Phyre^2

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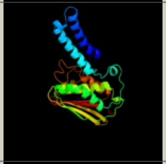
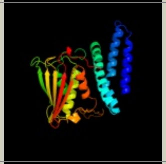
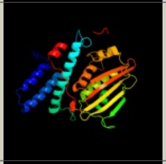
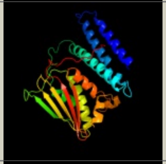
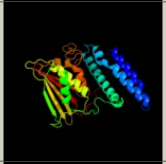
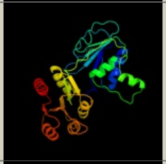
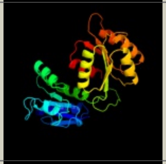
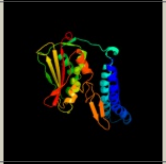
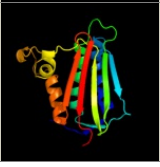
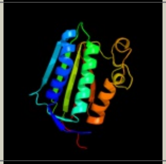
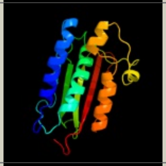
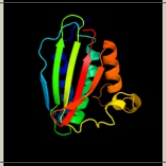
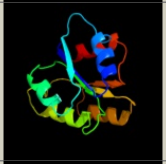
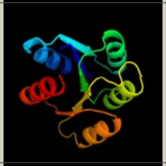
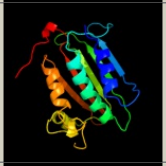
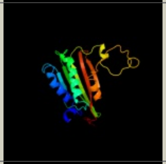
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c2aA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
2	c3d36B_	Alignment		100.0	25	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**sporulation kinase b; **PDBTitle:** how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
3	c2q8fA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
4	c3d2rB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; **PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
5	c2bu8A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase kinase isoenzyme 2; **PDBTitle:** crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
6	c1y8oA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
7	c1gjvA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[3-methyl-2-oxobutanoate dehydrogenase **PDBTitle:** branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complxed with atp-gamma-s
8	c2ayxA_	Alignment		100.0	22	**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
9	c3lufB_	Alignment		100.0	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
10	c3a0rA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
11	d2c2aa2	Alignment		100.0	27	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase

12	c1b3qA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
13	c3a0tA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal)
14	d1gkza2	Alignment		100.0	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
15	d1id0a_	Alignment		100.0	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
16	c3breA_	Alignment		100.0	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
17	c1w25B_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
18	d1jm6a2	Alignment		100.0	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
19	d1bxda_	Alignment		99.9	24	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
20	c3jz3B_	Alignment		99.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
21	c3i5aA_	Alignment	not modelled	99.9	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
22	c3eq2A_	Alignment	not modelled	99.9	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
23	d1k66a_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
24	c3gt7A_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
25	d1w25a1	Alignment	not modelled	99.9	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	c2zayA_	Alignment	not modelled	99.9	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
27	c3t6kB_	Alignment	not modelled	99.9	26	**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
28	c2ch4A	Alignment	not modelled	99.9	17	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea;

28	c2ch4A_	Alignment	not modelled	99.9	17	**PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
29	d1heya_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
30	d1ysra1	Alignment	not modelled	99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
31	d2ayxa1	Alignment	not modelled	99.9	31	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	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
33	c3mmnA_	Alignment	not modelled	99.9	35	**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+
34	c3gl9B_	Alignment	not modelled	99.9	24	**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
35	d2r25b1	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
36	d1p6qa_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	d1mb3a_	Alignment	not modelled	99.9	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
38	c3cnbC_	Alignment	not modelled	99.9	17	**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
39	d1jbea_	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
40	c2qvgA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
41	d1u0sy_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	d1peya_	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	d2pl1a1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	d1zesa1	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	d1ny5a1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	c3lteH_	Alignment	not modelled	99.9	22	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
47	d1i3ca_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	d1qkka_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	d1i58a_	Alignment	not modelled	99.9	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
50	d1s8na_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	c1ny5A_	Alignment	not modelled	99.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
52	c3c3mA_	Alignment	not modelled	99.9	26	**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
53	d1mvoa_	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:structural genomics, unknown function

54	c3cfyA_	Alignment	not modelled	99.9	26	**Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
55	c3khtA_	Alignment	not modelled	99.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
56	c3r0jA_	Alignment		99.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
57	c2zwmA_	Alignment	not modelled	99.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
58	c3n0rA_	Alignment	not modelled	99.9	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
59	d2a9pa1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	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
61	c3cg4A_	Alignment	not modelled	99.9	25	**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
62	d1zh2a1	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c3nhzA_	Alignment	not modelled	99.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
64	d1dcfa_	Alignment	not modelled	99.9	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
65	c3m6mF_	Alignment	not modelled	99.9	24	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
66	d1ys7a2	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3i42A_	Alignment	not modelled	99.9	23	**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
68	c2qzjC_	Alignment	not modelled	99.9	22	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
69	d1dbwa_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c3ilhA_	Alignment	not modelled	99.9	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
71	c2rjnA_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
72	d1zgza1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	c2qr3A_	Alignment	not modelled	99.9	23	**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
74	c3jteA_	Alignment	not modelled	99.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
75	d1yioa2	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	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
77	c3b2nA_	Alignment	not modelled	99.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus

78	c3hdgE_	Alignment	not modelled	99.9	21	**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
79	c3hv2B_	Alignment	not modelled	99.9	23	**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
80	d1xhfa1	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	d1a04a2	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c3luaA_	Alignment	not modelled	99.9	22	**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
83	c2gwrA_	Alignment	not modelled	99.9	20	**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
84	d1kgsa2	Alignment	not modelled	99.9	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	c2jrlA_	Alignment	not modelled	99.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
86	d1krwa_	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	d1dz3a_	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
88	d1k68a_	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	c3dzdA_	Alignment		99.9	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
90	c1ys7B_	Alignment	not modelled	99.9	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
91	c3c97A_	Alignment	not modelled	99.9	26	**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
92	c3grcD_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
93	c3cu5B_	Alignment	not modelled	99.9	22	**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
94	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
95	c2qxyB_	Alignment	not modelled	99.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
96	c1a2oB_	Alignment	not modelled	99.9	19	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
97	c3cg0A_	Alignment	not modelled	99.9	23	**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
98	c3eulB_	Alignment	not modelled	99.9	24	**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
99	c2j48A_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
100	d1w25a2	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:transcription regulator **Chain:** B: **PDB Molecule:**two-component response regulator, luxr

101	c3cz5B_	Alignment	not modelled	99.9	23	family; **PDBTitle:** crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
102	c3nhmA_	Alignment	not modelled	99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
103	c3rqiA_	Alignment	not modelled	99.9	19	**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
104	c3hzhA_	Alignment	not modelled	99.9	19	**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
105	c2qv0A_	Alignment	not modelled	99.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
106	c3eodA_	Alignment	not modelled	99.9	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
107	c1p2fA_	Alignment	not modelled	99.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
108	d2b4aa1	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c2jk1A_	Alignment	not modelled	99.9	22	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
110	d1r62a_	Alignment	not modelled	99.9	24	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
111	c1kgsA_	Alignment	not modelled	99.9	26	**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
112	c3h5iA_	Alignment	not modelled	99.9	30	**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
113	c2rdmB_	Alignment	not modelled	99.9	22	**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
114	d1qo0d_	Alignment	not modelled	99.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
115	d1p2fa2	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
116	c3f6cB_	Alignment	not modelled	99.9	18	**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
117	c3kcnA_	Alignment	not modelled	99.9	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
118	c3a0rB_	Alignment	not modelled	99.9	18	**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)
119	c2nt3A_	Alignment	not modelled	99.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
120	d2hkja3	Alignment	not modelled	99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain