bound to dna reveals a beta fold with a novel mode of3 binding
119	d1fmfa_	Alignment	not modelled	99.3	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
120	c3klnC_	Alignment	not modelled	99.0	9	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst