Phyre^2

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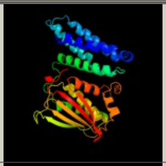
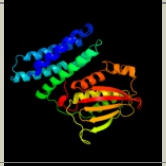
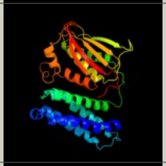
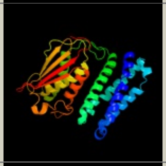
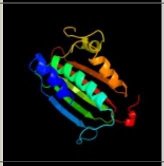
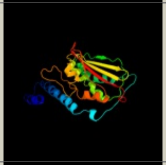
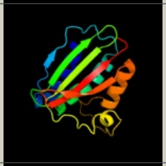
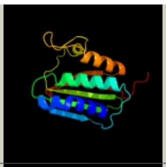
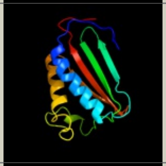
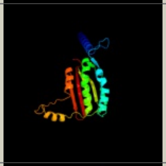
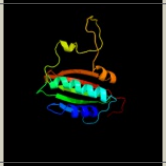
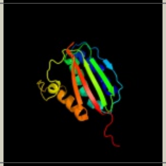
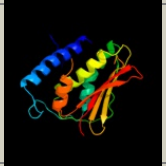
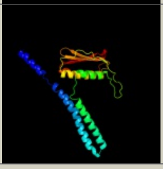
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c3d2rB_	Alignment		100.0	13	**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
3	c2bu8A_	Alignment		100.0	14	**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
4	c1y8oA_	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
5	c2c2aA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
6	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 stearothermophilus kinb with the inhibitor sda
7	c1gjvA_	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 complxed with atp-gamma-s
8	d1jm6a2	Alignment		99.9	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
9	c3a0rA_	Alignment		99.9	18	**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	d1id0a_	Alignment		99.9	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
11	d2c2aa2	Alignment		99.9	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	c3a0tA_	Alignment		99.9	23	**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)
13	d1gkza2	Alignment		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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
14	c1b3qA_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
15	d1bxda_	Alignment		99.9	29	**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	c2ch4A_	Alignment		99.9	20	**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
17	d1i58a_	Alignment		99.9	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
18	d1ysra1	Alignment		99.8	23	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
19	c3jz3B_	Alignment		99.8	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
20	c3gieA_	Alignment		99.7	19	**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	99.6	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
22	d2hkja3	Alignment	not modelled	99.6	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
23	c3ehgA_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase (yocf protein); **PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp
24	c2zbkB_	Alignment	not modelled	99.5	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
25	c3zxqA_	Alignment	not modelled	99.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost; **PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
26	c1mx0D_	Alignment	not modelled	99.4	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
27	c2q2eB_	Alignment	not modelled	99.4	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
						PDB header:transferase **Chain:** B: **PDB Molecule:**redox sensor histidine kinase response

28	c3zxoB_	Alignment	not modelled	99.4	20	regulator devs; **PDBTitle:** crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
29	d1h7sa2	Alignment	not modelled	99.3	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
30	d1th8a_	Alignment	not modelled	99.2	22	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
31	d1b63a2	Alignment	not modelled	99.0	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
32	d1bkna2	Alignment	not modelled	99.0	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
33	d1ixma_	Alignment	not modelled	98.8	20	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
34	d1y8oa2	Alignment	not modelled	98.8	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
35	c3na3A_	Alignment	not modelled	98.7	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
36	c3zrwB_	Alignment	not modelled	98.5	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
37	c3h4lB_	Alignment	not modelled	98.3	28	**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	97.7	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
39	d1kija2	Alignment	not modelled	97.7	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
40	d1ei1a2	Alignment	not modelled	97.6	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	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:**DNA gyrase/MutL, N-terminal domain
42	c3lnrA_	Alignment	not modelled	97.5	6	**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
43	c1ea6A_	Alignment	not modelled	97.5	19	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
44	d1s16a2	Alignment	not modelled	97.5	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
45	c3iedA_	Alignment	not modelled	97.3	20	**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
46	c1kijB_	Alignment	not modelled	97.2	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
47	c1ei1B_	Alignment	not modelled	97.1	22	**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
48	d2iwxa1	Alignment	not modelled	97.1	23	**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	c1zwhA_	Alignment	not modelled	97.0	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
50	c1zxnB_	Alignment	not modelled	97.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
						PDB header:chaperone

51	c1y4sA_	Alignment	not modelled	97.0	18	**Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
52	c3ke6A_	Alignment	not modelled	97.0	25	**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
53	c1qzrA_	Alignment	not modelled	96.9	14	**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)
54	c2cg9A_	Alignment	not modelled	96.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
55	d1uyla_	Alignment	not modelled	96.9	13	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
56	c2fwyA_	Alignment	not modelled	96.7	13	**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	c1s16B_	Alignment	not modelled	96.7	18	**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
58	c3g7bB_	Alignment	not modelled	96.7	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
59	c2akpA_	Alignment	not modelled	96.5	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
60	d2gqpa1	Alignment	not modelled	96.4	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
61	d1joya_	Alignment	not modelled	96.4	22	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
62	c2iorA_	Alignment	not modelled	96.4	16	**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
63	d2asxa1	Alignment	not modelled	96.2	23	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
64	d1s14a_	Alignment	not modelled	96.0	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
65	c3pehB_	Alignment	not modelled	95.9	19	**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
66	d1uyma_	Alignment	not modelled	95.9	13	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
67	c2o1wB_	Alignment	not modelled	95.6	13	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
68	d1qy5a_	Alignment	not modelled	95.3	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
69	c2iopD_	Alignment	not modelled	94.9	17	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
70	c3lnuA_	Alignment	not modelled	93.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
71	d2c2aa1	Alignment	not modelled	90.3	21	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
72	c2o1uA_	Alignment	not modelled	88.1	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
73	c3cwvB_	Alignment	not modelled	72.6	17	**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	c2rm8A_	Alignment	not modelled	67.3	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	c3n0rA_	Alignment	not modelled	37.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator;

75	[illegible]	Alignment	not modelled	37.5	13	**PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
76	d1g0oa_	Alignment	not modelled	30.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	d1h5qa_	Alignment	not modelled	30.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	c2z1nA_	Alignment	not modelled	24.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
79	c3s8mA_	Alignment	not modelled	24.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
80	c3o38D_	Alignment	not modelled	23.5	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
81	c3ctmH_	Alignment	not modelled	22.6	11	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
82	c3i1jB_	Alignment	not modelled	22.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
83	c2ntnB_	Alignment	not modelled	22.3	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of maba-c60v/g139a/s144l
84	c2o2sA_	Alignment	not modelled	22.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
85	c3s5pA_	Alignment	not modelled	21.7	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
86	c3rd5A_	Alignment	not modelled	21.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
87	d1oaaa_	Alignment	not modelled	20.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d1f6ga_	Alignment	not modelled	20.1	12	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
89	d1y5ma1	Alignment	not modelled	20.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	d1yxma1	Alignment	not modelled	19.1	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c1n9wA_	Alignment	not modelled	18.9	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
92	d1efub3	Alignment	not modelled	18.8	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
93	c3i7fA_	Alignment	not modelled	18.4	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
94	d1xb2b1	Alignment	not modelled	18.3	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
95	c2zpaB_	Alignment	not modelled	18.2	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein ypfi; **PDBTitle:** crystal structure of trna(met) cytidine acetyltransferase
96	c3sx2F_	Alignment	not modelled	18.0	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative 3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
97	c3qivA_	Alignment	not modelled	18.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase or 3-oxoacyl-[acyl-carrier- **PDBTitle:** crystal structure of a putative short-chain dehydrogenase or 3-2 oxoacyl-[acyl-carrier-protein] reductase from mycobacterium3 paratuberculosis atcc baa-968 / k-10
98	d1aipc1	Alignment	not modelled	17.4	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
99	d1qsga_	Alignment	not modelled	17.3	4	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases