

















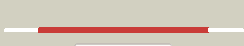



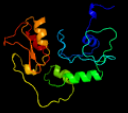










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0247c_(-)_298116_298862
Date	Tue Jul 23 14:50:31 BST 2019
Unique Job ID	36960ba8a0c80411

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xmjl_	 Alignment		100.0	27	PDB header: electron transport Chain: J; PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
2	c3vrbf_	 Alignment		100.0	23	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F; PDB Molecule: iron-sulfur subunit of succinate dehydrogenase; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
3	c2h89B_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: B; PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
4	c2bs2E_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: E; PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
5	c2b76N_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: N; PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
6	c1nekB_	 Alignment		100.0	27	PDB header: oxidoreductase/electron transport Chain: B; PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
7	d2bs2b2	 Alignment		100.0	35	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
8	d1kf6b2	 Alignment		100.0	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
9	d1nekb2	 Alignment		100.0	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
10	c5xf9F_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: F; PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
11	c1c4cA_	 Alignment		100.0	12	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 (cpl) from clostridium3 pasteurianum

12	c5lnk3	Alignment		100.0	16	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
13	c6gcsA	Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
14	c5ldxG	Alignment		100.0	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
15	c5ldwG	Alignment		100.0	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
16	c2fugC	Alignment		100.0	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
17	c5lc5G	Alignment		100.0	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
18	d1kfb1	Alignment		99.9	20	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
19	d1nekb1	Alignment		99.9	21	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
20	d2bs2b1	Alignment		99.8	22	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
21	d3c8ya2	Alignment	not modelled	99.6	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
22	c5g5ga	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative xanthine dehydrogenase yagt iron-sulfur-binding PDBTitle: escherichia coli periplasmic aldehyde oxidase
23	c5odcC	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
24	d1t3qa2	Alignment	not modelled	99.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
25	d1ffva2	Alignment	not modelled	99.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
26	d1rm6c2	Alignment	not modelled	99.5	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
27	d1dgja2	Alignment	not modelled	99.5	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
28	d1vlba2	Alignment	not modelled	99.5	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
						Fold: beta-Grasp (ubiquitin-like)

29	d1n62a2	Alignment	not modelled	99.5	19	Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
30	c1n60D	Alignment	not modelled	99.5	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
31	c5y6qA	Alignment	not modelled	99.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase small subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
32	c1rm6F	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: F: PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
33	c1t3qD	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
34	c3hrdH	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
35	c1ffuA	Alignment	not modelled	99.4	17	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
36	d2fug33	Alignment	not modelled	99.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
37	c4zohC	Alignment	not modelled	99.3	26	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
38	c3kwIA	Alignment	not modelled	99.2	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
39	c3b9jI	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: I: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
40	c3zyvA	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
41	d1jroa2	Alignment	not modelled	98.7	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
42	d1v97a2	Alignment	not modelled	98.6	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
43	c1vlbA	Alignment	not modelled	98.6	30	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
44	c4p6vA	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
45	c4uhxA	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
46	c2w3rG	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
47	c1dgiA	Alignment	not modelled	98.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
48	c3eubJ	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
49	d2fug34	Alignment	not modelled	98.5	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
50	d1czpa	Alignment	not modelled	98.4	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
51	d1frra	Alignment	not modelled	98.4	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
52	d1awda	Alignment	not modelled	98.4	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
53	d1offa	Alignment	not modelled	98.4	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
54	d1fxia	Alignment	not modelled	98.4	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like

						Family: 2Fe-2S ferredoxin-related
55	c3cf4A	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
56	d1iuea	Alignment	not modelled	98.4	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
57	d1doia	Alignment	not modelled	98.4	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
58	d1frda	Alignment	not modelled	98.3	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
59	d4fxca	Alignment	not modelled	98.3	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
60	d1e0za	Alignment	not modelled	98.3	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
61	d1pfda	Alignment	not modelled	98.3	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
62	d1a70a	Alignment	not modelled	98.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
63	d1gaqb	Alignment	not modelled	98.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
64	d1krha3	Alignment	not modelled	98.2	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
65	d1jq4a	Alignment	not modelled	98.1	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
66	c3zyyX	Alignment	not modelled	98.1	24	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
67	c1krhA	Alignment	not modelled	98.1	29	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray structure of benzoate dioxygenase reductase
68	c5ogxA	Alignment	not modelled	98.1	29	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
69	c1wygA	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
70	c5firtC	Alignment	not modelled	98.1	35	PDB header: oxidoreductase Chain: C: PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
71	d2c42a5	Alignment	not modelled	98.0	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
72	d2cjoa	Alignment	not modelled	98.0	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
73	c4itkA	Alignment	not modelled	98.0	18	PDB header: electron transport Chain: A: PDB Molecule: apoferredoxin; PDBTitle: the structure of c.reinhardtii ferredoxin 2
74	c4wqmA	Alignment	not modelled	98.0	26	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
75	c2wlbB	Alignment	not modelled	98.0	25	PDB header: electron transport Chain: B: PDB Molecule: electron transfer protein 1, mitochondrial; PDBTitle: adrenodoxin-like ferredoxin etp1fd(516-618) of schizosaccharomyces2 pombe mitochondria
76	c4n58A	Alignment	not modelled	98.0	30	PDB header: hydrolase Chain: A: PDB Molecule: pectocin m2; PDBTitle: crystal structure of pectocin m2 at 1.86 angstroms
77	d1wria	Alignment	not modelled	98.0	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
78	d1l5pa	Alignment	not modelled	98.0	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
79	c2y5cB	Alignment	not modelled	98.0	22	PDB header: electron transport Chain: B: PDB Molecule: adrenodoxin-like protein, mitochondrial; PDBTitle: structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster
80	d3c8ya3	Alignment	not modelled	97.9	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
						PDB header: electron transport

81	c5uj5A_	Alignment	not modelled	97.9	29	Chain: A: PDB Molecule: adrenodoxin; PDBTitle: solution structure of the oxidized iron-sulfur protein adrenodoxin2 from encephalitozoon cuniculi. seattle structural genomics center for3 infectious disease target encua.00705.a
82	c2mj3A_	Alignment	not modelled	97.9	21	PDB header: metal binding protein Chain: A: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments and structure of2 iron-sulfur cluster binding protein from ehrlichia chaffeensis
83	c6fahE_	Alignment	not modelled	97.9	39	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
84	c3lxfC_	Alignment	not modelled	97.8	17	PDB header: metal binding protein Chain: C: PDB Molecule: ferredoxin; PDBTitle: crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
85	c4ltuB_	Alignment	not modelled	97.8	16	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: crystal structure of ferredoxin from rhodopseudomonas palustris haa2
86	d1i7ha_	Alignment	not modelled	97.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
87	c3ah7A_	Alignment	not modelled	97.8	19	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
88	c2mjdA_	Alignment	not modelled	97.8	27	PDB header: metal binding protein Chain: A: PDB Molecule: adrenodoxin homolog, mitochondrial; PDBTitle: oxidized yeast adrenodoxin homolog 1
89	d2piaa3	Alignment	not modelled	97.8	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
90	c1gx7A_	Alignment	not modelled	97.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between cytochrome c3 and2 [fe]-hydrogenase
91	c5lc5I_	Alignment	not modelled	97.8	24	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
92	c3huiA_	Alignment	not modelled	97.7	30	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: crystal structure of the mutant a105r of [2fe-2s] ferredoxin in the2 class i cyp199a2 system from rhodopseudomonas palustris
93	c5t5iG_	Alignment	not modelled	97.7	17	PDB header: oxidoreductase Chain: G: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdg; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
94	c6gcsI_	Alignment	not modelled	97.7	22	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
95	d1b9ra_	Alignment	not modelled	97.7	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
96	c1hfeL_	Alignment	not modelled	97.7	31	PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.18.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
97	d1e9ma_	Alignment	not modelled	97.7	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
98	c4p6vF_	Alignment	not modelled	97.7	28	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
99	d1xlqa1	Alignment	not modelled	97.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
100	c5odhG_	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: G: PDB Molecule: heterodisulfide reductase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
101	c2piaA_	Alignment	not modelled	97.6	27	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]
102	c4heaO_	Alignment	not modelled	97.6	24	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
103	d2fug91	Alignment	not modelled	97.5	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
104	c2fugG_	Alignment	not modelled	97.5	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase chain 9; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
						Fold: Ferredoxin-like

105	d1jb0c_	Alignment	not modelled	97.5	24	Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
106	d2bt6a1	Alignment	not modelled	97.5	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
107	c5c4iB_	Alignment	not modelled	97.5	30	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
108	c3p1mG_	Alignment	not modelled	97.5	22	PDB header: electron transport Chain: G: PDB Molecule: adrenodoxin, mitochondrial; PDBTitle: crystal structure of human ferredoxin-1 (fdx1) in complex with iron-2 sulfur cluster
109	c6cfwN_	Alignment	not modelled	97.4	37	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
110	c2c3yA_	Alignment	not modelled	97.4	27	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of 2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
111	c6huml_	Alignment	not modelled	97.4	28	PDB header: proton transport Chain: I: PDB Molecule: nad(p)h-quinone oxidoreductase subunit i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
112	d1xera_	Alignment	not modelled	97.4	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
113	c6cipD_	Alignment	not modelled	97.4	23	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with 2 acetyl-tpg bound
114	d1bc6a_	Alignment	not modelled	97.3	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
115	d1hfel2	Alignment	not modelled	97.3	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
116	d1rgva_	Alignment	not modelled	97.2	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
117	d1gtea5	Alignment	not modelled	97.2	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
118	c2gmhA_	Alignment	not modelled	97.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
119	c5t5iN_	Alignment	not modelled	97.1	22	PDB header: oxidoreductase Chain: N: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from 2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
120	d1blua_	Alignment	not modelled	97.1	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins