Phyre^2

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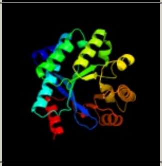
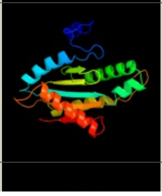
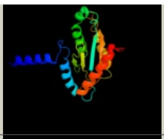
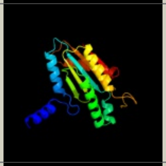
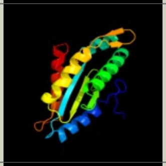
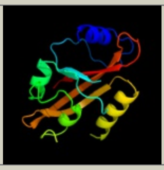
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	23	**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	22	**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	25	**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	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	Alignment		100.0	33	**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	25	**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	17	**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	34	**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	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	c3kzpA_	Alignment		100.0	21	**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
11	c1w25B_	Alignment		100.0	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp

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		99.9	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3iclA_	Alignment		99.9	39	**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	c3mtkA_	Alignment		99.9	25	**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
16	c3ignA_	Alignment		99.9	30	**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
17	c3i5bA_	Alignment		99.9	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
18	c3hvaA_	Alignment		99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
19	c3i5cA_	Alignment		99.9	28	**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
20	c3i5aA_	Alignment		99.9	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
21	c3qyyB_	Alignment	not modelled	99.9	28	**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	d1w25a3	Alignment	not modelled	99.9	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
23	c3hvwA_	Alignment	not modelled	99.9	20	**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	c3p7nB_	Alignment		99.8	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
25	c2wkqA_	Alignment	not modelled	99.7	15	**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
26	c2gj3A_	Alignment	not modelled	99.7	17	**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.
27	c3lyxA_	Alignment	not modelled	99.7	18	**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
28	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
29	c3bwlA_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
30	c2v1bA_	Alignment	not modelled	99.6	16	**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))
31	c3caxA_	Alignment	not modelled	99.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
32	d1ew0a_	Alignment	not modelled	99.6	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
33	c2l4rA_	Alignment	not modelled	99.6	10	**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
34	c3mxqC_	Alignment	not modelled	99.6	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
35	c3luqC_	Alignment	not modelled	99.6	15	**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
36	d1bywa_	Alignment	not modelled	99.6	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
37	d1p97a_	Alignment	not modelled	99.6	8	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain
38	c2r78D_	Alignment	not modelled	99.6	15	**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
39	d1n9la_	Alignment	not modelled	99.5	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
40	c3mfxA_	Alignment	not modelled	99.5	14	**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
41	c3f1oB_	Alignment	not modelled	99.5	13	**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
42	c2kdkA_	Alignment	not modelled	99.5	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	c3eehA_	Alignment	not modelled	99.5	10	**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
44	d1jnua_	Alignment	not modelled	99.5	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
45	c3h9wA_	Alignment	not modelled	99.5	10	**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
46	c2z6dB_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phototropin-2; **PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
47	c3oloB_	Alignment	not modelled	99.5	11	**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
48	c2pr6A_	Alignment	not modelled	99.5	18	**PDB header:**flavoprotein, signaling protein **Chain:** A: **PDB Molecule:**blue-light photoreceptor; **PDBTitle:** structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
49	c3k3dA_	Alignment	not modelled	99.5	11	**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
50	c3b33A_	Alignment	not modelled	99.5	16	**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

51	c2vlgD_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
52	c3mr0B_	Alignment	not modelled	99.5	14	**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
53	c1v9yA_	Alignment	not modelled	99.4	20	**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)
54	d1v9ya_	Alignment	not modelled	99.4	20	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
55	c2pdtD_	Alignment		99.4	16	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
56	c3mjqB_	Alignment	not modelled	99.4	12	**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.
57	c3kx0X_	Alignment	not modelled	99.4	11	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
58	d1y28a_	Alignment	not modelled	99.4	21	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
59	c3gdiB_	Alignment	not modelled	99.4	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**period circadian protein homolog 2; **PDBTitle:** mammalian clock protein mper2 - crystal struture of a pas2 domain fragment
60	d1xj3a1	Alignment	not modelled	99.3	20	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
61	c3fg8B_	Alignment	not modelled	99.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
62	c2qkpD_	Alignment	not modelled	99.3	9	**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
63	c3rtyA_	Alignment	not modelled	99.3	15	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
64	c3icyB_	Alignment	not modelled	99.3	10	**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
65	d1nwza_	Alignment	not modelled	99.3	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
66	c3njaC_	Alignment	not modelled	99.3	16	**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.
67	c2jheB_	Alignment	not modelled	99.2	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
68	c3gecA_	Alignment	not modelled	99.2	10	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of a tandem pas domain fragment of2 drosophila period
69	c3fc7B_	Alignment	not modelled	99.2	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
70	d1oj5a_	Alignment	not modelled	99.1	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1
71	c3ewkA_	Alignment	not modelled	99.1	18	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
72	d1otda_	Alignment	not modelled	99.1	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
73	d1ll8a_	Alignment	not modelled	99.1	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
74	d1mzua_	Alignment	not modelled	99.1	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
75	c3a0rA_	Alignment	not modelled	99.0	18	**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)
						PDB header:transferase

76	c3a0vA_	Alignment	not modelled	99.0	17	**Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
77	c2w0nA_	Alignment	not modelled	99.0	14	**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
78	c1wa9A_	Alignment	not modelled	99.0	10	**PDB header:**circadian rhythm **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of the pas repeat region of the2 drosophila clock protein period
79	d1xfna1	Alignment	not modelled	98.9	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
80	c3cloC_	Alignment	not modelled	98.8	16	**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
81	c2oolA_	Alignment	not modelled	98.4	14	**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	98.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
83	c2veaA_	Alignment	not modelled	97.3	12	**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	d1p6qa_	Alignment	not modelled	96.8	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	d1mvoa_	Alignment	not modelled	96.8	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	d1zesa1	Alignment	not modelled	96.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c2ayxA_	Alignment	not modelled	96.5	18	**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
88	c2zayA_	Alignment	not modelled	96.4	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
89	c3q58A_	Alignment	not modelled	96.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
90	d2ayxa1	Alignment	not modelled	96.3	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	c3khtA_	Alignment	not modelled	96.2	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
92	d1w25a1	Alignment	not modelled	96.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c3hebB_	Alignment	not modelled	96.1	15	**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
94	d1xhfa1	Alignment	not modelled	96.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	d2a9pa1	Alignment	not modelled	95.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	d1jbea_	Alignment	not modelled	95.9	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	d1krwa_	Alignment	not modelled	95.8	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	c2qr3A_	Alignment	not modelled	95.8	13	**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
99	d1qkka_	Alignment	not modelled	95.7	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
100	d1heya_	Alignment	not modelled	95.7	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:hydrolase

101	c3gt7A_	Alignment	not modelled	95.6	16	**Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
102	c2rjnA_	Alignment	not modelled	95.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
103	c3nhzA_	Alignment	not modelled	95.6	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
104	c2yxbA_	Alignment	not modelled	95.6	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
105	c3cnbC_	Alignment	not modelled	95.5	18	**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
106	c3t6kB_	Alignment	not modelled	95.4	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
107	c3c2wB_	Alignment	not modelled	95.4	8	**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
108	d1k66a_	Alignment	not modelled	95.2	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c3hv2B_	Alignment	not modelled	95.1	13	**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
110	c3cg0A_	Alignment	not modelled	95.1	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
111	c2jk1A_	Alignment	not modelled	95.1	13	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
112	d1mb3a_	Alignment	not modelled	95.0	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
113	d1yioa2	Alignment	not modelled	95.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
114	c3c97A_	Alignment	not modelled	95.0	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
115	d1dz3a_	Alignment	not modelled	95.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
116	c3crnA_	Alignment	not modelled	94.9	15	**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	c3i42A_	Alignment	not modelled	94.8	17	**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
118	d1ny5a1	Alignment	not modelled	94.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
119	c2zwmA_	Alignment	not modelled	94.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
120	c3b2nA_	Alignment	not modelled	94.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus