



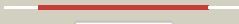

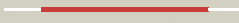


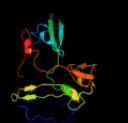





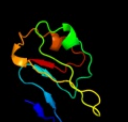








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fugG_	 Alignment		99.9	42	PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase chain 9; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
2	d2fug91	 Alignment		99.9	42	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
3	c1kqfB_	 Alignment		99.8	22	PDB header: oxidoreductase Chain: B; PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
4	d1y5ib1	 Alignment		99.8	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
5	d1kqfb1	 Alignment		99.7	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
6	c2ivfB_	 Alignment		99.7	29	PDB header: oxidoreductase Chain: B; PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
7	c2vpyB_	 Alignment		99.7	23	PDB header: oxidoreductase Chain: B; PDB Molecule: nrhc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
8	d1xera_	 Alignment		99.7	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
9	d2fug34	 Alignment		99.7	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
10	d1h0hb_	 Alignment		99.7	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
11	c1ti2F_	 Alignment		99.7	16	PDB header: oxidoreductase Chain: F; PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol 2 transhydroxylase from pelobacter acidigallici

12	c1gthD_	Alignment		99.6	20	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
13	c2gmhA_	Alignment		99.6	17	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
14	d1hfel2	Alignment		99.6	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
15	c2c3yA_	Alignment		99.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
16	d7fd1a_	Alignment		99.6	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
17	d1gtea5	Alignment		99.6	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
18	c2fugC_	Alignment		99.6	15	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
19	c3gyxl_	Alignment		99.6	23	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
20	d1h98a_	Alignment		99.6	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
21	d1jb0c_	Alignment	not modelled	99.6	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
22	d3c8ya3	Alignment	not modelled	99.6	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
23	d2gmha3	Alignment	not modelled	99.6	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
24	d1bc6a_	Alignment	not modelled	99.6	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
25	c1hfeL_	Alignment	not modelled	99.5	27	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
26	d1dura_	Alignment	not modelled	99.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
27	d2c42a5	Alignment	not modelled	99.5	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	d1jnrb_	Alignment	not modelled	99.5	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
						PDB header: electron transport

29	c2zvsB_	Alignment	not modelled	99.5	23	Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfhI; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
30	d2fdna_	Alignment	not modelled	99.5	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
31	d1rgva_	Alignment	not modelled	99.5	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
32	d1vlfm2	Alignment	not modelled	99.5	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
33	d1blua_	Alignment	not modelled	99.5	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
34	c1gx7A_	Alignment	not modelled	99.5	32	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
35	d1fcaa_	Alignment	not modelled	99.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	c1c4cA_	Alignment	not modelled	99.5	20	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
37	d1clfa_	Alignment	not modelled	99.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
38	c2fgoA_	Alignment	not modelled	99.5	28	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
39	d1vjwa_	Alignment	not modelled	99.4	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
40	c2v2kB_	Alignment	not modelled	99.4	23	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
41	d1iqza_	Alignment	not modelled	99.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
42	d1sj1a_	Alignment	not modelled	99.4	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
43	c3c7bE_	Alignment	not modelled	99.2	26	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
44	d3c7bb1	Alignment	not modelled	99.2	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
45	c1dwlA_	Alignment	not modelled	99.2	21	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
46	d1fxra_	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
47	c2v4jE_	Alignment	not modelled	99.2	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
48	c3c7bA_	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
49	c2v4jA_	Alignment	not modelled	98.9	19	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
50	c3bk7A_	Alignment	not modelled	98.6	25	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
51	d1kf6b1	Alignment	not modelled	98.4	21	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
52	d2bs2b1	Alignment	not modelled	98.4	14	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	c2b76N_	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein;

						PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
54	c1nekB_	Alignment	not modelled	98.3	23	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
55	c2bs2E_	Alignment	not modelled	98.3	24	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinetella succinogenes
56	c2h89B_	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
57	d1nekb1	Alignment	not modelled	98.0	34	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
58	c3cf4A_	Alignment	not modelled	97.5	31	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
59	d2v4jb1	Alignment	not modelled	97.4	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
60	d2v4ja1	Alignment	not modelled	93.1	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
61	d3c7ba1	Alignment	not modelled	93.0	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
62	d1fxda_	Alignment	not modelled	87.7	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
63	c2vdcl_	Alignment	not modelled	84.2	18	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
64	c1g8jC_	Alignment	not modelled	61.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
65	c1igrA_	Alignment	not modelled	32.3	25	PDB header: hormone receptor Chain: A: PDB Molecule: insulin-like growth factor receptor 1; PDBTitle: type 1 insulin-like growth factor receptor (domains 1-3)
66	d1i6ua_	Alignment	not modelled	20.3	13	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
67	c3rf2A_	Alignment	not modelled	19.4	26	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8; PDBTitle: crystal structure of 30s ribosomal protein s8 from aquifex aeolicus
68	d1gtea1	Alignment	not modelled	16.0	20	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
69	d2gy9h1	Alignment	not modelled	14.6	22	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
70	c3bbnH_	Alignment	not modelled	13.9	17	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
71	d1an7a_	Alignment	not modelled	13.1	17	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
72	c2xznH_	Alignment	not modelled	13.0	13	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
73	d1seia_	Alignment	not modelled	12.1	22	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
74	d1i94h_	Alignment	not modelled	12.1	17	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
75	c1s1hH_	Alignment	not modelled	11.7	22	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s22; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
76	d1ogyb_	Alignment	not modelled	11.0	15	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
77	c2bpbB_	Alignment	not modelled	10.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
78	c1moxB_	Alignment	not modelled	10.6	19	PDB header: transferase/growth factor Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: crystal structure of human epidermal growth factor receptor (residues2 1-501) in complex with tgf-alpha

