Phyre^2

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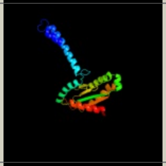
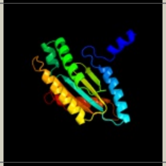
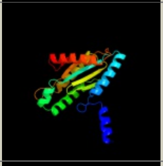
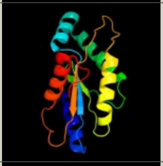
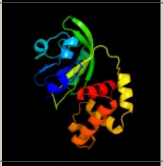
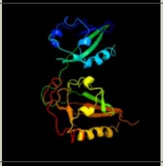
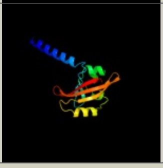
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	38	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
2	c3ezuA_	Alignment		100.0	27	**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
3	c3i5aA_	Alignment		100.0	41	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
4	c3breA_	Alignment		100.0	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
5	c3qyyB_	Alignment		100.0	31	**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
6	c3ignA_	Alignment		100.0	36	**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
7	c3i5cA_	Alignment		100.0	39	**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
8	c3i5bA_	Alignment		100.0	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
9	c3hvaA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
10	d1w25a3	Alignment		100.0	41	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
11	c3iclA_	Alignment		100.0	33	**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

12	c3mtkA_	Alignment		100.0	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
13	c3pjwA_	Alignment		99.9	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		99.9	15	**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
15	c3p7nB_	Alignment		99.7	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
16	c3gecA_	Alignment		99.6	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
17	c3gfzB_	Alignment		99.5	13	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
18	c3rtyA_	Alignment		99.5	10	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
19	c3gdiB_	Alignment		99.5	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
20	c3bwlA_	Alignment		99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
21	d1ew0a_	Alignment	not modelled	99.4	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
22	c1wa9A_	Alignment	not modelled	99.4	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
23	c2r78D_	Alignment	not modelled	99.3	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
24	c3mfxA_	Alignment	not modelled	99.3	13	**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
25	c3mjqB_	Alignment	not modelled	99.2	20	**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.
26	c2pr6A_	Alignment	not modelled	99.2	21	**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)
27	c3mqoB_	Alignment	not modelled	99.2	12	**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

28	c3caxA_	Alignment	not modelled	99.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
29	c2v1bA_	Alignment	not modelled	99.2	12	**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))
30	c3ewkA_	Alignment	not modelled	99.2	13	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
31	c3oloB_	Alignment	not modelled	99.2	12	**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
32	d1y28a_	Alignment	not modelled	99.2	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
33	d1p97a_	Alignment	not modelled	99.1	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain
34	c3b33A_	Alignment	not modelled	99.1	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
35	c2l4rA_	Alignment	not modelled	99.1	14	**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
36	d1bywa_	Alignment	not modelled	99.1	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
37	c3luqC_	Alignment	not modelled	99.1	14	**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
38	c1v9yA_	Alignment	not modelled	99.0	15	**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)
39	d1v9ya_	Alignment	not modelled	99.0	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
40	c3lyxA_	Alignment	not modelled	99.0	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
41	d1xj3a1	Alignment	not modelled	99.0	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
42	d1ll8a_	Alignment	not modelled	99.0	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
43	c2gj3A_	Alignment	not modelled	99.0	15	**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.
44	c2wkqA_	Alignment	not modelled	99.0	14	**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
45	c2z6dB_	Alignment	not modelled	99.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phototropin-2; **PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
46	c3mxqC_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
47	c3mr0B_	Alignment	not modelled	99.0	13	**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
48	c3f1oB_	Alignment	not modelled	99.0	10	**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
49	c2vlgD_	Alignment	not modelled	99.0	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
50	d1n9la_	Alignment	not modelled	99.0	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
51	c3kx0X_	Alignment	not modelled	98.9	12	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
52	c3k3dA_	Alignment	not modelled	98.9	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410;

52	c3k3dA_	Alignment	not modelled	98.9	14	**PDBTitle:** the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
53	c3h9wA_	Alignment	not modelled	98.9	6	**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
54	c3eehA_	Alignment	not modelled	98.9	14	**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	d1jnua_	Alignment	not modelled	98.9	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
56	c2kdkA_	Alignment	not modelled	98.8	10	**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
57	c3fg8B_	Alignment	not modelled	98.8	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
58	c2pdtD_	Alignment	not modelled	98.7	12	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
59	c2jheB_	Alignment	not modelled	98.6	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
60	d1otda_	Alignment	not modelled	98.5	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
61	d1oj5a_	Alignment	not modelled	98.4	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1
62	c2qkpD_	Alignment	not modelled	98.4	10	**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	d1nwza_	Alignment	not modelled	98.4	10	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
64	c3fc7B_	Alignment	not modelled	98.4	14	**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
65	d1xfna1	Alignment	not modelled	98.4	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
66	c3icyB_	Alignment	not modelled	98.4	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
67	c2o9bA_	Alignment	not modelled	98.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
68	d1mzua_	Alignment	not modelled	98.3	8	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
69	c3njaC_	Alignment	not modelled	98.2	12	**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.
70	c2w0nA_	Alignment	not modelled	98.2	13	**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
71	c3a0rA_	Alignment	not modelled	98.2	12	**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)
72	c3cloC_	Alignment	not modelled	98.1	8	**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
73	c2oolA_	Alignment	not modelled	98.1	7	**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
74	c3a0vA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
75	c2veaA_	Alignment	not modelled	97.7	7	**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.
76	c2qv6D_	Alignment	not modelled	97.2	17	**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
77	d1azsa_	Alignment	not modelled	95.0	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase

						Family: Adenylyl and guanylyl cyclase catalytic domain
78	c1cjkA_	Alignment	not modelled	94.9	13	**PDB header:**lyase/lyase/signaling protein **Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
79	c1y10C_	Alignment	not modelled	91.6	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
80	c3c2wB_	Alignment	not modelled	90.5	13	**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
81	c1yk9A_	Alignment	not modelled	89.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
82	c3uvjC_	Alignment	not modelled	89.2	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
83	c2w01C_	Alignment	not modelled	85.2	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
84	c3mr7B_	Alignment	not modelled	84.5	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
85	c1wc6B_	Alignment	not modelled	83.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
86	d1wc1a_	Alignment	not modelled	79.1	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
87	d2o9ca2	Alignment	not modelled	75.0	10	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
88	c1ybuA_	Alignment	not modelled	68.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
89	c3et6A_	Alignment	not modelled	67.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
90	d1fx4a_	Alignment	not modelled	66.2	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
91	d1fx2a_	Alignment	not modelled	57.5	12	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
92	c3gqcB_	Alignment	not modelled	43.8	22	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
93	c3pxpA_	Alignment	not modelled	39.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
94	d2veaa3	Alignment	not modelled	37.1	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
95	d1azsb_	Alignment	not modelled	35.9	11	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
96	c3onqB_	Alignment	not modelled	33.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
97	c2wz1B_	Alignment	not modelled	32.9	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
98	c2aq4A_	Alignment	not modelled	29.1	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
99	d3c2wa3	Alignment	not modelled	23.7	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like