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Description	P0AF59
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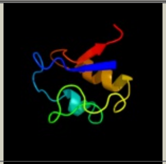
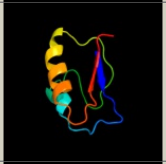
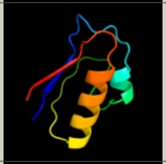
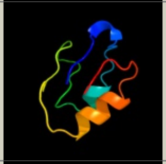
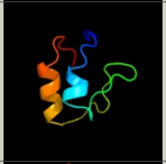
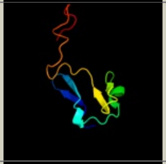
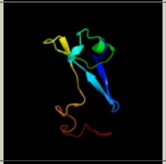
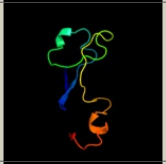
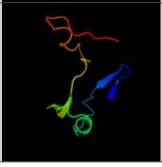
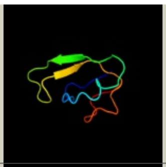
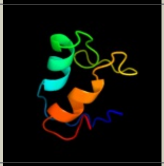
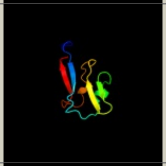
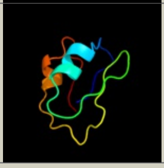
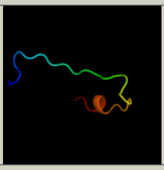
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fxra_	Alignment		99.5	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
2	d1iqza_	Alignment		99.3	12	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
3	d1sj1a_	Alignment		99.3	15	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
4	c1dwlA_	Alignment		99.2	16	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
5	d1vjwa_	Alignment		99.1	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
6	d1fxda_	Alignment		98.4	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
7	c1kqfB_	Alignment		97.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
8	d1kqfb1	Alignment		97.7	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c1ti2F_	Alignment		97.6	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
10	d1gtea5	Alignment		97.6	11	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
11	c2vpyB_	Alignment		97.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)

12	d1xera_	Alignment		97.4	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
13	d2fug34	Alignment		97.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
14	c1gthD_	Alignment		97.3	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
15	c3gyxJ_	Alignment		97.2	24	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
16	c1c4cA_	Alignment		97.2	25	**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
17	c2fugC_	Alignment		97.2	28	**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
18	d3c8ya3	Alignment		97.2	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
19	d1vlfn2	Alignment		96.9	10	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	d1jnrb_	Alignment		96.9	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
21	c2ivfB_	Alignment	not modelled	96.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
22	d1h0hb_	Alignment	not modelled	96.8	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
23	d2fug91	Alignment	not modelled	96.6	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
24	c2fugG_	Alignment	not modelled	96.6	14	**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
25	c2c3yA_	Alignment		96.5	29	**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	d1hfel2	Alignment	not modelled	96.2	15	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
27	d1jb0c_	Alignment	not modelled	96.1	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
						PDB header:hydrogenase

28	c1hfeL_	Alignment	not modelled	96.1	15	**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
29	d1dura_	Alignment	not modelled	96.0	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
30	c1gx7A_	Alignment	not modelled	95.7	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
31	c2fgoA_	Alignment	not modelled	95.7	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
32	c2zvsB_	Alignment	not modelled	95.2	11	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl; **PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
33	c2gmhA_	Alignment	not modelled	95.2	19	**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
34	d2fdna_	Alignment	not modelled	94.7	15	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	d1h98a_	Alignment	not modelled	94.5	11	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
36	d7fd1a_	Alignment	not modelled	94.5	13	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
37	c2v4jE_	Alignment	not modelled	94.5	15	**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
38	d1blua_	Alignment	not modelled	94.4	11	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
39	d1rgva_	Alignment	not modelled	93.8	15	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
40	c2v2kB_	Alignment	not modelled	93.7	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
41	d1y5ib1	Alignment	not modelled	93.5	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
42	d3c7bb1	Alignment	not modelled	93.2	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
43	d2c42a5	Alignment	not modelled	92.7	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
44	d1fcaa_	Alignment	not modelled	92.6	15	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
45	d2gmha3	Alignment	not modelled	92.2	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
46	c3c7bE_	Alignment	not modelled	92.0	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
47	c3bk7A_	Alignment	not modelled	91.0	23	**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 abysii
48	d1bc6a_	Alignment	not modelled	90.4	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
49	c2v4jA_	Alignment	not modelled	85.1	10	**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	c3c7bA_	Alignment	not modelled	84.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	d2v4jb1	Alignment	not modelled	80.2	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
52	d1clfa_	Alignment	not modelled	75.2	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins

53	d2bs2b1	Alignment	not modelled	48.2	25	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
54	d1kf6b1	Alignment	not modelled	46.6	16	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
55	c1nekB_	Alignment	not modelled	42.5	13	**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
56	c2bs2E_	Alignment	not modelled	36.0	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
57	d1nekb1	Alignment	not modelled	29.1	29	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
58	c2qwuB_	Alignment	not modelled	20.8	35	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**intracellular growth locus, subunit c; **PDBTitle:** crystal structure of f. tularensis pathogenicity island2 protein c
59	c3cf4A_	Alignment	not modelled	19.3	20	**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	c2vdcI_	Alignment	not modelled	17.4	21	**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.
61	c2b76N_	Alignment	not modelled	14.2	21	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
62	c2h89B_	Alignment	not modelled	13.5	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
63	d3c7ba1	Alignment	not modelled	13.3	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
64	d2v4ja1	Alignment	not modelled	11.0	11	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
65	c3d6rA_	Alignment	not modelled	7.7	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** structure of an avian influenza a virus ns1 protein2 effector domain
66	c2z8nB_	Alignment	not modelled	6.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**27.5 kda virulence protein; **PDBTitle:** structural basis for the catalytic mechanism of phosphothreonine lyase
67	d1ycya1	Alignment	not modelled	5.8	28	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**PF1955-like
68	c1icfA_	Alignment	not modelled	5.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (cathepsin l: heavy chain); **PDBTitle:** crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin l
69	c3ktbD_	Alignment	not modelled	5.3	38	**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