Phyre^2

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Description	P77510
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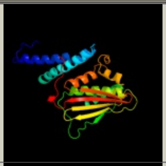
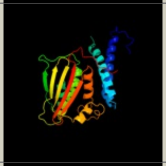
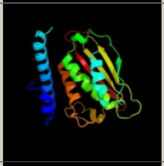
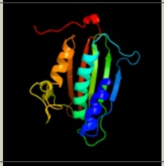
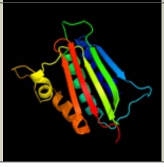
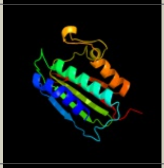
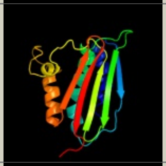
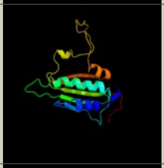
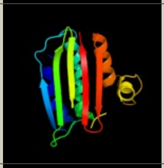
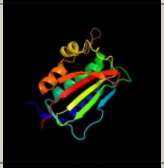
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2q8fA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
2	c3d2rB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; **PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
3	c2bu8A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase kinase isoenzyme 2; **PDBTitle:** crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
4	c1y8oA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
5	c3a0rA_	Alignment		100.0	17	**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)
6	c2c2aA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
7	c3d36B_	Alignment		100.0	18	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**sporulation kinase b; **PDBTitle:** how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
8	c1gjvA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[3-methyl-2-oxobutanoate dehydrogenase **PDBTitle:** branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complxed with atp-gamma-s
9	d1jm6a2	Alignment		100.0	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
10	d1gkza2	Alignment		100.0	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
11	d2c2aa2	Alignment		100.0	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase

12	c1b3qA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
13	c3a0tA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal)
14	d1id0a_	Alignment		99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
15	c2ch4A_	Alignment		99.9	22	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
16	d1bxda_	Alignment		99.9	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
17	d1i58a_	Alignment		99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
18	d1ysra1	Alignment		99.9	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
19	c3jz3B_	Alignment		99.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
20	d2hkja3	Alignment		99.8	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
21	d1r62a_	Alignment	not modelled	99.8	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
22	c3ehgA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase (yocf protein); **PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp
23	c3gieA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
24	c3zxqA_	Alignment	not modelled	99.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost; **PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
25	c1mx0D_	Alignment	not modelled	99.7	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
26	c2zbkB_	Alignment	not modelled	99.7	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
27	c2q2eB_	Alignment	not modelled	99.6	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
						PDB header:transferase **Chain:** B: **PDB Molecule:**redox sensor histidine kinase response

28	c3zxoB_	Alignment	not modelled	99.6	26	regulator devs; **PDBTitle:** crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
29	d1ixma_	Alignment	not modelled	99.6	17	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
30	d1th8a_	Alignment	not modelled	99.5	23	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
31	d1h7sa2	Alignment	not modelled	99.5	18	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
32	d1b63a2	Alignment	not modelled	99.4	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
33	d1bkna2	Alignment	not modelled	99.4	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
34	d1y8oa2	Alignment	not modelled	99.4	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
35	c3na3A_	Alignment	not modelled	99.1	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
36	d3by8a1	Alignment		99.1	25	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
37	d1p0za_	Alignment		99.1	37	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
38	c3h4lB_	Alignment	not modelled	98.8	19	**PDB header:**dna binding protein, protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
39	d1kija2	Alignment	not modelled	98.5	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
40	d1pvga2	Alignment	not modelled	98.4	29	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
41	d1ei1a2	Alignment	not modelled	98.4	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
42	c1kijB_	Alignment	not modelled	98.3	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
43	d1s16a2	Alignment	not modelled	98.3	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
44	c1bknA_	Alignment	not modelled	98.3	20	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
45	c1y4sA_	Alignment	not modelled	98.3	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
46	c1ei1B_	Alignment	not modelled	98.2	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase b; **PDBTitle:** dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center
47	c2cg9A_	Alignment	not modelled	98.1	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
48	d2iwxa1	Alignment	not modelled	98.1	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
49	c3ke6A_	Alignment	not modelled	98.1	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410;

		Alignment				**PDBTitle:** the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
50	c1s16B_	Alignment	not modelled	98.1	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
51	c1zwhA_	Alignment	not modelled	98.1	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
52	c1ea6A_	Alignment	not modelled	98.1	32	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
53	d1uyla_	Alignment	not modelled	98.0	18	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
54	c3iedA_	Alignment	not modelled	98.0	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein; **PDBTitle:** crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
55	c2iopD_	Alignment	not modelled	98.0	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
56	c2fwyA_	Alignment	not modelled	97.9	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
57	c1zxnB_	Alignment	not modelled	97.9	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
58	c3g7bB_	Alignment	not modelled	97.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
59	c2iorA_	Alignment	not modelled	97.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
60	c1qzrA_	Alignment	not modelled	97.9	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase ii; **PDBTitle:** crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
61	c2o1wB_	Alignment	not modelled	97.8	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
62	c3pehB_	Alignment	not modelled	97.8	22	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin homolog; **PDBTitle:** crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
63	d1uyma_	Alignment	not modelled	97.7	13	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
64	c2akpA_	Alignment	not modelled	97.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
65	d2gqpa1	Alignment	not modelled	97.6	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
66	d1s14a_	Alignment	not modelled	97.5	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
67	d1qy5a_	Alignment	not modelled	97.4	25	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
68	c2o1uA_	Alignment	not modelled	97.3	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
69	c3lnuA_	Alignment	not modelled	97.1	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
70	c2w0nA_	Alignment	not modelled	96.9	25	**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	c2jheB_	Alignment	not modelled	96.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
72	c2qkpD_	Alignment	not modelled	96.2	15	**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
73	c3lyxA_	Alignment	not modelled	96.0	15	**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
74	c3caxA_	Alignment	not modelled	95.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
75	c3mqoB_	Alignment	not modelled	95.5	14	**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
76	c3mxqC_	Alignment	not modelled	95.5	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
77	c3cwvB_	Alignment	not modelled	95.1	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase, b subunit, truncated; **PDBTitle:** crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
78	c3mfxA_	Alignment	not modelled	95.1	11	**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
79	c3b33A_	Alignment	not modelled	95.0	14	**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
80	d1nwza_	Alignment	not modelled	95.0	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
81	d1mzua_	Alignment	not modelled	94.5	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
82	c2gj3A_	Alignment	not modelled	94.3	13	**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.
83	c1v9yA_	Alignment	not modelled	93.9	9	**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)
84	d1v9ya_	Alignment	not modelled	93.9	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
85	d1otda_	Alignment	not modelled	93.7	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
86	c2pr6A_	Alignment	not modelled	93.7	13	**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)
87	c3fg8B_	Alignment	not modelled	93.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
88	c3oloB_	Alignment	not modelled	93.6	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
89	c3b42B_	Alignment	not modelled	93.4	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
90	c2v1bA_	Alignment	not modelled	93.2	13	**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))
91	c3fc7B_	Alignment	not modelled	93.1	12	**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
92	c3luqC_	Alignment	not modelled	91.9	12	**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
93	d1y28a_	Alignment	not modelled	91.8	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
94	c2r78D_	Alignment	not modelled	91.1	18	**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
95	c3mr0B_	Alignment	not modelled	90.5	8	**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
96	d1xfna1	Alignment	not modelled	90.4	20	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
97	c3a0vA_	Alignment	not modelled	90.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)

98	c3lmmA_	Alignment	not modelled	90.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
99	c3e4pB_	Alignment	not modelled	89.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of malonate occupied dctb
100	c3mjqB_	Alignment	not modelled	89.0	7	**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.
101	c3by9A_	Alignment	not modelled	88.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. cholerae histidine kinase dctb2 sensor domain
102	c3k3dA_	Alignment	not modelled	87.6	13	**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
103	c3fosA_	Alignment	not modelled	87.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
104	d1ew0a_	Alignment	not modelled	84.1	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
105	d1ll8a_	Alignment	not modelled	84.0	24	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
106	c2vlgD_	Alignment	not modelled	82.3	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
107	c3kx0X_	Alignment	not modelled	76.3	12	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
108	c3bwlA_	Alignment	not modelled	75.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
109	d2p7ja2	Alignment	not modelled	74.7	8	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
110	d1xj3a1	Alignment	not modelled	71.4	22	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
111	d1wmaa1	Alignment	not modelled	70.3	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	d1n9la_	Alignment	not modelled	69.4	8	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
113	c2l4rA_	Alignment	not modelled	66.9	11	**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
114	c2wkqA_	Alignment	not modelled	65.8	13	**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
115	c3c38A_	Alignment	not modelled	61.2	15	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**autoinducer 2 sensor kinase/phosphatase luxq; **PDBTitle:** crystal structure of the periplasmic domain of vibrio2 cholerae luxq
116	c3p7nB_	Alignment	not modelled	59.2	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
117	d2c2aa1	Alignment	not modelled	57.7	13	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
118	c3eehA_	Alignment	not modelled	55.8	13	**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
119	c3rtyA_	Alignment	not modelled	50.2	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
120	c3ewkA_	Alignment	not modelled	48.6	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos