


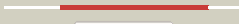



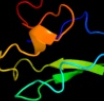













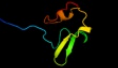
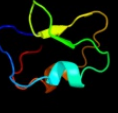





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gmha3	 Alignment		99.7	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
2	c2gmhA_	 Alignment		99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
3	c2ivfB_	 Alignment		99.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
4	d1y5ib1	 Alignment		99.5	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
5	d7fd1a_	 Alignment		99.4	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
6	d1bc6a_	 Alignment		99.4	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
7	c1ti2F_	 Alignment		99.4	12	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
8	c1gthD_	 Alignment		99.4	17	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
9	c3gyxJ_	 Alignment		99.3	17	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
10	d1hfel2	 Alignment		99.3	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
11	d1h98a_	 Alignment		99.3	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin

12	c1hfeL_	Alignment		99.3	13	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
13	c1gx7A_	Alignment		99.3	17	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
14	c2fugG_	Alignment		99.3	23	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
15	d2fug91	Alignment		99.3	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
16	c1kqfB_	Alignment		99.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
17	d1jnrb_	Alignment		99.3	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
18	d3c7bb1	Alignment		99.2	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
19	d1kqfb1	Alignment		99.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
20	d1xera_	Alignment		99.2	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
21	d1fcaa_	Alignment	not modelled	99.2	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
22	c2v2kB_	Alignment	not modelled	99.2	15	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
23	d2fdna_	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
24	d1dura_	Alignment	not modelled	99.2	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
25	c2vpyB_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
26	d1clfa_	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
27	d3c8ya3	Alignment	not modelled	99.1	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	c2zvsB_	Alignment	not modelled	99.1	20	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
29	d1jb0c_	Alignment	not modelled	99.1	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins

					Family: 7-Fe ferredoxin
30	d1gtea5	Alignment	not modelled	99.1	17 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
31	c2c3yA	Alignment	not modelled	99.1	22 PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of 2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
32	d1vlfn2	Alignment	not modelled	99.0	13 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
33	d1blua	Alignment	not modelled	99.0	19 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
34	d2fug34	Alignment	not modelled	99.0	14 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
35	d1rgva	Alignment	not modelled	99.0	17 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	c2fgoA	Alignment	not modelled	99.0	22 PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4Fe-4S] ferredoxin from pseudomonas2 aeruginosa
37	c1c4cA	Alignment	not modelled	98.9	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	c3bk7A	Alignment	not modelled	98.9	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
39	c3c7bE	Alignment	not modelled	98.9	25 PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
40	d1h0hb	Alignment	not modelled	98.9	7 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
41	d2c42a5	Alignment	not modelled	98.8	21 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
42	c3c7bA	Alignment	not modelled	98.8	25 PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
43	c2v4jE	Alignment	not modelled	98.7	17 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
44	d1iqza	Alignment	not modelled	98.7	15 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
45	d1vjwa	Alignment	not modelled	98.7	11 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
46	c2v4jA	Alignment	not modelled	98.6	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
47	c1dlwA	Alignment	not modelled	98.5	11 PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
48	c2fugC	Alignment	not modelled	98.4	14 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
49	d1sj1a	Alignment	not modelled	98.3	11 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
50	d1fxra	Alignment	not modelled	98.1	12 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
51	d2v4jb1	Alignment	not modelled	97.5	22 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
52	d1kf6b1	Alignment	not modelled	96.6	28 Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	d2bs2b1	Alignment	not modelled	96.3	22 Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
54	c2b76N	Alignment	not modelled	96.2	19 PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein;

						PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
55	d1nekb1	Alignment	not modelled	95.9	24	Fold:Globin-like Superfamily:alpha-helical ferredoxin Family:Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain PDB header:oxidoreductase Chain: E: PDB Molecule:quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinelia succinogenes
57	d3c7ba1	Alignment	not modelled	95.8	32	Fold:Ferredoxin-like Superfamily:4Fe-4S ferredoxins Family:Ferredoxin domains from multidomain proteins
58	d2v4ja1	Alignment	not modelled	95.8	26	Fold:Ferredoxin-like Superfamily:4Fe-4S ferredoxins Family:Ferredoxin domains from multidomain proteins
59	c1nekB_	Alignment	not modelled	95.7	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
60	c2h89B_	Alignment	not modelled	95.1	19	PDB header:oxidoreductase Chain: B: PDB Molecule:succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
61	c3cf4A_	Alignment	not modelled	95.1	24	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
62	c2vdcl_	Alignment	not modelled	79.4	35	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.
63	d1gtea1	Alignment	not modelled	25.9	29	Fold:Globin-like Superfamily:alpha-helical ferredoxin Family:Dihydropyrimidine dehydrogenase, N-terminal domain
64	c1g8jC_	Alignment	not modelled	24.9	24	PDB header:oxidoreductase Chain: C: PDB Molecule:arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
65	d1g8ka2	Alignment	not modelled	21.1	19	Fold:Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily:Formate dehydrogenase/DMSO reductase, domains 1-3 Family:Formate dehydrogenase/DMSO reductase, domains 1-3
66	d1fxda_	Alignment	not modelled	15.0	21	Fold:Ferredoxin-like Superfamily:4Fe-4S ferredoxins Family:Single 4Fe-4S cluster ferredoxin
67	c2pmzS_	Alignment	not modelled	14.6	22	PDB header:translation, transferase Chain: S: PDB Molecule:dna-directed rna polymerase subunit d; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
68	d1fra1	Alignment	not modelled	11.7	18	Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase
69	d2o5ha1	Alignment	not modelled	11.0	14	Fold:NMB0513-like Superfamily:NMB0513-like Family:NMB0513-like
70	d1m5ha1	Alignment	not modelled	10.9	14	Fold:Ferredoxin-like Superfamily:Formylmethanofuran:tetrahydromethanopterin formyltransferase Family:Formylmethanofuran:tetrahydromethanopterin formyltransferase
71	c2qasA_	Alignment	not modelled	10.1	20	PDB header:hydrolase activator Chain: A: PDB Molecule:hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus ssfb ortholog
72	c2fhjd_	Alignment	not modelled	9.6	18	PDB header:transferase Chain: D: PDB Molecule:formylmethanofuran--tetrahydromethanopterin PDBTitle: crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
73	c2esyA_	Alignment	not modelled	8.4	67	PDB header:lipid binding protein Chain: A: PDB Molecule:lung surfactant protein c; PDBTitle: structure and influence on stability and activity of the n-2 terminal propetide part of lung surfactant protein c
74	c2qazC_	Alignment	not modelled	7.8	21	PDB header:hydrolase activator Chain: C: PDB Molecule:ssfb protein; PDBTitle: structure of c. crescentus ssfb ortholog
75	c2fuga_	Alignment	not modelled	7.7	27	PDB header:oxidoreductase Chain: A: PDB Molecule:nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
76	d2nysa1	Alignment	not modelled	7.1	16	Fold:SspB-like Superfamily:SspB-like Family:AGR C 3712p-like
77	c2nysA_	Alignment	not modelled	7.1	16	PDB header:structural genomics, unknown function Chain: A: PDB Molecule:agr_c_3712p; PDBTitle: x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
78	d1h6ua1	Alignment	not modelled	6.2	6	Fold:Immunoglobulin-like beta-sandwich Superfamily:E set domains Family:Internalin Ig-like domain
						Fold:SspB-like

79	dlou9a_	Alignment	not modelled	6.2	11	Superfamily: SspB-like Family: Stringent starvation protein B, SspB
80	cligrA	Alignment	not modelled	5.9	23	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)
81	dlzszc1	Alignment	not modelled	5.7	11	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
82	dlh6ta1	Alignment	not modelled	5.5	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
83	dlfjra_	Alignment	not modelled	5.3	12	Fold: Methuselah ectodomain Superfamily: Methuselah ectodomain Family: Methuselah ectodomain
84	cly88A	Alignment	not modelled	5.2	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1548; PDBTitle: crystal structure of protein of unknown function af1548