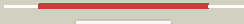



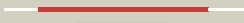
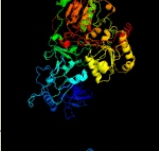



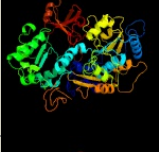






















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3151_(nuoG)_3516743_3519163
Date	Thu Aug 8 16:20:33 BST 2019
Unique Job ID	3ae01cd70a7c049f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fugC_	 Alignment		100.0	30	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
2	c5lnk3_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: 3; PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
3	c6gcsA_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A; PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
4	c2nyaF_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: F; PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
5	c1ogyA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
6	c2v45A_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A; PDB Molecule: periplasmic nitrate reductase; PDBTitle: a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
7	c2iv2X_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: X; PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
8	c1h0hA_	 Alignment		100.0	20	PDB header: electron transport Chain: A; PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
9	c1kqgA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
10	c2e7zA_	 Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
11	c2vpyE_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: E; PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)

12	c4aayE_	Alignment		100.0	18	PDB header: oxidoreductase Chain: E; PDB Molecule: araoa; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
13	c5ch7E_	Alignment		100.0	19	PDB header: oxidoreductase Chain: E; PDB Molecule: dmsmo reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
14	c6cz7C_	Alignment		100.0	20	PDB header: oxidoreductase Chain: C; PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
15	c1g8jC_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C; PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
16	c1y5iA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
17	c2ivfA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
18	c1tmoA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
19	c1h5nC_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C; PDB Molecule: dmsmo reductase; PDBTitle: dmsmo reductase modified by the presence of dms and air
20	d1kqfa2	Alignment		100.0	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
21	c1eu1A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: dimethyl sulfoxide reductase; PDBTitle: the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
22	c1vifQ_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: Q; PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
23	d1h0ha2	Alignment	not modelled	100.0	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
24	d2jioa2	Alignment	not modelled	100.0	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
25	d2iv2x2	Alignment	not modelled	100.0	25	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
26	d1ogya2	Alignment	not modelled	100.0	24	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
27	c6btmB_	Alignment	not modelled	100.0	14	PDB header: membrane protein Chain: B; PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
						PDB header: membrane protein

28	c6f0kB_	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
29	d1g8ka2	Alignment	not modelled	100.0	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
30	d1y5ia2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
31	d1dmra2	Alignment	not modelled	100.0	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
32	d1tmoa2	Alignment	not modelled	100.0	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
33	d1vlfm2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
34	d1eu1a2	Alignment	not modelled	100.0	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
35	c5ldwG_	Alignment	not modelled	100.0	43	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
36	c5ldxG_	Alignment	not modelled	100.0	43	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
37	c5lc5G_	Alignment	not modelled	100.0	43	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
38	c1c4cA_	Alignment	not modelled	100.0	23	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
39	c5t5mB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdb; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
40	d2fug32	Alignment	not modelled	100.0	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
41	c5xf9F_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
42	d3c8ya2	Alignment	not modelled	100.0	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
43	d2fug34	Alignment	not modelled	100.0	46	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
44	c5g5gA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative xanthine dehydrogenase yagt iron-sulfur-binding PDBTitle: escherichia coli periplasmic aldehyde oxidase
45	c2bs2E_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
46	c5xmjl_	Alignment	not modelled	99.9	19	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
47	c2b76N_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
48	d2fug33	Alignment	not modelled	99.9	42	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
49	c1nekB_	Alignment	not modelled	99.8	16	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
50	c2h89B_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
51	c3vrBF_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F: PDB Molecule: iron-sulfur subunit of succinate dehydrogenase; PDBTitle: mitochondrial rhoquoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
52	d2jioa1	Alignment	not modelled	99.7	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain

53	dlogya1	Alignment	not modelled	99.7	23	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
54	d1h0ha1	Alignment	not modelled	99.7	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
55	d1g8ka1	Alignment	not modelled	99.7	12	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
56	d1kqfa1	Alignment	not modelled	99.6	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
57	d1tmoa1	Alignment	not modelled	99.6	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
58	d2iv2x1	Alignment	not modelled	99.6	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
59	d1eu1a1	Alignment	not modelled	99.6	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
60	d1dmra1	Alignment	not modelled	99.6	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
61	d1vlfm1	Alignment	not modelled	99.5	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
62	d1y5ia1	Alignment	not modelled	99.5	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
63	c2ki8A_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
64	d3c8ya3	Alignment	not modelled	99.5	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
65	c5t5iL_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwd;, PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
66	c1hfeL_	Alignment	not modelled	99.2	14	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
67	d1iqza_	Alignment	not modelled	99.1	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
68	c1n60D_	Alignment	not modelled	99.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: carbon monoxide dehydrogenase small chain; PDBTitle: crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
69	c5odhG_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: G: PDB Molecule: heterodisulfide reductase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
70	c1gx7A_	Alignment	not modelled	98.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between cytochrome c3 and2 [fe]-hydrogenase
71	d1hfeI2	Alignment	not modelled	98.9	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
72	d1xera_	Alignment	not modelled	98.9	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
73	c6cfwN_	Alignment	not modelled	98.8	14	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
74	c5lc5I_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
75	c6humI_	Alignment	not modelled	98.8	15	PDB header: proton transport Chain: I: PDB Molecule: nad(p)h-quinone oxidoreductase subunit i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
76	d2fug91	Alignment	not modelled	98.7	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins

77	c2fugG	Alignment	not modelled	98.7	20	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
78	d1ffva2	Alignment	not modelled	98.7	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
79	d1t3qa2	Alignment	not modelled	98.7	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
80	c6gcsI	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
81	c4heaO	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
82	d1n62a2	Alignment	not modelled	98.7	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
83	c6fahE	Alignment	not modelled	98.6	21	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
84	d1gtea5	Alignment	not modelled	98.6	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
85	c2c3yA	Alignment	not modelled	98.6	23	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
86	d1jb0c	Alignment	not modelled	98.6	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
87	d1frra	Alignment	not modelled	98.6	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
88	c5ogxA	Alignment	not modelled	98.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
89	d1vlba2	Alignment	not modelled	98.6	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
90	c6cipD	Alignment	not modelled	98.5	26	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpb bound
91	d1awda	Alignment	not modelled	98.5	34	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
92	c1gthD	Alignment	not modelled	98.5	20	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
93	d1blua	Alignment	not modelled	98.5	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
94	c4z3zE	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: E: PDB Molecule: iron-sulfur cluster-binding oxidoreductase, putative PDBTitle: active site complex bambc of benzoyl coenzyme a reductase in complex2 with zinc
95	c5c4iB	Alignment	not modelled	98.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
96	c2ivfB	Alignment	not modelled	98.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
97	c1t3qD	Alignment	not modelled	98.5	25	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
98	d1doia	Alignment	not modelled	98.4	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
99	d1iuea	Alignment	not modelled	98.4	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
100	c5t5iN	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: N: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
101	c3ah7A	Alignment	not modelled	98.4	24	PDB header: metal binding protein Chain: A: PDB Molecule: [2fe-2s]ferredoxin; PDBTitle: crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
102	d1rm6c2	Alignment	not modelled	98.4	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like

						Family: 2Fe-2S ferredoxin domains from multidomain proteins
103	d1dgja2	Alignment	not modelled	98.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
104	d2c42a5	Alignment	not modelled	98.4	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
105	d1czpa	Alignment	not modelled	98.4	34	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
106	c5y6qA	Alignment	not modelled	98.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase small subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
107	d2piaa3	Alignment	not modelled	98.4	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
108	d1fxia	Alignment	not modelled	98.4	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
109	d1rgva	Alignment	not modelled	98.4	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
110	d4fxca	Alignment	not modelled	98.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
111	c6czaB	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4fe-4s ferredoxin, iron-sulfur binding domain protein; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate
112	c3gyxl	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
113	c2gmhA	Alignment	not modelled	98.4	18	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
114	c1dwlA	Alignment	not modelled	98.3	21	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
115	d1vjwa	Alignment	not modelled	98.3	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
116	d1sj1a	Alignment	not modelled	98.3	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
117	d1kqfb1	Alignment	not modelled	98.3	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
118	c4zohC	Alignment	not modelled	98.3	30	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
119	c3hrdH	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
120	d1jnrb	Alignment	not modelled	98.3	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins