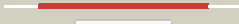



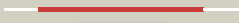


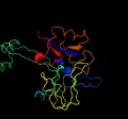











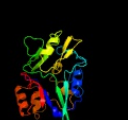


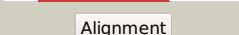





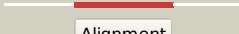






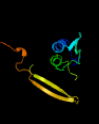






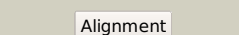
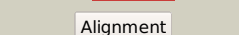
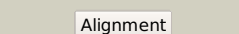
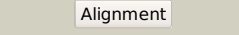




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1162_(narH)_1291070_1292746
Date	Wed Jul 31 22:05:25 BST 2019
Unique Job ID	c6b57c9156ed3f8b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ib1	 Alignment		100.0	53	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
2	c2ivfB_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
3	c4yddF_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: F: PDB Molecule: dmsO reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
4	c6btmB_	 Alignment		100.0	29	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
5	c6f0kB_	 Alignment		100.0	35	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
6	c1ti2F_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
7	c6czaB_	 Alignment		100.0	42	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
8	c2vpyB_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
9	d1kqfb1	 Alignment		100.0	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
10	d1vifn2	 Alignment		100.0	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
11	c1kqfB_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli

12	d1h0hb_	 Alignment		100.0	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
13	c4z3zE_	 Alignment		99.8	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
14	c5t5iN_	 Alignment		99.7	13	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	c1hfeL_	 Alignment		99.5	13	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
16	c1gx7A_	 Alignment		99.5	14	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
17	d1jnrb_	 Alignment		99.5	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
18	c3gyxJ_	 Alignment		99.4	14	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
19	d7fd1a_	 Alignment		99.3	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
20	d1h98a_	 Alignment		99.3	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
21	c5odhG_	 Alignment	not modelled	99.2	29	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
22	d3c7bb1	 Alignment	not modelled	99.2	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
23	c2v2kB_	 Alignment	not modelled	99.2	17	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
24	c1c4cA_	 Alignment	not modelled	99.2	17	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
25	d1bc6a_	 Alignment	not modelled	99.2	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
26	c6humI_	 Alignment	not modelled	99.1	17	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
27	c1gthD_	 Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
28	d1hfeI2	 Alignment	not modelled	99.1	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins

29	c6cfwN_	Alignment	not modelled	99.0	26	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
30	c6fahE_	Alignment	not modelled	99.0	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
31	c2gmhA_	Alignment	not modelled	99.0	13	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
32	d1clfa_	Alignment	not modelled	98.9	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
33	c3c7bE_	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
34	c5c4iB_	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
35	d1fcaa_	Alignment	not modelled	98.9	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	d1dura_	Alignment	not modelled	98.9	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
37	d2fug91	Alignment	not modelled	98.9	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
38	c2fugG_	Alignment	not modelled	98.9	21	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
39	c5lc5I_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
40	c4heaO_	Alignment	not modelled	98.8	25	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
41	d2fdna_	Alignment	not modelled	98.8	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
42	d2gmha3	Alignment	not modelled	98.8	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
43	c2c3yA_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
44	c6cipD_	Alignment	not modelled	98.8	24	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpp bound
45	d1gtea5	Alignment	not modelled	98.7	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
46	c6gcsI_	Alignment	not modelled	98.7	25	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
47	c2zvsB_	Alignment	not modelled	98.7	24	PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfhI; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
48	c3j16B_	Alignment	not modelled	98.7	23	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
49	d1blua_	Alignment	not modelled	98.7	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
50	c5t5iG_	Alignment	not modelled	98.7	27	PDB header: oxidoreductase Chain: G: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdg; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
51	d2c42a5	Alignment	not modelled	98.7	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
52	c2fgoA_	Alignment	not modelled	98.6	23	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
53	d1rgva_	Alignment	not modelled	98.6	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
						Fold: Ferredoxin-like

54	d1xera_	Alignment	not modelled	98.6	20	Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
55	c2v4jE_	Alignment	not modelled	98.6	24	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
56	d1jb0c_	Alignment	not modelled	98.6	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
57	c3bk7A_	Alignment	not modelled	98.5	23	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abyssi
58	c2v4jA_	Alignment	not modelled	98.3	18	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
59	d1vjwa_	Alignment	not modelled	98.3	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
60	c3c7bA_	Alignment	not modelled	98.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
61	d3c8ya3	Alignment	not modelled	98.3	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
62	c5d0bB_	Alignment	not modelled	98.0	36	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
63	c5xf9F_	Alignment	not modelled	98.0	11	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
64	d2fug34	Alignment	not modelled	98.0	14	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
65	c5d6sB_	Alignment	not modelled	97.9	27	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
66	d1iqza_	Alignment	not modelled	97.8	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
67	c2fugC_	Alignment	not modelled	97.8	22	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
68	c4rasC_	Alignment	not modelled	97.8	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
69	c3zfsB_	Alignment	not modelled	97.7	26	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
70	c1dwlA_	Alignment	not modelled	97.7	20	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
71	c6gcsA_	Alignment	not modelled	97.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
72	c4id8A_	Alignment	not modelled	97.5	19	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
73	c4ur1A_	Alignment	not modelled	97.5	30	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
74	d1fxra_	Alignment	not modelled	97.3	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
75	d1sj1a_	Alignment	not modelled	97.2	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
76	d2v4jb1	Alignment	not modelled	97.2	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
77	c5lnk3_	Alignment	not modelled	97.2	12	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
78	c5lc5G_	Alignment	not modelled	97.1	10	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit,

						PDBTitle: structure of mammalian respiratory complex i, class2 PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1 PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
79	c5ldwG_	Alignment	not modelled	96.9	10	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
80	c5ldxG_	Alignment	not modelled	96.9	10	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
81	c2b76N_	Alignment	not modelled	96.8	19	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
82	c2bs2E_	Alignment	not modelled	96.7	31	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
83	c5xmjl_	Alignment	not modelled	96.7	36	PDB header: oxidoreductase Chain: C: PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from 2 methanothermococcus thermolithotrophicus at 2.3 a resolution
84	c3cf4A_	Alignment	not modelled	96.6	25	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
85	c5odcC_	Alignment	not modelled	96.3	29	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
86	d2bs2b1	Alignment	not modelled	95.8	26	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)
87	d1nekb1	Alignment	not modelled	95.4	37	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
88	c5dqrA_	Alignment	not modelled	95.2	11	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
89	d1kf6b1	Alignment	not modelled	95.2	27	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
90	c2h89B_	Alignment	not modelled	94.7	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
91	c1nekB_	Alignment	not modelled	94.2	37	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
92	d2v4ja1	Alignment	not modelled	93.8	26	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
93	d3c7ba1	Alignment	not modelled	93.6	26	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
94	d3c8ya1	Alignment	not modelled	92.8	14	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
95	c3vrbf_	Alignment	not modelled	92.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
96	c3lx4B_	Alignment	not modelled	92.5	18	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
97	c4yifD_	Alignment	not modelled	91.9	22	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
98	d1hfel1	Alignment	not modelled	90.5	10	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
99	c4p6vA_	Alignment	not modelled	81.8	20	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.
100	c2vdcl_	Alignment	not modelled	78.9	31	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
101	d1ugpa_	Alignment	not modelled	78.4	35	PDB header: hydrolase Chain: R: PDB Molecule: thiocyanate hydrolase subunit gamma;
102	c2dyhb_	Alignment	not modelled	72.6	33	

102	c2uxvN_	Alignment	not modelled	72.0	35	PDBTitle: recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers PDB header: lyase
103	c3qyhG_	Alignment	not modelled	67.8	37	Chain: G: PDB Molecule: co-type nitrile hydratase alpha subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-h711 from2 pseudomonas putida.
104	c5jcaL_	Alignment	not modelled	64.1	25	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
105	c5fj8C_	Alignment	not modelled	61.9	15	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
106	c1g8jC_	Alignment	not modelled	57.3	26	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
107	c1m2oA_	Alignment	not modelled	55.2	19	PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
108	d2qw6a1	Alignment	not modelled	53.4	32	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
109	c2qw6A_	Alignment	not modelled	53.4	32	PDB header: hydrolase Chain: A: PDB Molecule: aaa atpase, central region; PDBTitle: crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
110	d1gtea1	Alignment	not modelled	52.8	33	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
111	c3pvsA_	Alignment	not modelled	52.0	24	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
112	c1m2vB_	Alignment	not modelled	48.6	21	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
113	d2d6fc2	Alignment	not modelled	45.3	12	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
114	d3ctda1	Alignment	not modelled	44.0	28	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
115	d2r9ga1	Alignment	not modelled	42.1	32	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
116	c4o5jA_	Alignment	not modelled	42.0	26	PDB header: cell adhesion Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of saba from helicobacter pylori
117	c3ctdB_	Alignment	not modelled	40.6	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative atpase, aaa family; PDBTitle: crystal structure of a putative aaa family atpase from prochlorococcus2 marinus subsp. pastoris
118	c6nmgB_	Alignment	not modelled	38.8	16	PDB header: signaling protein Chain: B: PDB Molecule: resistance to inhibitors of cholinesterase 8 homolog a (c. PDBTitle: crystal structure of rat ric-8a g alpha binding domain
119	c1dfsA_	Alignment	not modelled	37.8	59	PDB header: metal binding protein Chain: A: PDB Molecule: metallothionein-1; PDBTitle: solution structure of the alpha-domain of mouse2 metallothionein-1
120	c3mlgB_	Alignment	not modelled	35.6	13	PDB header: de novo protein Chain: B: PDB Molecule: 2x chimera of helicobacter pylori protein hp0242; PDBTitle: 2ouf-2x, a designed knotted protein