Phyre2

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Description	P0AAJ3
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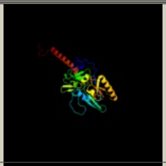
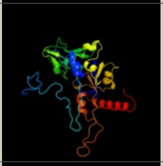
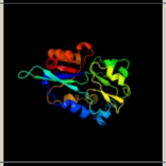
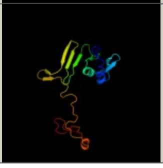
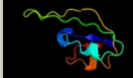
Unique Job ID	2a8c1ccd900434fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kqfB_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
2	d1kqfb1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
3	d1h0hb_	Alignment		100.0	34	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
4	c2ivfB_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
5	c1ti2F_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
6	c2vpyB_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
7	d1vlfn2	Alignment		100.0	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1y5ib1	Alignment		100.0	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c3gyxJ_	Alignment		99.4	26	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
10	d1xera_	Alignment		99.4	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
11	d1jnrb_	Alignment		99.4	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins

12	c2fgoA_	Alignment		99.4	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
13	c2v2kB_	Alignment		99.4	16	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
14	d7fd1a_	Alignment		99.4	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
15	c2zvsB_	Alignment		99.4	17	**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
16	d3c7bb1	Alignment		99.4	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
17	d1h98a_	Alignment		99.4	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
18	d1blua_	Alignment		99.3	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
19	d2fug91	Alignment		99.3	41	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	c2fugG_	Alignment		99.3	41	**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
21	d1rgva_	Alignment	not modelled	99.3	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
22	d1bc6a_	Alignment	not modelled	99.2	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
23	c1gthD_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
24	d1hfel2	Alignment	not modelled	99.1	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
25	c1hfeL_	Alignment	not modelled	99.1	25	**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
26	d2gmha3	Alignment	not modelled	99.1	12	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
27	c2gmhA_	Alignment	not modelled	99.0	16	**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	d1jb0c_	Alignment	not modelled	99.0	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
						PDB header:oxidoreductase

29	c2c3yA_	Alignment	not modelled	99.0	26	**Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
30	d1gtea5	Alignment	not modelled	99.0	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
31	c3c7bE_	Alignment	not modelled	99.0	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
32	d1clfa_	Alignment	not modelled	98.9	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
33	d1dura_	Alignment	not modelled	98.9	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
34	d2c42a5	Alignment	not modelled	98.9	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
35	d1fcaa_	Alignment	not modelled	98.9	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
36	d3c8ya3	Alignment	not modelled	98.9	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
37	c1gx7A_	Alignment	not modelled	98.8	30	**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
38	d2fug34	Alignment	not modelled	98.8	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
39	d1sj1a_	Alignment	not modelled	98.8	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
40	d2fdna_	Alignment	not modelled	98.8	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
41	d1vjwa_	Alignment	not modelled	98.8	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
42	c1dwlA_	Alignment	not modelled	98.8	25	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
43	d1fxra_	Alignment	not modelled	98.7	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
44	c1c4cA_	Alignment	not modelled	98.7	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
45	c3bk7A_	Alignment	not modelled	98.7	35	**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
46	d1iqza_	Alignment	not modelled	98.6	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
47	c2fugC_	Alignment	not modelled	98.6	19	**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	98.6	21	**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	c3c7bA_	Alignment	not modelled	98.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
50	d1kqfb2	Alignment	not modelled	98.2	100	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
51	c2v4jA_	Alignment	not modelled	98.2	21	**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
52	d1kf6b1	Alignment	not modelled	98.0	21	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	d2bs2b1	Alignment	not modelled	97.9	20	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur

						protein, C-terminal domain
54	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
55	c3cf4A_	Alignment	not modelled	97.7	35	**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
56	c1nekB_	Alignment	not modelled	97.6	16	**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
57	c2b76N_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
58	c2bs2E_	Alignment	not modelled	97.3	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
59	c2h89B_	Alignment	not modelled	97.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
60	d2v4jb1	Alignment	not modelled	97.2	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
61	c2vdcl_	Alignment	not modelled	94.7	28	**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.
62	d2v4ja1	Alignment	not modelled	90.9	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
63	d3c7ba1	Alignment	not modelled	90.3	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
64	d1gtea1	Alignment	not modelled	85.6	39	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
65	d1fxda_	Alignment	not modelled	72.3	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
66	c2kncA_	Alignment	not modelled	45.2	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
67	d2r4qa1	Alignment	not modelled	44.4	33	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
68	c2a91A_	Alignment	not modelled	25.0	22	**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
69	c1moxB_	Alignment	not modelled	22.1	20	**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
70	c2dtgE_	Alignment	not modelled	20.6	34	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
71	c1g8jC_	Alignment	not modelled	19.4	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
72	d1djqa3	Alignment	not modelled	18.3	38	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
73	c2fugA_	Alignment	not modelled	15.0	27	**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
74	d1yuza2	Alignment	not modelled	14.2	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
75	d2noca1	Alignment	not modelled	12.0	13	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
76	c2rhbD_	Alignment	not modelled	10.0	24	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure of nsp15-h234a mutant- hexamer in2 asymmetric unit
77	c2a45J_	Alignment	not modelled	9.9	32	**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	c2eqpA_	Alignment	not modelled	9.3	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
						Fold: Microbial ribonucleases

79	d1i0va_	Alignment	not modelled	9.2	20	**Superfamily:**Microbial ribonucleases **Family:**Fungal ribonucleases
80	d2r48a1	Alignment	not modelled	9.2	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
81	d1rdsa_	Alignment	not modelled	9.0	14	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Fungal ribonucleases
82	c1deqD_	Alignment	not modelled	9.0	29	**PDB header:** **PDB COMPND:**
83	c2a5hC_	Alignment	not modelled	8.3	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
84	c1skzA_	Alignment	not modelled	8.0	19	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**antistasin; **PDBTitle:** protease inhibitor
85	c2dxbR_	Alignment	not modelled	7.6	35	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
86	c2kn0A_	Alignment	not modelled	7.6	36	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fn14; **PDBTitle:** solution nmr structure of xenopus fn14
87	c3qyhG_	Alignment	not modelled	7.4	29	**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.
88	c1vbjB_	Alignment	not modelled	7.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
89	c2pmzS_	Alignment	not modelled	7.4	21	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
90	c3ghgD_	Alignment	not modelled	7.3	32	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
91	c2hr7B_	Alignment	not modelled	6.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (domains 1-3)
92	c3iufA_	Alignment	not modelled	6.8	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of2 human ubi-d4
93	d2dmda3	Alignment	not modelled	6.7	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
94	d1nnqa2	Alignment	not modelled	6.4	38	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
95	c3k7aM_	Alignment	not modelled	6.1	26	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
96	d1kbsa_	Alignment	not modelled	5.6	29	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
97	d1x5wa2	Alignment	not modelled	5.4	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
98	c1m1jA_	Alignment	not modelled	5.4	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
99	d2cs3a1	Alignment	not modelled	5.4	36	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain