Phyre^2

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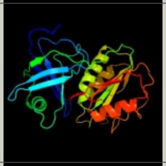
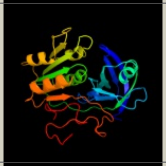
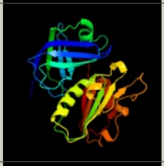
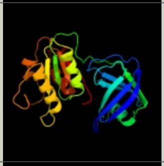
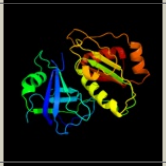
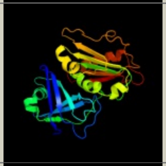
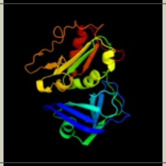
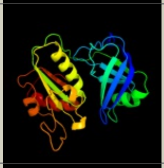
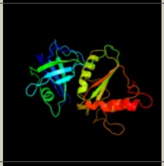
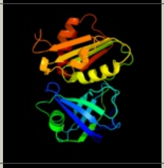
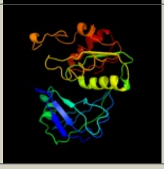
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2piaA_	Alignment		100.0	23	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
2	c1gvhA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
3	c1ep3B_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
4	c1krhA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
5	c1cqxB_	Alignment		100.0	23	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
6	c2r6hC_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
7	c2ok8D_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp+ reductase from plasmodium falciparum
8	c2bgjB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
9	c1tvcA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
10	c1a8pA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
11	c1qfjD_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (flavin reductase); **PDBTitle:** crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli

12	c2eixA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of physarum polycephalum cytochrome b5 reductase
13	c1fncA_	Alignment		100.0	21	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
14	c3fpkB_	Alignment		100.0	17	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
15	c1umkA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of human erythrocyte nadh-cytochrome b52 reductase
16	c2b5oA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
17	c1qgyA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
18	c1jb9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
19	c2rc5D_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** refined structure of fnr from leptospira interrogans
20	c1cneA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase; **PDBTitle:** structural studies on corn nitrate reductase: refined2 structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and4 modeling of the cytochrome b domain
21	c2gpjA_	Alignment	not modelled	100.0	16	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
22	c1ddiA_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha- **PDBTitle:** crystal structure of sir-fp60
23	c1tllA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
24	c1j9zB_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
25	c3qftA_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase; **PDBTitle:** crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
26	c1f20A_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
27	d1ep3b2	Alignment	not modelled	99.9	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
28	c2bpoA_	Alignment	not modelled	99.9	24	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.

29	c2qtzA_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
30	d1tvca2	Alignment	not modelled	99.9	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
31	d1qfja2	Alignment	not modelled	99.9	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
32	d1gvha3	Alignment	not modelled	99.9	24	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
33	d1krha2	Alignment	not modelled	99.9	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
34	d1cqxa3	Alignment	not modelled	99.9	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
35	d2piaa2	Alignment	not modelled	99.9	27	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
36	d1a8pa2	Alignment	not modelled	99.9	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
37	d1umka2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
38	c3a1fA_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b-245 heavy chain; **PDBTitle:** the crystal structure of nadph binding domain of gp91(phox)
39	d2piaa3	Alignment	not modelled	99.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
40	d2cnda2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
41	d1sm4a1	Alignment	not modelled	99.8	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
42	d1qx4a2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
43	d1doia_	Alignment	not modelled	99.8	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
44	d1a70a_	Alignment	not modelled	99.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
45	d2bmwa1	Alignment	not modelled	99.8	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
46	d1frda_	Alignment	not modelled	99.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
47	d1fdra2	Alignment	not modelled	99.8	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
48	d1e0za_	Alignment	not modelled	99.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
49	d1frra_	Alignment	not modelled	99.8	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
50	d2bmwa2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
51	d1offa_	Alignment	not modelled	99.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
52	d1awda_	Alignment	not modelled	99.8	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
53	d1gawa1	Alignment	not modelled	99.8	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
54	d1qx4a1	Alignment	not modelled	99.8	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
55	d1fxia_	Alignment	not modelled	99.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin-related
56	d1iuea_	Alignment	not modelled	99.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
57	d1pfda_	Alignment	not modelled	99.8	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
58	d1qfza2	Alignment	not modelled	99.8	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
59	d1ndha2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
60	d1f20a2	Alignment	not modelled	99.8	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
61	d1fnda1	Alignment	not modelled	99.8	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
62	c3lrxC_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
63	d1gawa2	Alignment	not modelled	99.8	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
64	d1wria_	Alignment	not modelled	99.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
65	d1gvha2	Alignment	not modelled	99.8	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
66	d1czpa_	Alignment	not modelled	99.8	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
67	d2cjoa_	Alignment	not modelled	99.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
68	d1a8pa1	Alignment	not modelled	99.8	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
69	d2piaa1	Alignment	not modelled	99.8	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
70	d1qfza1	Alignment	not modelled	99.8	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
71	d1fdra1	Alignment	not modelled	99.8	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
72	d1gaqb_	Alignment	not modelled	99.8	34	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
73	d1krha1	Alignment	not modelled	99.8	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
74	d1fnda2	Alignment	not modelled	99.8	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
75	d4fxca_	Alignment	not modelled	99.7	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
76	d1umka1	Alignment	not modelled	99.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
77	d1ddga2	Alignment	not modelled	99.7	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
78	d1cqxa2	Alignment	not modelled	99.7	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
79	d1ep3b1	Alignment	not modelled	99.7	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
80	d1qfja1	Alignment	not modelled	99.7	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
81	d2cnda1	Alignment	not modelled	99.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
82	d1jb9a2	Alignment	not modelled	99.7	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked

82	d1jb9a2	Alignment	not modelled	99.7	12	domain **Family:**Reductases
83	d1sm4a2	Alignment	not modelled	99.7	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
84	d1tvca1	Alignment	not modelled	99.7	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
85	d1ndha1	Alignment	not modelled	99.7	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
86	d1ja1a3	Alignment	not modelled	99.7	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
87	d1jq4a_	Alignment	not modelled	99.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
88	d1krha3	Alignment	not modelled	99.7	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
89	d1jb9a1	Alignment	not modelled	99.6	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
90	c3ah7A_	Alignment	not modelled	99.4	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
91	d1i7ha_	Alignment	not modelled	99.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
92	d1l5pa_	Alignment	not modelled	99.1	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
93	c2wlbB_	Alignment	not modelled	99.1	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
94	c3huiA_	Alignment	not modelled	99.0	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of the mutant a105r of [2fe-2s] ferredoxin2 in the class i cyp199a2 system from rhodopseudomonas3 palustris
95	d1e9ma_	Alignment	not modelled	98.9	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
96	d1xlqa1	Alignment	not modelled	98.9	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
97	c3lxfC_	Alignment	not modelled	98.9	20	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
98	d1b9ra_	Alignment	not modelled	98.8	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
99	d2bt6a1	Alignment	not modelled	98.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
100	d2fug33	Alignment	not modelled	98.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
101	d1ddga1	Alignment	not modelled	98.4	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
102	c1l6vA_	Alignment	not modelled	98.1	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
103	d3c8ya2	Alignment	not modelled	98.0	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
104	c1c4cA_	Alignment	not modelled	98.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
105	d1t3qa2	Alignment	not modelled	97.9	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
106	d1vlba2	Alignment	not modelled	97.8	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
107	d1ffva2	Alignment	not modelled	97.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
108	d1dgja2	Alignment	not modelled	97.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins

109	d1n62a2	Alignment	not modelled	97.7	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
110	c1t3qD_	Alignment	not modelled	97.6	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
111	d2bs2b2	Alignment	not modelled	97.5	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
112	d1kf6b2	Alignment	not modelled	97.5	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
113	d1rm6c2	Alignment	not modelled	97.5	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
114	c3hrdH_	Alignment	not modelled	97.5	23	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
115	c1rm6F_	Alignment	not modelled	97.4	32	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
116	c1n60D_	Alignment	not modelled	97.4	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
117	c1ffuA_	Alignment	not modelled	97.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
118	c2fugC_	Alignment	not modelled	97.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
119	c2b76N_	Alignment	not modelled	97.1	32	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
120	c1vlbA_	Alignment	not modelled	97.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a