Phyre2

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Description	P20083
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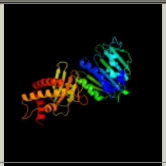
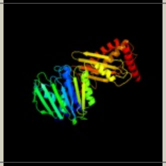
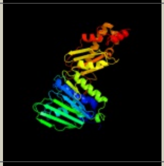
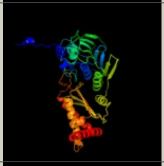
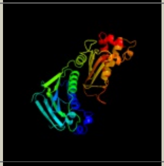
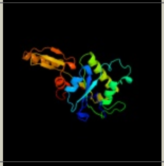
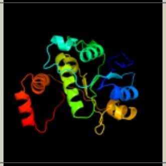
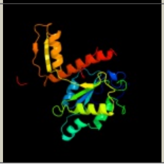
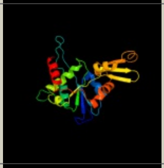
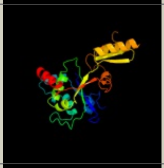
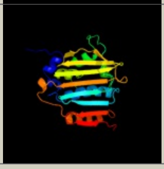
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lnuA_	Alignment		100.0	61	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
2	c1zxnB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
3	c1s16B_	Alignment		100.0	100	**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
4	c1qzrA_	Alignment		100.0	23	**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)
5	c1ei1B_	Alignment		100.0	36	**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
6	c2xkjE_	Alignment		100.0	71	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**topoisomerase iv; **PDBTitle:** crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate)
7	c1kijB_	Alignment		100.0	39	**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
8	c3cwvB_	Alignment		100.0	28	**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
9	c2xcqA_	Alignment		100.0	48	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
10	c2xcsD_	Alignment		100.0	45	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
11	d1bjta_	Alignment		100.0	25	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase

12	c1bjtA_	Alignment		100.0	25	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
13	c3fofD_	Alignment		100.0	47	**PDB header:**isomerase/dna **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit b; **PDBTitle:** structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
14	c3nuhB_	Alignment		100.0	55	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
15	c3qx3B_	Alignment		100.0	32	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
16	c2zjtB_	Alignment		100.0	44	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation
17	d1pvga2	Alignment		100.0	24	**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
18	d1ei1a2	Alignment		100.0	46	**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
19	d1s16a2	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:**DNA gyrase/MutL, N-terminal domain
20	d1kija2	Alignment		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:**DNA gyrase/MutL, N-terminal domain
21	c3g7bB_	Alignment	not modelled	100.0	45	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
22	d1s16a1	Alignment	not modelled	100.0	100	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
23	d1kija1	Alignment	not modelled	100.0	28	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
24	d1ei1a1	Alignment	not modelled	100.0	23	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
25	d1s14a_	Alignment	not modelled	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:**DNA gyrase/MutL, N-terminal domain
26	d1pvga1	Alignment	not modelled	100.0	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
27	c2q2eB_	Alignment	not modelled	99.8	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
28	c3h4lB_	Alignment	not modelled	99.8	18	**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

29	c2zbkB_	Alignment	not modelled	99.8	20	**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
30	c1mx0D_	Alignment	not modelled	99.8	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
31	d2hkja3	Alignment	not modelled	99.7	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
32	d1b63a2	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
33	c3na3A_	Alignment	not modelled	99.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
34	c1bknA_	Alignment	not modelled	99.5	18	**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
35	d1h7sa2	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
36	d1bkna2	Alignment	not modelled	99.4	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
37	c1ea6A_	Alignment	not modelled	99.3	25	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
38	c2akpA_	Alignment	not modelled	99.2	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
39	d2iwxa1	Alignment	not modelled	99.0	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
40	c1zwhA_	Alignment	not modelled	98.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
41	c2fwyA_	Alignment	not modelled	98.9	21	**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
42	d1uyla_	Alignment	not modelled	98.9	21	**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
43	c3iedA_	Alignment	not modelled	98.9	25	**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
44	c2o1wB_	Alignment	not modelled	98.8	17	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
45	d1uyma_	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:**Heat shock protein 90, HSP90, N-terminal domain
46	c2iorA_	Alignment	not modelled	98.7	24	**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
47	c3pehB_	Alignment	not modelled	98.6	16	**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
48	d1qy5a_	Alignment	not modelled	98.6	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
49	c1y4sA_	Alignment	not modelled	98.6	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
50	d2gqpa1	Alignment	not modelled	98.5	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
51	c2cg9A_	Alignment	not modelled	98.5	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex

52	c2bu8A_	Alignment	not modelled	98.2	16	**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
53	c3d2rB_	Alignment	not modelled	98.2	17	**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
54	c2q8fA_	Alignment	not modelled	98.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
55	c2iopD_	Alignment	not modelled	98.1	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
56	c1y8oA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
57	c1gjvA_	Alignment	not modelled	98.0	12	**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
58	d1jm6a2	Alignment	not modelled	97.6	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
59	c3d36B_	Alignment	not modelled	97.5	18	**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
60	c2c2aA_	Alignment	not modelled	97.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
61	c2o1uA_	Alignment	not modelled	97.4	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
62	d1gkza2	Alignment	not modelled	97.2	15	**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	c2ch4A_	Alignment	not modelled	97.2	25	**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
64	d1th8a_	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
65	c1b3qA_	Alignment	not modelled	96.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
66	d2c2aa2	Alignment	not modelled	96.5	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
67	d1y8oa2	Alignment	not modelled	96.5	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
68	c3a0rA_	Alignment	not modelled	96.3	12	**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	c3a0tA_	Alignment	not modelled	96.3	15	**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)
70	d1bxda_	Alignment	not modelled	96.0	14	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
71	d1i58a_	Alignment	not modelled	95.9	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
72	c3jz3B_	Alignment	not modelled	95.8	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
73	d1ysra1	Alignment	not modelled	95.7	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
74	d1id0a_	Alignment	not modelled	95.7	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

75	c3ehgA_	Alignment	not modelled	95.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase (yocf protein); **PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp
76	c3ke6A_	Alignment	not modelled	95.0	31	**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
77	d1ixma_	Alignment	not modelled	93.4	11	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
78	c3giеA_	Alignment	not modelled	92.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
79	c3zxqA_	Alignment	not modelled	91.3	29	**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
80	c3zxoB_	Alignment	not modelled	87.5	37	**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
81	c3ssoE_	Alignment	not modelled	76.6	34	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methyltransferase; **PDBTitle:** myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
82	d1mw9x_	Alignment	not modelled	75.5	20	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
83	d2fcja1	Alignment	not modelled	69.8	22	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
84	c2gajA_	Alignment	not modelled	54.4	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
85	c3ggqA_	Alignment	not modelled	48.6	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** dimerization of hepatitis e virus capsid protein e2s domain is2 essential for virus-host interaction
86	d1r62a_	Alignment	not modelled	48.4	14	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
87	d2hkja2	Alignment	not modelled	43.0	13	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
88	d1ecwa_	Alignment	not modelled	37.3	43	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
89	c3dmaA_	Alignment	not modelled	36.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
90	d1hiwa_	Alignment	not modelled	35.6	43	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
91	d1x87a_	Alignment	not modelled	35.5	12	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
92	d2gola1	Alignment	not modelled	34.7	43	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
93	d1tama_	Alignment	not modelled	33.8	46	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
94	d1l6na1	Alignment	not modelled	33.3	46	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Immunodeficiency virus matrix proteins
95	d1jmca1	Alignment	not modelled	33.2	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
96	d1h72c1	Alignment	not modelled	32.4	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
97	c3lmmA_	Alignment	not modelled	31.7	26	**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
98	d1gkub3	Alignment	not modelled	30.3	23	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
99	d1uwka_	Alignment	not modelled	29.5	9	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
						PDB header:heme-binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein, distantly related

100	c3fm2A_	Alignment	not modelled	29.4	22	to a heme **PDBTitle:** crystal structure of a putative heme-binding protein (ava_4353) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
101	c2fknC_	Alignment	not modelled	25.4	9	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
102	d2jdid1	Alignment	not modelled	23.7	15	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
103	c1nuiA_	Alignment	not modelled	22.5	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
104	d1i7da_	Alignment	not modelled	22.3	16	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
105	d1k92a2	Alignment	not modelled	21.6	28	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain