













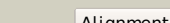


























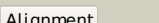



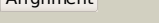

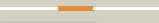


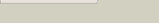
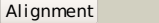
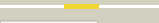


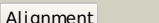
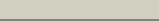
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f0xA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
2	c1ahuB_	 Alignment		100.0	17	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
3	c2uuvC_	 Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: alkyl dihydroxyacetonephosphate synthase; PDBTitle: alkyl dihydroxyacetonephosphate synthase in p1
4	c3pm9A_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
5	c1wveB_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
6	c3bw7A_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
7	c2exrA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
8	c2bvfa_	 Alignment		100.0	22	PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
9	c3fwaA_	 Alignment		100.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
10	c3d2hA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
11	c1zr6A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation

12	c2ipiD_	Alignment		100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
13	c2wdwB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
14	c3popD_	Alignment		100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
15	d1f0xa2	Alignment		100.0	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
16	c2y3rC_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
17	c2vfva_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
18	c1i19B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
19	d1e8ga2	Alignment		100.0	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
20	c3js8A_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
21	d1wvfa2	Alignment	not modelled	100.0	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
22	d1w1oa2	Alignment	not modelled	100.0	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
23	d2i0ka2	Alignment	not modelled	100.0	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
24	d1f0xa1	Alignment	not modelled	100.0	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
25	d1hska1	Alignment	not modelled	100.0	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
26	d1luxa1	Alignment	not modelled	100.0	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
27	d1e8ga1	Alignment	not modelled	100.0	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
28	d1wvfa1	Alignment	not modelled	100.0	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
29	c1hska	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine

29	c1t8vA_	Alignment	not modelled	100.0	19	reductase; PDBTitle: crystal structure of s. aureus murB
30	c2yvsA_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
31	c1mbbA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
32	c3i99A_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: the crystal structure of the udp-n-acetylenolpyruvylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
33	c2gquA_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
34	c3kwlA_	Alignment		99.6	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
35	d1nekb1	Alignment		99.4	25	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
36	c2h89B_	Alignment		99.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
37	c2b76N_	Alignment		99.2	17	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
38	c3cf4A_	Alignment		99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acids complex
39	c1nekB_	Alignment		99.2	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
40	d1kf6b1	Alignment		99.2	20	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
41	d2bs2b1	Alignment	not modelled	99.2	17	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
42	c2bs2E_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinetella succinogenes
43	d1w1oa1	Alignment	not modelled	98.7	17	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
44	c1gx7A_	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
45	c1c4cA_	Alignment	not modelled	98.1	18	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
46	c1hfeL_	Alignment	not modelled	98.0	21	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
47	d1ffvc2	Alignment	not modelled	97.7	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
48	c1ffuF	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: F: PDB Molecule: cutm, flavoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
49	c1n62C	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: carbon monoxide dehydrogenase medium chain; PDBTitle: crystal structure of the mo,co-cu dehydrogenase (codh), n-2 butylisocyanide-bound state
50	c2vdcl	Alignment	not modelled	97.6	9	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadh] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
51	c1t3qF	Alignment	not modelled	97.5	22	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
52	c3hrdC	Alignment	not modelled	97.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
53	d1t3qc2	Alignment	not modelled	97.4	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
54	d2c42a5	Alignment	not modelled	97.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
55	d1v97a6	Alignment	not modelled	97.4	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
56	d1n62c2	Alignment	not modelled	97.4	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
57	c1gthD	Alignment	not modelled	97.3	14	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
58	d1gtea5	Alignment	not modelled	97.3	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
59	d3b9jb2	Alignment	not modelled	97.3	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
60	c3etrM	Alignment	not modelled	97.2	11	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with2 lumazine
61	c3b9jl	Alignment	not modelled	97.2	11	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
62	c2c3yA	Alignment	not modelled	97.2	32	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
63	c2w3rG	Alignment	not modelled	97.1	18	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
64	d1jroa4	Alignment	not modelled	97.0	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
65	c1rm6E	Alignment	not modelled	96.9	24	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
66	d3c8ya3	Alignment	not modelled	96.9	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
67	c1wygA	Alignment	not modelled	96.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
68	d2fug91	Alignment	not modelled	96.7	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
69	c2fugG	Alignment	not modelled	96.7	31	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
70	d1hfel2	Alignment	not modelled	96.6	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
71	d1rm6b2	Alignment	not modelled	96.6	25	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
						Fold: Ferredoxin-like

72	d2fug34	Alignment	not modelled	96.5	12	Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
73	d1jb0c	Alignment	not modelled	96.4	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
74	c2gmhA	Alignment	not modelled	96.4	21	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
75	d1xera	Alignment	not modelled	96.3	34	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
76	d7fd1a	Alignment	not modelled	96.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
77	d1clfa	Alignment	not modelled	95.9	38	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
78	d2fdna	Alignment	not modelled	95.9	38	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
79	c1kqfB	Alignment	not modelled	95.9	34	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
80	d1y5b1	Alignment	not modelled	95.8	37	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
81	d1bc6a	Alignment	not modelled	95.7	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
82	d1fcaa	Alignment	not modelled	95.4	40	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
83	d1blua	Alignment	not modelled	95.4	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
84	d1rgva	Alignment	not modelled	95.3	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
85	c2fugC	Alignment	not modelled	95.2	13	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
86	d1dura	Alignment	not modelled	95.2	39	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
87	c2zvsB	Alignment	not modelled	95.2	36	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
88	c2ivfB	Alignment	not modelled	95.2	37	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
89	d1h98a	Alignment	not modelled	95.1	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
90	c2fgoA	Alignment	not modelled	95.1	29	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
91	d1jnrb	Alignment	not modelled	94.5	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
92	c2v2kB	Alignment	not modelled	94.5	27	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
93	d1gtea1	Alignment	not modelled	94.5	18	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
94	c3gyxj	Alignment	not modelled	93.8	29	PDB header: oxidoreductase Chain: J: PDB Molecule: adenyllysulfate reductase; PDBTitle: crystal structure of adenyllysulfate reductase from2 desulfovibrio gigas
95	c3c7bE	Alignment	not modelled	93.1	25	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
96	c2v4jE	Alignment	not modelled	93.1	43	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
97	d2gmha3	Alignment	not modelled	93.1	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like

98	c2vpyB_	 Alignment	not modelled	92.9	47	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
99	d1kqfb1	 Alignment	not modelled	92.6	41	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
100	d1h0hb_	 Alignment	not modelled	92.6	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
101	c1ti2F_	 Alignment	not modelled	92.2	30	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
102	d1iqza_	 Alignment	not modelled	91.9	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
103	c3c7bA_	 Alignment	not modelled	91.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
104	c1dwlA_	 Alignment	not modelled	91.5	28	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
105	d1vjwa_	 Alignment	not modelled	88.3	38	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
106	d2i0ka1	 Alignment	not modelled	87.3	15	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
107	d1sj1a_	 Alignment	not modelled	86.2	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
108	c2v4iA_	 Alignment	not modelled	85.2	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
109	d3c7bb1	 Alignment	not modelled	85.0	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
110	d1fxra_	 Alignment	not modelled	84.9	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
111	c2fugA_	 Alignment	not modelled	84.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nahd-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
112	d1vlfu2	 Alignment	not modelled	83.8	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
113	c3hlyA_	 Alignment	not modelled	77.3	11	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
114	c3bk7A_	 Alignment	not modelled	76.9	33	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-l inhibitor protein2 from pyrococcus abyssi
115	d1jfla1	 Alignment	not modelled	76.4	2	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
116	c2uval_	 Alignment	not modelled	75.5	19	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
117	c2vkzH_	 Alignment	not modelled	74.4	22	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
118	d2plsa1	 Alignment	not modelled	67.8	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
119	c2vdcF_	 Alignment	not modelled	60.2	27	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
120	c3fniA_	 Alignment	not modelled	58.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a