Phyre^2

Email	l.a.kelley@imperial.ac.uk
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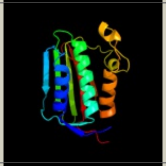
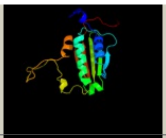
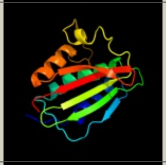
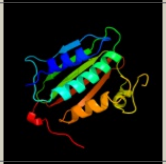
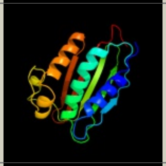
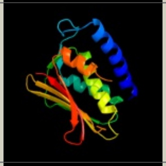
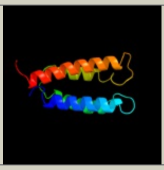
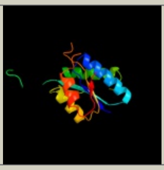
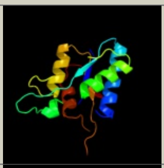
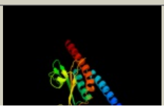
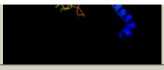
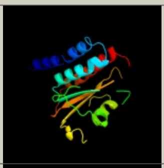
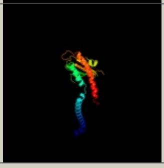
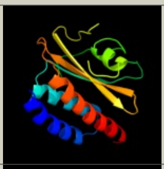
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r8rB_	Alignment		100.0	61	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
2	c2c2aA_	Alignment		99.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
3	c3d36B_	Alignment		99.9	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
4	c3d2rB_	Alignment		99.9	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
5	c2q8fA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
6	c2bu8A_	Alignment		99.9	17	**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
7	c1gjvA_	Alignment		99.9	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	c1y8oA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
9	c3a0rA_	Alignment		99.8	25	**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)
10	c3a0tA_	Alignment		99.7	24	**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	d2c2aa2	Alignment		99.7	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

12	d1bxda_	Alignment		99.7	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		99.7	17	**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		99.7	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
15	d1jm6a2	Alignment		99.7	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
16	d1gkza2	Alignment		99.6	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
17	d1ysra1	Alignment		99.6	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
18	c3jz3B_	Alignment		99.6	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
19	c2ch4A_	Alignment		99.6	21	**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
20	d1i58a_	Alignment		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
21	c3gieA_	Alignment	not modelled	99.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
22	d1r62a_	Alignment	not modelled	99.3	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
23	c3ehgA_	Alignment	not modelled	99.1	20	**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
24	d2hkja3	Alignment	not modelled	99.1	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
25	c3zxqA_	Alignment	not modelled	99.0	28	**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
26	c3zxoB_	Alignment	not modelled	98.9	25	**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
27	c1mx0D_	Alignment	not modelled	98.9	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
28	c2zbkB_	Alignment	not modelled	98.9	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;

28	c2zbkB_	Alignment	not modelled	98.9	21	**PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
29	d1ixma_	Alignment	not modelled	98.8	16	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
30	c2ksfA_	Alignment		98.8	98	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c
31	c2q2eB_	Alignment	not modelled	98.8	17	**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
32	d1th8a_	Alignment	not modelled	98.7	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
33	d1y8oa2	Alignment	not modelled	98.6	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	d1h7sa2	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
35	d1bkna2	Alignment	not modelled	98.3	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
36	d2c2aa1	Alignment	not modelled	98.3	22	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
37	c3hgmD_	Alignment		98.2	21	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
38	d1b63a2	Alignment	not modelled	98.2	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
39	c3dloC_	Alignment		98.2	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
40	c3s3tD_	Alignment		98.2	15	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
41	d2z3va1	Alignment		98.1	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
42	c3loqA_	Alignment		98.0	13	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
43	d1mjha_	Alignment		98.0	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
44	c2pfsA_	Alignment	not modelled	97.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
45	c3ibjB_	Alignment		97.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase;

						**PDBTitle:** x-ray structure of pde2a
46	c3mt0A_	Alignment	not modelled	97.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
47	d1tq8a_	Alignment	not modelled	97.9	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
48	c3p01A_	Alignment		97.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
49	c3olqA_	Alignment	not modelled	97.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein e; **PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
50	c3na3A_	Alignment	not modelled	97.8	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
51	d1jmva_	Alignment	not modelled	97.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
52	c3p01C_	Alignment		97.8	14	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
53	c1mc0A_	Alignment		97.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
54	c3fh0A_	Alignment	not modelled	97.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative universal stress protein kpn_01444; **PDBTitle:** crystal structure of putative universal stress protein kpn_01444 -2 atpase
55	d2gm3a1	Alignment	not modelled	97.6	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
56	c3mmhA_	Alignment		97.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
57	d2o9ca1	Alignment		97.6	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
58	c3fg9B_	Alignment	not modelled	97.6	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of universal stress protein uspa family; **PDBTitle:** the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
59	c3trcA_	Alignment	not modelled	97.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
60	c3ci6B_	Alignment	not modelled	97.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
61	d2oola1	Alignment	not modelled	97.5	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
62	d2veaa1	Alignment	not modelled	97.5	18	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
63	d1joya_	Alignment	not modelled	97.3	29	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
64	c3oovA_	Alignment	not modelled	97.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
						PDB header:dna binding protein, protein binding

65	c3h4lB_	Alignment	not modelled	97.3	16	**Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
66	c3mf0A_	Alignment	not modelled	97.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
67	c2dumD_	Alignment	not modelled	97.3	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
68	c3zrwB_	Alignment	not modelled	97.2	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
69	c1vhmB_	Alignment	not modelled	97.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
70	c3ab8B_	Alignment	not modelled	97.2	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
71	c3k2nB_	Alignment	not modelled	97.2	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator; **PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls
72	d1pvga2	Alignment	not modelled	97.1	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
73	c2vjwA_	Alignment	not modelled	97.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
74	c3e98B_	Alignment	not modelled	97.1	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
75	d1kija2	Alignment	not modelled	97.1	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
76	d1vhma_	Alignment	not modelled	97.1	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
77	d1q77a_	Alignment	not modelled	97.0	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
78	c3e0yA_	Alignment	not modelled	97.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
79	c2zmfA_	Alignment	not modelled	96.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
80	c2e21A_	Alignment	not modelled	96.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
81	c3eeaB_	Alignment	not modelled	96.8	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
82	c3a2kB_	Alignment	not modelled	96.8	14	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
83	d1ei1a2	Alignment	not modelled	96.8	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
84	c1zxnB_	Alignment	not modelled	96.8	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
85	c1ea6A_	Alignment	not modelled	96.8	19	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
86	c1y4sA_	Alignment	not modelled	96.7	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
87	d1s16a2	Alignment	not modelled	96.7	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
88	d1mc0a1	Alignment	not modelled	96.7	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
						PDB header:dna repair

89	c1bknA_	Alignment	not modelled	96.7	23	**Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
90	c3idfA_	Alignment	not modelled	96.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
91	c2jaxA_	Alignment	not modelled	96.6	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein tb31.7; **PDBTitle:** universal stress protein rv2623 from mycobaterium2 tuberculosis
92	c3ke6A_	Alignment	not modelled	96.6	29	**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
93	c3ksiA_	Alignment	not modelled	96.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
94	c3dbaB_	Alignment	not modelled	96.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
95	c1ei1B_	Alignment	not modelled	96.5	23	**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
96	c1ykdB_	Alignment	not modelled	96.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization
97	c1kijB_	Alignment	not modelled	96.4	26	**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
98	c3iedA_	Alignment	not modelled	96.4	18	**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
99	c2w3gA_	Alignment	not modelled	96.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf **PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
100	c2ja1A_	Alignment	not modelled	96.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
101	c1qzrA_	Alignment	not modelled	96.2	21	**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)
102	c3o5yA_	Alignment	not modelled	96.2	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
103	d1uyla_	Alignment	not modelled	96.2	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
104	c1s16B_	Alignment	not modelled	96.1	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
105	c2iopD_	Alignment	not modelled	96.1	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
106	c2qybA_	Alignment	not modelled	96.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein, putative; **PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
107	c2fwyA_	Alignment	not modelled	96.0	17	**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
108	d1wy5a1	Alignment	not modelled	95.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
109	c3hcyB_	Alignment	not modelled	95.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
110	c2akpA_	Alignment	not modelled	95.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
111	c2cg9A_	Alignment	not modelled	95.8	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
112	d1mc0a2	Alignment	not modelled	95.7	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
						PDB header:chaperone

113	c2o1wB_	Alignment	not modelled	95.7	20	**Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
114	d1xp8a1	Alignment	not modelled	95.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
115	d2k2na1	Alignment	not modelled	95.6	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
116	d1xbta1	Alignment	not modelled	95.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
117	c2lb5A_	Alignment	not modelled	95.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
118	c1xx6B_	Alignment	not modelled	95.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
119	c3g7bB_	Alignment	not modelled	95.5	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
120	d2iwxa1	Alignment	not modelled	95.4	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain