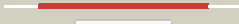



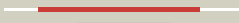


















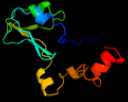









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1177_(fdxC)_1309010_1309336
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	52fc949e4a473898


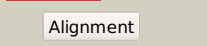
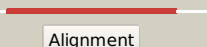
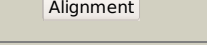
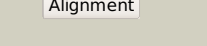
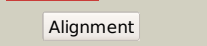



Detailed template information

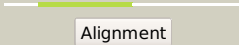
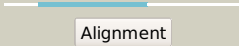


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v2kB_	 Alignment		100.0	88	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
2	d1bc6a_	 Alignment		99.9	60	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
3	d7fd1a_	 Alignment		99.9	43	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
4	d1h98a_	 Alignment		99.8	54	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
5	d1blua_	 Alignment		99.7	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
6	c5odhG_	 Alignment		99.7	21	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
7	c2zvsB_	 Alignment		99.7	23	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
8	c2ivfB_	 Alignment		99.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
9	c2fgoA_	 Alignment		99.7	27	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
10	d1clfa_	 Alignment		99.7	47	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
11	d2fdna_	 Alignment		99.7	45	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins

12	dlfcaa_	Alignment		99.7	47	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
13	c4yddF_	Alignment		99.7	24	PDB header: oxidoreductase Chain: F: PDB Molecule: dmsio reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
14	dlrgva_	Alignment		99.7	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
15	dljnrB_	Alignment		99.6	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
16	dlidura_	Alignment		99.6	45	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
17	c6fahE_	Alignment		99.6	27	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
18	c5c4iB_	Alignment		99.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
19	c3gyxJ_	Alignment		99.6	33	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
20	c6humI_	Alignment		99.6	18	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
21	c1gthD_	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dhd) from pig, ternary complex with2 nadph and 5-iodouracil
22	c2fugG_	Alignment	not modelled	99.6	36	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
23	d2fug91	Alignment	not modelled	99.6	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
24	c6czaB_	Alignment	not modelled	99.6	23	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
25	c5lc5I_	Alignment	not modelled	99.6	38	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
26	c4heaO_	Alignment	not modelled	99.6	35	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
27	c5t5iN_	Alignment	not modelled	99.5	32	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
28	c6gcsI_	Alignment	not modelled	99.5	39	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia

						lipolytica
29	c1kqfB_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
30	d1y5ib1	Alignment	not modelled	99.5	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
31	c1ti2F_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
32	d1hfeI2	Alignment	not modelled	99.5	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
33	c1gx7A_	Alignment	not modelled	99.5	23	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
34	c2gmhA_	Alignment	not modelled	99.5	23	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
35	d1jb0c_	Alignment	not modelled	99.5	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
36	c6cfwN_	Alignment	not modelled	99.5	26	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
37	c2c3yA_	Alignment	not modelled	99.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
38	d2gmha3	Alignment	not modelled	99.5	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
39	d1xera_	Alignment	not modelled	99.4	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
40	d1gtea5	Alignment	not modelled	99.4	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
41	c6cipD_	Alignment	not modelled	99.4	25	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with2 acetyl-tpg bound
42	d1kqfb1	Alignment	not modelled	99.4	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
43	c1hfeL_	Alignment	not modelled	99.4	23	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
44	c2vpyB_	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
45	d2c42a5	Alignment	not modelled	99.4	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
46	c5t5iG_	Alignment	not modelled	99.3	41	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
47	c1c4cA_	Alignment	not modelled	99.3	16	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
48	c6btmB_	Alignment	not modelled	99.3	22	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
49	d3c8ya3	Alignment	not modelled	99.3	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
50	d1vjwa_	Alignment	not modelled	99.3	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
51	c6f0kB_	Alignment	not modelled	99.2	21	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
52	c4z3zE_	Alignment	not modelled	99.2	36	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
53	c2i1eB_	Alignment	not modelled	99.2	26	PDB header: ribosome Chain: B: PDB Molecule: rli1p;

53	c9j10b_	Alignment	not modelled	99.2	20	PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
54	d1h0hb_	Alignment	not modelled	99.2	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
55	d3c7bb1	Alignment	not modelled	99.2	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
56	d1v1fn2	Alignment	not modelled	99.2	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
57	d1iqza_	Alignment	not modelled	99.2	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
58	d2fug34	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
59	c3c7bE_	Alignment	not modelled	99.2	21	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
60	c5xf9F_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
61	c3bk7A_	Alignment	not modelled	99.1	26	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
62	c2v4jE_	Alignment	not modelled	99.1	25	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
63	c3c7bA_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
64	c4id8A_	Alignment	not modelled	99.1	16	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
65	c1dw1A_	Alignment	not modelled	99.0	24	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
66	d1sj1a_	Alignment	not modelled	99.0	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
67	d1fxra_	Alignment	not modelled	99.0	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
68	c2v4jA_	Alignment	not modelled	99.0	22	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
69	c51c5G_	Alignment	not modelled	98.9	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
70	c51dxG_	Alignment	not modelled	98.8	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
71	c51dwG_	Alignment	not modelled	98.8	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
72	c6gcsA_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
73	c51nk3_	Alignment	not modelled	98.7	21	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
74	c3zfsB_	Alignment	not modelled	98.7	20	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
75	c2fugC_	Alignment	not modelled	98.6	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
76	c5d0bB_	Alignment	not modelled	98.5	24	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
77	c5d6sB_	Alignment	not modelled	98.5	25	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.

78	c4rasC	 Alignment	not modelled	98.3	33	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
79	c5odcC	 Alignment	not modelled	98.1	22	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
80	c4ur1A	 Alignment	not modelled	98.1	37	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
81	d2bs2b1	 Alignment	not modelled	98.0	22	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
82	d1kf6b1	 Alignment	not modelled	97.8	24	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
83	d2v4jb1	 Alignment	not modelled	97.7	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
84	d1nekB1	 Alignment	not modelled	97.7	24	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
85	c1nekB	 Alignment	not modelled	97.7	24	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
86	c4yifD	 Alignment	not modelled	97.6	16	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
87	c2b76N	 Alignment	not modelled	97.6	24	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
88	c5xmij	 Alignment	not modelled	97.5	29	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
89	c3cf4A	 Alignment	not modelled	97.5	33	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	c2bs2E	 Alignment	not modelled	97.5	28	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinella succinogenes
91	d2v4ja1	 Alignment	not modelled	97.5	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
92	d3c7ba1	 Alignment	not modelled	97.4	32	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
93	c2h89B	 Alignment	not modelled	97.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
94	c4p6vA	 Alignment	not modelled	97.2	20	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
95	c3vrBf	 Alignment	not modelled	97.2	23	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
96	c2vdcl	 Alignment	not modelled	96.5	19	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.
97	c5jcaL	 Alignment	not modelled	95.7	23	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
98	c5dqrA	 Alignment	not modelled	94.1	13	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)
99	d1fxda	 Alignment	not modelled	81.2	37	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
100	d1gtea1	 Alignment	not modelled	67.8	32	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain

101	c4zxbE	 Alignment	not modelled	60.5	32	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
102	c2a91A	 Alignment	not modelled	34.8	16	PDB header: signaling protein,transferase,membrane p Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: crystal structure of erbb2 domains 1-3
103	d1skza1	 Alignment	not modelled	34.7	25	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Huristasin-like
104	c1igrA	 Alignment	not modelled	33.6	23	PDB header: hormone receptor Chain: A: PDB Molecule: insulin-like growth factor receptor 1; PDBTitle: type 1 insulin-like growth factor receptor (domains 1-3)