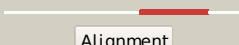
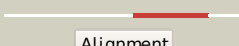
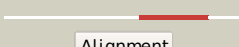
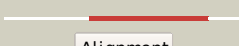
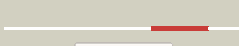


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bu8A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
2	c2q8fA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
3	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
4	c3a0rA_	 Alignment		100.0	15	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)
5	c1y8oA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
6	c1g1vA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
7	c3d36B_	 Alignment		100.0	17	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	c2c2aA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
9	d1jm6a2	 Alignment		100.0	20	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	c3a0tA_	 Alignment		100.0	20	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)
11	d1gkza2	 Alignment		100.0	21	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

12	d2c2aa2	Alignment		100.0	28	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
13	c1b3qA	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
14	d1id0a	Alignment		100.0	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	d1bxda	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
16	c2ch4A	Alignment		99.9	30	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
17	d1i58a	Alignment		99.9	32	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	20	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		99.9	18	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
20	d1r62a	Alignment		99.8	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
21	d2hkja3	Alignment	not modelled	99.8	23	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
22	c3ehgA	Alignment	not modelled	99.8	17	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	99.8	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	99.8	21	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	c2zkbB	Alignment	not modelled	99.7	23	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
26	c1mx0D	Alignment	not modelled	99.7	22	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
27	c3zxoB	Alignment	not modelled	99.7	21	PDB header: transferase Chain: B: PDB Molecule: redox sensor histidine kinase response regulator devs; PDBTitle: crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
28	c2q2eB	Alignment	not modelled	99.6	21	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
29	d1h7sa2	Alignment	not modelled	99.6	19 Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
30	d1th8a_	Alignment	not modelled	99.6	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
31	dlixma_	Alignment	not modelled	99.5	20 Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
32	d1bkna2	Alignment	not modelled	99.5	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
33	d1y8oa2	Alignment	not modelled	99.4	15 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
34	d1b63a2	Alignment	not modelled	99.4	22 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
35	c3na3A_	Alignment	not modelled	99.1	23 PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
36	c3h4lB_	Alignment	not modelled	98.9	22 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
37	d3by8a1	Alignment		98.8	100 Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
38	d1kija2	Alignment	not modelled	98.6	25 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
39	c1kijB_	Alignment	not modelled	98.6	19 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
40	c1bknA_	Alignment	not modelled	98.6	24 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
41	d1p0za_	Alignment	not modelled	98.5	28 Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
42	d1ei1a2	Alignment	not modelled	98.5	24 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
43	d1s16a2	Alignment	not modelled	98.5	23 Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
44	d1pvga2	Alignment	not modelled	98.4	23 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
45	c1ei1B_	Alignment	not modelled	98.4	30 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
46	c1ea6A_	Alignment	not modelled	98.3	20 PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
47	c1s16B_	Alignment	not modelled	98.3	28 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
48	c3g7bB_	Alignment	not modelled	98.2	19 PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with inhibitor
49	d2iwxal	Alignment	not modelled	98.2	26 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
50	d2gqpa1	Alignment	not modelled	98.2	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

51	c1y4sA	Alignment	not modelled	98.2	25	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
52	c3iedA	Alignment	not modelled	98.2	16	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
53	c1zwhA	Alignment	not modelled	98.2	26	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
54	c2o1uA	Alignment	not modelled	98.1	24	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
55	c1zxnB	Alignment	not modelled	98.1	25	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
56	d1uylA	Alignment	not modelled	98.1	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
57	c2fwyA	Alignment	not modelled	98.1	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
58	c2iorA	Alignment	not modelled	98.0	30	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
59	c3ke6A	Alignment	not modelled	98.0	24	PDB header: unknown function Chain: A: PDB Molecule: protein rv1364c/mt1410; PDBTitle: the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
60	c2cg9A	Alignment	not modelled	98.0	25	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
61	c1qzrA	Alignment	not modelled	97.9	25	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)
62	c2akpA	Alignment	not modelled	97.9	19	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
63	c3pehB	Alignment	not modelled	97.9	21	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
64	d1s14a	Alignment	not modelled	97.9	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
65	c3lnuA	Alignment	not modelled	97.8	21	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
66	d1uyma	Alignment	not modelled	97.7	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
67	d1qy5a	Alignment	not modelled	97.6	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	c2o1wB	Alignment	not modelled	97.4	24	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
69	c2iopD	Alignment	not modelled	97.4	31	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
70	c2w0nA	Alignment	not modelled	96.9	99	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	c3cwvB	Alignment	not modelled	96.1	10	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
72	c1v9yA	Alignment	not modelled	95.6	17	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)
73	d1v9ya	Alignment	not modelled	95.6	17	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
74	c3oloB	Alignment	not modelled	95.0	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
						PDB header: transferase

75	c3a0vA_	Alignment	not modelled	94.4	17	Chain: A: PDB Molecule: sensor protein; PDBTitle: pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
76	c2jheB_	Alignment	not modelled	94.2	16	PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1 -2 190)
77	c3mfxA_	Alignment	not modelled	94.0	15	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
78	c3mxqC_	Alignment	not modelled	92.1	9	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
79	c3lyxA_	Alignment	not modelled	91.8	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
80	d1nwza_	Alignment	not modelled	91.7	16	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
81	c2gj3A_	Alignment	not modelled	91.6	14	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.
82	c3b33A_	Alignment	not modelled	90.9	21	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
83	d1mzua_	Alignment	not modelled	90.5	14	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
84	c3fc7B_	Alignment	not modelled	88.9	15	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
85	c2vlgD_	Alignment	not modelled	88.1	9	PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
86	d1otda_	Alignment	not modelled	87.8	15	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
87	c2r78D_	Alignment	not modelled	87.6	10	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
88	c3luqC_	Alignment	not modelled	86.6	7	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
89	c3fg8B_	Alignment	not modelled	86.5	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790
90	d1xfna1	Alignment	not modelled	85.6	16	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
91	c2pr6A_	Alignment	not modelled	85.1	16	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)
92	c3mqoB_	Alignment	not modelled	85.0	8	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
93	d1y28a_	Alignment	not modelled	83.8	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
94	d1ew0a_	Alignment	not modelled	83.8	11	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
95	c2v1bA_	Alignment	not modelled	83.3	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))
96	c3mr0B_	Alignment	not modelled	82.2	6	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
97	d1l18a_	Alignment	not modelled	81.9	22	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: N-terminal PAS domain of Pas kinase
98	c3bwlA_	Alignment	not modelled	81.3	12	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
99	c3mjgB_	Alignment	not modelled	80.6	16	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. PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
100	c3p7nB_	Alignment	not modelled	80.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695
101	c3caxA_	Alignment	not modelled	80.4	16	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
102	d1xj3a1	Alignment	not modelled	79.3	12	PDB header: transferase Chain: B: PDB Molecule: c4-dicarboxylate transport sensor protein dctb; PDBTitle: crystal structure of malonate occupied dctb
103	c3e4pB_	Alignment	not modelled	79.1	17	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
104	c3lmmA_	Alignment	not modelled	75.1	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
105	c2qkpD_	Alignment	not modelled	73.9	12	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
106	c2wkqA_	Alignment	not modelled	72.1	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the v. cholerae histidine kinase dctb2 sensor domain
107	c3by9A_	Alignment	not modelled	70.9	10	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
108	c3fosA_	Alignment	not modelled	67.5	6	Fold: Profilin-like Superfamily: Sensory domain-like Family: Ykul C-terminal domain-like
109	d2p7ja2	Alignment	not modelled	63.4	7	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
110	d1n9la_	Alignment	not modelled	62.7	7	PDB header: flavoprotein Chain: A: PDB Molecule: sensor protein; PDBTitle: structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
111	c3ewkA_	Alignment	not modelled	58.4	14	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
112	c3f1oB_	Alignment	not modelled	56.7	7	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
113	c3eehA_	Alignment	not modelled	55.6	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
114	c3k3dA_	Alignment	not modelled	49.8	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	d1g0oa_	Alignment	not modelled	44.3	24	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
116	d1jnua_	Alignment	not modelled	41.7	15	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
117	c1wa9A_	Alignment	not modelled	36.0	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
118	c3rtyA_	Alignment	not modelled	34.7	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
119	c2kdkA_	Alignment	not modelled	33.9	9	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
120	c3n0rA_	Alignment	not modelled	33.6	14	