



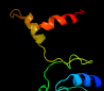






Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v2kB_	Alignment		99.9	61	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
2	d7fd1a_	Alignment		99.9	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
3	d1bc6a_	Alignment		99.9	47	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
4	d1h98a_	Alignment		99.9	49	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
5	c2ivfB_	Alignment		99.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
6	d1blua_	Alignment		99.7	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
7	c1qx7A_	Alignment		99.7	22	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
8	c4yddF_	Alignment		99.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: dms0 reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
9	d1clfa_	Alignment		99.7	40	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
10	c1ti2F_	Alignment		99.7	14	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
11	d1jnrb_	Alignment		99.7	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins

12	c2zvsB	Alignment		99.7	24	PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfhI; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
13	d1y5ib1	Alignment		99.7	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
14	d1fcaa	Alignment		99.7	42	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
15	c2fgoA	Alignment		99.7	23	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
16	c1hfeL	Alignment		99.7	22	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
17	c5odhG	Alignment		99.7	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
18	d2fdna	Alignment		99.6	40	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
19	d1rgva	Alignment		99.6	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
20	d1dura	Alignment		99.6	40	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
21	c6czaB	Alignment	not modelled	99.6	31	PDB header: oxidoreductase Chain: B: PDB Molecule: 4fe-4s ferredoxin, iron-sulfur binding domain protein; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate
22	c3gyxJ	Alignment	not modelled	99.6	34	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
23	c1gthD	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
24	c1c4cA	Alignment	not modelled	99.6	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
25	c1kqfB	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
26	c6btmB	Alignment	not modelled	99.6	20	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
27	d1kqfb1	Alignment	not modelled	99.6	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	c6fahE	Alignment	not modelled	99.6	36	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
29	c5c4iB	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
30	c6huml	Alignment	not modelled	99.6	17	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
31	c5t5iN	Alignment	not modelled	99.5	26	PDB header: oxidoreductase Chain: N: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
32	c6f0kB	Alignment	not modelled	99.5	17	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
33	d2fug91	Alignment	not modelled	99.5	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
34	c2fugG	Alignment	not modelled	99.5	36	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
35	c4heaO	Alignment	not modelled	99.5	34	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
36	c2gmhA	Alignment	not modelled	99.5	26	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
37	d1hfeI2	Alignment	not modelled	99.5	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
38	c5lc5I	Alignment	not modelled	99.5	38	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
39	c6gcsI	Alignment	not modelled	99.5	30	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
40	d2gmha3	Alignment	not modelled	99.5	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
41	c6cfwN	Alignment	not modelled	99.5	21	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
42	c2vpyB	Alignment	not modelled	99.4	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
43	c2c3yA	Alignment	not modelled	99.4	27	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
44	d1jb0c	Alignment	not modelled	99.4	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
45	c6cipD	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
46	d1gtea5	Alignment	not modelled	99.4	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
47	d1vlfN2	Alignment	not modelled	99.4	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
48	d1xera	Alignment	not modelled	99.4	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
49	d3c7bb1	Alignment	not modelled	99.3	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
50	d2c42a5	Alignment	not modelled	99.3	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
51	c5t5iG	Alignment	not modelled	99.3	39	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
52	d1h0hb	Alignment	not modelled	99.3	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
53	c4z3zE	Alignment	not modelled	99.2	29	PDB header: oxidoreductase Chain: E: PDB Molecule: iron-sulfur cluster-binding oxidoreductase, putative PDBTitle: active site complex bambc of benzoyl coenzyme a reductase in complex2 with zinc
						Fold: Ferredoxin-like

54	d3c8ya3	Alignment	not modelled	99.2	27	Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
55	c3c7bE	Alignment	not modelled	99.2	19	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
56	c2v4jE	Alignment	not modelled	99.1	23	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
57	c3c7bA	Alignment	not modelled	99.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
58	d1vjwa	Alignment	not modelled	99.1	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
59	c3j16B	Alignment	not modelled	99.1	27	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
60	d1iqza	Alignment	not modelled	99.0	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
61	c5xf9F	Alignment	not modelled	99.0	10	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [Nife]-hydrogenase in the air-2 oxidized state
62	d2fug34	Alignment	not modelled	99.0	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
63	c2v4jA	Alignment	not modelled	99.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
64	c1dwlA	Alignment	not modelled	98.9	28	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
65	c4id8A	Alignment	not modelled	98.9	18	PDB header: electron transport Chain: A: PDB Molecule: putative ferredoxin; PDBTitle: the crystal structure of a [3Fe-4s] ferredoxin associated with2 cyp194a4 from r. palustris haa2
66	c3bk7A	Alignment	not modelled	98.8	26	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-l inhibitor protein from2 pyrococcus abyssi
67	d1fxra	Alignment	not modelled	98.8	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
68	d1sj1a	Alignment	not modelled	98.8	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
69	c3zfsB	Alignment	not modelled	98.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
70	c5lc5G	Alignment	not modelled	98.5	20	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
71	c6gcsA	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
72	c5ldxG	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
73	c5ldwG	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
74	c5d0bB	Alignment	not modelled	98.4	25	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
75	c5d6sB	Alignment	not modelled	98.4	25	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
76	c5lnk3	Alignment	not modelled	98.3	18	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
77	c4rasC	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, nad-binding/iron-sulfur cluster-binding PDBTitle: reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
78	c2fugC	Alignment	not modelled	98.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3;

78	c2rfgC_	Alignment	not modelled	98.1	15	PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus Fold: Globin-like
79	d2bs2b1	Alignment	not modelled	98.1	16	Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
80	c4ur1A_	Alignment	not modelled	98.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: tetrachloroethene reductive dehalogenase catalytic subunit PDBTitle: crystal structure of the pce reductive dehalogenase from s.2 multivorans in complex with dibromoethene
81	c5odcC_	Alignment	not modelled	97.9	17	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
82	d1kf6b1	Alignment	not modelled	97.6	22	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
83	c2bs2E_	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
84	c1nekB_	Alignment	not modelled	97.6	25	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
85	d2v4jb1	Alignment	not modelled	97.6	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
86	c3cf4A_	Alignment	not modelled	97.5	27	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
87	d3c7ba1	Alignment	not modelled	97.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
88	d2v4ja1	Alignment	not modelled	97.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
89	d1nekb1	Alignment	not modelled	97.5	22	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
90	c2b76N_	Alignment	not modelled	97.4	22	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
91	c5xmjl_	Alignment	not modelled	97.1	24	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
92	c2h89B_	Alignment	not modelled	97.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
93	c3vrbf_	Alignment	not modelled	96.9	22	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
94	c4p6vA_	Alignment	not modelled	96.5	14	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
95	c4y1fD_	Alignment	not modelled	96.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase subunit a; PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
96	c2vdcI_	Alignment	not modelled	94.0	16	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
97	c5dqrA_	Alignment	not modelled	92.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: 7-hydroxymethyl chlorophyll a reductase, chloroplastic; PDBTitle: the crystal structure of arabidopsis 7-hydroxymethyl chlorophyll a2 reductase (hcar)
98	c5jcaL_	Alignment	not modelled	90.3	22	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
99	d1fxda_	Alignment	not modelled	82.9	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
100	d1gtea1	Alignment	not modelled	69.3	26	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
101	c4zxbE_	Alignment	not modelled	34.5	34	PDB header: hormone receptor/immune system Chain: E: PDB Molecule: insulin receptor; PDBTitle: structure of the human insulin receptor ectodomain,

