Phyre2

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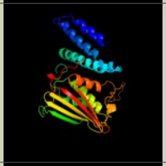
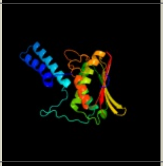
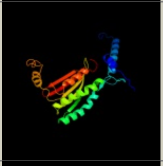
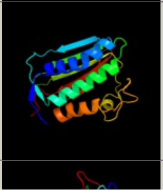
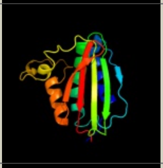
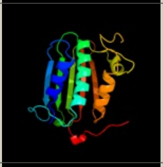
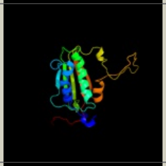
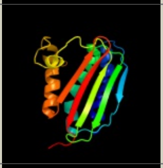
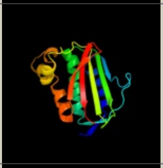
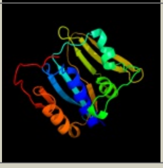
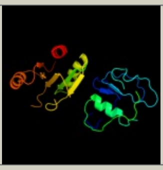
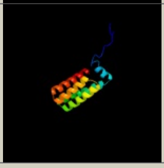
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c2aA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
2	c3d2rB_	Alignment		100.0	16	**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
3	c2q8fA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
4	c3d36B_	Alignment		100.0	17	**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
5	c1y8oA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
6	c2bu8A_	Alignment		100.0	16	**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
7	c1gjvA_	Alignment		100.0	16	**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	c3a0rA_	Alignment		100.0	16	**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)
9	d2c2aa2	Alignment		100.0	18	**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
10	c1b3qA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
11	c3a0tA_	Alignment		100.0	15	**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)
						

12	d1gkza2	Alignment		100.0	18	**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
13	d1id0a_	Alignment		100.0	14	**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
14	d1jm6a2	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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
15	d1bxda_	Alignment		100.0	13	**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	c2ch4A_	Alignment		100.0	15	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
17	d1ysra1	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
18	c3jz3B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
19	d1i58a_	Alignment		100.0	13	**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	d2hkja3	Alignment		99.9	14	**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
21	d1r62a_	Alignment	not modelled	99.9	17	**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
22	c3gieA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
23	c2ayxA_	Alignment		99.8	12	**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
24	c2zbkB_	Alignment	not modelled	99.8	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
25	c1mx0D_	Alignment	not modelled	99.8	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
26	c3ehgA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase (yocf protein); **PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp
27	c3zxqA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost; **PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost

28	c2q2eB_	Alignment	not modelled	99.7	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
29	d1ixma_	Alignment	not modelled	99.7	10	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
30	d1h7sa2	Alignment	not modelled	99.6	9	**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
31	c3zxoB_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**redox sensor histidine kinase response regulator devs; **PDBTitle:** crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
32	d1bkna2	Alignment	not modelled	99.6	13	**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
33	c3n0rA_	Alignment		99.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
34	d1sr2a_	Alignment		99.5	100	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Sensor-like histidine kinase YojN, C-terminal domain
35	d1dcfa_	Alignment	not modelled	99.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
36	d1b63a2	Alignment	not modelled	99.5	13	**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
37	c1w25B_	Alignment	not modelled	99.5	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
38	c3mmnA_	Alignment	not modelled	99.5	16	**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+
39	c3eq2A_	Alignment	not modelled	99.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
40	c3breA_	Alignment	not modelled	99.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
41	d1th8a_	Alignment	not modelled	99.4	12	**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
42	d1y8oa2	Alignment	not modelled	99.4	15	**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
43	d2r25b1	Alignment	not modelled	99.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	d2ayxa1	Alignment	not modelled	99.4	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	d2pl1a1	Alignment	not modelled	99.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	c3i5aA_	Alignment	not modelled	99.4	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
47	d1s8na_	Alignment	not modelled	99.4	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3c97A_	Alignment	not modelled	99.4	14	**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
49	d1qo0d_	Alignment	not modelled	99.4	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR

50	c3t6kB_	Alignment	not modelled	99.4	10	**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
51	c3lteH_	Alignment	not modelled	99.4	10	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
52	d1peya_	Alignment	not modelled	99.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
53	c3gt7A_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
54	d1jbea_	Alignment	not modelled	99.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	d2c2aa1	Alignment	not modelled	99.4	19	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
56	c2gwrA_	Alignment	not modelled	99.4	12	**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
57	c3c3mA_	Alignment	not modelled	99.4	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
58	d1u0sy_	Alignment	not modelled	99.4	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	d1qkka_	Alignment	not modelled	99.4	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	c3r0jA_	Alignment	not modelled	99.4	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
61	c3lufB_	Alignment	not modelled	99.4	13	**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
62	d1w25a1	Alignment	not modelled	99.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	d1k66a_	Alignment	not modelled	99.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
64	c3h1gA_	Alignment	not modelled	99.4	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
65	c3nhzA_	Alignment	not modelled	99.4	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
66	c3cg4A_	Alignment	not modelled	99.4	16	**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
67	c2zwmA_	Alignment	not modelled	99.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
68	c2zayA_	Alignment	not modelled	99.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
69	d1i3ca_	Alignment	not modelled	99.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d1dbwa_	Alignment	not modelled	99.4	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d1ny5a1	Alignment	not modelled	99.3	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c3cnbC_	Alignment	not modelled	99.3	15	**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
73	d1p6qa_	Alignment	not modelled	99.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	d1mvoa_	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:signaling protein

75	c3gl9B_	Alignment	not modelled	99.3	18	**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
76	d1zgza1	Alignment	not modelled	99.3	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d1ys7a2	Alignment	not modelled	99.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	c1ny5A_	Alignment	not modelled	99.3	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
79	d1yioa2	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c3jteA_	Alignment	not modelled	99.3	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
81	d1heya_	Alignment	not modelled	99.3	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c3i42A_	Alignment	not modelled	99.3	16	**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
83	d1zh2a1	Alignment	not modelled	99.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	c3cfyA_	Alignment	not modelled	99.3	7	**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
85	c2qr3A_	Alignment	not modelled	99.3	12	**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
86	d1mb3a_	Alignment	not modelled	99.3	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c2qzjC_	Alignment	not modelled	99.3	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
88	d1zesa1	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	d1a04a2	Alignment	not modelled	99.3	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
90	c3hv2B_	Alignment	not modelled	99.3	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
91	c3h5iA_	Alignment	not modelled	99.3	14	**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
92	d1krwa_	Alignment	not modelled	99.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c2qvgA_	Alignment	not modelled	99.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
94	c3khtA_	Alignment	not modelled	99.3	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
95	d1xhfa1	Alignment	not modelled	99.3	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	c2rjnA_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
97	c3hdvB_	Alignment	not modelled	99.3	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
98	d1w25a2	Alignment	not modelled	99.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	c3hebB_	Alignment	not modelled	99.3	11	**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
100	c3hdgE_	Alignment	not modelled	99.3	13	**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
101	d2a9pa1	Alignment	not modelled	99.3	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
102	c3cg0A_	Alignment	not modelled	99.3	17	**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
103	d1kgsa2	Alignment	not modelled	99.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
104	c1p2fA_	Alignment	not modelled	99.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
105	c2jrlA_	Alignment	not modelled	99.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
106	c3eodA_	Alignment	not modelled	99.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
107	c3ilhA_	Alignment	not modelled	99.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
108	c3f6cB_	Alignment	not modelled	99.3	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
109	c3luaA_	Alignment	not modelled	99.3	12	**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
110	c2rdmB_	Alignment	not modelled	99.3	13	**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
111	c3dzdA_	Alignment	not modelled	99.2	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
112	c3eulB_	Alignment	not modelled	99.2	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
113	c2kx7A_	Alignment	not modelled	99.2	99	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sensor-like histidine kinase yojn; **PDBTitle:** solution structure of the e.coli rcsd-abl domain (residues 688-795)
114	c2qxyB_	Alignment	not modelled	99.2	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
115	c3m6mF_	Alignment	not modelled	99.2	19	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
116	c3crnA_	Alignment	not modelled	99.2	9	**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
117	c3b2nA_	Alignment	not modelled	99.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
118	c3rqiA_	Alignment	not modelled	99.2	14	**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
119	c1ys7B_	Alignment	not modelled	99.2	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
120	d2b4aa1	Alignment	not modelled	99.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related