


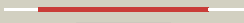










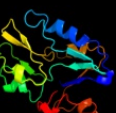






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ti2F_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
2	c2ivfB_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
3	c1kqfB_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
4	d1kqfb1	 Alignment		100.0	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
5	c2vpyB_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
6	d1h0hb_	 Alignment		100.0	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
7	d1vlfn2	 Alignment		100.0	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
8	d1y5ib1	 Alignment		100.0	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
9	d7fd1a_	 Alignment		99.5	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
10	c3gyxl_	 Alignment		99.4	25	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
11	c2v2kB_	 Alignment		99.4	22	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis

12	c2zvsB_	Alignment		99.4	25	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	d1h98a_	Alignment		99.4	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
14	d1bc6a_	Alignment		99.4	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
15	c1gthD_	Alignment		99.3	26	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
16	d3c8ya3	Alignment		99.3	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
17	d2fug91	Alignment		99.3	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
18	c2fugG_	Alignment		99.3	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
19	d1blua_	Alignment		99.3	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
20	c2fgoA_	Alignment		99.2	29	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
21	d1rgva_	Alignment	not modelled	99.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
22	d1hfel2	Alignment	not modelled	99.2	41	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
23	d2fug34	Alignment	not modelled	99.2	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
24	d1gtea5	Alignment	not modelled	99.2	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
25	d1xera_	Alignment	not modelled	99.2	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
26	d2c42a5	Alignment	not modelled	99.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
27	d1jnrb_	Alignment	not modelled	99.1	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	d3c7bb1	Alignment	not modelled	99.1	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
29	d1clfa_	Alignment	not modelled	99.1	41	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins

30	d2gmha3	Alignment	not modelled	99.1	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
31	c2gmhA	Alignment	not modelled	99.0	22	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
32	c1gx7A	Alignment	not modelled	99.0	43	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
33	d1iqza	Alignment	not modelled	99.0	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
34	d2fdna	Alignment	not modelled	99.0	39	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
35	d1jb0c	Alignment	not modelled	99.0	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
36	d1fcaa	Alignment	not modelled	99.0	35	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
37	c1c4cA	Alignment	not modelled	99.0	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
38	d1dura	Alignment	not modelled	99.0	35	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
39	c1hfeL	Alignment	not modelled	99.0	28	PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.1.8.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
40	c2fugC	Alignment	not modelled	99.0	19	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
41	c2c3yA	Alignment	not modelled	98.9	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
42	d1vjwa	Alignment	not modelled	98.8	38	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
43	d1sj1a	Alignment	not modelled	98.5	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
44	c1dw1A	Alignment	not modelled	98.5	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	98.5	17	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	d1fxra	Alignment	not modelled	98.3	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
47	c3bk7A	Alignment	not modelled	98.2	40	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
48	c2v4jA	Alignment	not modelled	98.2	15	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	c2v4jE	Alignment	not modelled	98.2	24	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
50	c3c7bA	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	d2bs2b1	Alignment	not modelled	97.6	21	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
52	d1nekb1	Alignment	not modelled	97.6	17	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	d1kf6b1	Alignment	not modelled	97.5	21	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	97.4	17	Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
55	c2h89B_	Alignment	not modelled	97.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
56	c2b76N_	Alignment	not modelled	96.8	17	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
57	c2bs2E_	Alignment	not modelled	96.7	22	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinetella succinogenes
58	d2v4jb1	Alignment	not modelled	96.3	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
59	c3cf4A_	Alignment	not modelled	96.2	32	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
60	d3c7ba1	Alignment	not modelled	93.7	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
61	d2v4ja1	Alignment	not modelled	93.4	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
62	c2vdcl_	Alignment	not modelled	84.0	19	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.
63	d1gtea1	Alignment	not modelled	50.0	41	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
64	d1fxda_	Alignment	not modelled	44.7	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
65	c2a91A_	Alignment	not modelled	24.6	27	PDB header: signaling protein,transferase,membrane p Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: crystal structure of erbb2 domains 1-3
66	d1djqa3	Alignment	not modelled	17.6	33	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
67	d2r4qa1	Alignment	not modelled	11.7	32	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
68	c1moxB_	Alignment	not modelled	9.4	32	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
69	d2hfqa1	Alignment	not modelled	8.9	19	Fold: NE1680-like Superfamily: NE1680-like Family: NE1680-like
70	c2hfqa_	Alignment	not modelled	8.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
71	d2r48a1	Alignment	not modelled	7.8	23	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
72	c2eqpA_	Alignment	not modelled	7.3	27	PDB header: transcription Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the str_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
73	d2i76a2	Alignment	not modelled	5.9	5	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
74	c2kn0A_	Alignment	not modelled	5.7	27	PDB header: apoptosis Chain: A: PDB Molecule: fn14; PDBTitle: solution nmr structure of xenopus fn14