Phyre2

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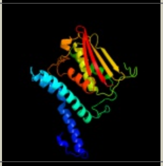
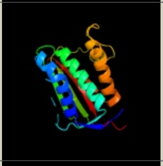
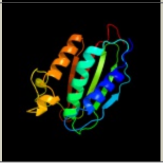
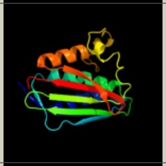
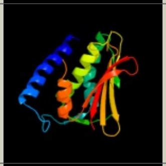
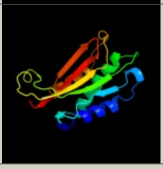
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d36B_	Alignment		100.0	21	**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
2	c2c2aA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
3	c3d2rB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; **PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
4	c2q8fA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
5	c2bu8A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase kinase isoenzyme 2; **PDBTitle:** crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
6	c1y8oA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
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	c3a0rA_	Alignment		100.0	23	**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)
9	c3a0tA_	Alignment		100.0	30	**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)
10	d2c2aa2	Alignment		100.0	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
11	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

12	c1b3qA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase
13	d1id0a_	Alignment		99.9	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
14	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
15	d1bxda_	Alignment		99.9	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
16	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
17	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
18	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
19	c3jz3B_	Alignment		99.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
20	d1r62a_	Alignment		99.8	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
21	d2hkja3	Alignment	not modelled	99.8	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
22	c3gieA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase desk; **PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp
23	c3ehgA_	Alignment	not modelled	99.7	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	c1mx0D_	Alignment	not modelled	99.7	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
25	c2zbkB_	Alignment	not modelled	99.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
26	c3zxqA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost; **PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
27	c3zxoB_	Alignment	not modelled	99.6	22	**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
						PDB header:isomerase

28	c2q2eB_	Alignment	not modelled	99.6	22	**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
29	d1h7sa2	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
30	d1th8a_	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:**Histidine kinase
31	d1ixma_	Alignment	not modelled	99.4	14	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
32	d1bkna2	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
33	d1y8oa2	Alignment	not modelled	99.3	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
34	d1b63a2	Alignment	not modelled	99.3	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
35	c3na3A_	Alignment	not modelled	98.9	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
36	c3h4lB_	Alignment	not modelled	98.6	17	**PDB header:**dna binding protein, protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
37	c3zrwB_	Alignment	not modelled	98.3	21	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
38	c1bknA_	Alignment	not modelled	98.3	20	**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	98.3	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
40	d1pvga2	Alignment	not modelled	98.3	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
41	d1ei1a2	Alignment	not modelled	98.3	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
42	d1s16a2	Alignment	not modelled	98.2	15	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
43	c1ei1B_	Alignment	not modelled	98.1	21	**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
44	c1kijB_	Alignment	not modelled	98.1	16	**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
45	c1zxnB_	Alignment	not modelled	98.0	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
46	c1y4sA_	Alignment	not modelled	98.0	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
47	c1ea6A_	Alignment	not modelled	98.0	23	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
48	c1s16B_	Alignment	not modelled	98.0	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
49	d1uyla_	Alignment	not modelled	97.9	11	**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
50	c3iedA_	Alignment	not modelled	97.9	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein; **PDBTitle:** crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
51	c2fwyA_	Alignment	not modelled	97.8	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-alpha;

51	c2iwyA_	Alignment	not modelled	97.8	11	**PDBTitle:** structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
52	c1qzrA_	Alignment	not modelled	97.8	26	**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)
53	c3ke6A_	Alignment	not modelled	97.8	22	**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
54	c2cg9A_	Alignment	not modelled	97.8	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
55	d2c2aa1	Alignment	not modelled	97.7	28	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
56	c2akpA_	Alignment	not modelled	97.7	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
57	c3pehB_	Alignment	not modelled	97.6	14	**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
58	c3g7bB_	Alignment	not modelled	97.6	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
59	d2iwxa1	Alignment	not modelled	97.6	15	**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
60	d1uyma_	Alignment	not modelled	97.6	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
61	d1joya_	Alignment	not modelled	97.6	25	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
62	c1zwhA_	Alignment	not modelled	97.6	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
63	d1s14a_	Alignment	not modelled	97.5	11	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
64	c3lnuA_	Alignment	not modelled	97.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
65	c2iopD_	Alignment	not modelled	97.4	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
66	c2iorA_	Alignment	not modelled	97.4	18	**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
67	c2o1wB_	Alignment	not modelled	97.3	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
68	d2gqpa1	Alignment	not modelled	97.2	18	**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	d1qy5a_	Alignment	not modelled	97.2	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
70	c3lnrA_	Alignment	not modelled	96.9	7	**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
71	c2o1uA_	Alignment	not modelled	96.9	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
72	c3cwvB_	Alignment	not modelled	95.0	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
73	d2asxa1	Alignment	not modelled	92.6	15	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
74	c3lmmA_	Alignment	not modelled	74.4	18	**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
						PDB header:signaling protein

75	c2rm8A_	Alignment	not modelled	69.8	9	**Chain:** A: **PDB Molecule:**sensory rhodopsin ii transducer; **PDBTitle:** the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
76	d1g0oa_	Alignment	not modelled	64.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c3s8mA_	Alignment	not modelled	60.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
78	c3n0rA_	Alignment	not modelled	59.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
79	d1y5ma1	Alignment	not modelled	51.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
80	c3rd5A_	Alignment	not modelled	47.9	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
81	c3ctmH_	Alignment	not modelled	47.3	14	**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	d1vr7a1	Alignment	not modelled	45.3	10	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**Bacterial S-adenosylmethionine decarboxylase
83	c3i1jB_	Alignment	not modelled	44.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
84	c2zpaB_	Alignment	not modelled	44.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein ypfi; **PDBTitle:** crystal structure of trna(met) cytidine acetyltransferase
85	d1yxma1	Alignment	not modelled	43.7	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	c3o38D_	Alignment	not modelled	42.0	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
87	c1vr7A_	Alignment	not modelled	41.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**s-adenosylmethionine decarboxylase proenzyme; **PDBTitle:** crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
88	c3r1iB_	Alignment	not modelled	39.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
89	d1xsea_	Alignment	not modelled	39.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	d2bela_	Alignment	not modelled	39.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c3kvoB_	Alignment	not modelled	37.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxysteroid dehydrogenase-like protein 2; **PDBTitle:** crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
92	d1w6ua_	Alignment	not modelled	35.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	d1h5qa_	Alignment	not modelled	35.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	c1zn0B_	Alignment	not modelled	34.3	15	**PDB header:**translation/biosynthetic protein/rna **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf
95	d1xg5a_	Alignment	not modelled	34.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	c3r3sD_	Alignment	not modelled	33.6	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
97	c3t6oA_	Alignment	not modelled	31.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter/antisigma-factor antagonist stas; **PDBTitle:** the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
98	c1ybyB_	Alignment	not modelled	31.4	11	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium2 thermocellum
99	d2c07a1	Alignment	not modelled	29.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
100	c2c07A_	Alignment	not modelled	29.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum

101	d1fmca_	Alignment	not modelled	29.6	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	c3ijrF_	Alignment	not modelled	29.1	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
103	d1xu9a_	Alignment	not modelled	28.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
104	c3sx2F_	Alignment	not modelled	28.5	18	**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
105	c3rkuC_	Alignment	not modelled	27.8	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase ymr226c; **PDBTitle:** substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
106	c2vz8B_	Alignment	not modelled	27.3	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
107	c2b4qB_	Alignment	not modelled	27.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
108	c3pt5A_	Alignment	not modelled	27.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; **PDBTitle:** crystal structure of nans
109	c2vx8D_	Alignment	not modelled	26.2	11	**PDB header:**endocytosis,exocytosis **Chain:** D: **PDB Molecule:**nucleoporin-like protein rip, vesicle-associated **PDBTitle:** vamp7 longin domain hrb peptide complex
110	c1qr0A_	Alignment	not modelled	25.9	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
111	c3v2gA_	Alignment	not modelled	25.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
112	c3gdfA_	Alignment	not modelled	25.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
113	c2rdo7_	Alignment	not modelled	25.2	19	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
114	c3oyyA_	Alignment	not modelled	24.9	3	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
115	c3k31B_	Alignment	not modelled	24.5	21	**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
116	c2wdzD_	Alignment	not modelled	24.3	38	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
117	d1dsya_	Alignment	not modelled	23.4	12	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**Synaptotagmin-like (S variant)
118	d1efub3	Alignment	not modelled	23.0	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
119	d2fr1a1	Alignment	not modelled	22.9	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	c3nnhA_	Alignment	not modelled	22.9	12	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**cugbp elav-like family member 1; **PDBTitle:** crystal structure of the cugbp1 rrm1 with guuguuuuguuu rna