Phyre^2

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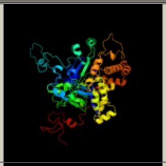
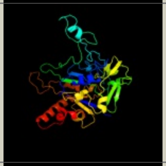
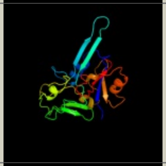
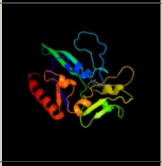
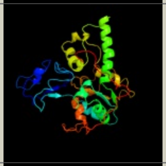
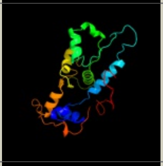
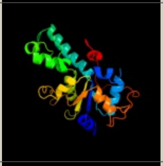
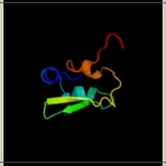
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ib1	Alignment		100.0	78	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
2	c2ivfB_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
3	c1ti2F_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
4	c2vpyB_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
5	d1kqfb1	Alignment		100.0	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
6	c1kqfB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
7	d1vlfn2	Alignment		100.0	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1h0hb_	Alignment		100.0	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c1gx7A_	Alignment		100.0	13	**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
10	c1hfeL_	Alignment		100.0	16	**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
11	c1c4cA_	Alignment		100.0	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

12	d3c8ya1	Alignment		99.9	13	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
13	c3lx4B_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fe-hydrogenase; **PDBTitle:** stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
14	d1hfel1	Alignment		99.9	11	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
15	c3gyxJ_	Alignment		99.4	18	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
16	d1jnrb_	Alignment		99.4	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
17	c2v2kB_	Alignment		99.3	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
18	d7fd1a_	Alignment		99.3	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
19	d3c7bb1	Alignment		99.3	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	d1h98a_	Alignment		99.3	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
21	c1gthD_	Alignment	not modelled	99.2	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
22	d1bc6a_	Alignment	not modelled	99.2	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
23	d1hfel2	Alignment	not modelled	99.1	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
24	d2c42a5	Alignment	not modelled	99.0	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
25	d1clfa_	Alignment	not modelled	98.9	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
26	c2zvsB_	Alignment	not modelled	98.9	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl; **PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
27	c2gmhA_	Alignment	not modelled	98.9	15	**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
28	d1dura_	Alignment	not modelled	98.9	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins

29	d1gtea5	Alignment	not modelled	98.9	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
30	d1fcaa_	Alignment	not modelled	98.9	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
31	c3c7bE_	Alignment	not modelled	98.8	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
32	d2fdna_	Alignment	not modelled	98.8	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
33	d1xera_	Alignment	not modelled	98.8	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
34	c2c3yA_	Alignment	not modelled	98.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
35	d2gmha3	Alignment	not modelled	98.8	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
36	d2fug91	Alignment	not modelled	98.8	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
37	c2fugG_	Alignment	not modelled	98.8	30	**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
38	d1blua_	Alignment	not modelled	98.7	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
39	c2fgoA_	Alignment	not modelled	98.6	28	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
40	d1rgva_	Alignment	not modelled	98.6	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
41	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
42	d1jb0c_	Alignment	not modelled	98.6	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
43	d2fug34	Alignment	not modelled	98.5	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
44	c3bk7A_	Alignment	not modelled	98.5	28	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
45	d1vjwa_	Alignment	not modelled	98.4	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
46	d3c8ya3	Alignment	not modelled	98.4	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
47	c3c7bA_	Alignment	not modelled	98.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
48	c2v4jA_	Alignment	not modelled	98.3	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
49	c2fugC_	Alignment	not modelled	97.8	29	**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
50	d1fxra_	Alignment	not modelled	97.8	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
51	d1sj1a_	Alignment	not modelled	97.8	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
52	d1iqza_	Alignment	not modelled	97.7	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
53	c1dwlA_	Alignment	not modelled	97.7	23	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
						Fold: Ferredoxin-like

54	d2v4jb1	Alignment	not modelled	97.5	31	**Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
55	c2b76N_	Alignment	not modelled	96.9	24	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
56	c3cf4A_	Alignment	not modelled	96.8	25	**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
57	c2bs2E_	Alignment	not modelled	96.8	31	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
58	c1nekB_	Alignment	not modelled	96.0	26	**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
59	d2bs2b1	Alignment	not modelled	95.9	18	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
60	d1nekb1	Alignment	not modelled	95.7	31	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
61	d1kf6b1	Alignment	not modelled	95.4	26	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
62	c2h89B_	Alignment	not modelled	94.8	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
63	d3c7ba1	Alignment	not modelled	93.8	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
64	d2v4ja1	Alignment	not modelled	93.6	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
65	c2vdcI_	Alignment	not modelled	90.8	23	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
66	c2dxbR_	Alignment	not modelled	70.3	22	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
67	d1gtea1	Alignment	not modelled	63.3	28	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
68	c3qyhG_	Alignment	not modelled	59.8	16	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
69	c2z6vA_	Alignment	not modelled	57.6	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of sulfotransferase stf9 from2 mycobacterium avium
70	d1ugpa_	Alignment	not modelled	48.7	21	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
71	d2igsa1	Alignment	not modelled	36.4	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PA2222-like
72	c1m2oA_	Alignment	not modelled	30.8	24	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
73	c1m2vB_	Alignment	not modelled	29.7	22	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
74	c1g8jC_	Alignment	not modelled	28.9	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
75	d1v29a_	Alignment	not modelled	21.8	22	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
76	d1djqa3	Alignment	not modelled	21.0	33	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
77	d1seda_	Alignment	not modelled	16.1	18	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
78	d1pyfa_	Alignment	not modelled	14.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
79	c2a91A_	Alignment	not modelled	14.6	15	**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
80	c3eg9B_	Alignment	not modelled	14.5	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d;

80	c3eg9B_	Alignment	not modelled	14.5	19	**PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
81	c2fugA_	Alignment	not modelled	14.4	29	**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
82	c2yqfA_	Alignment	not modelled	13.1	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
83	c2ldiA_	Alignment	not modelled	12.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
84	d1fxda_	Alignment	not modelled	11.7	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
85	d2qw6a1	Alignment	not modelled	11.1	23	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
86	c2qw6A_	Alignment	not modelled	11.1	23	**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
87	d2d6fc2	Alignment	not modelled	10.0	24	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
88	c1s6wA_	Alignment	not modelled	9.8	50	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hybrid white striped bass hepcidin
89	d2hyec1	Alignment	not modelled	9.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
90	c2dtgE_	Alignment	not modelled	9.3	23	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
91	d2ouwa1	Alignment	not modelled	9.3	23	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
92	c2qkdA_	Alignment	not modelled	9.2	14	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
93	c2hjpA_	Alignment	not modelled	9.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
94	d3c7bb3	Alignment	not modelled	8.9	18	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
95	c3c6fD_	Alignment	not modelled	8.9	12	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yetf protein; **PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis
96	d1zq1c2	Alignment	not modelled	8.8	24	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
97	c3k30B_	Alignment	not modelled	8.7	45	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
98	c3egxB_	Alignment	not modelled	8.5	34	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
99	c2pmzS_	Alignment	not modelled	8.0	19	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus