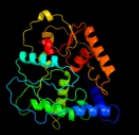
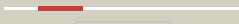
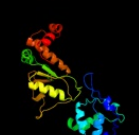
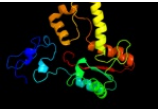


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kwlA_	 Alignment		99.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
2	c2h89B_	 Alignment		99.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
3	d1nekb1	 Alignment		99.4	19	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
4	c2b76N_	 Alignment		99.4	24	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
5	c1nekb_	 Alignment		99.3	18	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
6	d1kf6b1	 Alignment		99.3	26	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
7	c2bs2E_	 Alignment		99.3	20	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
8	d2bs2b1	 Alignment		99.3	18	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
9	c3cf4A_	 Alignment		99.1	19	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
10	c1c4cA_	 Alignment		98.5	15	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
11	c1gx7A_	 Alignment		98.3	18	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

12	c1hfeL_	Alignment		98.2	17	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
13	d2c42a5	Alignment		98.2	28	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
14	c2fugG_	Alignment		97.7	27	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
15	d2fug91	Alignment		97.7	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
16	d3c8ya3	Alignment		97.7	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
17	d1jb0c_	Alignment		97.6	37	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
18	d1xera_	Alignment		97.4	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
19	c2c3yA_	Alignment		97.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
20	d1gtea5	Alignment		97.3	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
21	d2fug34	Alignment	not modelled	97.2	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
22	d1hfel2	Alignment	not modelled	97.1	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
23	d7fd1a_	Alignment	not modelled	97.0	40	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
24	d2fdna_	Alignment	not modelled	97.0	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
25	d1clfa_	Alignment	not modelled	97.0	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
26	d1dura_	Alignment	not modelled	96.9	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
27	c2vdcl_	Alignment	not modelled	96.9	11	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.
28	d1blua_	Alignment	not modelled	96.9	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
29	d1bc6a_	Alignment	not modelled	96.8	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin

30	c2gmhA_	Alignment	not modelled	96.8	22	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
31	d1rgva_	Alignment	not modelled	96.8	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
32	c1kqfB_	Alignment	not modelled	96.8	27	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
33	c2fgoA_	Alignment	not modelled	96.8	29	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
34	c1gthD_	Alignment	not modelled	96.8	28	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
35	d1fcaa_	Alignment	not modelled	96.7	38	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	c2zvsB_	Alignment	not modelled	96.6	29	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
37	c3c7bE_	Alignment	not modelled	96.5	20	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
38	d1y5ib1	Alignment	not modelled	96.5	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
39	c2fugC_	Alignment	not modelled	96.5	20	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
40	d1h98a_	Alignment	not modelled	96.5	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
41	c2ivfB_	Alignment	not modelled	96.4	32	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
42	c3gyxl_	Alignment	not modelled	96.4	29	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
43	d1jnrb_	Alignment	not modelled	96.4	33	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
44	d2gmha3	Alignment	not modelled	96.2	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
45	d1h0hb_	Alignment	not modelled	96.1	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
46	d1kqfb1	Alignment	not modelled	96.1	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
47	c2v2kB_	Alignment	not modelled	96.0	32	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
48	c2v4jE_	Alignment	not modelled	95.9	19	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
49	c1ti2F_	Alignment	not modelled	95.7	26	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
50	d1vlfm2	Alignment	not modelled	95.5	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
51	c2vpyB_	Alignment	not modelled	95.2	38	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
52	c1dwIA_	Alignment	not modelled	95.0	34	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
53	d1vjwa_	Alignment	not modelled	94.6	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
54	dliqza_	Alignment	not modelled	94.4	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin

55	d3c7bb1	Alignment	not modelled	94.2	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
56	d1gtea1	Alignment	not modelled	92.9	19	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
57	d1sj1a	Alignment	not modelled	92.8	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
58	c3c7bA	Alignment	not modelled	91.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
59	c2dwuA	Alignment	not modelled	90.6	12	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
60	c2gzmB	Alignment	not modelled	88.8	12	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus2 anthracis
61	d1fxra	Alignment	not modelled	88.7	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
62	d1jfla1	Alignment	not modelled	88.0	20	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
63	c2fugA	Alignment	not modelled	86.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
64	c3ojcD	Alignment	not modelled	85.7	13	PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis
65	c2v4jA	Alignment	not modelled	84.3	16	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
66	c3bk7A	Alignment	not modelled	83.7	25	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-l inhibitor protein2 from pyrococcus abyssi
67	c2zskA	Alignment	not modelled	80.5	13	PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
68	c2jfbB	Alignment	not modelled	80.4	11	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
69	c1zuwA	Alignment	not modelled	76.6	12	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
70	c3hfrA	Alignment	not modelled	75.4	13	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
71	c2ohoA	Alignment	not modelled	74.4	10	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
72	c3outC	Alignment	not modelled	73.4	13	PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
73	c2jfoB	Alignment	not modelled	71.4	13	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
74	c2dx7B	Alignment	not modelled	70.0	16	PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
75	c1b74A	Alignment	not modelled	69.4	9	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
76	c2jfqA	Alignment	not modelled	68.2	15	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
77	c3s81A	Alignment	not modelled	66.6	14	PDB header: isomerase Chain: A: PDB Molecule: putative aspartate racemase; PDBTitle: crystal structure of putative aspartate racemase from salmonella2 typhimurium
78	c2jfnA	Alignment	not modelled	65.6	11	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
79	d2v4jb1	Alignment	not modelled	53.3	36	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
						PDB header: oxidoreductase

80	c2vdcF_	Alignment	not modelled	49.7	40	Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
81	c1lm1A_	Alignment	not modelled	46.6	40	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
82	d1ofda2	Alignment	not modelled	43.7	40	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c1g8jC_	Alignment	not modelled	42.9	33	PDB header: oxidoreductase Chain: C: PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
84	d1b74a1	Alignment	not modelled	31.6	11	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
85	d1ea0a2	Alignment	not modelled	31.2	40	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
86	c3lp6D_	Alignment	not modelled	30.1	16	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
87	c2eq5D_	Alignment	not modelled	28.5	11	PDB header: isomerase Chain: D: PDB Molecule: 228aa long hypothetical hydantoin racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
88	d1qcza_	Alignment	not modelled	28.3	12	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
89	c2yv4A_	Alignment	not modelled	25.7	18	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein ph0435; PDBTitle: crystal structure of c-terminal sua5 domain from pyrococcus horikoshii2 hypothetical sua5 protein ph0435
90	c3qvjB_	Alignment	not modelled	25.2	10	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
91	c3ucoB_	Alignment	not modelled	24.4	15	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
92	c3lx4B_	Alignment	not modelled	23.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
93	c2gksB_	Alignment	not modelled	23.1	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
94	c3rggD_	Alignment	not modelled	22.1	17	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
95	d1lxja_	Alignment	not modelled	19.8	13	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
96	c3fniA_	Alignment	not modelled	18.3	9	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
97	d1jfla2	Alignment	not modelled	17.4	16	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
98	c1xnjB_	Alignment	not modelled	17.3	11	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
99	c2kvgA_	Alignment	not modelled	17.2	33	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein