Phyre2

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Description	Q06065
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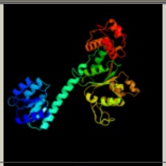
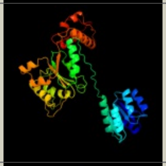
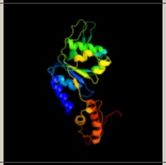
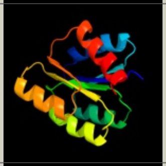
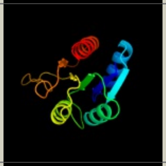
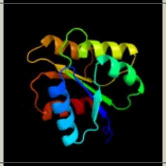
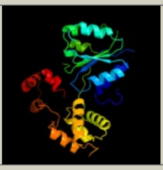
Unique Job ID	11788e3ddcd53b11

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	Alignment		100.0	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	Alignment		100.0	43	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2c99A_	Alignment		100.0	45	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
4	d1ny5a2	Alignment		100.0	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	c1ojlF_	Alignment		100.0	55	**PDB header:**response regulator **Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
6	c3co5B_	Alignment		99.9	26	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
7	c2ayxA_	Alignment		99.9	31	**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
8	c1w25B_	Alignment		99.9	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
9	c3eq2A_	Alignment		99.9	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
10	d1qkka_	Alignment		99.9	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
11	c2rjnA_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis

12	c2qr3A_	Alignment		99.9	27	**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
13	d1ny5a1	Alignment		99.9	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
14	c2jrlA_	Alignment		99.9	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
15	d1ys7a2	Alignment		99.9	35	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
16	d1dbwa_	Alignment		99.9	31	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
17	c3cfyA_	Alignment		99.9	23	**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
18	c3jteA_	Alignment		99.9	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
19	d1w25a1	Alignment		99.9	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
20	c3breA_	Alignment		99.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
21	d1peya_	Alignment	not modelled	99.9	41	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
22	d1mvoa_	Alignment	not modelled	99.9	33	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	c3crnA_	Alignment	not modelled	99.9	25	**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
24	d2a9pa1	Alignment	not modelled	99.8	35	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
25	c3r0jA_	Alignment	not modelled	99.8	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
26	d2pl1a1	Alignment	not modelled	99.8	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
27	d2ayxa1	Alignment	not modelled	99.8	31	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	d1yioa2	Alignment	not modelled	99.8	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:transcription

29	c2zwmA_	Alignment	not modelled	99.8	36	**Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
30	d1krwa_	Alignment	not modelled	99.8	41	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	c3i5aA_	Alignment	not modelled	99.8	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
32	d1kgsa2	Alignment	not modelled	99.8	34	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c3hv2B_	Alignment	not modelled	99.8	28	**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
34	c3b2nA_	Alignment	not modelled	99.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
35	c3c3mA_	Alignment	not modelled	99.8	24	**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
36	c3gt7A_	Alignment	not modelled	99.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
37	c3nhzA_	Alignment	not modelled	99.8	35	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
38	d1u0sy_	Alignment	not modelled	99.8	36	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
39	c1a2oB_	Alignment	not modelled	99.8	22	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
40	d1zesa1	Alignment	not modelled	99.8	31	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c2jk1A_	Alignment	not modelled	99.8	23	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
42	c3kcnA_	Alignment	not modelled	99.8	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
43	d1zh2a1	Alignment	not modelled	99.8	35	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	d1jbea_	Alignment	not modelled	99.8	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	c3rqiA_	Alignment	not modelled	99.8	20	**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
46	c3cu5B_	Alignment	not modelled	99.8	31	**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
47	c1ys7B_	Alignment	not modelled	99.8	33	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
48	d1s8na_	Alignment	not modelled	99.8	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c2qzjC_	Alignment	not modelled	99.8	26	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
50	c3lteH_	Alignment	not modelled	99.8	26	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
51	c3t6kB_	Alignment	not modelled	99.8	31	**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
52	c2zayA_	Alignment	not modelled	99.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
53	c3hdgE_	Alignment	not modelled	99.8	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
						PDB header:lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated

54	c3cg0A_	Alignment	not modelled	99.8	26	diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
55	c3hdvB_	Alignment	not modelled	99.8	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
56	d1zgza1	Alignment	not modelled	99.8	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	d1xhfa1	Alignment	not modelled	99.8	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	d1p6qa_	Alignment	not modelled	99.8	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	c3eulB_	Alignment	not modelled	99.8	32	**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
60	c3cz5B_	Alignment	not modelled	99.8	27	**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
61	d1dz3a_	Alignment	not modelled	99.8	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	d1a04a2	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c2qxyB_	Alignment	not modelled	99.8	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
64	c2gwrA_	Alignment	not modelled	99.8	31	**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
65	c1kgsA_	Alignment	not modelled	99.8	28	**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
66	c3cnbC_	Alignment	not modelled	99.8	25	**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
67	c3h1gA_	Alignment	not modelled	99.8	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
68	d1k66a_	Alignment	not modelled	99.8	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	d1heya_	Alignment	not modelled	99.8	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c3a0rB_	Alignment	not modelled	99.8	36	**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)
71	c3pfiB_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
72	c3cg4A_	Alignment	not modelled	99.8	24	**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
73	c3khtA_	Alignment	not modelled	99.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
74	d1p2fa2	Alignment	not modelled	99.8	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
75	d1w25a2	Alignment	not modelled	99.8	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	d2r25b1	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	c3gl9B_	Alignment	not modelled	99.8	34	**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

78	c3grcD_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
79	c2qv0A_	Alignment	not modelled	99.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
80	d1mb3a_	Alignment	not modelled	99.8	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	c3q9sA_	Alignment	not modelled	99.8	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
82	c3eqzB_	Alignment	not modelled	99.8	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from colwellia2 psychrerythraea
83	c3t8yA_	Alignment	not modelled	99.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
84	c1zn2A_	Alignment	not modelled	99.8	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
85	c3hzhA_	Alignment	not modelled	99.8	26	**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
86	c3eodA_	Alignment	not modelled	99.8	34	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
87	c1p2fA_	Alignment	not modelled	99.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
88	d1r6bx3	Alignment	not modelled	99.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
89	c2rdmB_	Alignment	not modelled	99.8	23	**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
90	c2oqrA_	Alignment	not modelled	99.8	29	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
91	c3hebB_	Alignment	not modelled	99.8	22	**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
92	d1a2oa1	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c2hqoA_	Alignment	not modelled	99.8	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
94	c3nhmA_	Alignment	not modelled	99.7	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
95	c2qvgA_	Alignment	not modelled	99.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
96	d1i3ca_	Alignment	not modelled	99.7	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	c2j48A_	Alignment	not modelled	99.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
98	c3i42A_	Alignment	not modelled	99.7	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
99	c3f6cB_	Alignment	not modelled	99.7	19	**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
100	c3luaA_	Alignment	not modelled	99.7	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
101	d1dcfa_	Alignment	not modelled	99.7	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
102	c3snkA_	Alignment	not modelled	99.7	20	**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

103	c3ktoA_	Alignment	not modelled	99.7	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
104	c3h5iA_	Alignment	not modelled	99.7	29	**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
105	c3ilhA_	Alignment	not modelled	99.7	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
106	c3m6mF_	Alignment	not modelled	99.7	28	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
107	c2hqrA_	Alignment	not modelled	99.7	14	**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
108	c3mmnA_	Alignment	not modelled	99.7	31	**PDB header:**transferase **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+
109	c3n0rA_	Alignment	not modelled	99.7	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
110	d2b4aa1	Alignment	not modelled	99.7	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
111	c1qvrB_	Alignment	not modelled	99.7	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
112	c1in8A_	Alignment	not modelled	99.7	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
113	c1r6bX_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
114	c3c97A_	Alignment	not modelled	99.7	30	**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
115	d1k68a_	Alignment	not modelled	99.7	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
116	c3lufB_	Alignment	not modelled	99.7	16	**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
117	c2nt3A_	Alignment	not modelled	99.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
118	c3pxiB_	Alignment	not modelled	99.7	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
119	d1um8a_	Alignment	not modelled	99.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
120	d1qvra3	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain