



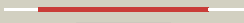






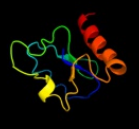





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2zvsB_</a>	 Alignment		99.9	100	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ferredoxin-like protein yfhI; <b>PDBTitle:</b> crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
2	<a href="#">d1blua_</a>	 Alignment		99.8	59	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
3	<a href="#">d1rgva_</a>	 Alignment		99.8	47	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
4	<a href="#">c2fgoA_</a>	 Alignment		99.8	54	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> structure of the 2[4fe-4s] ferredoxin from pseudomonas aeruginosa
5	<a href="#">d7fd1a_</a>	 Alignment		99.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
6	<a href="#">d1bc6a_</a>	 Alignment		99.7	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
7	<a href="#">c2vpyB_</a>	 Alignment		99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nrhc protein; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
8	<a href="#">c1ti2F_</a>	 Alignment		99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> pyrogallol hydroxytransferase small subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
9	<a href="#">c2ivfB_</a>	 Alignment		99.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
10	<a href="#">c1kqfB_</a>	 Alignment		99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
11	<a href="#">d1fcaa_</a>	 Alignment		99.6	45	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins

12	<a href="#">d1h98a_</a>	Alignment		99.6	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
13	<a href="#">c2v2kB_</a>	Alignment		99.6	23	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
14	<a href="#">d1clfa_</a>	Alignment		99.6	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
15	<a href="#">d2fdna_</a>	Alignment		99.6	46	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
16	<a href="#">c2fugG_</a>	Alignment		99.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 9; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
17	<a href="#">c1gthD_</a>	Alignment		99.6	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
18	<a href="#">d2fug91</a>	Alignment		99.6	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
19	<a href="#">d1h0hb_</a>	Alignment		99.5	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
20	<a href="#">d1kqfb1</a>	Alignment		99.5	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
21	<a href="#">d1dura_</a>	Alignment	not modelled	99.5	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
22	<a href="#">d1vlfn2</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
23	<a href="#">d1jb0c_</a>	Alignment	not modelled	99.5	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
24	<a href="#">d1jnrb_</a>	Alignment	not modelled	99.4	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
25	<a href="#">c3gyxl_</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> adenylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
26	<a href="#">c2gmhA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
27	<a href="#">d1gtea5</a>	Alignment	not modelled	99.4	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
28	<a href="#">d1hfel2</a>	Alignment	not modelled	99.4	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [fe] hydrogenase large

29	<a href="#">c1qx7A_</a>	Alignment	not modelled	99.4	30	subunit; <b>PDBTitle:</b> best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
30	<a href="#">d1xera_</a>	Alignment	not modelled	99.3	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Archaeal ferredoxins
31	<a href="#">c2c3yA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
32	<a href="#">d1y5b1_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
33	<a href="#">d2c42a5_</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
34	<a href="#">c1hfeL_</a>	Alignment	not modelled	99.2	28	<b>PDB header:</b> hydrogenase <b>Chain:</b> L: <b>PDB Molecule:</b> protein (fe-only hydrogenase (e.c.1.18.99.1) <b>PDBTitle:</b> 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
35	<a href="#">d3c8ya3_</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
36	<a href="#">d2gmha3_</a>	Alignment	not modelled	99.1	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> ETF-QO domain-like
37	<a href="#">d1vjwa_</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
38	<a href="#">d2fug34_</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
39	<a href="#">d1iqza_</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
40	<a href="#">d3c7bb1_</a>	Alignment	not modelled	98.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
41	<a href="#">d1sj1a_</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
42	<a href="#">c3c7bE_</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
43	<a href="#">c1c4cA_</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fe-only hydrogenase); <b>PDBTitle:</b> binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
44	<a href="#">c1dw1A_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> electron transfer <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin i; <b>PDBTitle:</b> the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
45	<a href="#">c3c7bA_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	<a href="#">c2v4jE_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
47	<a href="#">c2v4jA_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
48	<a href="#">d1fxra_</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
49	<a href="#">c2fugC_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
50	<a href="#">c3bk7A_</a>	Alignment	not modelled	98.2	32	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
51	<a href="#">d2bs2b1_</a>	Alignment	not modelled	97.2	27	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
52	<a href="#">d1kf6b1_</a>	Alignment	not modelled	97.0	33	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	<a href="#">c1nekB_</a>	Alignment	not modelled	96.9	29	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur protein;

						<b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
54	<a href="#">d1nekb1</a>	Alignment	not modelled	96.9	30	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
55	<a href="#">c2b76N</a>	Alignment	not modelled	96.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> fumarate reductase iron-sulfur protein; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda e49q mutation
56	<a href="#">c2bs2E</a>	Alignment	not modelled	96.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b; <b>PDBTitle:</b> quinol:fumarate reductase from wolinetella succinogenes
57	<a href="#">d3c7ba1</a>	Alignment	not modelled	96.7	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
58	<a href="#">d2v4ja1</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
59	<a href="#">d2v4jb1</a>	Alignment	not modelled	96.5	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
60	<a href="#">c2h89B</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase ip subunit; <b>PDBTitle:</b> avian respiratory complex ii with malonate bound
61	<a href="#">c3cf4A</a>	Alignment	not modelled	96.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase alpha subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
62	<a href="#">d1fxda</a>	Alignment	not modelled	90.7	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
63	<a href="#">c2vdcl</a>	Alignment	not modelled	68.9	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
64	<a href="#">d1g8ka2</a>	Alignment	not modelled	20.7	17	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
65	<a href="#">c1igrA</a>	Alignment	not modelled	17.2	23	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> insulin-like growth factor receptor 1; <b>PDBTitle:</b> type 1 insulin-like growth factor receptor (domains 1-3)
66	<a href="#">d1gtea1</a>	Alignment	not modelled	10.8	33	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Dihydropyrimidine dehydrogenase, N-terminal domain
67	<a href="#">c1g8jC</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
68	<a href="#">c3ag7A</a>	Alignment	not modelled	8.2	15	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein f9e10.5; <b>PDBTitle:</b> an auxilin-like j-domain containing protein, jac1 j-domain
69	<a href="#">c2npbA</a>	Alignment	not modelled	7.5	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> selenoprotein w; <b>PDBTitle:</b> nmr solution structure of mouse selw
70	<a href="#">d2apob1</a>	Alignment	not modelled	7.5	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
71	<a href="#">d1nz6a</a>	Alignment	not modelled	7.0	26	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
72	<a href="#">d2ey4e1</a>	Alignment	not modelled	7.0	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
73	<a href="#">c1eu1A</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
74	<a href="#">c2a91A</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> signaling protein,transferase,membrane p <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> crystal structure of erbb2 domains 1-3
75	<a href="#">d1kbsa</a>	Alignment	not modelled	6.7	42	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins
76	<a href="#">d2vgna1</a>	Alignment	not modelled	6.4	20	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Dom34/Pelota N-terminal domain-like <b>Family:</b> Dom34/Pelota N-terminal domain-like
77	<a href="#">d1cdta</a>	Alignment	not modelled	6.0	42	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins
78	<a href="#">d2cdxa</a>	Alignment	not modelled	5.5	42	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins