







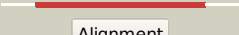

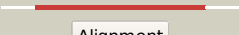


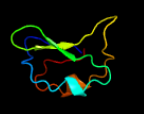







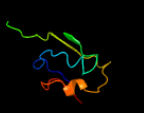
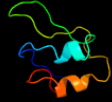


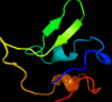
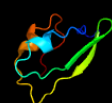
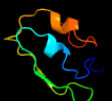
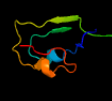
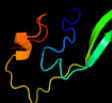
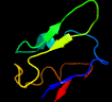


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3503c\_(fdxD)\_3922244\_3922435  
 Date Fri Aug 9 18:20:18 BST 2019  
 Unique Job ID aff7af79d835e771

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4id8A_</a>	 Alignment		99.7	40	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> putative ferredoxin; <b>PDBTitle:</b> the crystal structure of a [3Fe-4S] ferredoxin associated with2 cyp194a4 from r. palustris haa2
2	<a href="#">dlfxra_</a>	 Alignment		99.6	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
3	<a href="#">dliqza_</a>	 Alignment		99.6	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
4	<a href="#">dlsj1a_</a>	 Alignment		99.6	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
5	<a href="#">dlvjwa_</a>	 Alignment		99.5	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
6	<a href="#">c1dw1A_</a>	 Alignment		99.3	28	<b>PDB header:</b> electron transfer <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin i; <b>PDBTitle:</b> the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
7	<a href="#">c5odhG_</a>	 Alignment		98.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> heterodisulfide reductase, subunit a; <b>PDBTitle:</b> heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
8	<a href="#">dlxera_</a>	 Alignment		98.8	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Archaeal ferredoxins
9	<a href="#">c3gyxJ_</a>	 Alignment		98.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> adenylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
10	<a href="#">c5c4iB_</a>	 Alignment		98.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> oxalate oxidoreductase subunit delta; <b>PDBTitle:</b> structure of an oxalate oxidoreductase
11	<a href="#">c6humL_</a>	 Alignment		98.8	23	<b>PDB header:</b> proton transport <b>Chain:</b> I; <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit i; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus

12	<a href="#">d2fug34</a>	Alignment		98.8	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
13	<a href="#">d3c8ya3</a>	Alignment		98.7	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
14	<a href="#">d1jnrb_</a>	Alignment		98.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
15	<a href="#">d1gtea5</a>	Alignment		98.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
16	<a href="#">c2fugG_</a>	Alignment		98.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 9; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
17	<a href="#">d2fug91</a>	Alignment		98.7	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
18	<a href="#">c5lc5I_</a>	Alignment		98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I; <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
19	<a href="#">c6qcsl_</a>	Alignment		98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I; <b>PDB Molecule:</b> tyky subunit (nuim); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
20	<a href="#">c6cfwN_</a>	Alignment		98.6	20	<b>PDB header:</b> membrane protein <b>Chain:</b> N; <b>PDB Molecule:</b> nadh-plastoquinone oxidoreductase subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
21	<a href="#">d1hfel2</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
22	<a href="#">c5t5iG_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdg; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
23	<a href="#">c5lc5G_</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
24	<a href="#">c4heaO_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 9; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
25	<a href="#">c2gmaA_</a>	Alignment	not modelled	98.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
26	<a href="#">c5lnk3_</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 3; <b>PDB Molecule:</b> mitochondrial complex i, 75 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
27	<a href="#">c2vpyB_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nrfc protein; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
28	<a href="#">c1gthD_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil

29	<a href="#">d2fdna_</a>	Alignment	not modelled	98.5	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
30	<a href="#">d1jb0c_</a>	Alignment	not modelled	98.5	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
31	<a href="#">c2fugC_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
32	<a href="#">c5xf9F_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
33	<a href="#">c5ldwG_</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
34	<a href="#">c5ldxG_</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.
35	<a href="#">d1blua_</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
36	<a href="#">c1hfeL_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrogenase <b>Chain:</b> L: <b>PDB Molecule:</b> protein (fe-only hydrogenase (e.c.1.18.99.1) <b>PDBTitle:</b> 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
37	<a href="#">c6cipD_</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
38	<a href="#">c1c4cA_</a>	Alignment	not modelled	98.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fe-only hydrogenase); <b>PDBTitle:</b> binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
39	<a href="#">d1dura_</a>	Alignment	not modelled	98.5	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
40	<a href="#">c6gcsA_</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 75-kda protein (nuam); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
41	<a href="#">d1fxda_</a>	Alignment	not modelled	98.4	34	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
42	<a href="#">c2fgoA_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
43	<a href="#">c2zvsB_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ferredoxin-like protein yfh1; <b>PDBTitle:</b> crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
44	<a href="#">c5t5iN_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdf; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
45	<a href="#">c1kqfB_</a>	Alignment	not modelled	98.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
46	<a href="#">d1fcaa_</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
47	<a href="#">d1rgva_</a>	Alignment	not modelled	98.4	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
48	<a href="#">d1kqfb1</a>	Alignment	not modelled	98.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
49	<a href="#">d1bc6a_</a>	Alignment	not modelled	98.3	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
50	<a href="#">d1h98a_</a>	Alignment	not modelled	98.3	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
51	<a href="#">c2c3yA_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
52	<a href="#">c1gx7A_</a>	Alignment	not modelled	98.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [fe] hydrogenase large subunit; <b>PDBTitle:</b> best model of the electron transfer complex between cytochrome c3 and2 [fe]-hydrogenase
53	<a href="#">d7fd1a_</a>	Alignment	not modelled	98.3	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4fe-4s ferredoxin. iron-sulfur binding

54	<a href="#">c6czaB_</a>	Alignment	not modelled	98.3	15	domain protein; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate <b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> iron-sulfur cluster-binding oxidoreductase, putative <b>PDBTitle:</b> active site complex bambc of benzoyl coenzyme a reductase in complex2 with zinc <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> pyrogallol hydroxytransferase small subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici <b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
55	<a href="#">c4z3zE_</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> ETF-QO domain-like
56	<a href="#">c1ti2F_</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
57	<a href="#">c2v2kB_</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
58	<a href="#">d2gmha3</a>	Alignment	not modelled	98.0	7	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit care; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
59	<a href="#">d1clfa_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dms0 reductase family type ii enzyme, iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
60	<a href="#">d1h0hb_</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
61	<a href="#">c6fahE_</a>	Alignment	not modelled	98.0	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
62	<a href="#">c2ivfB_</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
63	<a href="#">c4yddF_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
64	<a href="#">d1vifn2</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
65	<a href="#">d2c42a5</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> fe-s-cluster-containing hydrogenase; <b>PDBTitle:</b> alternative complex iii
66	<a href="#">d3c7bb1</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
67	<a href="#">d1y5ib1</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
68	<a href="#">c3c7bE_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
69	<a href="#">c6f0kB_</a>	Alignment	not modelled	96.9	25	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
70	<a href="#">c2v4jE_</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
71	<a href="#">c6btmB_</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur protein; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
72	<a href="#">c3c7bA_</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> f420-reducing hydrogenase, subunit gamma; <b>PDBTitle:</b> cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate <b>Fold:</b> Globin-like
73	<a href="#">c3j16B_</a>	Alignment	not modelled	95.9	23	
74	<a href="#">c2v4jA_</a>	Alignment	not modelled	95.9	19	
75	<a href="#">c1nekB_</a>	Alignment	not modelled	95.7	21	
76	<a href="#">c3zfsB_</a>	Alignment	not modelled	95.7	15	

77	<a href="#">d2bs2b1</a>	Alignment	not modelled	95.0	29	<b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
78	<a href="#">c2bs2E_</a>	Alignment	not modelled	94.7	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b; <b>PDBTitle:</b> quinol:fumarate reductase from wolinella succinogenes
79	<a href="#">c5odcC_</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> heterodisulfide reductase, subunit c; <b>PDBTitle:</b> heterodisulfide reductase / [nife]-hydrogenase complex from 2 methanothermococcus thermolithotrophicus at 2.3 a resolution
80	<a href="#">d1kf6b1</a>	Alignment	not modelled	94.6	15	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
81	<a href="#">c5xmij_</a>	Alignment	not modelled	94.6	25	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
82	<a href="#">c3bk7A_</a>	Alignment	not modelled	94.5	25	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A; <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abc1/rnaase-i inhibitor protein from 2 pyrococcus abyssi
83	<a href="#">c3vrbf_</a>	Alignment	not modelled	94.5	23	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> F; <b>PDB Molecule:</b> iron-sulfur subunit of succinate dehydrogenase; <b>PDBTitle:</b> mitochondrial rholoquinol-fumarate reductase from the parasitic 2 nematode ascaris suum with the specific inhibitor flutolanil and 3 substrate fumarate
84	<a href="#">c4ur1A_</a>	Alignment	not modelled	94.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> tetrachloroethene reductive dehalogenase catalytic subunit <b>PDBTitle:</b> crystal structure of the pce reductive dehalogenase from s.2 multivorans in complex with dibromoethene
85	<a href="#">d1nekb1</a>	Alignment	not modelled	94.1	21	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
86	<a href="#">c2h89B_</a>	Alignment	not modelled	94.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> succinate dehydrogenase ip subunit; <b>PDBTitle:</b> avian respiratory complex ii with malonate bound
87	<a href="#">d2v4jb1</a>	Alignment	not modelled	92.7	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
88	<a href="#">c2b76N_</a>	Alignment	not modelled	91.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N; <b>PDB Molecule:</b> fumarate reductase iron-sulfur protein; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda e49q mutation
89	<a href="#">c5dqrA_</a>	Alignment	not modelled	91.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 7-hydroxymethyl chlorophyll a reductase, chloroplastic; <b>PDBTitle:</b> the crystal structure of arabidopsis 7-hydroxymethyl chlorophyll a2 reductase (hcar)
90	<a href="#">c4rasC_</a>	Alignment	not modelled	90.9	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> oxidoreductase, nad-binding/iron-sulfur cluster-binding <b>PDBTitle:</b> reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
91	<a href="#">c3cf4A_</a>	Alignment	not modelled	88.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase alpha subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
92	<a href="#">c5d0bB_</a>	Alignment	not modelled	87.8	22	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> B; <b>PDB Molecule:</b> epoxyqueuosine reductase; <b>PDBTitle:</b> crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
93	<a href="#">c5d6sB_</a>	Alignment	not modelled	80.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> epoxyqueuosine reductase; <b>PDBTitle:</b> structure of epoxyqueuosine reductase from streptococcus thermophilus.
94	<a href="#">d2v4ja1</a>	Alignment	not modelled	72.3	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
95	<a href="#">d3c7ba1</a>	Alignment	not modelled	71.9	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
96	<a href="#">c4p6vA_</a>	Alignment	not modelled	61.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit a; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
97	<a href="#">c2vdcl_</a>	Alignment	not modelled	48.5	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I; <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
98	<a href="#">c4ylfD_</a>	Alignment	not modelled	35.2	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase subunit a; <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent 2 reduced ferredoxin-nadp oxidoreductase structure
99	<a href="#">c5jcaL_</a>	Alignment	not modelled	30.8	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L; <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (nfni) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus