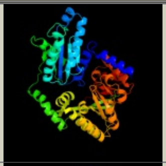
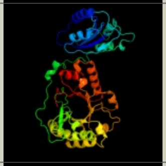
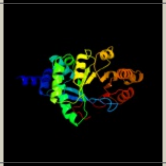
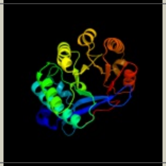
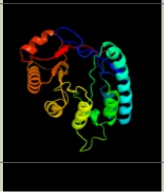
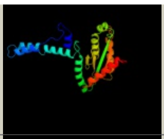
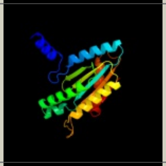
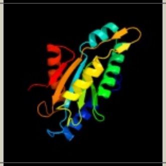
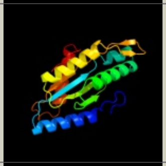
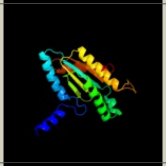
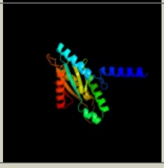
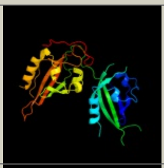
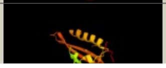
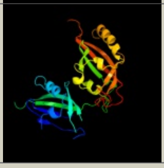
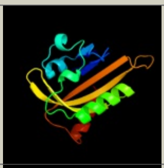
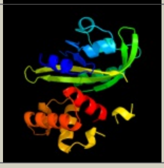
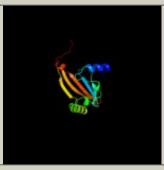
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P38097
Date	Thu Jan 5 11:57:56 GMT 2012
Unique Job ID	623c96788c4fa1d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
2	c3gfzB_	Alignment		100.0	13	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
3	c3hvbB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
4	c3hv9A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	Alignment		100.0	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
6	c3pfmA_	Alignment		100.0	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
7	c2w27A_	Alignment		100.0	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ykui protein; **PDBTitle:** crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
8	c2r6oB_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase (ggdef & eal **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
9	d2basa1	Alignment		100.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	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
11	c3kzpA_	Alignment		100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase; **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes

12	c3ezuA_	Alignment		100.0	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
13	c3breA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3iclA_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
15	c3ignA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
16	c3i5bA_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
17	c3i5aA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
18	c3hvaA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
19	d1w25a3	Alignment		100.0	32	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
20	c3i5cA_	Alignment		100.0	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
21	c3qyyB_	Alignment	not modelled	99.9	26	**PDB header:**signaling protein/inhibitor **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
22	c3mtkA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
23	c3hvwA_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
24	c3rtyA_	Alignment		99.9	12	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
25	c3gecA_	Alignment		99.8	13	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of a tandem pas domain fragment of2 drosophila period
						**PDB header:**circadian rhythm

26	c1wa9A_	Alignment		99.8	11	**Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of the pas repeat region of the2 drosophila clock protein period
27	c3gdiB_	Alignment		99.8	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**period circadian protein homolog 2; **PDBTitle:** mammalian clock protein mper2 - crystal struture of a pas2 domain fragment
28	c3ewkA_	Alignment	not modelled	99.8	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
29	c2wkqA_	Alignment		99.7	19	**PDB header:**transferase, cell adhesion **Chain:** A: **PDB Molecule:**nph1-1, ras-related c3 botulinum toxin substrate **PDBTitle:** structure of a photoactivatable rac1 containing the lov22 c450a mutant
30	c3p7nB_	Alignment		99.7	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
31	d1ew0a_	Alignment	not modelled	99.7	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
32	c3caxA_	Alignment		99.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
33	c2gj3A_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nitrogen fixation regulatory protein; **PDBTitle:** crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.
34	c3bwlA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
35	c2v1bA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nph1-1; **PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
36	c2r78D_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
37	c3f1oB_	Alignment	not modelled	99.6	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator; **PDBTitle:** crystal structure of the high affinity heterodimer of hif22 alpha and arnt c-terminal pas domains, with an internally-3 bound artificial ligand
38	c3lyxA_	Alignment	not modelled	99.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef domain protein; **PDBTitle:** crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
39	d1p97a_	Alignment	not modelled	99.6	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain
40	c3mqoB_	Alignment	not modelled	99.6	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
41	c3luqC_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a
42	c2kdkA_	Alignment	not modelled	99.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator-like protein **PDBTitle:** structure of human circadian clock protein bmal2 c-terminal pas domain
43	c3mr0B_	Alignment	not modelled	99.6	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sensory box histidine kinase/response regulator; **PDBTitle:** crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
44	c3mxqC_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
45	c2pr6A_	Alignment	not modelled	99.6	19	**PDB header:**flavoprotein, signaling protein **Chain:** A: **PDB Molecule:**blue-light photoreceptor;

45	c2pr6A_	Alignment	not modelled	99.6	19	**PDBTitle:** structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
46	c3mfxA_	Alignment	not modelled	99.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
47	d1n9la_	Alignment	not modelled	99.6	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
48	c2vlgD_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
49	d1bywa_	Alignment	not modelled	99.6	21	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
50	c2l4rA_	Alignment	not modelled	99.5	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h member 2; **PDBTitle:** nmr solution structure of the n-terminal pas domain of herg
51	d1jnua_	Alignment	not modelled	99.5	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
52	c3h9wA_	Alignment	not modelled	99.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diguanylate cyclase with pas/pac sensor; **PDBTitle:** crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
53	c3mjqB_	Alignment	not modelled	99.5	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
54	c3eehA_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative light and redox sensing histidine kinase; **PDBTitle:** the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
55	c2z6dB_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phototropin-2; **PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
56	c3k3dA_	Alignment	not modelled	99.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410; **PDBTitle:** the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
57	c1v9yA_	Alignment	not modelled	99.5	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
58	d1v9ya_	Alignment	not modelled	99.5	22	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
59	d1y28a_	Alignment	not modelled	99.5	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
60	c3icyB_	Alignment	not modelled	99.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 tls
61	c3kx0X_	Alignment	not modelled	99.4	13	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
62	c3oloB_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**two-component sensor histidine kinase; **PDBTitle:** crystal structure of a pas domain from two-component sensor histidine2 kinase
63	c3njaC_	Alignment	not modelled	99.4	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**probable ggdef family protein; **PDBTitle:** the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
64	d1xj3a1	Alignment	not modelled	99.4	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
65	c3b33A_	Alignment	not modelled	99.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
66	c2pdtD_	Alignment	not modelled	99.4	15	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
67	c2qkpD_	Alignment	not modelled	99.3	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
68	c3fg8B_	Alignment	not modelled	99.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
69	d1oj5a_	Alignment	not modelled	99.3	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1
70	d1nwza_	Alignment	not modelled	99.3	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain)

						Family:PYP-like
71	c2jheB_	Alignment	not modelled	99.3	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
72	c3fc7B_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**htr-like protein; **PDBTitle:** the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
73	d1ll8a_	Alignment	not modelled	99.2	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
74	c3cloC_	Alignment	not modelled	99.2	14	**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
75	d1otda_	Alignment	not modelled	99.2	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
76	d1mzua_	Alignment	not modelled	99.1	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
77	c3a0rA_	Alignment	not modelled	99.1	14	**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)
78	c3a0vA_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
79	c2w0nA_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein dcus; **PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
80	d1xfna1	Alignment	not modelled	98.9	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
81	c2oolA_	Alignment	not modelled	98.7	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
82	c2o9bA_	Alignment	not modelled	98.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
83	c2veaA_	Alignment	not modelled	98.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phytochrome-like protein cph1; **PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
84	c3c2wB_	Alignment	not modelled	96.4	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
85	c3eulB_	Alignment	not modelled	95.9	13	**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
86	c2qv6D_	Alignment	not modelled	95.8	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
87	c3khtA_	Alignment	not modelled	95.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
88	c3hebB_	Alignment	not modelled	95.4	12	**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
89	c2zayA_	Alignment	not modelled	95.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
90	d1mvoa_	Alignment	not modelled	95.3	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	d1p6qa_	Alignment	not modelled	95.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	d1w25a1	Alignment	not modelled	95.0	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c3b2nA_	Alignment	not modelled	94.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
94	d1krwa_	Alignment	not modelled	94.8	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	c2ayxA_	Alignment	not modelled	94.5	15	**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

96	d2oola2	Alignment	not modelled	94.4	10	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
97	c2qr3A_	Alignment	not modelled	94.4	10	**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
98	c3t6kB_	Alignment	not modelled	94.3	14	**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
99	d2o9ca2	Alignment	not modelled	94.3	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
100	d1ny5a1	Alignment	not modelled	94.2	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
101	c3cg0A_	Alignment	not modelled	94.2	18	**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
102	d1jbea_	Alignment	not modelled	94.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
103	d1heya_	Alignment	not modelled	94.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
104	d1u0sy_	Alignment	not modelled	93.8	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c2rjnA_	Alignment	not modelled	93.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
106	c3lteH_	Alignment	not modelled	93.1	11	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
107	c2jrlA_	Alignment	not modelled	93.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
108	d1dz3a_	Alignment	not modelled	92.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	d1i3ca_	Alignment	not modelled	92.8	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
110	d1dbwa_	Alignment	not modelled	92.7	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
111	d1zesa1	Alignment	not modelled	92.7	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
112	d2ayxa1	Alignment	not modelled	92.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
113	c2jk1A_	Alignment	not modelled	92.7	10	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
114	d1qkka_	Alignment	not modelled	92.6	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
115	c3gt7A_	Alignment	not modelled	92.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
116	c2yxbA_	Alignment	not modelled	92.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
117	d2pl1a1	Alignment	not modelled	92.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
118	c3gl9B_	Alignment	not modelled	92.4	8	**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
119	c3hv2B_	Alignment	not modelled	92.1	11	**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
120	c2qxyB_	Alignment	not modelled	91.9	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima