Phyre^2

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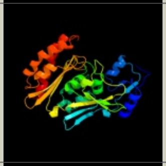
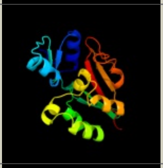
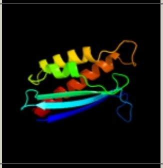
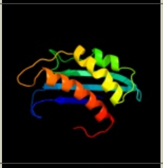
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n62C_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
2	c3hrdC_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
3	c1t3qF_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
4	c1ffuF_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
5	c1rm6E_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
6	c1wygA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	c2w3rG_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
8	c3b9jJ_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
9	c3etrM_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of xanthine oxidase in complex with2 lumazine
10	d1ffvc2	Alignment		100.0	35	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
11	d1n62c2	Alignment		100.0	31	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like

12	d1t3qc2	Alignment		100.0	30	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
13	d1rm6b2	Alignment		100.0	40	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
14	d1v97a6	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
15	d3b9jb2	Alignment		100.0	24	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
16	d1jroa4	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
17	d1v97a4	Alignment		99.9	20	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
18	d1jroa3	Alignment		99.9	26	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
19	d1n62c1	Alignment		99.9	22	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
20	d1t3qc1	Alignment		99.9	23	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
21	d1ffvc1	Alignment	not modelled	99.9	24	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
22	d1rm6b1	Alignment	not modelled	99.9	18	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
23	c1hskA_	Alignment	not modelled	97.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
24	c1mbbA_	Alignment	not modelled	97.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
25	c3i99A_	Alignment	not modelled	97.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
26	c1zr6A_	Alignment	not modelled	97.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
27	c2wdwB_	Alignment	not modelled	97.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative hexose oxidase; **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
28	c2ipiD_	Alignment	not modelled	97.5	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox);

						PDBTitle: crystal structure of aclacinomycin oxidoreductase
29	c3fwaA_	Alignment	not modelled	97.5	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
30	d1uxya1	Alignment	not modelled	97.5	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
31	c2vfvA_	Alignment	not modelled	97.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
32	c2y3rC_	Alignment	not modelled	97.3	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
33	d1hska1	Alignment	not modelled	97.3	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
34	c3d2hA_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
35	c2gquA_	Alignment	not modelled	97.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvylglucosamine reductase; **PDBTitle:** crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
36	c3bw7A_	Alignment	not modelled	96.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
37	c3pm9A_	Alignment	not modelled	96.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
38	c1f0xA_	Alignment	not modelled	96.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
39	c2uuvC_	Alignment	not modelled	96.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
40	d1f0xa2	Alignment	not modelled	96.7	19	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
41	c3popD_	Alignment	not modelled	96.5	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gilr oxidase; **PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
42	d2i0ka2	Alignment	not modelled	96.4	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
43	c2bvfA_	Alignment	not modelled	96.2	16	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
44	c2exrA_	Alignment	not modelled	96.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
45	c1wveB_	Alignment	not modelled	96.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
46	c1i19B_	Alignment	not modelled	95.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum
47	c3js8A_	Alignment	not modelled	95.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
48	d1wvfa2	Alignment	not modelled	95.5	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
49	c1ahuB_	Alignment	not modelled	94.5	12	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
50	d1w1oa2	Alignment	not modelled	93.9	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
51	d1e8ga2	Alignment	not modelled	92.8	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
52	d1x2ga1	Alignment	not modelled	89.9	16	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
53	d1vqza1	Alignment	not modelled	89.6	2	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
						PDB header:ligase

54	c2e5aA_	Alignment	not modelled	75.4	9	**Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
55	c1x2gB_	Alignment	not modelled	75.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
56	d1su0b_	Alignment	not modelled	69.2	14	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
57	d1li4a2	Alignment	not modelled	67.0	13	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
58	d1xjsa_	Alignment	not modelled	65.7	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
59	c1vqzA_	Alignment	not modelled	63.1	2	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
60	c2yvsA_	Alignment	not modelled	59.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce; **PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
61	d1v8ba2	Alignment	not modelled	56.1	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
62	c2qq4A_	Alignment	not modelled	50.3	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
63	c3d64A_	Alignment	not modelled	44.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
64	c3dhyC_	Alignment	not modelled	43.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
65	c1v8bA_	Alignment	not modelled	42.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
66	c3oneA_	Alignment	not modelled	41.1	16	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
67	d1wfza_	Alignment	not modelled	35.9	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
68	d1r9pa_	Alignment	not modelled	35.5	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
69	c3n58D_	Alignment	not modelled	32.7	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
70	d1frfl_	Alignment	not modelled	31.7	13	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
71	d1e3db_	Alignment	not modelled	29.8	17	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
72	d1wuil1	Alignment	not modelled	28.0	13	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
73	c2z7eB_	Alignment	not modelled	25.8	9	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
74	c2wpnB_	Alignment	not modelled	23.4	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
75	d1yq9h1	Alignment	not modelled	22.8	15	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
76	c1h2aL_	Alignment	not modelled	22.1	14	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
77	d1j3ka_	Alignment	not modelled	20.1	24	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
78	c3ix9B_	Alignment	not modelled	19.3	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
						PDB header:oxidoreductase, transferase **Chain:** B: **PDB Molecule:**bifunctional dihydrofolate reductase-

79	c3dg8B_	Alignment	not modelled	18.8	24	thymidylate **PDBTitle:** quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
80	d2ji7a1	Alignment	not modelled	18.7	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
81	d1fmta1	Alignment	not modelled	18.0	13	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
82	c2blcA_	Alignment	not modelled	17.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
83	c1zdrB_	Alignment	not modelled	17.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** dhfr from bacillus stearothermophilus
84	d2qdya1	Alignment	not modelled	17.5	20	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
85	c2qyaA_	Alignment	not modelled	17.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from methanopyrus kandleri
86	c1d4fD_	Alignment	not modelled	14.8	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
87	c3qyhG_	Alignment	not modelled	14.5	11	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
88	d1ozha1	Alignment	not modelled	14.2	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
89	d2djia1	Alignment	not modelled	13.8	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
90	d1aoea_	Alignment	not modelled	13.0	21	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
91	d1oj7a_	Alignment	not modelled	12.8	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
92	c2dyoB_	Alignment	not modelled	12.3	56	**PDB header:**protein turnover/protein turnover **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
93	d1cc1l_	Alignment	not modelled	12.2	10	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
94	d1jr1a4	Alignment	not modelled	12.0	29	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
95	c3gxxB_	Alignment	not modelled	11.9	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
96	d2fug41	Alignment	not modelled	11.2	11	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
97	c2fug4_	Alignment	not modelled	11.2	11	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
98	d1ybha1	Alignment	not modelled	11.0	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
99	c1b7gO_	Alignment	not modelled	11.0	19	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase