Phyre2

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Description	P0A6Z3
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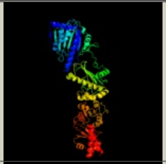
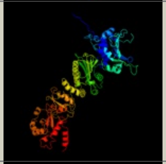
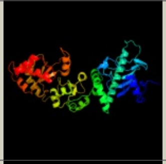
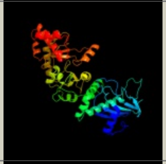
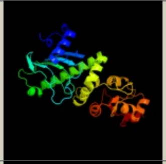
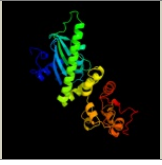
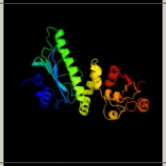
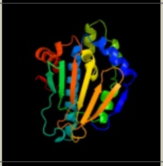
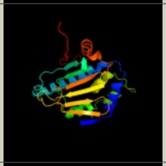
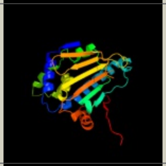
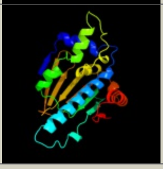
Unique Job ID	cc39b1aa0dc0c1e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iopD_	Alignment		100.0	99	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
2	c2cg9A_	Alignment		100.0	41	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
3	c2o1uA_	Alignment		100.0	41	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
4	c1y4sA_	Alignment		100.0	100	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
5	c2o1wB_	Alignment		100.0	46	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
6	c2cgeD_	Alignment		100.0	38	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
7	c2o1tB_	Alignment		100.0	38	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of middle plus c-terminal domains (m+c) of grp94
8	c3hjcA_	Alignment		100.0	37	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 83-1; **PDBTitle:** crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
9	c3q6nF_	Alignment		100.0	38	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** crystal structure of human mc-hsp90 in p21 space group
10	c2gq0B_	Alignment		100.0	100	**PDB header:**chaperone, hydrolase **Chain:** B: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the middle domain of htpg, the e. coli2 hsp90
11	c3pryA_	Alignment		100.0	45	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-beta; **PDBTitle:** crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution

12	d1usua_	Alignment		100.0	44	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Hsp90 middle domain
13	c1hk7A_	Alignment		100.0	45	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp82; **PDBTitle:** middle domain of hsp90
14	c1y6zA_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
15	c3pehB_	Alignment		100.0	41	**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
16	c2iorA_	Alignment		100.0	100	**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
17	d1qy5a_	Alignment		100.0	47	**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
18	d2iwxa1	Alignment		100.0	45	**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
19	c1zwhA_	Alignment		100.0	45	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
20	c3iedA_	Alignment		100.0	46	**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
21	d1uyla_	Alignment	not modelled	100.0	49	**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
22	c2fwyA_	Alignment	not modelled	100.0	49	**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
23	d1uyma_	Alignment	not modelled	100.0	48	**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
24	d2gqpa1	Alignment	not modelled	100.0	47	**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
25	c2akpA_	Alignment	not modelled	100.0	46	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
26	d1sf8a_	Alignment	not modelled	100.0	97	**Fold:**HSP90 C-terminal domain **Superfamily:**HSP90 C-terminal domain **Family:**HSP90 C-terminal domain
27	c2q2eB_	Alignment	not modelled	99.9	18	**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
						PDB header:dna binding protein, protein binding

28	c3h4lB_	Alignment	not modelled	99.8	16	**Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
29	c3na3A_	Alignment	not modelled	99.8	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
30	c2zbkB_	Alignment	not modelled	99.8	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
31	d1b63a2	Alignment	not modelled	99.7	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
32	c1bknA_	Alignment	not modelled	99.7	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
33	c1mx0D_	Alignment	not modelled	99.7	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
34	d1bkna2	Alignment	not modelled	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:**DNA gyrase/MutL, N-terminal domain
35	d2hkja3	Alignment	not modelled	99.6	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
36	c1ea6A_	Alignment	not modelled	99.5	18	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
37	d1kija2	Alignment	not modelled	99.5	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
38	d1h7sa2	Alignment	not modelled	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:**DNA gyrase/MutL, N-terminal domain
39	c1kijB_	Alignment	not modelled	99.4	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
40	d1s16a2	Alignment	not modelled	99.4	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
41	d1pvga2	Alignment	not modelled	99.4	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	c1ei1B_	Alignment	not modelled	99.4	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
43	d1ei1a2	Alignment	not modelled	99.2	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
44	c1s16B_	Alignment	not modelled	99.2	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
45	d1s14a_	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:**DNA gyrase/MutL, N-terminal domain
46	c3g7bB_	Alignment	not modelled	98.5	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
47	c1y8oA_	Alignment	not modelled	98.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
48	c2q8fA_	Alignment	not modelled	98.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
49	c1qzrA_	Alignment	not modelled	98.5	18	**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)
50	c3d36B_	Alignment	not modelled	98.2	26	**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
51	c1zxnB_	Alignment	not modelled	98.2	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp

52	c1gjvA_	Alignment	not modelled	98.2	25	**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
53	c2bu8A_	Alignment	not modelled	98.2	22	**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
54	d1gkza2	Alignment	not modelled	98.1	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
55	c3d2rB_	Alignment	not modelled	98.1	22	**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
56	d1jm6a2	Alignment	not modelled	98.1	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
57	c3lnuA_	Alignment	not modelled	98.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
58	c1b3qA_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
59	c2c2aA_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
60	d2c2aa2	Alignment	not modelled	97.5	16	**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
61	c2ch4A_	Alignment	not modelled	97.5	22	**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
62	d1y8oa2	Alignment	not modelled	97.4	25	**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
63	d1i58a_	Alignment	not modelled	97.1	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
64	c3a0tA_	Alignment	not modelled	97.1	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)
65	d1ysra1	Alignment	not modelled	97.1	18	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
66	d1id0a_	Alignment	not modelled	96.9	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
67	d1th8a_	Alignment	not modelled	96.7	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
68	c3a0rA_	Alignment	not modelled	96.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
69	d1bxda_	Alignment	not modelled	96.6	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
70	c3ehgA_	Alignment	not modelled	96.4	25	**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
71	c3gieA_	Alignment	not modelled	96.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
72	c3cwvB_	Alignment	not modelled	95.3	15	**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
73	c3jz3B_	Alignment	not modelled	95.2	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
74	d1ixma_	Alignment	not modelled	92.3	12	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
						PDB header:transferase

75	c3zxqA_	Alignment	not modelled	86.0	22	**Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost; **PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
76	c3zxoB_	Alignment	not modelled	61.3	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
77	d1r62a_	Alignment	not modelled	61.2	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
78	d2cwqa1	Alignment	not modelled	56.6	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
79	c3b9qA_	Alignment	not modelled	40.2	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
80	c2qy9A_	Alignment	not modelled	33.1	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
81	c3ndhA_	Alignment	not modelled	32.0	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**restriction endonuclease thai; **PDBTitle:** restriction endonuclease in complex with substrate dna
82	c3lmmA_	Alignment	not modelled	28.8	24	**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
83	d1i5ga_	Alignment	not modelled	26.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
84	c2kxxA_	Alignment	not modelled	26.4	45	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
85	d2p0sa1	Alignment	not modelled	25.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**PG0945 N-terminal domain-like
86	d2g2ub1	Alignment	not modelled	23.7	35	**Fold:**BLIP-like **Superfamily:**beta-lactamase-inhibitor protein, BLIP **Family:**beta-lactamase-inhibitor protein, BLIP
87	c2ayaA_	Alignment	not modelled	21.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit tau; **PDBTitle:** solution structure of the c-terminal 14 kda domain of the2 tau subunit from escherichia coli dna polymerase iii
88	d1j20a2	Alignment	not modelled	21.0	28	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
89	d1toaa_	Alignment	not modelled	19.9	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
90	c1toaA_	Alignment	not modelled	19.9	14	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
91	c2pxgA_	Alignment	not modelled	18.9	43	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
92	c3gk0H_	Alignment	not modelled	17.7	24	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
93	c1p8cD_	Alignment	not modelled	17.4	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
94	d1k25a2	Alignment	not modelled	16.6	19	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
95	c2yhsA_	Alignment	not modelled	16.4	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
96	c3ke6A_	Alignment	not modelled	15.8	19	**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
97	c2x48B_	Alignment	not modelled	15.6	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
98	c2qeuA_	Alignment	not modelled	14.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
99	c2xhfA_	Alignment	not modelled	14.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana