Phyre^2

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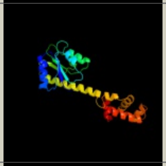
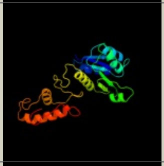
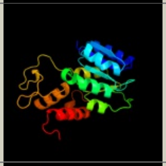
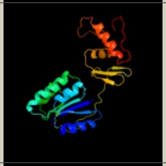
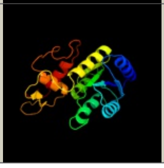
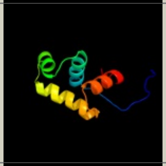
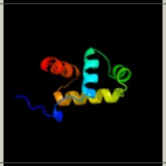
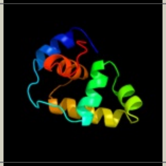
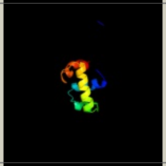
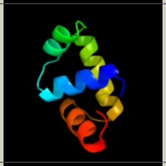
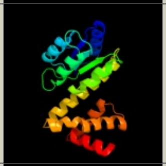
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rnlA_	Alignment		100.0	18	**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
2	c3c3wB_	Alignment		100.0	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
3	c1zn2A_	Alignment		100.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
4	c3klnC_	Alignment		99.9	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
5	c1kgsA_	Alignment		99.9	15	**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
6	c3q9sA_	Alignment		99.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
7	c2gwrA_	Alignment		99.8	14	**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
8	c3r0jA_	Alignment		99.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
9	c2oqrA_	Alignment		99.8	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
10	c2hqrA_	Alignment		99.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
11	c1ys7B_	Alignment		99.8	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+

12	c3sztB_	Alignment		99.7	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
13	c1h0mD_	Alignment		99.7	21	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
14	c2q0oA_	Alignment		99.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
15	d1p4wa_	Alignment		99.7	91	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
16	c3qp5C_	Alignment		99.7	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
17	c1p2fA_	Alignment		99.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
18	c3cloC_	Alignment		99.6	31	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
19	d1s8na_	Alignment		99.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
20	c1x3uA_	Alignment		99.6	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
21	c2krfB_	Alignment	not modelled	99.6	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
22	c1zljE_	Alignment	not modelled	99.6	22	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
23	d1l3la1	Alignment	not modelled	99.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
24	d1fsea_	Alignment	not modelled	99.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
25	d1a04a1	Alignment	not modelled	99.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
26	c1a2oB_	Alignment	not modelled	99.6	16	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
27	c2rnjA_	Alignment	not modelled	99.6	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
28	c2jpcA_	Alignment	not modelled	99.5	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
						Fold:DNA/RNA-binding 3-helical bundle

29	d1yioa1	Alignment	not modelled	99.5	25	**Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
30	d1a2oa1	Alignment	not modelled	99.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	c3eulB_	Alignment	not modelled	99.4	26	**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
32	d1dz3a_	Alignment	not modelled	99.4	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c3b2nA_	Alignment	not modelled	99.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
34	c3cz5B_	Alignment	not modelled	99.3	24	**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
35	c3t8yA_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
36	d1a04a2	Alignment	not modelled	99.3	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	c3eq2A_	Alignment	not modelled	99.3	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
38	c2ayxA_	Alignment	not modelled	99.3	19	**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
39	c3breA_	Alignment	not modelled	99.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
40	d1dbwa_	Alignment	not modelled	99.3	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c3i5aA_	Alignment	not modelled	99.3	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
42	c1w25B_	Alignment	not modelled	99.3	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
43	d1jbea_	Alignment	not modelled	99.3	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	c3cu5B_	Alignment	not modelled	99.2	21	**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
45	c3rqiA_	Alignment	not modelled	99.2	16	**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	d1p6qa_	Alignment	not modelled	99.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c2qv0A_	Alignment	not modelled	99.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
48	d1krwa_	Alignment	not modelled	99.2	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c2rjnA_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
50	c3nhzA_	Alignment	not modelled	99.2	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
51	d1mvoa_	Alignment	not modelled	99.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	d1u0sy_	Alignment	not modelled	99.2	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						Fold: Flavodoxin-like

53	d1ny5a1	Alignment	not modelled	99.2	17	**Superfamily:**CheY-like **Family:**CheY-related
54	c3khtA_	Alignment	not modelled	99.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
55	c3cfyA_	Alignment	not modelled	99.2	14	**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
56	c3f6cB_	Alignment	not modelled	99.2	21	**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
57	c3cnbC_	Alignment	not modelled	99.2	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
58	c3t6kB_	Alignment	not modelled	99.2	17	**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
59	c3kyiB_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**chey6 protein; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
60	c1ny5A_	Alignment	not modelled	99.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
61	d1heya_	Alignment	not modelled	99.2	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	d1kgsa2	Alignment	not modelled	99.2	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c3hebB_	Alignment	not modelled	99.2	18	**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
64	c2qvgA_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
65	d1k66a_	Alignment	not modelled	99.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	d2ayxa1	Alignment	not modelled	99.1	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3mmnA_	Alignment	not modelled	99.1	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+
68	d1ys7a2	Alignment	not modelled	99.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	d2a9pa1	Alignment	not modelled	99.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c3grcD_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
71	c3h1gA_	Alignment	not modelled	99.1	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
72	d1peya_	Alignment	not modelled	99.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	c3ilhA_	Alignment	not modelled	99.1	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
74	c3hdgE_	Alignment	not modelled	99.1	16	**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
75	d1w25a1	Alignment	not modelled	99.1	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c2jrlA_	Alignment	not modelled	99.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
77	c3lteH_	Alignment	not modelled	99.1	17	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
78	c2qr3A	Alignment	not modelled	99.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**two-component system response regulator;

78	c2qr3A_	Alignment	not modelled	99.1	19	**PDBTitle:** crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
79	d2pl1a1	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c2zwmA_	Alignment	not modelled	99.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
81	c3hv2B_	Alignment	not modelled	99.1	17	**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
82	d1i3ca_	Alignment	not modelled	99.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
83	c3cg4A_	Alignment	not modelled	99.1	22	**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
84	c3gt7A_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
85	c2qzjC_	Alignment	not modelled	99.1	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
86	c3c3mA_	Alignment	not modelled	99.1	15	**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
87	d1zh2a1	Alignment	not modelled	99.1	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
88	d1qkka_	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	c3crnA_	Alignment	not modelled	99.0	14	**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
90	c3cg0A_	Alignment	not modelled	99.0	19	**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
91	d2r25b1	Alignment	not modelled	99.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	c3hzhA_	Alignment	not modelled	99.0	13	**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
93	c3c97A_	Alignment	not modelled	99.0	18	**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
94	c3dzdA_	Alignment	not modelled	99.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
95	d1yioa2	Alignment	not modelled	99.0	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	d1zgza1	Alignment	not modelled	99.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	c2zayA_	Alignment	not modelled	99.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
98	d1zesa1	Alignment	not modelled	99.0	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	c3m6mF_	Alignment	not modelled	99.0	21	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
100	c3jteA_	Alignment	not modelled	99.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
101	d1xhfa1	Alignment	not modelled	99.0	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
102	c3a0rB_	Alignment	not modelled	99.0	14	**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)
103	c3kcnA_	Alignment	not modelled	99.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog;

103	c3kchA_	Alignment	not modelled	99.0	19	**PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
104	d1mb3a_	Alignment	not modelled	99.0	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c3i42A_	Alignment	not modelled	99.0	12	**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
106	c3hdvB_	Alignment	not modelled	99.0	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
107	c3luaA_	Alignment	not modelled	99.0	17	**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
108	c3eodA_	Alignment	not modelled	98.9	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
109	c3n0rA_	Alignment	not modelled	98.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
110	c2qxyB_	Alignment	not modelled	98.9	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
111	c3gl9B_	Alignment	not modelled	98.9	17	**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
112	c2rdmB_	Alignment	not modelled	98.9	19	**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
113	c3nhmA_	Alignment	not modelled	98.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
114	c3n53B_	Alignment	not modelled	98.9	16	**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	c2nt3A_	Alignment	not modelled	98.9	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
116	d1dcfa_	Alignment	not modelled	98.9	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
117	d2b4aa1	Alignment	not modelled	98.8	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
118	c2qsjB_	Alignment	not modelled	98.8	25	**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
119	c3snkA_	Alignment	not modelled	98.8	13	**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
120	d1k68a_	Alignment	not modelled	98.8	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related