Phyre^2

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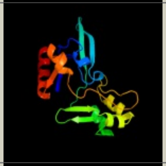
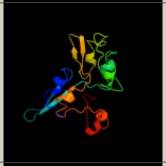
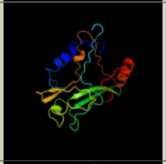
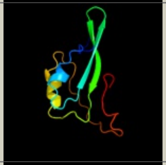
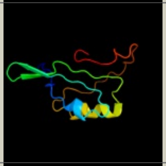
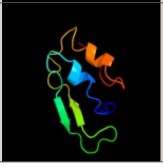
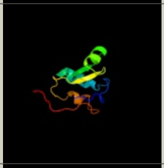
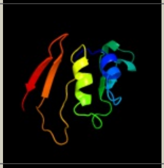
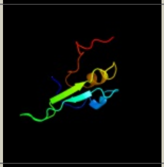
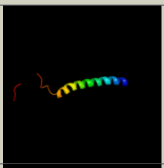
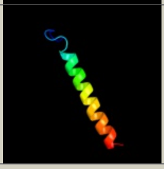
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kqfB_	Alignment		99.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
2	c2ivfB_	Alignment		99.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
3	d1kqfb1	Alignment		99.9	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
4	c2vpyB_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
5	d1h0hb_	Alignment		99.9	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
6	c1ti2F_	Alignment		99.9	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
7	d1y5ib1	Alignment		99.9	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
8	d1vlfn2	Alignment		99.8	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c2fugG_	Alignment		99.4	18	**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
10	d2fug91	Alignment		99.4	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
11	d1xera_	Alignment		99.3	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins

12	c2c3yA_	Alignment		99.2	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
13	d2c42a5	Alignment		99.2	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
14	c1gthD_	Alignment		99.1	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
15	c2gmhA_	Alignment		99.1	17	**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
16	d1jb0c_	Alignment		99.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
17	c3gyxJ_	Alignment		99.0	26	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
18	d7fd1a_	Alignment		99.0	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
19	d1blua_	Alignment		99.0	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
20	d1hfel2	Alignment		99.0	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
21	c2zvsB_	Alignment	not modelled	99.0	21	**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
22	c2fgoA_	Alignment	not modelled	99.0	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
23	d1rgva_	Alignment	not modelled	99.0	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
24	d1bc6a_	Alignment	not modelled	99.0	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
25	d2fug34	Alignment	not modelled	99.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
26	d1gtea5	Alignment	not modelled	99.0	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
27	d1jnrb_	Alignment	not modelled	98.9	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
28	d1dura_	Alignment	not modelled	98.9	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
						PDB header:hydrolyase/translation

29	c3bk7A_	Alignment	not modelled	98.9	32	**Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
30	d2fdna_	Alignment	not modelled	98.9	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
31	d1h98a_	Alignment	not modelled	98.9	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
32	d1clfa_	Alignment	not modelled	98.9	38	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
33	c1hfeL_	Alignment	not modelled	98.9	18	**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
34	d1fcaa_	Alignment	not modelled	98.9	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	c2fugC_	Alignment	not modelled	98.8	21	**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
36	d3c8ya3	Alignment	not modelled	98.8	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
37	d2gmha3	Alignment	not modelled	98.8	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
38	c3c7bE_	Alignment	not modelled	98.8	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
39	c1c4cA_	Alignment	not modelled	98.7	27	**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
40	d3c7bb1	Alignment	not modelled	98.7	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
41	c2v2kB_	Alignment	not modelled	98.7	26	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
42	c2v4jE_	Alignment	not modelled	98.6	14	**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
43	d1iqza_	Alignment	not modelled	98.6	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
44	c1gx7A_	Alignment	not modelled	98.6	27	**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
45	d1vjwa_	Alignment	not modelled	98.6	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
46	c3c7bA_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
47	c1dwlA_	Alignment	not modelled	98.2	24	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
48	d1sj1a_	Alignment	not modelled	98.1	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
49	c2v4jA_	Alignment	not modelled	98.1	15	**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	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
51	d1fxra_	Alignment	not modelled	97.9	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
52	d1kf6b1	Alignment	not modelled	97.8	23	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	c2b76N_	Alignment	not modelled	97.8	20	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein;

						PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
54	c2bs2E_	Alignment	not modelled	97.7	20	**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	97.7	20	**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	d1nekb1	Alignment	not modelled	97.6	19	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
57	c2h89B_	Alignment	not modelled	97.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
58	c3cf4A_	Alignment	not modelled	97.3	23	**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	97.3	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
60	c2vdcI_	Alignment	not modelled	96.7	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	c2e76D_	Alignment		95.8	23	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
62	c1p84E_	Alignment		92.7	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
63	d2v4ja1	Alignment	not modelled	91.7	26	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
64	d3c7ba1	Alignment	not modelled	91.7	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
65	c2fynO_	Alignment	not modelled	86.1	25	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
66	c2fyuE_	Alignment	not modelled	81.0	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
67	d1gtea1	Alignment	not modelled	77.3	47	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
68	d1fxda_	Alignment	not modelled	76.7	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
69	d2e74d2	Alignment	not modelled	62.2	24	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
70	c2pq4B_	Alignment	not modelled	59.7	27	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
71	d1q90r_	Alignment	not modelled	57.5	27	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
72	c1q90R_	Alignment	not modelled	57.5	27	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
73	c1g8jC_	Alignment	not modelled	49.2	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
74	c3o0rC_	Alignment	not modelled	36.9	11	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
75	c2dtgE_	Alignment	not modelled	26.9	30	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
76	d1rhzb_	Alignment	not modelled	26.7	25	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit

						Family: Preprotein translocase SecE subunit
77	c1moxB_	Alignment	not modelled	22.9	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
78	c2ww9B_	Alignment	not modelled	22.3	24	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
79	c2htfA_	Alignment	not modelled	17.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
80	c2a91A_	Alignment	not modelled	16.3	20	**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
81	d1ssla_	Alignment	not modelled	11.9	40	**Fold:**Trefoil/Plexin domain-like **Superfamily:**Plexin repeat **Family:**Plexin repeat
82	c2wwbB_	Alignment	not modelled	10.8	33	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
83	c2o01H_	Alignment	not modelled	7.5	17	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosystem i reaction center subunit vi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
84	c2p0gB_	Alignment	not modelled	7.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
85	d1djqa3	Alignment	not modelled	7.5	21	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
86	c3dexA_	Alignment	not modelled	7.4	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
87	d2fa8a1	Alignment	not modelled	7.3	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
88	c2obkE_	Alignment	not modelled	7.2	36	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**selt/selw/selh selenoprotein domain; **PDBTitle:** x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
89	c2jz2A_	Alignment	not modelled	6.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
90	d1m3va1	Alignment	not modelled	5.4	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
91	c2ojlB_	Alignment	not modelled	5.4	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
92	c3lw5H_	Alignment	not modelled	5.2	12	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** improved model of plant photosystem i