Phyre2

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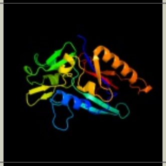
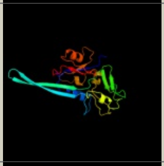
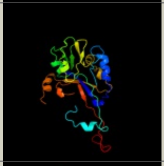
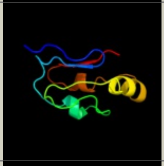
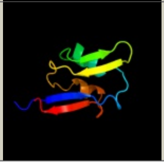
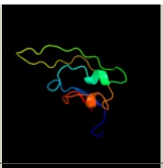
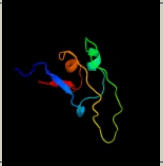
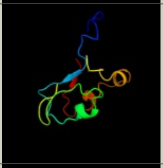
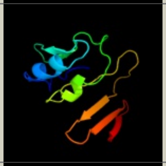
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ivfB_	Alignment		100.0	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
2	c1ti2F_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
3	d1kqfb1	Alignment		100.0	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
4	c2vpyB_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
5	c1kqfB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
6	d1y5ib1	Alignment		100.0	34	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
7	d1h0hb_	Alignment		100.0	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1vlfn2	Alignment		100.0	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	d1xera_	Alignment		99.3	37	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
10	c2zvsB_	Alignment		99.3	18	**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
11	c1gthD_	Alignment		99.3	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil

12	c2fugG_	Alignment		99.3	35	**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
13	d2fug91	Alignment		99.3	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
14	d1hfel2	Alignment		99.3	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
15	d1jnrb_	Alignment		99.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
16	c2v2kB_	Alignment		99.2	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
17	d7fd1a_	Alignment		99.2	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
18	c3gyxJ_	Alignment		99.2	28	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
19	d3c8ya3	Alignment		99.2	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	d2c42a5	Alignment		99.2	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
21	c2fgoA_	Alignment	not modelled	99.2	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
22	d1h98a_	Alignment	not modelled	99.2	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
23	d1bc6a_	Alignment	not modelled	99.1	34	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
24	d1blua_	Alignment	not modelled	99.1	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
25	d1jb0c_	Alignment	not modelled	99.1	38	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
26	c1hfeL_	Alignment	not modelled	99.1	33	**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
27	d1gtea5	Alignment	not modelled	99.1	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
28	d1rgva_	Alignment	not modelled	99.1	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
						Fold: Ferredoxin-like

29	d3c7bb1	Alignment	not modelled	99.1	29	**Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
30	c2gmhA_	Alignment	not modelled	99.1	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	c1gx7A_	Alignment	not modelled	99.1	38	**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
32	d2fdna_	Alignment	not modelled	99.0	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
33	c2c3yA_	Alignment	not modelled	99.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
34	d1iqza_	Alignment	not modelled	99.0	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
35	d1fcaa_	Alignment	not modelled	98.9	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
36	d2fug34	Alignment	not modelled	98.9	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
37	d1dura_	Alignment	not modelled	98.9	37	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
38	d2gmha3	Alignment	not modelled	98.9	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
39	d1clfa_	Alignment	not modelled	98.9	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
40	d1vjwa_	Alignment	not modelled	98.8	36	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
41	c1c4cA_	Alignment	not modelled	98.7	22	**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
42	d1sj1a_	Alignment	not modelled	98.7	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
43	d1fxra_	Alignment	not modelled	98.7	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
44	c1dwlA_	Alignment	not modelled	98.7	25	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
45	c3c7bE_	Alignment	not modelled	98.6	30	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	c3bk7A_	Alignment	not modelled	98.3	32	**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
47	c2fugC_	Alignment	not modelled	98.3	26	**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
48	c2v4jE_	Alignment	not modelled	98.2	26	**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	c2v4jA_	Alignment	not modelled	98.1	17	**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
50	c3c7bA_	Alignment	not modelled	97.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	d1kf6b1	Alignment	not modelled	97.9	19	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
52	d2bs2b1	Alignment	not modelled	97.9	18	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	d1nekb1	Alignment	not modelled	97.5	14	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain

54	c2bs2E_	Alignment	not modelled	97.5	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
55	c1nekB_	Alignment	not modelled	97.4	14	**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
56	c2h89B_	Alignment	not modelled	97.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
57	d2v4jb1	Alignment	not modelled	97.1	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
58	c2b76N_	Alignment	not modelled	97.0	19	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
59	c3cf4A_	Alignment	not modelled	95.8	38	**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
60	d2v4ja1	Alignment	not modelled	85.4	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
61	d3c7ba1	Alignment	not modelled	84.3	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
62	c2vdcI_	Alignment	not modelled	80.4	25	**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.
63	d1fxda_	Alignment	not modelled	59.1	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
64	d1gtea1	Alignment	not modelled	43.8	41	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
65	d1yuza2	Alignment	not modelled	19.0	24	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
66	d1djqa3	Alignment	not modelled	18.9	33	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
67	c2a91A_	Alignment	not modelled	17.1	25	**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
68	d1nnqa2	Alignment	not modelled	17.0	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
69	d2r4qa1	Alignment	not modelled	14.6	32	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
70	c2kn0A_	Alignment	not modelled	11.7	36	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fn14; **PDBTitle:** solution nmr structure of xenopus fn14
71	c2eqpA_	Alignment	not modelled	11.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the stn_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
72	c1moxB_	Alignment	not modelled	11.4	25	**PDB header:**transferase/growth factor **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of human epidermal growth factor receptor (residues2 1-501) in complex with tgf-alpha
73	d2cs3a1	Alignment	not modelled	10.0	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
74	c1deqD_	Alignment	not modelled	9.8	24	**PDB header:** **PDB COMPND:**
75	c2dtgE_	Alignment	not modelled	9.3	25	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
76	d1exta3	Alignment	not modelled	8.9	40	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
77	c2a45J_	Alignment	not modelled	8.9	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
78	d1ncfb3	Alignment	not modelled	8.3	42	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
79	c4a1eT_	Alignment	not modelled	8.1	27	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1

80	c3iz5Z_	Alignment	not modelled	7.9	14	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
81	c1g8jC_	Alignment	not modelled	7.7	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
82	d1lkoa2	Alignment	not modelled	7.6	21	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
83	c1s1iS_	Alignment	not modelled	7.1	8	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l24-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
84	c2zkru_	Alignment	not modelled	7.0	15	**PDB header:**ribosomal protein/rna **Chain:** U: **PDB Molecule:**rna expansion segment es41; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
85	c3izcZ_	Alignment	not modelled	7.0	7	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
86	d2r48a1	Alignment	not modelled	6.8	33	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
87	d1rutx1	Alignment	not modelled	6.7	31	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
88	c1m1jA_	Alignment	not modelled	6.5	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands