Phyre2

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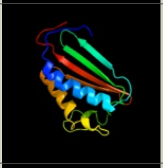
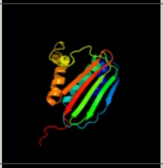
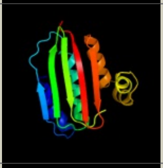
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c2q8fA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
3	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
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	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
6	c2c2aA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
7	c1gjvA_	Alignment		100.0	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
8	d1bxda_	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:**Histidine kinase
9	c3a0rA_	Alignment		100.0	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	d1jm6a2	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
11	c1b3qA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea); **PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase

12	c3a0tA_	Alignment		100.0	22	**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	d1id0a_	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:**Histidine kinase
14	d2c2aa2	Alignment		99.9	24	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
15	d1gkza2	Alignment		99.9	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
16	d1ysra1	Alignment		99.9	24	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
17	c2ch4A_	Alignment		99.9	27	**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	d1i58a_	Alignment		99.9	28	**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	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec
20	c3gieA_	Alignment		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
21	d2hkja3	Alignment	not modelled	99.8	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
22	d1r62a_	Alignment	not modelled	99.8	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
23	c3ehgA_	Alignment	not modelled	99.7	16	**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	99.7	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	c1mx0D_	Alignment	not modelled	99.7	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
26	c3zxqA_	Alignment	not modelled	99.7	23	**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	18	**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	21	**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	99.6	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	d1bkna2	Alignment	not modelled	99.5	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
31	d1th8a_	Alignment	not modelled	99.5	20	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
32	d1b63a2	Alignment	not modelled	99.5	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
33	d1y8oa2	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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
34	d1ixma_	Alignment	not modelled	99.2	9	**Fold:**Sporulation response regulatory protein Spo0B **Superfamily:**Sporulation response regulatory protein Spo0B **Family:**Sporulation response regulatory protein Spo0B
35	c3na3A_	Alignment	not modelled	99.0	22	**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	99.0	61	**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	98.7	19	**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	c3lnrA_	Alignment	not modelled	98.5	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
39	c1bknA_	Alignment	not modelled	98.4	19	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
40	d1pvga2	Alignment	not modelled	98.3	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
41	c1ea6A_	Alignment	not modelled	98.2	24	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
42	d1kija2	Alignment	not modelled	98.2	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
43	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
44	d1ei1a2	Alignment	not modelled	98.2	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
45	c1ei1B_	Alignment	not modelled	98.1	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
46	c1y4sA_	Alignment	not modelled	98.0	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
47	c1kijB_	Alignment	not modelled	98.0	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
48	c1s16B_	Alignment	not modelled	98.0	16	**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	12	**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
						PDB header:chaperone

51	c2fwyA_	Alignment	not modelled	97.9	11	**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
52	c1qzrA_	Alignment	not modelled	97.9	27	**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	d2asxa1	Alignment	not modelled	97.8	15	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
54	d2iwxa1	Alignment	not modelled	97.8	18	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
55	c1zwhA_	Alignment	not modelled	97.8	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
56	c3ke6A_	Alignment	not modelled	97.8	23	**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
57	c1zxnB_	Alignment	not modelled	97.8	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
58	c2cg9A_	Alignment	not modelled	97.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
59	c2iopD_	Alignment	not modelled	97.7	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
60	c2akpA_	Alignment	not modelled	97.7	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** hsp90 delta24-n210 mutant
61	c3pehB_	Alignment	not modelled	97.7	20	**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
62	c2iorA_	Alignment	not modelled	97.6	22	**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	d1uyma_	Alignment	not modelled	97.5	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
64	c3g7bB_	Alignment	not modelled	97.5	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor
65	d2gqpa1	Alignment	not modelled	97.5	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
66	d1s14a_	Alignment	not modelled	97.4	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
67	c2o1wB_	Alignment	not modelled	97.2	15	**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	97.1	19	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
69	d1joya_	Alignment	not modelled	96.7	100	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
70	c2o1uA_	Alignment	not modelled	96.1	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
71	c3lnuA_	Alignment	not modelled	96.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
72	c2rm8A_	Alignment	not modelled	94.7	15	**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
73	c3cwvB_	Alignment	not modelled	92.3	7	**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	d2c2aa1	Alignment	not modelled	90.2	24	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
						PDB header:structural genomics, unknown function

75	c3lmmA_	Alignment	not modelled	84.3	17	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
76	d1wmaa1	Alignment	not modelled	78.9	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c3s8mA_	Alignment	not modelled	59.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
78	d1g0oa_	Alignment	not modelled	59.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
79	c2b4qB_	Alignment	not modelled	54.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
80	d2o23a1	Alignment	not modelled	53.8	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
81	d1zema1	Alignment	not modelled	50.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c2z1nA_	Alignment	not modelled	47.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
83	c3h7aC_	Alignment	not modelled	46.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of short-chain dehydrogenase from2 rhodopseudomonas palustris
84	d1oaaa_	Alignment	not modelled	46.4	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
85	c3n0rA_	Alignment	not modelled	45.2	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
86	c2crqA_	Alignment	not modelled	45.1	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**mitochondrial translational initiation factor 3; **PDBTitle:** solution structure of c-terminal domain of riken cdna2 2810012l14
87	d1spxa_	Alignment	not modelled	44.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d1y5ma1	Alignment	not modelled	43.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c3ctmH_	Alignment	not modelled	43.5	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
90	c2p68A_	Alignment	not modelled	41.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
91	c3o38D_	Alignment	not modelled	39.9	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
92	c3rd5A_	Alignment	not modelled	39.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
93	c3i1jB_	Alignment	not modelled	39.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
94	c2jahB_	Alignment	not modelled	38.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
95	c3imfA_	Alignment	not modelled	38.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
96	c3qivA_	Alignment	not modelled	38.2	19	**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
97	c3afnC_	Alignment	not modelled	37.9	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
98	d1gz6a_	Alignment	not modelled	37.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c3ftpD_	Alignment	not modelled	37.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
100	d2bela_	Alignment	not modelled	36.9	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
101	c3f5sA_	Alignment	not modelled	36.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of putatitve short chain dehydrogenase from shigella2 flexneri 2a str. 301
102	d2h7ma1	Alignment	not modelled	36.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
103	c3sx2F_	Alignment	not modelled	35.9	14	**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
104	c3tfoD_	Alignment	not modelled	35.7	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative 3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
105	c2o2sA_	Alignment	not modelled	35.1	28	**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
106	c3uf0A_	Alignment	not modelled	34.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
107	c3gafF_	Alignment	not modelled	34.7	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
108	d1e7wa_	Alignment	not modelled	34.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
109	c2fwmX_	Alignment	not modelled	34.4	17	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; **PDBTitle:** crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
110	d1h5qa_	Alignment	not modelled	34.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
111	c3ksuA_	Alignment	not modelled	34.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-acyl carrier protein reductase; **PDBTitle:** crystal structure of short-chain dehydrogenase from2 oenococcus oeni psu-1
112	c3tjrA_	Alignment	not modelled	34.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
113	c3s55F_	Alignment	not modelled	33.9	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
114	d1yxma1	Alignment	not modelled	33.9	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
115	c3f9iB_	Alignment	not modelled	33.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
116	c3pxxE_	Alignment	not modelled	33.6	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
117	c3ai3A_	Alignment	not modelled	33.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-sorbose reductase; **PDBTitle:** the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
118	d1xsea_	Alignment	not modelled	33.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	d1odka_	Alignment	not modelled	33.1	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
120	c3r1iB_	Alignment	not modelled	33.0	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