Phyre^2

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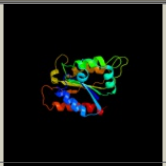
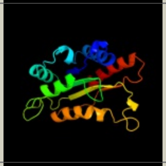
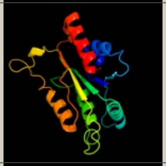
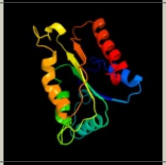
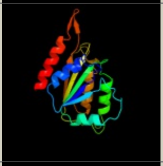
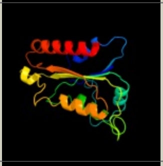
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eywA_	Alignment		100.0	100	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
2	c3f2vA_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
3	d1dxqa_	Alignment		100.0	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
4	d1qrda_	Alignment		100.0	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
5	c3ha2B_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
6	d1d4aa_	Alignment		100.0	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
7	c2amjD_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
8	c3rpeA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
9	d2qwxa1	Alignment		100.0	33	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
10	c3lcmB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
11	c3p0rA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne

12	c2hpvA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
13	c2v9cA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1; **PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
14	d2z98a1	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
15	d1t5ba_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
16	d1rlia_	Alignment		100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
17	d1nni1_	Alignment		99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
18	d1rtta_	Alignment		99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
19	c3fvwA_	Alignment		99.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
20	d1sqsa_	Alignment		99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
21	c2q62A_	Alignment	not modelled	99.9	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
22	c3k1yE_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
23	d1t0ia_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
24	d1ydga_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
25	c2vzhA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
26	c2fzvC_	Alignment	not modelled	99.9	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
27	d2fzva1	Alignment	not modelled	99.8	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
28	c3b6iB_	Alignment	not modelled	99.8	18	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure

29	d2a5la1	Alignment	not modelled	99.8	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
30	c2zkiH_	Alignment	not modelled	99.8	22	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
31	c3d7nA_	Alignment	not modelled	99.8	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
32	d1e5da1	Alignment	not modelled	99.7	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
33	d1ycga1	Alignment	not modelled	99.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
34	d2arka1	Alignment	not modelled	99.7	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
35	c1ychD_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
36	c2ohiB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
37	d1vmea1	Alignment	not modelled	99.6	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
38	c2q9uB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
39	c1e5dA_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
40	c3fniA_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
41	c3klbA_	Alignment	not modelled	99.4	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
42	c1vmeB_	Alignment	not modelled	99.3	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
43	c3hlyA_	Alignment	not modelled	99.3	22	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
44	c3edoA_	Alignment	not modelled	99.3	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
45	d2fz5a1	Alignment	not modelled	99.2	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
46	d5nula_	Alignment	not modelled	99.0	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
47	c3f6sI_	Alignment	not modelled	98.8	12	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
48	d1ag9a_	Alignment	not modelled	98.6	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
49	c3hr4C_	Alignment	not modelled	98.5	8	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
50	d1tlla2	Alignment	not modelled	98.5	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
51	d1oboa_	Alignment	not modelled	98.5	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
52	d1ykga1	Alignment	not modelled	98.4	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
53	d1czna_	Alignment	not modelled	98.4	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
						PDB header:oxidoreductase

54	c1bvyF_	Alignment	not modelled	98.4	12	**Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
55	d1bvyf_	Alignment	not modelled	98.4	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
56	d1b1ca_	Alignment	not modelled	98.2	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
57	c2wc1A_	Alignment	not modelled	98.2	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
58	d1f4pa_	Alignment	not modelled	98.1	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
59	d2fcra_	Alignment	not modelled	98.0	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	c1tlIA_	Alignment	not modelled	98.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
61	d1yoba1	Alignment	not modelled	97.9	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
62	d1fuea_	Alignment	not modelled	97.9	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
63	d1ja1a2	Alignment	not modelled	97.9	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
64	c2hnbA_	Alignment	not modelled	97.7	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
65	c2bpoA_	Alignment	not modelled	94.7	13	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
66	c1j9zB_	Alignment	not modelled	94.3	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
67	c2x2oA_	Alignment	not modelled	90.6	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
68	d1rlja_	Alignment	not modelled	78.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
69	d1yrba1	Alignment	not modelled	77.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
70	d1yqea1	Alignment	not modelled	65.4	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
71	c1q7tA_	Alignment	not modelled	56.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
72	d1q74a_	Alignment	not modelled	56.0	15	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
73	c3dfiA_	Alignment	not modelled	55.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pseudoaglycone deacetylase dbv21; **PDBTitle:** the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
74	c3mw8A_	Alignment	not modelled	50.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
75	d2r4qa1	Alignment	not modelled	42.8	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
76	c3dfmA_	Alignment	not modelled	40.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teicoplanin pseudoaglycone deacetylase orf2; **PDBTitle:** the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
77	d1uana_	Alignment	not modelled	38.5	11	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
78	c2kokA_	Alignment	not modelled	30.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
79	c3l4eA_	Alignment	not modelled	29.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
						Fold:P-loop containing nucleoside triphosphate hydrolases

80	d1jala1	Alignment	not modelled	29.6	15	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
81	d1mv8a3	Alignment	not modelled	22.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain **Family:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
82	c3iprC_	Alignment	not modelled	21.8	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
83	c2ixdB_	Alignment	not modelled	21.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
84	c2gedB_	Alignment	not modelled	20.8	7	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
85	d1jr2a_	Alignment	not modelled	20.0	5	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
86	c1jr2A_	Alignment	not modelled	20.0	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
87	d1ir6a_	Alignment	not modelled	18.8	10	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
88	c1ir6A_	Alignment	not modelled	18.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
89	c3gg2B_	Alignment	not modelled	17.4	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
90	d1z3ea1	Alignment	not modelled	15.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
91	c2gfqC_	Alignment	not modelled	15.3	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
92	c3n39D_	Alignment	not modelled	15.2	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
93	c3mtqA_	Alignment	not modelled	15.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
94	d1t4za_	Alignment	not modelled	13.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
95	d2r48a1	Alignment	not modelled	12.3	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
96	c3l78A_	Alignment	not modelled	11.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
97	c3g79A_	Alignment	not modelled	11.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; **PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
98	d1t3ta3	Alignment	not modelled	10.4	18	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**FGAM synthase PurL, PurS-like domain
99	c2yvuA_	Alignment	not modelled	10.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195