
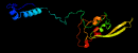

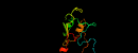




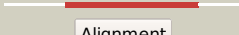



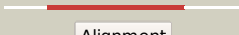
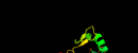


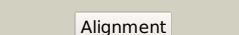




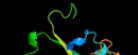
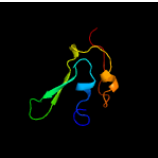

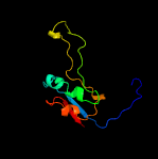



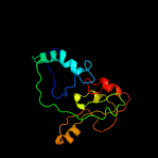




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3153_(nuo)_3520504_3521139
 Date Thu Aug 8 16:20:34 BST 2019
 Unique Job ID 2eca482360501992

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gcsI_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
2	c5lc5I_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
3	c4heaO_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
4	c6humI_	 Alignment		100.0	30	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
5	d2fug91	 Alignment		100.0	56	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
6	c2fugG_	 Alignment		100.0	56	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
7	c6cfwN_	 Alignment		99.9	31	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
8	c5c4iB_	 Alignment		99.6	35	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
9	c5odhG_	 Alignment		99.6	33	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
10	d2fug34	 Alignment		99.5	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
11	c6cipD_	 Alignment		99.5	30	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound

12	c2gmhA_	Alignment		99.5	25	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
13	d1jb0c_	Alignment		99.5	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
14	c5t5iN_	Alignment		99.4	26	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
15	d1xera_	Alignment		99.4	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
16	c1c4cA_	Alignment		99.4	20	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	c2c3yA_	Alignment		99.4	35	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
18	c5lc5G_	Alignment		99.4	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
19	c5lnk3_	Alignment		99.4	22	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
20	d7fd1a_	Alignment		99.4	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
21	d1hfel2	Alignment	not modelled	99.3	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
22	c6fahE_	Alignment	not modelled	99.3	42	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
23	c3gyxl_	Alignment	not modelled	99.3	31	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
24	c5ldxG_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
25	c5ldwG_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
26	c1gthD_	Alignment	not modelled	99.3	31	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
27	d2gmha3	Alignment	not modelled	99.3	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
28	c5t5iG_	Alignment	not modelled	99.3	33	PDB header: oxidoreductase Chain: G: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase

					from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
29	c2zvsB_	Alignment	not modelled	99.3	28 PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfh1; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
30	d2c42a5	Alignment	not modelled	99.3	37 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
31	c5xf9F_	Alignment	not modelled	99.3	19 PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
32	d1gtea5	Alignment	not modelled	99.3	21 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
33	c2fugC_	Alignment	not modelled	99.3	19 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
34	c6gcsA_	Alignment	not modelled	99.3	22 PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
35	d1blua_	Alignment	not modelled	99.3	29 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	d1rgva_	Alignment	not modelled	99.2	31 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
37	c6czaB_	Alignment	not modelled	99.2	31 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
38	d1bc6a_	Alignment	not modelled	99.2	35 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
39	c1hfeL_	Alignment	not modelled	99.2	26 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
40	d1h98a_	Alignment	not modelled	99.2	38 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
41	d3c8ya3	Alignment	not modelled	99.2	22 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
42	d1jnrb_	Alignment	not modelled	99.2	28 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
43	c2fgoA_	Alignment	not modelled	99.2	28 PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
44	d2fdna_	Alignment	not modelled	99.2	42 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
45	c1kqfB_	Alignment	not modelled	99.2	29 PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
46	d1fcaa_	Alignment	not modelled	99.2	48 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
47	d1dura_	Alignment	not modelled	99.2	35 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
48	c1gx7A_	Alignment	not modelled	99.1	33 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
49	d1clfa_	Alignment	not modelled	99.1	35 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
50	c1ti2F_	Alignment	not modelled	99.1	24 PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidgallici
51	d1kqfb1	Alignment	not modelled	99.1	29 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
52	d1h0hb_	Alignment	not modelled	99.1	25 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
53	c2vpyB_	Alignment	not modelled	99.1	33 PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp) PDB header: electron transport

54	c2v2kB_	Alignment	not modelled	99.0	31	Chain: B; PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
55	d1y5ib1	Alignment	not modelled	99.0	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
56	c2ivfB_	Alignment	not modelled	99.0	35	PDB header: oxidoreductase Chain: B; PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
57	d1iqza_	Alignment	not modelled	99.0	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
58	d1vfn2	Alignment	not modelled	99.0	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
59	c4z3zE_	Alignment	not modelled	99.0	20	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
60	c3c7bE_	Alignment	not modelled	98.9	26	PDB header: oxidoreductase Chain: E; PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
61	c6btmB_	Alignment	not modelled	98.9	23	PDB header: membrane protein Chain: B; PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
62	c4yddF_	Alignment	not modelled	98.9	29	PDB header: oxidoreductase Chain: F; PDB Molecule: dms0 reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
63	c6f0kB_	Alignment	not modelled	98.9	23	PDB header: membrane protein Chain: B; PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
64	c2v4jE_	Alignment	not modelled	98.9	21	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
65	d1vjwa_	Alignment	not modelled	98.8	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
66	d3c7bb1	Alignment	not modelled	98.7	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
67	c3j16B_	Alignment	not modelled	98.7	35	PDB header: ribosome Chain: B; PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
68	d1sj1a_	Alignment	not modelled	98.7	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
69	c4id8A_	Alignment	not modelled	98.7	20	PDB header: electron transport Chain: A; PDB Molecule: putative ferredoxin; PDBTitle: the crystal structure of a [3fe-4s] ferredoxin associated with2 cyp194a4 from r. palustris haa2
70	c1dwIA_	Alignment	not modelled	98.7	28	PDB header: electron transfer Chain: A; PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
71	c3c7bA_	Alignment	not modelled	98.6	32	PDB header: oxidoreductase Chain: A; PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
72	c4ur1A_	Alignment	not modelled	98.6	34	PDB header: oxidoreductase Chain: A; PDB Molecule: tetrachloroethene reductive dehalogenase catalytic subunit PDBTitle: crystal structure of the pce reductive dehalogenase from s.2 multivorans in complex with dibromoethene
73	d1fxra_	Alignment	not modelled	98.5	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
74	c2v4jA_	Alignment	not modelled	98.5	20	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
75	c4rasC_	Alignment	not modelled	98.4	28	PDB header: oxidoreductase Chain: C; PDB Molecule: oxidoreductase, nad-binding/iron-sulfur cluster-binding PDBTitle: reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
76	c5odcC_	Alignment	not modelled	98.4	21	PDB header: oxidoreductase Chain: C; PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
77	d2hc2h1	Alignment	not modelled	98.4	15	Fold: Globin-like Superfamily: alpha-helical ferredoxin

77	c2s201	Alignment	not modelled	98.4	13	Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain PDB header: hydrolyase/translation
78	c3bk7A	Alignment	not modelled	98.4	40	Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abcE1/rnaase-I inhibitor protein from2 pyrococcus abyssi
79	d1kf6b1	Alignment	not modelled	98.2	18	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
80	c5d0bB	Alignment	not modelled	98.2	45	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
81	c5d6sB	Alignment	not modelled	98.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
82	d1nekB1	Alignment	not modelled	98.1	24	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
83	c3zfsB	Alignment	not modelled	98.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
84	c1nekB	Alignment	not modelled	98.0	23	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
85	c5xmjl	Alignment	not modelled	97.9	22	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
86	c2bs2E	Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
87	c2h89B	Alignment	not modelled	97.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
88	c2b76N	Alignment	not modelled	97.8	25	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
89	c3cf4A	Alignment	not modelled	97.8	27	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
90	c3vrBf	Alignment	not modelled	97.7	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F: PDB Molecule: iron-sulfur subunit of succinate dehydrogenase; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
91	d2v4jb1	Alignment	not modelled	97.4	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
92	c4p6vA	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
93	c5dqrA	Alignment	not modelled	97.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 7-hydroxymethyl chlorophyll a reductase, chloroplastic; PDBTitle: the crystal structure of arabidopsis 7-hydroxymethyl chlorophyll a2 reductase (hcar)
94	c4yIfD	Alignment	not modelled	95.8	21	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase subunit a; PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
95	c2vdcl	Alignment	not modelled	94.1	22	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
96	d2v4ja1	Alignment	not modelled	90.9	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
97	d3c7ba1	Alignment	not modelled	89.6	44	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
98	c5jcaL	Alignment	not modelled	87.2	20	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
99	d1fxda	Alignment	not modelled	75.5	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
100	c1g8jC	Alignment	not modelled	71.4	9	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis

101	d1gtea1	Alignment	not modelled	52.5	44	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
102	c5fj8C_	Alignment	not modelled	47.8	5	PDB header: transcription Chain: C: PDB Molecule: dna-directed rna polymerases i and iii subunit rpac1; PDBTitle: cryo-em structure of yeast rna polymerase iii elongation complex at 3.2 9 a
103	c3mk7B_	Alignment	not modelled	36.5	26	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit o; PDBTitle: the structure of cbb3 cytochrome oxidase
104	c4aayE_	Alignment	not modelled	32.2	38	PDB header: oxidoreductase Chain: E: PDB Molecule: aroa; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
105	c2dtgE_	Alignment	not modelled	32.1	20	PDB header: hormone receptor/immune system Chain: E: PDB Molecule: insulin receptor; PDBTitle: insulin receptor (ir) ectodomain in complex with fab's
106	c4zxbE_	Alignment	not modelled	31.2	35	PDB header: hormone receptor/immune system Chain: E: PDB Molecule: insulin receptor; PDBTitle: structure of the human insulin receptor ectodomain, irdeltabeta2 construct, in complex with four fab molecules
107	c2pmzS_	Alignment	not modelled	26.1	20	PDB header: translation, transferase Chain: S: PDB Molecule: dna-directed rna polymerase subunit d; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
108	c2kn0A_	Alignment	not modelled	23.9	33	PDB header: apoptosis Chain: A: PDB Molecule: fn14; PDBTitle: solution nmr structure of xenopus fn14
109	d1ogyb_	Alignment	not modelled	20.9	22	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif