Phyre^2

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Description	P0AAK4
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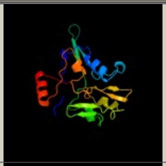
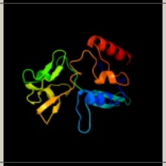
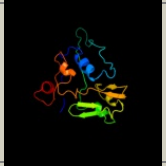
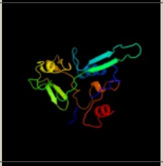
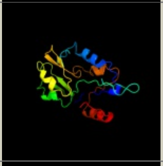
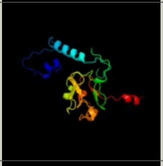
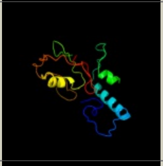
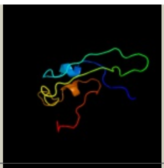
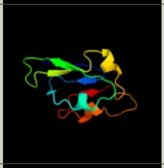
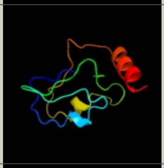
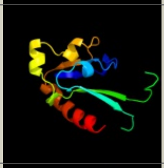
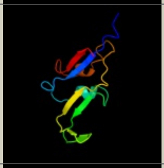
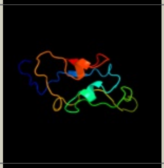
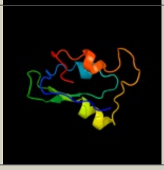
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ti2F_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
2	c1kqfB_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
3	c2ivfB_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
4	d1h0hb_	Alignment		100.0	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
5	c2vpyB_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
6	d1kqfb1	Alignment		100.0	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
7	d1vlfn2	Alignment		100.0	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1y5ib1	Alignment		100.0	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c1c4cA_	Alignment		99.6	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
10	c2fugC_	Alignment		99.6	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
11	d2fug91	Alignment		99.5	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins

12	c2fugG_	Alignment		99.5	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
13	d1xera_	Alignment		99.5	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
14	c2zvsB_	Alignment		99.5	22	**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
15	c2c3yA_	Alignment		99.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
16	c1gthD_	Alignment		99.5	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
17	d3c8ya3	Alignment		99.4	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
18	d1hfel2	Alignment		99.4	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
19	d2fug34	Alignment		99.4	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	d1jb0c_	Alignment		99.4	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
21	d2c42a5	Alignment	not modelled	99.4	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
22	d1gtea5	Alignment	not modelled	99.4	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
23	c2gmhA_	Alignment	not modelled	99.4	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
24	c2fgoA_	Alignment	not modelled	99.4	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
25	d1blua_	Alignment	not modelled	99.4	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
26	d1rgva_	Alignment	not modelled	99.3	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
27	d7fd1a_	Alignment	not modelled	99.3	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
28	c3gyxJ_	Alignment	not modelled	99.3	30	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
						PDB header:hydrogenase **Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase

29	c1hfeL_	Alignment	not modelled	99.3	26	(e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
30	d1h98a_	Alignment	not modelled	99.3	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
31	d1bc6a_	Alignment	not modelled	99.3	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
32	c1gx7A_	Alignment	not modelled	99.3	28	**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
33	d1dura_	Alignment	not modelled	99.2	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
34	d1jnrb_	Alignment	not modelled	99.2	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
35	d2fdna_	Alignment	not modelled	99.2	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
36	d1fcaa_	Alignment	not modelled	99.2	36	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
37	d2gmha3	Alignment	not modelled	99.1	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
38	d1clfa_	Alignment	not modelled	99.1	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
39	d1iqza_	Alignment	not modelled	99.1	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
40	d1vjwa_	Alignment	not modelled	99.0	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
41	c2v2kB_	Alignment	not modelled	99.0	31	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
42	d1sj1a_	Alignment	not modelled	98.9	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
43	d3c7bb1	Alignment	not modelled	98.8	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
44	c1dwlA_	Alignment	not modelled	98.8	22	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
45	d1fxra_	Alignment	not modelled	98.7	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
46	c3c7bE_	Alignment	not modelled	98.6	33	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
47	c2v4jE_	Alignment	not modelled	98.6	20	**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
48	c2b76N_	Alignment	not modelled	98.4	19	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
49	c2v4jA_	Alignment	not modelled	98.2	18	**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	98.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	d2bs2b1	Alignment	not modelled	98.0	23	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
52	d1kf6b1	Alignment	not modelled	98.0	22	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	c3bk7A_	Alignment	not modelled	98.0	27	**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
						PDB header:oxidoreductase/electron transport

54	c1nekB_	Alignment	not modelled	97.9	17	**Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
55	c2h89B_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
56	d1nekb1	Alignment	not modelled	97.7	16	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
57	c2bs2E_	Alignment	not modelled	97.6	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
58	c3cf4A_	Alignment	not modelled	97.1	20	**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
59	d2v4jb1	Alignment	not modelled	95.6	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
60	c2vdcI_	Alignment	not modelled	87.7	21	**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.
61	d3c8ya2	Alignment	not modelled	83.0	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
62	d3c7ba1	Alignment	not modelled	81.8	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
63	d2v4ja1	Alignment	not modelled	81.5	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
64	d1gtea1	Alignment	not modelled	57.1	25	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
65	d1fxda_	Alignment	not modelled	46.0	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
66	c3ktbD_	Alignment	not modelled	38.5	22	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
67	c1g8jC_	Alignment	not modelled	35.8	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
68	c3m1yA_	Alignment	not modelled	23.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
69	d2r48a1	Alignment	not modelled	22.2	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
70	d2r4qa1	Alignment	not modelled	17.6	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
71	d1djqa3	Alignment	not modelled	17.0	35	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
72	c2kn0A_	Alignment	not modelled	13.5	45	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fn14; **PDBTitle:** solution nmr structure of xenopus fn14
73	c2eqpA_	Alignment	not modelled	12.9	45	**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
74	c2kyrA_	Alignment	not modelled	12.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
75	c3kgkA_	Alignment	not modelled	10.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
76	c2kslA_	Alignment	not modelled	10.7	40	**PDB header:**toxin **Chain:** A: **PDB Molecule:**u1-agatoxin-ta1a; **PDBTitle:** structure of the insecticidal toxin taitx-1
77	d1l6ra_	Alignment	not modelled	9.5	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
78	d1dxga_	Alignment	not modelled	7.0	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Desulforedoxin

79	c3cw2M_	Alignment	not modelled	6.8	27	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
80	c1ghqC_	Alignment	not modelled	6.1	30	**PDB header:**immune system/viral protein receptor **Chain:** C: **PDB Molecule:**cr2/cd121/c3d/epstein-barr virus receptor; **PDBTitle:** cr2-c3d complex structure
81	c1neeA_	Alignment	not modelled	5.7	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
82	c4a1aI_	Alignment	not modelled	5.5	13	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
83	d1rutx1	Alignment	not modelled	5.4	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
84	c2xzn5_	Alignment	not modelled	5.4	16	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2