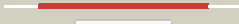



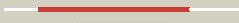




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3230c_(-)_3607109_3608251
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	b9b789a705d76317

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2piaA_	 Alignment		100.0	20	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	c1gvhA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: flavoheomprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
3	c6o0aA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: flavoheomoglobin; PDBTitle: crystal structure of flavohemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing
4	c4g1bB_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B; PDB Molecule: flavoheomoglobin; PDBTitle: x-ray structure of yeast flavohemoglobin in complex with econazole
5	c4p6vF_	 Alignment		100.0	17	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	c1krhA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray structure of benzoate dioxygenase reductase
7	c1cqxB_	 Alignment		100.0	23	PDB header: lipid binding protein Chain: B; PDB Molecule: flavoheomprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
8	c5ogxA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
9	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 (nadh+ form)
10	c4wqmA_	 Alignment		100.0	18	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
11	c2r6hC_	 Alignment		100.0	21	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

12	c1ep3B_	Alignment		100.0	16	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.
13	c4u9uB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of nqrf fad-binding domain from vibrio cholerae
14	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)
15	c2ok8D_	Alignment		100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: putative ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp+ reductase from plasmodium falciparum
16	c4eh1A_	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheмоprotein; PDBTitle: crystal structure of the flavohem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor
17	c5jcaS_	Alignment		100.0	13	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
18	c2eixA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of physarum polycephalum cytochrome b5 reductase
19	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
20	c4ylfA_	Alignment		100.0	16	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
21	c3fpkB_	Alignment	not modelled	100.0	22	PDB header: flavoprotein, oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
22	c1fncA_	Alignment	not modelled	100.0	25	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
23	c1a8pA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh\ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii
24	c1qgyA_	Alignment	not modelled	100.0	22	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	22	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	c4b4dA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of fad-containing ferredoxin-nadp reductase from2 xanthomonas axonopodis pv. citri
27	c1jb9A_	Alignment	not modelled	100.0	22	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
28	c2rc5D_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: refined structure of fnr from leptospira interrogans
						PDB header: oxidoreductase

29	c1umkA_	Alignment	not modelled	100.0	23	Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of human erythrocyte nadh-cytochrome b52 reductase
30	c1qfjD_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
31	c2b5oA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
32	c5thxA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of a ferredoxin nadp+ reductase from neisseria2 gonorrhoeae with bound nadp and fad
33	c2bgjB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(h) reductase; PDBTitle: x-ray structure of the ferredoxin-nadp(h) reductase from rhodobacter2 capsulatus at 2.1 angstroms
34	c5vj7B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(+) reductase subunit alpha; PDBTitle: ferredoxin nadp oxidoreductase (xfn)
35	c5o0xA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative ferric reductase; PDBTitle: crystal structure of dehydrogenase domain of cylindrospermum stagnale2 nadph-oxidase 5 (nox5)
36	c4f7dA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from burkholderia2 thailandensis e264
37	c1cneA_	Alignment	not modelled	100.0	18	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
38	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 t. fusca
39	c6gehA_	Alignment	not modelled	100.0	13	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 the2 marine bacterium shewanella reveals unanticipated functional3 versatility.
40	c6k2IA_	Alignment	not modelled	100.0	12	PDB header: flavoprotein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of the siderophore-interacting protein sips from2 aeromonas hydrophila
41	c2gpiA_	Alignment	not modelled	100.0	12	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
42	c6efvA_	Alignment	not modelled	100.0	22	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
43	c1tllA_	Alignment	not modelled	100.0	22	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.
44	c1ddiA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: crystal structure of sir-fp60
45	c5gxuA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase 2; PDBTitle: cystal structure of arabidopsis atr2
46	c1f20A_	Alignment	not modelled	100.0	19	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.
47	c1j9zB_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
48	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 domain2 and r457h mutant)
49	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
50	c4dqkA_	Alignment	not modelled	99.9	18	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
51	c2qtzA_	Alignment	not modelled	99.9	17	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
52	d1gvha3	Alignment	not modelled	99.9	25	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
53	c2hpaA_	Alignment	not modelled	99.9	10	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase;

53	c2upvA	Alignment	not modelled	99.9	19	PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a. Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
54	d1qfja2	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: Reductases
55	d1ep3b2	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: Dihydroorotate dehydrogenase B, PyrK subunit
56	d1krha2	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: Aromatic dioxygenase reductase-like
57	d1cqxa3	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
58	d2piaa2	Alignment	not modelled	99.9	18	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
59	c6j7aB_	Alignment	not modelled	99.9	20	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)
60	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
61	d1umka2	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: Reductases
62	d2cnda2	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: Reductases
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	d1f20a2	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: NADPH-cytochrome p450 reductase-like
65	c3a1fA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b-245 heavy chain; PDBTitle: the crystal structure of nadph binding domain of gp91(phox)
66	c4n58A_	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A: PDB Molecule: pectocin m2; PDBTitle: crystal structure of pectocin m2 at 1.86 angstroms
67	d2bmwa2	Alignment	not modelled	99.8	25	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
68	d2piaa3	Alignment	not modelled	99.8	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
69	d1ddga2	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: NADPH-cytochrome p450 reductase-like
70	d1fdra2	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
71	d1ja1a3	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: NADPH-cytochrome p450 reductase-like
72	d1gawa2	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
73	d1qfza2	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
74	d1ndha2	Alignment	not modelled	99.8	24	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
75	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
76	d1fnda2	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
77	d1sm4a1	Alignment	not modelled	99.8	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
78	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
						Fold: Reductase/isomerase/elongation factor common domain

79	d1gvha2	Alignment	not modelled	99.8	31	Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
80	c3lrxC_	Alignment	not modelled	99.8	19	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
81	d1cqxa2	Alignment	not modelled	99.7	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
82	d1krha1	Alignment	not modelled	99.7	27	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
83	d1a8pa1	Alignment	not modelled	99.7	27	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
84	d1fdra1	Alignment	not modelled	99.7	30	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
85	d1a70a_	Alignment	not modelled	99.7	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
86	d1sm4a2	Alignment	not modelled	99.7	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
87	d1gawa1	Alignment	not modelled	99.7	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
88	d1doia_	Alignment	not modelled	99.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
89	d1fnda1	Alignment	not modelled	99.7	30	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
90	d1frra_	Alignment	not modelled	99.7	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
91	d1e0za_	Alignment	not modelled	99.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
92	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
93	d1offa_	Alignment	not modelled	99.7	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
94	d1frda_	Alignment	not modelled	99.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
95	d2piaa1	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
96	d1fxia_	Alignment	not modelled	99.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
97	d1qfza1	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
98	d1awda_	Alignment	not modelled	99.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
99	d1iuea_	Alignment	not modelled	99.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
100	d1qx4a1	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
101	d1czpa_	Alignment	not modelled	99.7	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
102	d1ep3b1	Alignment	not modelled	99.7	16	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
103	d1tvca1	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
104	d1pfda_	Alignment	not modelled	99.7	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
105	d1umka1	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
106	d2cjoa_	Alignment	not modelled	99.6	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related

107	d1qfja1	Alignment	not modelled	99.6	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
108	d1wria	Alignment	not modelled	99.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
109	d1ndha1	Alignment	not modelled	99.6	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
110	d1gaqb	Alignment	not modelled	99.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
111	d4fxca	Alignment	not modelled	99.6	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
112	c4itkA	Alignment	not modelled	99.6	30	PDB header: electron transport Chain: A: PDB Molecule: apoferrredoxin; PDBTitle: the structure of c.reinhardtii ferredoxin 2
113	d1jq4a	Alignment	not modelled	99.6	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
114	d1krha3	Alignment	not modelled	99.5	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
115	d1jb9a1	Alignment	not modelled	99.5	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
116	c5frtC	Alignment	not modelled	99.4	26	PDB header: oxidoreductase Chain: C: PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
117	c3zyyX	Alignment	not modelled	99.4	30	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
118	c3ah7A	Alignment	not modelled	99.3	17	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
119	d1i7ha	Alignment	not modelled	99.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
120	d1l5pa	Alignment	not modelled	99.1	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related