

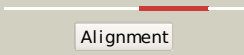

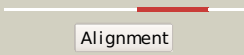



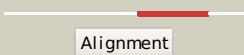

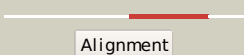



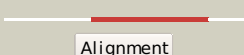



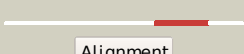

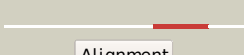














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c2aA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
2	c3d36B_	 Alignment		100.0	20	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearotherophilus kinb with the inhibitor sda
3	c2q8fA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
4	c3d2rB_	 Alignment		99.9	12	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	c1y8oA_	 Alignment		99.9	13	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
6	c1g1vA_	 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 complexed with atp-gamma-s
7	c2bu8A_	 Alignment		99.9	10	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
8	c3a0rA_	 Alignment		99.9	8	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)
9	c1b3qA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
10	d2c2aa2	 Alignment		99.9	15	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
11	c3a0tA_	 Alignment		99.9	12	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	d1gkza2	Alignment		99.9	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
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	c3jz3B_	Alignment		99.8	13	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
15	c2ch4A_	Alignment		99.8	19	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		99.8	18	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	d1jm6a2	Alignment		99.8	10	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
18	d1i58a_	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: Histidine kinase
19	d1ysra1	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
20	c3gieA_	Alignment		99.8	15	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of deskc_h188e in complex with amp-pcp
21	d1r62a_	Alignment	not modelled	99.7	14	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	14	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	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
24	c3zxoB_	Alignment	not modelled	99.6	20	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
25	d2hkja3	Alignment	not modelled	99.5	22	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
26	d1ixma_	Alignment	not modelled	99.4	9	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
27	d1th8a_	Alignment	not modelled	99.3	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 PDB header: isomerase

28	c2zbkB	Alignment	not modelled	99.3	24	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
29	c1mx0D	Alignment	not modelled	99.3	23	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
30	c2q2eB	Alignment	not modelled	99.3	14	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
31	d1h7sa2	Alignment	not modelled	99.0	8	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	d1y8oa2	Alignment	not modelled	98.9	13	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
33	d1bknA2	Alignment	not modelled	98.7	13	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
34	d1b63a2	Alignment	not modelled	98.6	13	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	c3h4lB	Alignment	not modelled	98.0	21	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
36	c3na3A	Alignment	not modelled	98.0	13	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
37	c1ea6A	Alignment	not modelled	98.0	12	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
38	d1pvga2	Alignment	not modelled	97.9	12	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	c3ke6A	Alignment	not modelled	97.9	21	PDB header: unknown function Chain: A: PDB Molecule: protein rv1364c/mtl1410; PDBTitle: the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
40	c1zxnB	Alignment	not modelled	97.9	18	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
41	d1kija2	Alignment	not modelled	97.8	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
42	d1ei1a2	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: DNA gyrase/MutL, N-terminal domain
43	c1qzrA	Alignment	not modelled	97.7	12	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)
44	c1bknA	Alignment	not modelled	97.6	19	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	c2iopD	Alignment	not modelled	97.6	21	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
46	c1ei1B	Alignment	not modelled	97.6	15	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	c1s16B	Alignment	not modelled	97.6	16	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	c1y4sA	Alignment	not modelled	97.6	23	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
49	d1s16a2	Alignment	not modelled	97.5	12	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
50	c1kijB	Alignment	not modelled	97.5	18	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
51	c3lnuA	Alignment	not modelled	97.5	11	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
						PDB header: isomerase

52	c3g7bB_	Alignment	not modelled	97.4	11	Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with inhibitor
53	dls14a_	Alignment	not modelled	97.4	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
54	c2o1uA_	Alignment	not modelled	97.4	26	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
55	c2w1tB_	Alignment	not modelled	97.4	18	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
56	c3iedA_	Alignment	not modelled	97.4	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
57	c2w1rA_	Alignment	not modelled	97.2	17	PDB header: transcription Chain: A: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of the c-terminal domain of b. subtilis2 spovt
58	d2c2aa1	Alignment	not modelled	97.1	24	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
59	dlqy5a_	Alignment	not modelled	97.1	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
60	c2fwyA_	Alignment	not modelled	97.0	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
61	c2cg9A_	Alignment	not modelled	96.9	21	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
62	c2akpA_	Alignment	not modelled	96.8	19	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
63	c3pehB_	Alignment	not modelled	96.6	24	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pf1070c in the presence of a thienopyrimidine derivative
64	dluy1a_	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
65	d2gqpa1	Alignment	not modelled	96.4	15	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
66	dluyma_	Alignment	not modelled	96.4	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
67	c1zwhA_	Alignment	not modelled	96.3	20	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
68	d2iwxal	Alignment	not modelled	96.3	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
69	c2iorA_	Alignment	not modelled	96.2	20	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
70	dljoya_	Alignment	not modelled	96.0	19	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
71	c2o1wB_	Alignment	not modelled	96.0	12	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
72	c3zrwB_	Alignment	not modelled	95.7	13	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
73	c3cwvB_	Alignment	not modelled	94.1	7	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
74	c3lmma_	Alignment	not modelled	89.3	10	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
						PDB header: structural genomics, unknown function

75	c1vhmB_	Alignment	not modelled	87.6	14	Chain: B: PDB Molecule: protein yebr; PDBTitle: crystal structure of an hypothetical protein
76	c3eeaB_	Alignment	not modelled	86.9	12	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
77	c3hcyB_	Alignment	not modelled	86.5	13	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
78	d1vhma_	Alignment	not modelled	84.1	11	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
79	c3mmhA_	Alignment	not modelled	82.0	16	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
80	d1f5ma_	Alignment	not modelled	81.8	15	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
81	c2zmfA_	Alignment	not modelled	80.5	12	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
82	c2vjwA_	Alignment	not modelled	80.2	17	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
83	c3p5nA_	Alignment		78.7	9	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
84	c3ksiA_	Alignment	not modelled	70.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of frmrs of staphylococcus aureus (complex with 2-propanol)
85	c3oovA_	Alignment	not modelled	67.9	14	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
86	c2w3gA_	Alignment	not modelled	66.6	11	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
87	c1mc0A_	Alignment		65.6	10	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
88	c3o5yA_	Alignment	not modelled	64.1	14	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
89	c3ibjB_	Alignment	not modelled	59.4	14	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
90	c3p01C_	Alignment	not modelled	55.5	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
91	c2oolA_	Alignment	not modelled	54.7	25	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
92	c3k2nB_	Alignment	not modelled	53.8	19	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 t1s
93	d2veaa1	Alignment	not modelled	52.8	12	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
94	c3dbaB_	Alignment	not modelled	51.5	11	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	d1mc0a1	Alignment	not modelled	46.6	11	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
96	d2k2na1	Alignment	not modelled	46.3	19	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
						PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein

97	c3ci6B_	Alignment	not modelled	46.0	9	phosphotransferase; PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
98	c1ykdB_	Alignment	not modelled	45.9	16	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
99	c2qybA_	Alignment	not modelled	45.8	15	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
100	c3trcA_	Alignment	not modelled	44.0	13	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
101	c3k7pA_	Alignment	not modelled	41.6	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
102	c3m1pA_	Alignment	not modelled	41.6	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
103	c2lb5A_	Alignment	not modelled	40.4	25	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
104	c3s6fA_	Alignment	not modelled	38.1	20	PDB header: transferase Chain: A: PDB Molecule: hypothetical acetyltransferase; PDBTitle: crystal structure of a hypotetical acetyltransferase (dr_1678) from2 deinococcus radiodurans at 1.19 a resolution
105	d2o9ca1	Alignment	not modelled	37.9	12	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
106	d1xmta_	Alignment	not modelled	33.4	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
107	d1hh2p2	Alignment	not modelled	31.0	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
108	d1mc0a2	Alignment	not modelled	30.4	6	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
109	d1b74a1	Alignment	not modelled	29.9	17	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
110	c3mf0A_	Alignment	not modelled	28.5	15	PDB header: hydrolase Chain: A: PDB Molecule: cgm-p-specific 3',5'-cyclic phosphodiesterase; PDBTitle: crystal structure of pde5a gaf domain (89-518)
111	c3p01A_	Alignment	not modelled	27.7	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
112	d2asba2	Alignment	not modelled	26.9	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
113	c3mxqC_	Alignment	not modelled	26.6	10	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
114	c2crqA_	Alignment	not modelled	24.0	15	PDB header: translation Chain: A: PDB Molecule: mitochondrial translational initiation factor 3; PDBTitle: solution structure of c-terminal domain of riken cdna2 2810012114
115	c2o9bA_	Alignment	not modelled	24.0	23	PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
116	d1p0ha_	Alignment	not modelled	22.2	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
117	c3c26A_	Alignment	not modelled	21.9	15	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase ta0821; PDBTitle: crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
118	c3e0yA_	Alignment	not modelled	21.8	17	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
119	c3onoA_	Alignment	not modelled	21.6	16	PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpiB from2 vibrio parahaemolyticus
120	c2pc1A_	Alignment	not modelled	21.4	9	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase gnat family (np_688560.1) from2 streptococcus agalactiae 2603 at 1.28 a resolution