





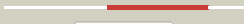
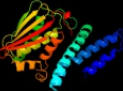








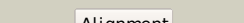



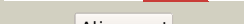



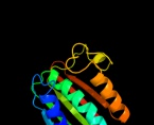





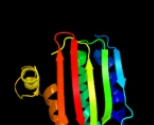


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c2aA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
2	c3d36B_	 Alignment		100.0	15	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	c3d2rB_	 Alignment		100.0	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
4	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
5	c2bu8A_	 Alignment		100.0	13	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
6	c1y8aA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
7	c1qjvA_	 Alignment		100.0	14	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
8	d1id0a_	 Alignment		100.0	100	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
9	c3a0rA_	 Alignment		100.0	14	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		100.0	18	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		100.0	27	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	d1jm6a2	Alignment		100.0	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
13	c1b3qA	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
14	d1gkza2	Alignment		100.0	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
15	d1bxda	Alignment		100.0	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
16	c3jz3B	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
17	d1ysra1	Alignment		100.0	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
18	c2ch4A	Alignment		99.9	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
19	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
20	c3gieA	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of desck_h188e in complex with amp-pcp
21	d1r62a	Alignment	not modelled	99.9	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
22	c3ehgA	Alignment	not modelled	99.8	16	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	d2hkja3	Alignment	not modelled	99.8	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
24	c3zxaA	Alignment	not modelled	99.8	19	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	c3zxoB	Alignment	not modelled	99.7	17	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
26	c1mx0D	Alignment	not modelled	99.7	18	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
27	c2zkbB	Alignment	not modelled	99.7	18	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
28	c2zkbB	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b;

28	c2q2eB	Alignment	not modelled	99.6	19	PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei 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	d1h7sa2	Alignment	not modelled	99.6	11	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	d1ixma	Alignment	not modelled	99.6	13	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
31	d1th8a	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: Histidine kinase
32	d1bkna2	Alignment	not modelled	99.5	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
33	d1b63a2	Alignment	not modelled	99.5	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
34	d1y8oa2	Alignment	not modelled	99.4	18	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
35	c3zrwB	Alignment	not modelled	99.4	21	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
36	c3na3A	Alignment	not modelled	99.3	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	c3h4lB	Alignment	not modelled	99.0	17	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
38	c1bkna	Alignment	not modelled	98.7	16	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
39	c3lnrA	Alignment	not modelled	98.7	10	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
40	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
41	d1pvga2	Alignment	not modelled	98.6	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
42	d1ei1a2	Alignment	not modelled	98.6	27	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	d1joya	Alignment	not modelled	98.6	12	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
44	c1ei1B	Alignment	not modelled	98.5	24	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
45	c1ea6A	Alignment	not modelled	98.5	11	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp
46	d1s16a2	Alignment	not modelled	98.5	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
47	c1kijB	Alignment	not modelled	98.4	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
48	c1y4sA	Alignment	not modelled	98.4	16	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
49	c1s16B	Alignment	not modelled	98.4	21	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
50	c3iedA	Alignment	not modelled	98.4	14	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
51	d2iwxal	Alignment	not modelled	98.3	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
52	c1zwhA_	Alignment	not modelled	98.3	17	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
53	d2c2aa1	Alignment	not modelled	98.3	14	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
54	d1uylA_	Alignment	not modelled	98.3	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
55	c1zxnB_	Alignment	not modelled	98.3	16	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp
56	c2fwyA_	Alignment	not modelled	98.2	12	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
57	c2cg9A_	Alignment	not modelled	98.2	17	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
58	c1qzrA_	Alignment	not modelled	98.2	19	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)
59	c3g7bB_	Alignment	not modelled	98.2	14	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with inhibitor
60	c3ke6A_	Alignment	not modelled	98.2	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
61	d1s14a_	Alignment	not modelled	98.1	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
62	c2akpA_	Alignment	not modelled	98.1	13	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
63	c2o1wB_	Alignment	not modelled	98.0	16	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
64	d1uyma_	Alignment	not modelled	98.0	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
65	c2iorA_	Alignment	not modelled	98.0	14	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
66	c3pehB_	Alignment	not modelled	98.0	19	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
67	d1qy5a_	Alignment	not modelled	97.9	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
68	d2asxa1	Alignment	not modelled	97.9	24	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
69	c2o1uA_	Alignment	not modelled	97.9	14	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
70	c2iopD_	Alignment	not modelled	97.9	16	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
71	c3lnuA_	Alignment	not modelled	97.8	22	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
72	d2gqpa1	Alignment	not modelled	97.8	16	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
73	c1yaxB_	Alignment		96.8	80	PDB header: transferase, signaling protein Chain: B: PDB Molecule: virulence sensor protein phoq, sensor domain; PDBTitle: cystal structure analysis of s.typhimurium phoq sensor domain with2 calcium
74	c2rm8A_	Alignment	not modelled	96.4	13	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2

					htrII linker region from natronomonas pharaonis
75	c3cwvB_	Alignment	not modelled	94.9	11 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
76	c3lmmA_	Alignment	not modelled	84.5	19 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
77	c2yv4A_	Alignment	not modelled	32.4	13 PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein ph0435; PDBTitle: crystal structure of c-terminal sua5 domain from pyrococcus horikoshii2 hypothetical sua5 protein ph0435
78	c2kseA_	Alignment	not modelled	30.6	32 PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmg) target 4311c
79	c3n0rA_	Alignment	not modelled	22.3	9 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
80	d1g0oa_	Alignment	not modelled	21.6	23 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	c3s8mA_	Alignment	not modelled	20.7	16 PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl reductase; PDBTitle: the crystal structure of fabv
82	d1y13a_	Alignment	not modelled	20.2	11 Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
83	d1j0ga_	Alignment	not modelled	17.7	16 Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
84	d1o57a1	Alignment	not modelled	17.6	21 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of Bacillus PurR
85	d1qfha2	Alignment	not modelled	16.8	19 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
86	d1efub3	Alignment	not modelled	15.1	21 Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
87	c2z1nA_	Alignment	not modelled	15.0	19 PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
88	c1qr0A_	Alignment	not modelled	15.0	12 PDB header: transferase Chain: A: PDB Molecule: 4'-phosphopantetheinyl transferase sfp; PDBTitle: crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
89	d1oaaa_	Alignment	not modelled	14.6	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	d1xb2b1	Alignment	not modelled	14.6	16 Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
91	d2cp9a1	Alignment	not modelled	13.6	16 Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
92	c3o38D_	Alignment	not modelled	13.0	25 PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
93	c2ojlB_	Alignment	not modelled	12.8	9 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1 borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
94	d1aipc1	Alignment	not modelled	12.7	16 Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
95	c3ctmH_	Alignment	not modelled	12.6	19 PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
96	d1y5ma1	Alignment	not modelled	11.8	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c2jnvA_	Alignment	not modelled	11.7	12 PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
98	c3rd5A_	Alignment	not modelled	11.6	19 PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
99	d2i14a2	Alignment	not modelled	11.4	17 Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRase N-terminal domain-like Family: NadC N-terminal domain-like