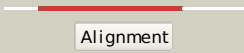
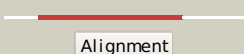
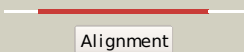
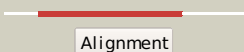
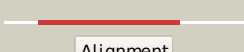
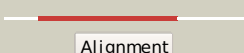
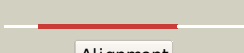
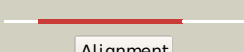
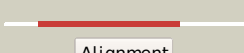
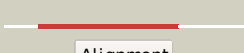
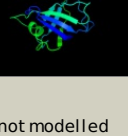


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2piaA_	 Alignment		100.0	34	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
2	c1gvhA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheomprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
3	c1krhA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray stucture of benzoate dioxygenase reductase
4	c1ep3B_	 Alignment		100.0	19	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.
5	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
6	c2r6hC_	 Alignment		100.0	20	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	c2eixA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of physarum polycephalum cytochrome b5 reductase
8	c1umkA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-cytochrome b5 reductase; PDBTitle: the structure of human erythrocyte nadh-cytochrome b52 reductase
9	c1tvcA_	 Alignment		100.0	22	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	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
11	c2ok8D_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: putative ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp+ reductase from plasmodium falciparum

12	c1a8pA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph\;ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii
13	c1fncA_	Alignment		100.0	18	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	c1qgyA_	Alignment		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)
15	c1qfjD_	Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
16	c2bgjB_	Alignment		100.0	17	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
17	c1cneA_	Alignment		100.0	20	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
18	c2b5oA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
19	c1jb9A_	Alignment		100.0	23	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
20	c2rc5D_	Alignment		100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: refined structure of fnr from leptospira interrogans
21	c2gpiA_	Alignment	not modelled	100.0	11	PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (spu2cn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
22	c1ddiA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha- PDBTitle: crystal structure of sir-fp60
23	c1t1IA_	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	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
25	d1ep3b2	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: Dihydroorotate dehydrogenase B, PyrK subunit
26	c1f20A_	Alignment	not modelled	99.9	22	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	d2piaa2	Alignment	not modelled	99.9	37	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
28	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)

29	d1gvha3	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
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	16	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
32	c2qtzA_	Alignment	not modelled	99.9	21	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
33	d1krha2	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
34	d1cqxa3	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: Flavohemoglobin, C-terminal domain
35	c2bpoA_	Alignment	not modelled	99.9	23	PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
36	d1umka2	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: Reductases
37	d2piaa3	Alignment	not modelled	99.9	41	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
38	d2cnda2	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
39	d1qx4a2	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: Reductases
40	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
41	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)
42	d1a70a_	Alignment	not modelled	99.8	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
43	c3lrxC_	Alignment	not modelled	99.8	14	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
44	d1doia_	Alignment	not modelled	99.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
45	d2piaa1	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
46	d1offa_	Alignment	not modelled	99.8	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
47	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
48	d1iuea_	Alignment	not modelled	99.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
49	d1awda_	Alignment	not modelled	99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
50	d1frra_	Alignment	not modelled	99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
51	d1gvha2	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
52	d1fxia_	Alignment	not modelled	99.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
53	d1ndha2	Alignment	not modelled	99.8	23	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
54	d2bmwa2	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
						Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain

55	dlqfza2	Alignment	not modelled	99.8	17	Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
56	dlf20a2	Alignment	not modelled	99.8	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
57	dlfrda	Alignment	not modelled	99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
58	dlcqa2	Alignment	not modelled	99.8	26	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
59	dlpfda	Alignment	not modelled	99.8	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
60	dle0za	Alignment	not modelled	99.8	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
61	dlqx4a1	Alignment	not modelled	99.8	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
62	dlwria	Alignment	not modelled	99.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
63	dlczpa	Alignment	not modelled	99.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
64	dlgawa2	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
65	dlkrha1	Alignment	not modelled	99.8	27	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
66	d2cjoa	Alignment	not modelled	99.8	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
67	dlfnda2	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
68	dljb9a2	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
69	dliddga2	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: NADPH-cytochrome p450 reductase-like
70	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
71	dlumka1	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
72	dlfdra1	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
73	dlgaqb	Alignment	not modelled	99.7	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
74	dla8pa1	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
75	dlsm4a2	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
76	d4fxca	Alignment	not modelled	99.7	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
77	d1ndha1	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
78	d2bmwa1	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
79	dlja1a3	Alignment	not modelled	99.7	22	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
80	dltvca1	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	dlepb3l	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

82	dism4a1	Alignment	not modelled	99.7	20	Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
83	dljq4a	Alignment	not modelled	99.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
84	dlqfja1	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
85	dlkrha3	Alignment	not modelled	99.6	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
86	dlgawa1	Alignment	not modelled	99.6	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
87	dlfnda1	Alignment	not modelled	99.6	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
88	dlqfza1	Alignment	not modelled	99.6	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
89	dljb9a1	Alignment	not modelled	99.4	25	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	20	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	dli7ha	Alignment	not modelled	99.4	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
92	dl15pa	Alignment	not modelled	99.1	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
93	c2wlbB	Alignment	not modelled	99.0	15	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	18	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	dlxlqa1	Alignment	not modelled	98.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
96	c3lxfC	Alignment	not modelled	98.9	18	PDB header: metal binding protein Chain: C: PDB Molecule: ferredoxin; PDBTitle: crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
97	dle9ma	Alignment	not modelled	98.9	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
98	dlb9ra	Alignment	not modelled	98.8	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
99	d2bt6a1	Alignment	not modelled	98.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
100	d2fug33	Alignment	not modelled	98.2	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
101	cll6vA	Alignment	not modelled	97.9	15	PDB header: electron transport Chain: A: PDB Molecule: adrenodoxin 1; PDBTitle: structure of reduced bovine adrenodoxin
102	dliddga1	Alignment	not modelled	97.9	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
103	dl1t3qa2	Alignment	not modelled	97.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
104	dlv1ba2	Alignment	not modelled	97.7	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
105	clc4cA	Alignment	not modelled	97.7	19	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
106	dlffva2	Alignment	not modelled	97.7	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
107	d2bs2b2	Alignment	not modelled	97.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
108	dl1dgja2	Alignment	not modelled	97.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins

109	d3c8ya2	Alignment	not modelled	97.6	18	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	19	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
111	d1n62a2	Alignment	not modelled	97.6	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
112	d1rm6c2	Alignment	not modelled	97.4	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
113	c3hrdH_	Alignment	not modelled	97.4	21	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
114	c1n60D_	Alignment	not modelled	97.4	17	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
115	c1rm6F_	Alignment	not modelled	97.4	26	PDB header: oxidoreductase Chain: F: PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
116	d1kf6b2	Alignment	not modelled	97.3	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
117	c1ffuA_	Alignment	not modelled	97.3	16	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	c2h89B_	Alignment	not modelled	96.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
119	c1vlbA_	Alignment	not modelled	96.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
120	c2bs2E_	Alignment	not modelled	96.8	28	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes