Phyre2

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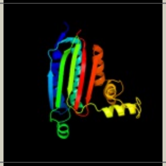
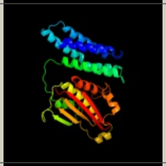
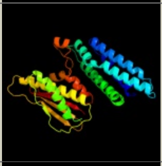
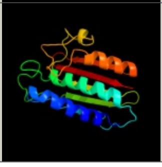
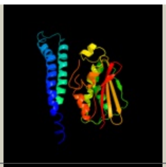
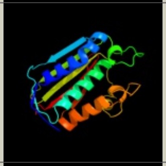
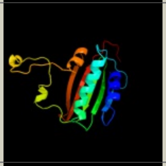
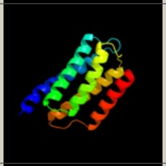
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ch4A_	Alignment		100.0	44	**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
2	c1b3qA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
3	d1i58a_	Alignment		100.0	50	**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
4	c2q8fA_	Alignment		100.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
5	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
6	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
7	c1gjvA_	Alignment		100.0	15	**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	c1y8oA_	Alignment		100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
9	c3d36B_	Alignment		100.0	23	**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
10	c2c2aA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
11	d1gkza2	Alignment		100.0	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain

12	c3a0rA_	Alignment		99.9	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)
13	d2c2aa2	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:**Histidine kinase
14	d1jm6a2	Alignment		99.9	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
15	c3a0tA_	Alignment		99.9	19	**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)
16	d1b3qa2	Alignment		99.9	36	**Fold:**OB-fold **Superfamily:**CheW-like **Family:**CheW-like
17	d1id0a_	Alignment		99.9	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
18	d1bxda_	Alignment		99.9	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
19	d1i5na_	Alignment		99.9	90	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
20	d1ysra1	Alignment		99.9	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
21	c3kyiA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative histidine protein kinase; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
22	c2lchA_	Alignment	not modelled	99.9	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or38; **PDBTitle:** solution nmr structure of a protein with a redesigned hydrophobic2 core, northeast structural genomics consortium target or38
23	d1tqga_	Alignment	not modelled	99.8	33	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
24	c3gieA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
25	c3jz3B_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
26	d1r62a_	Alignment	not modelled	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
27	c3zxqA_	Alignment	not modelled	99.7	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
						PDB header:transferase

28	c3ehgA_	Alignment	not modelled	99.7	17	**Chain:** A: **PDB Molecule:**sensor kinase (yocf protein); **PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp
29	d2hkja3	Alignment	not modelled	99.7	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
30	c3zxoB_	Alignment	not modelled	99.7	28	**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
31	c2ho9A_	Alignment	not modelled	99.6	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chew; **PDBTitle:** solution structure of chemotaxi protein chew from2 escherichia coli
32	d2ch4w1	Alignment	not modelled	99.5	15	**Fold:**OB-fold **Superfamily:**CheW-like **Family:**CheW-like
33	c2zbkB_	Alignment	not modelled	99.5	16	**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
34	d1th8a_	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:**Histidine kinase
35	c2qdlB_	Alignment	not modelled	99.5	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**chemotaxis signal transduction protein; **PDBTitle:** crystal structure of scaffolding protein ttchew from2 thermoanaerobacter tengcongensis
36	c1mx0D_	Alignment	not modelled	99.5	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
37	c2q2eB_	Alignment	not modelled	99.5	24	**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
38	d1h7sa2	Alignment	not modelled	99.4	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
39	d1bkna2	Alignment	not modelled	99.3	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
40	d1b63a2	Alignment	not modelled	99.3	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
41	d1ixma_	Alignment	not modelled	99.0	10	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
42	d1y8oa2	Alignment	not modelled	99.0	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
43	d2r25a1	Alignment	not modelled	98.8	23	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
44	c3na3A_	Alignment	not modelled	98.7	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
45	d1wn0a1	Alignment	not modelled	98.6	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
46	d1y6da_	Alignment	not modelled	98.5	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein luxU
47	d1yvia1	Alignment	not modelled	98.5	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
48	c3myfB_	Alignment	not modelled	98.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
49	c3iqtA_	Alignment	not modelled	98.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**signal transduction histidine-protein kinase bara; **PDBTitle:** structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
50	c3h4lB_	Alignment	not modelled	98.3	20	**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
51	d2a0ba_	Alignment	not modelled	98.3	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Aerobic respiration control sensor protein, ArcB
						Fold: Four-helical up-and-down bundle

52	d1sr2a_	Alignment	not modelled	98.2	16	**Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Sensor-like histidine kinase YojN, C-terminal domain
53	d1kija2	Alignment	not modelled	98.1	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
54	c1kijB_	Alignment	not modelled	98.1	24	**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
55	d1ei1a2	Alignment	not modelled	98.0	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
56	d1pvga2	Alignment	not modelled	98.0	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
57	d2ooca1	Alignment	not modelled	98.0	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**SphA-like
58	c3ke6A_	Alignment	not modelled	98.0	32	**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
59	c1bknA_	Alignment	not modelled	97.9	26	**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
60	c1ei1B_	Alignment	not modelled	97.8	25	**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
61	d1s16a2	Alignment	not modelled	97.8	21	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
62	c1ea6A_	Alignment	not modelled	97.8	27	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
63	c1s16B_	Alignment	not modelled	97.7	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
64	c3iedA_	Alignment	not modelled	97.7	23	**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
65	c1y4sA_	Alignment	not modelled	97.6	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
66	c1zxnB_	Alignment	not modelled	97.6	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
67	c3pehB_	Alignment	not modelled	97.6	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
68	c1qzrA_	Alignment	not modelled	97.6	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)
69	c2cg9A_	Alignment	not modelled	97.6	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
70	c2iopD_	Alignment	not modelled	97.5	28	**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	d1uyla_	Alignment	not modelled	97.5	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
72	c2akpA_	Alignment	not modelled	97.4	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
73	c2fwyA_	Alignment	not modelled	97.4	17	**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
74	c2iorA_	Alignment	not modelled	97.4	25	**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
75	c3lnuA_	Alignment	not modelled	97.4	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
						Fold:ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase

76	d1uyma_	Alignment	not modelled	97.4	18	**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
77	c3g7bB_	Alignment	not modelled	97.3	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
78	d1qy5a_	Alignment	not modelled	97.2	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
79	d2iwxa1	Alignment	not modelled	97.2	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
80	c2o1uA_	Alignment	not modelled	97.1	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
81	c1zwhA_	Alignment	not modelled	97.1	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
82	d2gqpa1	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:**Heat shock protein 90, HSP90, N-terminal domain
83	d1s14a_	Alignment	not modelled	97.0	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
84	c2o1wB_	Alignment	not modelled	96.0	26	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
85	c3cwvB_	Alignment	not modelled	94.2	13	**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
86	d1b3qa1	Alignment	not modelled	93.6	39	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
87	c2v6ll_	Alignment	not modelled	61.8	19	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**mxih; **PDBTitle:** molecular model of a type iii secretion system needle
88	c1qr0A_	Alignment	not modelled	61.4	18	**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	c3o38D_	Alignment	not modelled	56.9	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
90	d1wmaa1	Alignment	not modelled	50.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c3ck6E_	Alignment	not modelled	47.8	14	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**putative membrane transport protein; **PDBTitle:** crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
92	d2g0ua1	Alignment	not modelled	41.9	14	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
93	c2jowA_	Alignment	not modelled	40.6	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein prgi; **PDBTitle:** differences in the electrostatic surfaces of the type iii2 secretion needle proteins
94	c2cg5A_	Alignment	not modelled	39.8	15	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**l-aminoadipate-semialdehyde dehydrogenase- **PDBTitle:** structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic3 acyl carrier protein and coenzyme a
95	d1eyba_	Alignment	not modelled	38.1	27	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
96	c2o98P_	Alignment	not modelled	37.0	44	**PDB header:**protein binding **Chain:** P: **PDB Molecule:**plasma membrane h+ atpase; **PDBTitle:** structure of the 14-3-3 / h+-atpase plant complex
97	c3k31B_	Alignment	not modelled	36.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
98	d2ca5a1	Alignment	not modelled	33.7	21	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
99	c3gdfA_	Alignment	not modelled	33.7	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
						PDB header:oxidoreductase

100	c3gr6A_	Alignment	not modelled	33.2	20	**Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabi) in complex with nadp and3 triclosan
101	c1ey2A_	Alignment	not modelled	32.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
102	d1d7oa_	Alignment	not modelled	30.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
103	d1g0oa_	Alignment	not modelled	28.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
104	c3itdA_	Alignment	not modelled	27.7	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**17beta-hydroxysteroid dehydrogenase; **PDBTitle:** crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
105	c2qioA_	Alignment	not modelled	26.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
106	c3m51P_	Alignment	not modelled	25.4	50	**PDB header:**protein binding **Chain:** P: **PDB Molecule:**n.plumbaginifolia h+-translocating atpase mrna; **PDBTitle:** structure of the 14-3-3/pma2 complex stabilized by pyrrolidone1
107	d1aipc1	Alignment	not modelled	25.4	37	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
108	d1efub3	Alignment	not modelled	25.1	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
109	c2k42A_	Alignment	not modelled	25.1	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
110	d1ej5a_	Alignment	not modelled	25.0	27	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
111	d1xb2b1	Alignment	not modelled	25.0	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
112	d2o23a1	Alignment	not modelled	24.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
113	c3clwF_	Alignment	not modelled	24.1	18	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**conserved exported protein; **PDBTitle:** crystal structure of conserved exported protein from bacteroides2 fragilis
114	d1xmta_	Alignment	not modelled	24.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
115	c3fmsA_	Alignment	not modelled	23.8	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
116	c2o2sA_	Alignment	not modelled	23.7	25	**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
117	d1pn0a3	Alignment	not modelled	23.1	19	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
118	d1b74a1	Alignment	not modelled	23.0	38	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
119	c3zr6A_	Alignment	not modelled	22.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**galactocerebrosidase; **PDBTitle:** structure of galactocerebrosidase from mouse in complex with2 galactose
120	d2bela_	Alignment	not modelled	22.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases