Phyre^2

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Description	P08400
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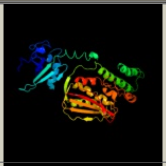
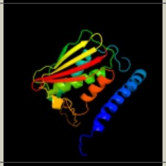
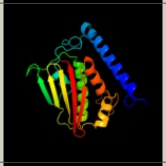
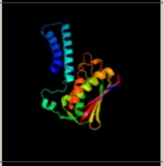
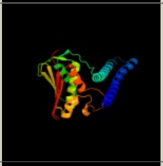
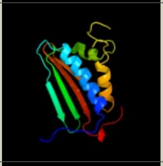
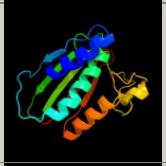
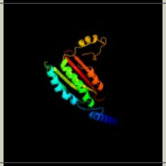
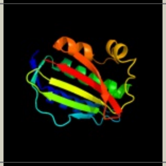
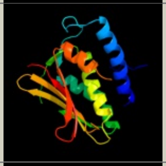
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a0rA_	Alignment		100.0	21	**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)
2	c2q8fA_	Alignment		100.0	19	**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	20	**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	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
5	c3d36B_	Alignment		100.0	25	**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
6	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
7	c1gjvA_	Alignment		100.0	15	**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
8	c2c2aA_	Alignment		100.0	31	**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		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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
10	d1gkza2	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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
11	c3a0tA_	Alignment		99.9	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)

12	d2c2aa2	Alignment		99.9	30	**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	d1id0a_	Alignment		99.9	19	**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
14	c1b3qA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
15	c2ch4A_	Alignment		99.9	23	**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	29	**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	24	**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	25	**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	27	**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	21	**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	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
22	c1mx0D_	Alignment	not modelled	99.7	26	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
23	c2zbkB_	Alignment	not modelled	99.7	27	**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
24	c3gieA_	Alignment	not modelled	99.6	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
25	c3ehgA_	Alignment	not modelled	99.6	22	**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
26	c3zxqA_	Alignment	not modelled	99.6	18	**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
27	c2q2eB_	Alignment	not modelled	99.5	25	**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
28	d1h7sa2	Alignment	not modelled	99.4	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
29	c3zxoB_	Alignment	not modelled	99.4	23	**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
30	d1bkna2	Alignment	not modelled	99.4	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
31	d1th8a_	Alignment	not modelled	99.4	23	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
32	d1b63a2	Alignment	not modelled	99.3	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
33	d1y8oa2	Alignment	not modelled	99.2	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
34	c3na3A_	Alignment	not modelled	98.9	31	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
35	c2r78D_	Alignment	not modelled	98.7	17	**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
36	c3mfxA_	Alignment	not modelled	98.7	19	**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
37	d1ixma_	Alignment	not modelled	98.7	10	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
38	d1ew0a_	Alignment	not modelled	98.6	21	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
39	c3bwlA_	Alignment	not modelled	98.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
40	c2jheB_	Alignment	not modelled	98.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
41	c3mxqC_	Alignment	not modelled	98.6	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
42	c3mqoB_	Alignment	not modelled	98.4	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
43	c3h4lB_	Alignment	not modelled	98.4	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
44	c3oloB_	Alignment	not modelled	98.3	8	**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
45	c1v9yA_	Alignment	not modelled	98.3	16	**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)
46	d1v9ya_	Alignment	not modelled	98.3	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
47	c3fg8B_	Alignment	not modelled	98.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
48	c2gj3A_	Alignment	not modelled	98.3	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.
49	c3b33A_	Alignment	not modelled	98.3	15	**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
50	c2w0nA_	Alignment	not modelled	98.2	19	**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
51	d1nwza_	Alignment	not modelled	98.2	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
52	c3luqC_	Alignment	not modelled	98.2	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
53	c2v1bA_	Alignment	not modelled	98.2	15	**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))
54	c3caxA_	Alignment	not modelled	98.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
55	c3lyxA_	Alignment	not modelled	98.1	19	**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
56	c1bknA_	Alignment	not modelled	98.1	22	**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
57	d1kija2	Alignment	not modelled	98.0	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
58	d1mzua_	Alignment	not modelled	98.0	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
59	c3k3dA_	Alignment	not modelled	98.0	15	**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
60	d1otda_	Alignment	not modelled	98.0	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
61	c3mjqB_	Alignment	not modelled	97.9	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.
62	c3kx0X_	Alignment	not modelled	97.9	15	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
63	c2pr6A_	Alignment	not modelled	97.9	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)
64	d1s16a2	Alignment	not modelled	97.9	17	**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	c3iedA_	Alignment	not modelled	97.9	17	**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
66	d1y28a_	Alignment	not modelled	97.9	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
67	c1ea6A_	Alignment	not modelled	97.9	28	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
68	c1y4sA_	Alignment	not modelled	97.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
69	c3mr0B_	Alignment	not modelled	97.8	15	**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
70	d1xfna1	Alignment	not modelled	97.8	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
71	c3p7nB_	Alignment	not modelled	97.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
72	d1ei1a2	Alignment	not modelled	97.8	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
73	d1pvga2	Alignment	not modelled	97.8	15	**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
74	c3fc7B_	Alignment	not modelled	97.7	20	**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
75	d1uyla_	Alignment	not modelled	97.7	11	**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
76	d1xj3a1	Alignment	not modelled	97.7	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain)

						Family: Heme-binding PAS domain
77	c2qkpD_	Alignment	not modelled	97.7	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
78	c2fwyA_	Alignment	not modelled	97.6	11	**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
79	c1kijB_	Alignment	not modelled	97.6	23	**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
80	c2l4rA_	Alignment	not modelled	97.6	12	**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
81	c1ei1B_	Alignment	not modelled	97.6	19	**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
82	c3a0vA_	Alignment	not modelled	97.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
83	c2iopD_	Alignment	not modelled	97.6	20	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
84	d2gqpa1	Alignment	not modelled	97.5	22	**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
85	c2cg9A_	Alignment	not modelled	97.5	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
86	c2vlgD_	Alignment	not modelled	97.5	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
87	c2akpA_	Alignment	not modelled	97.5	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
88	c2o1wB_	Alignment	not modelled	97.5	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
89	c3pehB_	Alignment	not modelled	97.4	20	**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
90	c1s16B_	Alignment	not modelled	97.4	19	**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
91	c3eehA_	Alignment	not modelled	97.4	21	**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
92	c3f1oB_	Alignment	not modelled	97.4	9	**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
93	c2iorA_	Alignment	not modelled	97.4	26	**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
94	d2iwxa1	Alignment	not modelled	97.4	14	**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
95	c2wkqA_	Alignment	not modelled	97.3	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
96	c3ewkA_	Alignment	not modelled	97.3	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
97	c1zwhA_	Alignment	not modelled	97.3	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
98	d1ll8a_	Alignment	not modelled	97.3	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
99	d1p97a_	Alignment	not modelled	97.2	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain

100	d1uyma_	Alignment	not modelled	97.2	12	**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
101	c3rtyA_	Alignment	not modelled	97.2	11	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
102	d1s14a_	Alignment	not modelled	97.2	16	**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
103	c1zxnB_	Alignment	not modelled	97.1	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
104	c3g7bB_	Alignment	not modelled	97.1	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
105	d1n9la_	Alignment	not modelled	97.1	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
106	c3gecA_	Alignment	not modelled	97.0	6	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of a tandem pas domain fragment of2 drosophila period
107	c1wa9A_	Alignment	not modelled	97.0	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
108	c2z6dB_	Alignment	not modelled	96.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phototropin-2; **PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
109	d1bywa_	Alignment	not modelled	96.9	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
110	c3lnuA_	Alignment	not modelled	96.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
111	d1jnua_	Alignment	not modelled	96.8	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
112	c2kdkA_	Alignment	not modelled	96.8	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
113	c2oolA_	Alignment	not modelled	96.6	9	**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
114	d1qy5a_	Alignment	not modelled	96.5	20	**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
115	c3ke6A_	Alignment	not modelled	96.4	26	**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
116	c3icyB_	Alignment	not modelled	96.4	12	**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
117	c1qzrA_	Alignment	not modelled	96.4	15	**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)
118	c2o1uA_	Alignment	not modelled	96.3	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
119	c2o9bA_	Alignment	not modelled	95.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
120	c3h9wA_	Alignment	not modelled	94.9	11	**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