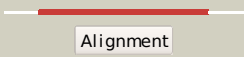
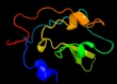
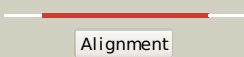

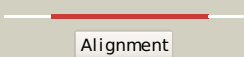

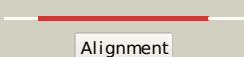
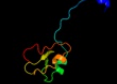
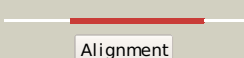

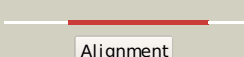
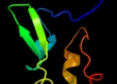
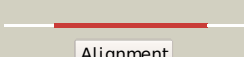

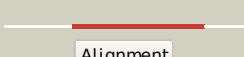

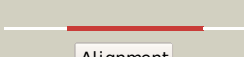

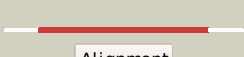
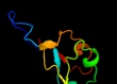





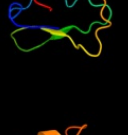
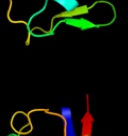
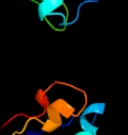
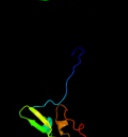

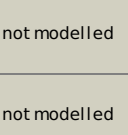


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gmha3	 Alignment		99.8	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
2	c2gmhA_	 Alignment		99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
3	c2ivfB_	 Alignment		99.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
4	d1y5ib1	 Alignment		99.4	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
5	c1gthD_	 Alignment		99.3	9	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
6	c1ti2F_	 Alignment		99.3	12	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
7	d1hfeL2	 Alignment		99.3	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
8	d7fd1a_	 Alignment		99.3	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
9	c3gyxJ_	 Alignment		99.2	19	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
10	c1hfeL_	 Alignment		99.2	10	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
11	d3c7bb1	 Alignment		99.2	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins

12	c2fugG_	Alignment		99.2	22	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
13	d2fug91	Alignment		99.2	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
14	d1jnrb_	Alignment		99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
15	d1bc6a_	Alignment		99.2	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
16	d1h98a_	Alignment		99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
17	c1gx7A_	Alignment		99.2	12	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
18	dlxera_	Alignment		99.2	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
19	c1kqfB_	Alignment		99.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
20	d1kqfb1	Alignment		99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
21	c3bk7A_	Alignment	not modelled	99.1	22	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein2 from pyrococcus abyssi
22	c2vpyB_	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nrhc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
23	d3c8ya3	Alignment	not modelled	99.1	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
24	d1fcaa_	Alignment	not modelled	99.1	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
25	d2fdna_	Alignment	not modelled	99.1	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
26	d1gtea5	Alignment	not modelled	99.1	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
27	c2c3yA_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
28	c2v2kB_	Alignment	not modelled	99.1	16	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
						Fold: Ferredoxin-like

54	d1kf6b1	Alignment	not modelled	96.3	23	Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
55	d2bs2b1	Alignment	not modelled	96.2	17	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
56	d1nekB1	Alignment	not modelled	95.7	15	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
57	c2bs2E_	Alignment	not modelled	95.5	14	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
58	c1nekB_	Alignment	not modelled	95.4	15	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
59	c2b76N_	Alignment	not modelled	95.1	25	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
60	c3cf4A_	Alignment	not modelled	94.7	17	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
61	c2h89B_	Alignment	not modelled	87.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
62	d1fxda_	Alignment	not modelled	79.8	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
63	c2vdcl_	Alignment	not modelled	68.5	29	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	37.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
65	c2pmzS_	Alignment	not modelled	25.7	22	PDB header: translation, transferase Chain: S: PDB Molecule: dna-directed rna polymerase subunit d; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
66	d1g8ka2	Alignment	not modelled	17.3	17	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	d1gtea1	Alignment	not modelled	15.6	24	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
68	d1h6ua1	Alignment	not modelled	14.9	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
69	d1h6ta1	Alignment	not modelled	11.7	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
70	d1j9ia_	Alignment	not modelled	10.6	40	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
71	d2omza1	Alignment	not modelled	10.2	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
72	c1igrA_	Alignment	not modelled	8.2	24	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)
73	d1qpma_	Alignment	not modelled	6.2	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like