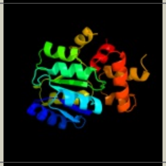
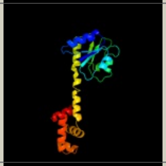
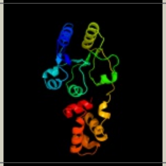
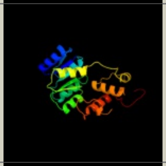
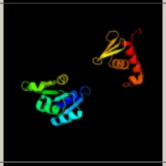
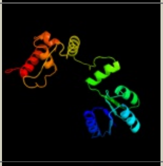
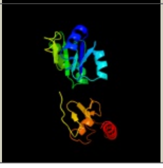
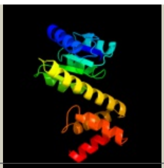
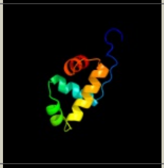
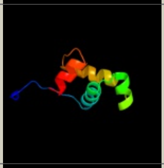
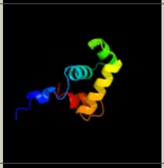
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AGA6
Date	Thu Jan 5 11:28:37 GMT 2012
Unique Job ID	cc9c9c0e826a7ec2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c3wB_	Alignment		100.0	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
2	c1rnlA_	Alignment		100.0	26	**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
3	c1zn2A_	Alignment		100.0	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
4	c3klnC_	Alignment		99.9	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
5	c1kgsA_	Alignment		99.9	21	**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	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
7	c3r0jA_	Alignment		99.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
8	c2oqrA_	Alignment		99.8	24	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
9	c1ys7B_	Alignment		99.8	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
10	c2gwrA_	Alignment		99.7	21	**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
11	c2hqrA_	Alignment		99.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism

12	d1s8na_	Alignment		99.7	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
13	c1p2fA_	Alignment		99.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
14	c3sztB_	Alignment		99.7	28	**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
15	c2q0oA_	Alignment		99.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
16	c1h0mD_	Alignment		99.6	18	**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
17	c3qp5C_	Alignment		99.6	30	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
18	c3cloC_	Alignment		99.6	35	**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	c2krfB_	Alignment		99.6	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
20	d1fsea_	Alignment		99.5	44	**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)
21	d1p4wa_	Alignment	not modelled	99.5	31	**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)
22	c1zljE_	Alignment	not modelled	99.5	29	**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	d1a04a1	Alignment	not modelled	99.5	31	**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	d1l3la1	Alignment	not modelled	99.5	19	**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	c2rnjA_	Alignment	not modelled	99.5	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
26	c3b2nA_	Alignment	not modelled	99.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
27	c1x3uA_	Alignment	not modelled	99.5	35	**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
28	c1a2oB_	Alignment	not modelled	99.5	26	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain

29	c2jpcA_	Alignment	not modelled	99.5	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
30	c3t8yA_	Alignment	not modelled	99.5	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
31	d1yioa1	Alignment	not modelled	99.5	41	**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)
32	c3eq2A_	Alignment	not modelled	99.4	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
33	d1dz3a_	Alignment	not modelled	99.4	24	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
34	c3breA_	Alignment	not modelled	99.4	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
35	c3cz5B_	Alignment	not modelled	99.4	28	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two-component response regulator, luxr family; **PDBTitle:** crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
36	c3eulB_	Alignment	not modelled	99.4	33	**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
37	d1a04a2	Alignment	not modelled	99.4	33	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
38	c3i5aA_	Alignment	not modelled	99.4	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
39	c2ayxA_	Alignment	not modelled	99.4	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
40	d1a2oa1	Alignment	not modelled	99.4	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c1w25B_	Alignment	not modelled	99.3	23	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
42	c3cu5B_	Alignment	not modelled	99.3	19	**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
43	c3f6cB_	Alignment	not modelled	99.3	25	**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
44	c2qv0A_	Alignment	not modelled	99.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
45	c2qr3A_	Alignment	not modelled	99.3	18	**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
46	d1jbea_	Alignment	not modelled	99.3	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	d1u0sy_	Alignment	not modelled	99.3	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3rqiA_	Alignment	not modelled	99.3	21	**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
49	c1ny5A_	Alignment	not modelled	99.3	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
50	c3cnbC_	Alignment	not modelled	99.2	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
51	c3khtA_	Alignment	not modelled	99.2	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
						PDB header:signaling protein

52	c3c3mA_	Alignment	not modelled	99.2	17	**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	d1ny5a1	Alignment	not modelled	99.2	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
54	c3kyiB_	Alignment	not modelled	99.2	28	**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
55	c3cg0A_	Alignment	not modelled	99.2	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
56	c3h1gA_	Alignment	not modelled	99.2	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
57	d1kgsa2	Alignment	not modelled	99.2	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	d1p6qa_	Alignment	not modelled	99.2	26	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	c2jrlA_	Alignment	not modelled	99.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
60	c2zwmA_	Alignment	not modelled	99.2	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
61	d1ys7a2	Alignment	not modelled	99.2	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	d2a9pa1	Alignment	not modelled	99.2	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	d1dbwa_	Alignment	not modelled	99.2	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
64	d1k66a_	Alignment	not modelled	99.2	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	c2rjnA_	Alignment	not modelled	99.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
66	d1peya_	Alignment	not modelled	99.2	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3hebB_	Alignment	not modelled	99.2	17	**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
68	c3nhzA_	Alignment	not modelled	99.2	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
69	c3ilhA_	Alignment	not modelled	99.2	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
70	c3hdgE_	Alignment	not modelled	99.2	22	**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
71	c3jteA_	Alignment	not modelled	99.2	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
72	c3m6mF_	Alignment	not modelled	99.2	27	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
73	c3crnA_	Alignment	not modelled	99.1	24	**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
74	c2qsjB_	Alignment	not modelled	99.1	28	**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
75	d2ayxa1	Alignment	not modelled	99.1	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c3i42A_	Alignment	not modelled	99.1	20	**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

77	d1zesa1	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	d2pl1a1	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
79	c3gt7A_	Alignment	not modelled	99.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
80	c3lteH_	Alignment	not modelled	99.1	22	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
81	c3t6kB_	Alignment	not modelled	99.1	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
82	d2r25b1	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
83	d1heya_	Alignment	not modelled	99.1	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	c2qvgA_	Alignment	not modelled	99.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
85	d1i3ca_	Alignment	not modelled	99.1	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	d1mvoa_	Alignment	not modelled	99.1	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	d1qkka_	Alignment	not modelled	99.1	33	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
88	d1w25a1	Alignment	not modelled	99.1	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	c3dzdA_	Alignment	not modelled	99.1	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
90	d1zgza1	Alignment	not modelled	99.1	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	c3hzhA_	Alignment	not modelled	99.1	22	**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
92	c2qzjC_	Alignment	not modelled	99.1	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
93	c3c97A_	Alignment	not modelled	99.1	24	**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	d1zh2a1	Alignment	not modelled	99.1	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	d1krwa_	Alignment	not modelled	99.1	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	d1xhfa1	Alignment	not modelled	99.1	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	d1mb3a_	Alignment	not modelled	99.1	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	c3cfyA_	Alignment	not modelled	99.1	27	**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
99	c3cg4A_	Alignment	not modelled	99.1	20	**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
100	c3hv2B_	Alignment	not modelled	99.1	25	**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
101	d1yioa2	Alignment	not modelled	99.1	29	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
102	c2zayA_	Alignment	not modelled	99.1	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans

103	c3mmnA_	Alignment	not modelled	99.0	25	**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+
104	c3n53B_	Alignment	not modelled	99.0	22	**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
105	c3lufB_	Alignment	not modelled	99.0	20	**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
106	c3a0rB_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
107	c3grcD_	Alignment	not modelled	99.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
108	c2jk1A_	Alignment	not modelled	99.0	27	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
109	c2j48A_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
110	c3n0rA_	Alignment	not modelled	99.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
111	c3kcnA_	Alignment	not modelled	99.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
112	c3snkA_	Alignment	not modelled	98.9	17	**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
113	c2qxyB_	Alignment	not modelled	98.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
114	c3nhmA_	Alignment	not modelled	98.9	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
115	c3luaA_	Alignment	not modelled	98.9	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
116	c3gl9B_	Alignment	not modelled	98.9	28	**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
117	c3eqzB_	Alignment	not modelled	98.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from colwellia2 psychrerythraea
118	c2rdmB_	Alignment	not modelled	98.9	20	**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
119	c3cwoX_	Alignment	not modelled	98.9	23	**PDB header:**de novo protein **Chain:** X: **PDB Molecule:**beta/alpha-barrel protein based on 1thf and 1tmy; **PDBTitle:** a beta/alpha-barrel built by the combination of fragments2 from different folds
120	c2hqoA_	Alignment	not modelled	98.9	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