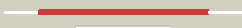



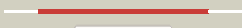



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2776c_(-)_3083384_3084313
Date	Wed Aug 7 12:50:43 BST 2019
Unique Job ID	93d8138dfc268ea8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2piaA_	 Alignment		100.0	32	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for electron2 transfer from pyridine nucleotides to [2fe-2s]
2	c1ep3B_	 Alignment		100.0	21	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.
3	c5jcaS_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: S: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
4	c4yifA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase b (nad(+)), electron transfer PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
5	c4p6vF_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: F: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
6	c4wqmA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene-4-monooxygenase electron transfer component; PDBTitle: structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
7	c1krhA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray structure of benzoate dioxygenase reductase
8	c6o0aA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoglobin; PDBTitle: crystal structure of flavo-hemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing
9	c1gvhA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: flavo-hemoprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavo-hemoglobin reveals an unsuspected geometry of the3 distal heme pocket
10	c5ogxA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
11	c4g1bB_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: flavo-hemoglobin; PDBTitle: x-ray structure of yeast flavo-hemoglobin in complex with econazole

12	c5vj7B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(+) reductase subunit alpha; PDBTitle: ferredoxin nadp oxidoreductase (xfn)
13	c1cqxB_	Alignment		100.0	25	PDB header: lipid binding protein Chain: B: PDB Molecule: flavoheomprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
14	c2r6hC_	Alignment		100.0	19	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
15	c6mv2A_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b5 reductase 4; PDBTitle: 2.05a resolution structure of the cs-b5r domains of human ncb5or2 (nadp+ form)
16	c4eh1A_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheomprotein; PDBTitle: crystal structure of the flavohem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor
17	c4u9uB_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of nqr fad-binding domain from vibrio cholerae
18	c5ylyB_	Alignment		100.0	22	PDB header: flavoprotein Chain: B: PDB Molecule: nitrate reductase; PDBTitle: crystal structure of the cytochrome b5 reductase domain of ulva2 prolifera nitrate reductase
19	c1qfjD_	Alignment		100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
20	c1tvcA_	Alignment		100.0	23	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)
21	c2eixA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of physarum polycephalum cytochrome b5 reductase
22	c2ok8D_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: putative ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp+ reductase from plasmodium falciparum
23	c1fncA_	Alignment	not modelled	100.0	15	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
24	c1qgyA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp+ reductase; PDBTitle: ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
25	c5tr9A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of a ferredoxin nadp+ reductase from neisseria2 gonorrhoeae with bound fad
26	c2b5oA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
27	c3fpkB_	Alignment	not modelled	100.0	19	PDB header: flavoprotein, oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
28	c1jb9A_	Alignment	not modelled	100.0	17	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

29	c4b4dA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of fad-containing ferredoxin-nadp reductase from <i>Xanthomonas axonopodis</i> pv. citri
30	c2bgjB	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(h) reductase; PDBTitle: x-ray structure of the ferredoxin-nadp(h) reductase from <i>Rhodobacter2 capsulatus</i> at 2.1 angstroms
31	c1a8pA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph\ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from <i>Azotobacter vinelandii</i>
32	c5o0xA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative ferric reductase; PDBTitle: crystal structure of dehydrogenase domain of <i>Cylindrospermum stagnale2</i> nadph-oxidase 5 (nox5)
33	c1umkA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of human erythrocyte nadh-cytochrome b52 reductase
34	c5thxA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of a ferredoxin nadp+ reductase from <i>Neisseria2 gonorrhoeae</i> with bound nadp and fad
35	c4f7dA	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from <i>Burkholderia2 thailandensis</i> e264
36	c6gehA	Alignment	not modelled	100.0	16	PDB header: metal transport Chain: A: PDB Molecule: fad-binding 9, siderophore-interacting domain protein; PDBTitle: structure and reactivity of a siderophore-interacting protein from the <i>2</i> marine bacterium <i>Shewanella</i> reveals unanticipated functional <i>3</i> versatility.
37	c4yhBA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-chelator utilization protein; PDBTitle: crystal structure of a siderophore utilization protein from <i>T. fusca</i>
38	c1cneA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrate reductase; PDBTitle: structural studies on corn nitrate reductase: refined <i>2</i> structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and <i>4</i> modeling of the cytochrome b domain
39	c2rc5D	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: refined structure of fnr from <i>Leptospira interrogans</i>
40	c6k2IA	Alignment	not modelled	100.0	18	PDB header: flavoprotein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of the siderophore-interacting protein sips from <i>2</i> <i>Aeromonas hydrophila</i>
41	c2gpiA	Alignment	not modelled	100.0	14	PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (spu32_0076) <i>2</i> from <i>Shewanella putrefaciens</i> cn-32 at 2.20 a resolution
42	d1ep3b2	Alignment	not modelled	100.0	24	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
43	c6efvA	Alignment	not modelled	100.0	20	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended <i>2</i> conformation that is unique to this diflavin reductase
44	c1ddiA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: crystal structure of sir-fp60
45	c1j9zB	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
46	c4dqkA	Alignment	not modelled	99.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional p-450/nadph-p450 reductase; PDBTitle: crystal structure of the fad binding domain of cytochrome p450 bm3
47	c5gxuA	Alignment	not modelled	99.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase 2; PDBTitle: crystal structure of <i>Arabidopsis atr2</i>
48	c1tllA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase <i>2</i> reductase module at 2.3 a resolution.
49	c1f20A	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase fad/nadp+ <i>2</i> domain at 1.9a resolution.
50	d2piaa2	Alignment	not modelled	99.9	26	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
51	c3qftA	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase; PDBTitle: crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain <i>2</i> and r457h mutant)
52	c2qtzA	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine synthase reductase; PDBTitle: crystal structure of the nadp+-bound fad-containing fnr-like module of <i>2</i> human methionine synthase reductase Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain

53	d1qfja2	Alignment	not modelled	99.9	20	Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
54	c4n58A	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: pectocin m2; PDBTitle: crystal structure of pectocin m2 at 1.86 angstroms
55	d1tvca2	Alignment	not modelled	99.9	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
56	d1gvha3	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: Flavo-hemoglobin, C-terminal domain
57	c2bpoA	Alignment	not modelled	99.9	20	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
58	d2piaa3	Alignment	not modelled	99.9	37	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
59	d1cqxa3	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: Flavo-hemoglobin, C-terminal domain
60	d1krha2	Alignment	not modelled	99.9	30	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
61	d1lumka2	Alignment	not modelled	99.8	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
62	c6j7aB	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1,nadph--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
63	d1qx4a2	Alignment	not modelled	99.8	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
64	d2cnda2	Alignment	not modelled	99.8	22	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
65	d1a8pa2	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
66	d2piaa1	Alignment	not modelled	99.8	36	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
67	d2bmwa2	Alignment	not modelled	99.8	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
68	c3lrxC	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: putative hydrogenase; PDBTitle: crystal structure of the c-terminal domain (residues 78-226) of pf19112 hydrogenase from pyrococcus furiosus, northeast structural genomics3 consortium target pfr246a
69	c3a1fA	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b-245 heavy chain; PDBTitle: the crystal structure of nadph binding domain of gp91(phox)
70	d1qfza2	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
71	d1a70a	Alignment	not modelled	99.8	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
72	d1e0za	Alignment	not modelled	99.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
73	d1doja	Alignment	not modelled	99.8	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
74	d1fxia	Alignment	not modelled	99.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
75	d1fdra2	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: Reductases
76	d1f20a2	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: NADPH-cytochrome p450 reductase-like
77	d1gawa2	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: Reductases
78	d1offa	Alignment	not modelled	99.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related

79	d1frra_	Alignment	not modelled	99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
80	d1jb9a2	Alignment	not modelled	99.8	14	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
81	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
82	d1frda_	Alignment	not modelled	99.8	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
83	d1czpa_	Alignment	not modelled	99.8	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
84	d1awda_	Alignment	not modelled	99.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
85	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
86	d1iuea_	Alignment	not modelled	99.7	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
87	d1fnda2	Alignment	not modelled	99.7	17	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
88	d1pfda_	Alignment	not modelled	99.7	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
89	d1ja1a3	Alignment	not modelled	99.7	21	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
90	d1wrja_	Alignment	not modelled	99.7	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
91	d1gvha2	Alignment	not modelled	99.7	28	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
92	d1ndha2	Alignment	not modelled	99.7	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
93	d1cqxa2	Alignment	not modelled	99.7	26	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
94	d1gaqb_	Alignment	not modelled	99.7	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
95	d2cjoa_	Alignment	not modelled	99.7	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
96	d1sm4a2	Alignment	not modelled	99.7	18	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
97	d1krha1	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
98	c4itkA_	Alignment	not modelled	99.7	25	PDB header: electron transport Chain: A: PDB Molecule: apoferradoxin; PDBTitle: the structure of c.reinhardtii ferredoxin 2
99	d4fxca_	Alignment	not modelled	99.7	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
100	d2cnda1	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
101	d1qfja1	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
102	d1qx4a1	Alignment	not modelled	99.7	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
103	d2bmwa1	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
104	d1tvca1	Alignment	not modelled	99.7	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
105	d1a8pa1	Alignment	not modelled	99.7	13	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
						Fold: Reductase/isomerase/elongation factor common domain

106	d1umka1	Alignment	not modelled	99.6	21	Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
107	d1sm4a1	Alignment	not modelled	99.6	16	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
108	d1krha3	Alignment	not modelled	99.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
109	d1gawa1	Alignment	not modelled	99.6	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
110	d1jq4a_	Alignment	not modelled	99.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
111	c5frtC_	Alignment	not modelled	99.6	22	PDB header: oxidoreductase Chain: C: PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
112	d1fnda1	Alignment	not modelled	99.6	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
113	d1ep3b1	Alignment	not modelled	99.6	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
114	d1ndha1	Alignment	not modelled	99.6	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
115	d1qfza1	Alignment	not modelled	99.6	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
116	c3ah7A_	Alignment	not modelled	99.4	15	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
117	c3zyyX_	Alignment	not modelled	99.4	19	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
118	d1i7ha_	Alignment	not modelled	99.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
119	d1jb9a1	Alignment	not modelled	99.4	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
120	c2mjdA_	Alignment	not modelled	99.1	22	PDB header: metal binding protein Chain: A: PDB Molecule: adrenodoxin homolog, mitochondrial; PDBTitle: oxidized yeast adrenodoxin homolog 1