





















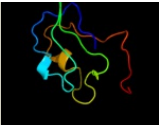


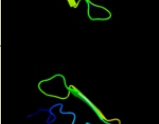
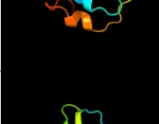
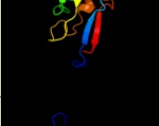





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ti2F_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
2	c1kqfB_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
3	c2vpyB_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: nrhc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
4	d1kqfb1	 Alignment		100.0	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
5	d1h0hb_	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
6	c2ivfB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
7	d1vlfm2	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
8	d1y5ib1	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
9	d1blua_	 Alignment		99.7	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
10	d1rgva_	 Alignment		99.7	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
11	c2fgoA_	 Alignment		99.6	22	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4Fe-4S] ferredoxin from pseudomonas2 aeruginosa

12	c2zvsB_	Alignment		99.6	23	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	d1xera_	Alignment		99.6	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
14	d2fug91	Alignment		99.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
15	c2fugG_	Alignment		99.5	32	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
16	c1gthD_	Alignment		99.5	16	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
17	d1hfel2	Alignment		99.5	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
18	c2gmhA_	Alignment		99.4	16	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
19	c3gyxl_	Alignment		99.4	27	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
20	d3c8ya3	Alignment		99.4	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
21	d1jnrb_	Alignment	not modelled	99.4	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
22	d1jb0c_	Alignment	not modelled	99.4	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
23	d7fd1a_	Alignment	not modelled	99.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
24	c1hfeL_	Alignment	not modelled	99.4	18	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
25	c2c3yA_	Alignment	not modelled	99.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
26	d1gtea5	Alignment	not modelled	99.4	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
27	d2fug34	Alignment	not modelled	99.4	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	d2c42a5	Alignment	not modelled	99.3	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
29	d2fdna_	Alignment	not modelled	99.3	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins

					Family: Short-chain ferredoxins
30	d1dura_	Alignment	not modelled	99.3	28 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
31	d1iqza_	Alignment	not modelled	99.3	19 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
32	d1fcaa_	Alignment	not modelled	99.3	33 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
33	d1bc6a_	Alignment	not modelled	99.3	25 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
34	c1gx7A_	Alignment	not modelled	99.3	24 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	d2gmha3	Alignment	not modelled	99.2	14 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
36	d1h98a_	Alignment	not modelled	99.2	27 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
37	d1clfa_	Alignment	not modelled	99.2	25 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
38	d1sj1a_	Alignment	not modelled	99.2	21 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
39	d1vjwa_	Alignment	not modelled	99.2	23 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
40	c1c4cA_	Alignment	not modelled	99.2	22 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
41	c2v2kB_	Alignment	not modelled	99.1	24 PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
42	d1fxra_	Alignment	not modelled	99.0	26 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
43	d3c7bb1	Alignment	not modelled	99.0	22 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
44	c1dwlA_	Alignment	not modelled	98.9	26 PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
45	c3c7bE_	Alignment	not modelled	98.9	13 PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	c2fugC_	Alignment	not modelled	98.9	20 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
47	c2v4jE_	Alignment	not modelled	98.7	10 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	c2v4iA_	Alignment	not modelled	98.4	16 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
49	c3c7bA_	Alignment	not modelled	98.4	19 PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
50	c3bk7A_	Alignment	not modelled	98.4	20 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	d2bs2b1	Alignment	not modelled	98.2	17 Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
52	d1kf6b1	Alignment	not modelled	98.1	13 Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	d1nekb1	Alignment	not modelled	98.0	17 Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain PDB header: oxidoreductase/electron transport

54	c1nekB_	Alignment	not modelled	98.0	18	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	98.0	25	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	97.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
57	c2b76N_	Alignment	not modelled	97.5	21	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
58	c3cf4A_	Alignment	not modelled	96.7	30	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	95.2	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
60	d3c7ba1	Alignment	not modelled	94.3	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
61	d2v4ja1	Alignment	not modelled	94.1	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
62	d1fxda_	Alignment	not modelled	91.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
63	c2vdcl_	Alignment	not modelled	91.1	18	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadh] 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	d1gtea1	Alignment	not modelled	60.6	15	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
65	c3ktbD_	Alignment	not modelled	11.8	22	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
66	d1g8ka2	Alignment	not modelled	10.7	11	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
67	d1djqa3	Alignment	not modelled	8.4	40	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
68	c2eqpA_	Alignment	not modelled	7.3	45	PDB header: transcription Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the stn_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
69	c2kn0A_	Alignment	not modelled	7.0	45	PDB header: apoptosis Chain: A: PDB Molecule: fn14; PDBTitle: solution nmr structure of xenopus fn14