Phyre^2

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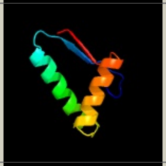
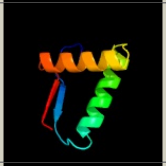
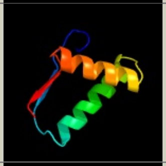
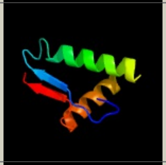
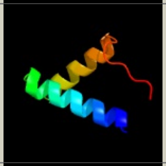
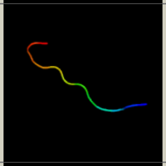
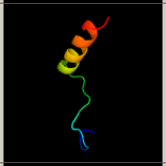
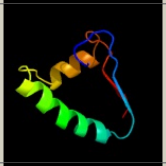
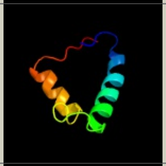
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qftA_	Alignment		94.9	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase; **PDBTitle:** crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
2	c2qtzA_	Alignment		94.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
3	c6j7aB_	Alignment		93.9	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**heme oxygenase 1,nadph--cytochrome p450 reductase; **PDBTitle:** fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
4	c2bpoA_	Alignment		93.8	28	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
5	c1ddiA_	Alignment		93.7	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha-component; **PDBTitle:** crystal structure of sir-fp60
6	c6efvA_	Alignment		93.1	32	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha-component; **PDBTitle:** the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
7	c5gxuA_	Alignment		92.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase 2; **PDBTitle:** cystal structure of arabidopsis atr2
8	c1j9zB_	Alignment		92.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
9	c1f20A_	Alignment		91.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
10	c4dqkA_	Alignment		91.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bifunctional p-450/nadph-p450 reductase; **PDBTitle:** crystal structure of the fad binding domain of cytochrome p450 bm3
11	d1ddga2	Alignment		88.6	32	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like

12	d1ja1a3	Alignment		88.1	28	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
13	c1tllA_	Alignment		87.6	21	**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.
14	d1f20a2	Alignment		80.8	26	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
15	c4u3qA_	Alignment		56.7	67	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**17 kda lipoprotein; **PDBTitle:** crystal structure of recombinant tp0435 from treponema pallidum
16	c6drfA_	Alignment		55.8	34	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein rd3; **PDBTitle:** structure of human retinal degeneration 3(rd3) protein
17	c1fncA_	Alignment		45.2	19	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
18	c1jb9A_	Alignment		45.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
19	d1jb9a2	Alignment		36.2	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
20	c2rc5D_	Alignment		35.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** refined structure of fnr from leptospira interrogans
21	c1qgyA_	Alignment	not modelled	34.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
22	c4nexA_	Alignment	not modelled	32.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** structure of the n-acetyltransferase domain of x. fastidiosa nags/k
23	d2proc1	Alignment	not modelled	31.5	33	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
24	d1sm4a2	Alignment	not modelled	27.5	19	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
25	d1wi3a_	Alignment	not modelled	25.9	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	d1dvoa_	Alignment	not modelled	24.1	32	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
27	d1qfza2	Alignment	not modelled	24.0	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
28	c3ltiA_	Alignment	not modelled	18.3	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
						Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain

29	d1fnda2	Alignment	not modelled	18.0	19	**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
30	c2b5oA_	Alignment	not modelled	12.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
31	d1s3ia2	Alignment	not modelled	12.2	60	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
32	d1ei5a1	Alignment	not modelled	11.6	46	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
33	c3kcqA_	Alignment	not modelled	11.3	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
34	c3shgB_	Alignment	not modelled	11.2	50	**PDB header:**transferase/protein binding **Chain:** B: **PDB Molecule:**vbha; **PDBTitle:** vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
35	d2bw0a2	Alignment	not modelled	10.9	60	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
36	c1yrwA_	Alignment	not modelled	9.7	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
37	d1fmta2	Alignment	not modelled	9.6	50	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
38	c1zghA_	Alignment	not modelled	9.5	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
39	d1zgha2	Alignment	not modelled	9.5	50	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
40	c4s1nA_	Alignment	not modelled	9.4	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
41	c3aufA_	Alignment	not modelled	8.5	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycinamide ribonucleotide transformylase 1; **PDBTitle:** crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
42	c5uaiA_	Alignment	not modelled	8.4	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
43	c3tqrA_	Alignment	not modelled	8.4	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
44	c3iz5d_	Alignment	not modelled	8.3	75	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4 (l4p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
45	c3izrd_	Alignment	not modelled	8.3	75	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4 (l4p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
46	c6ci2A_	Alignment	not modelled	8.2	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formyltransferase psej; **PDBTitle:** crystal structure of the formyltransferase psej from anoxybacillus2 kamchatkensis
47	c3tqqA_	Alignment	not modelled	8.1	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
48	c4ds3A_	Alignment	not modelled	7.9	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
49	c3rfoA_	Alignment	not modelled	7.8	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
50	c4npgA_	Alignment	not modelled	7.6	43	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of a hypothetical protein (bt1938) from bacteroides2 thetaiotaomicron vpi-5482 at 2.50 a resolution
51	c2ibjA_	Alignment	not modelled	7.2	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome b5; **PDBTitle:** structure of house fly cytochrome b5
52	c1fmtA_	Alignment	not modelled	7.1	56	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
53	c5vytD_	Alignment	not modelled	7.1	78	**PDB header:**transferase **Chain:** D: **PDB Molecule:**gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- **PDBTitle:** crystal structure of the wbkc n-formyltransferase (f142a

						variant) from2 brucella melitensis
54	c4faoI_	Alignment	not modelled	7.1	39	**PDB header:**signaling protein/signaling protein **Chain:** I: **PDB Molecule:**serine/threonine-protein kinase receptor r3; **PDBTitle:** specificity and structure of a high affinity activin-like 1 (alk1)2 signaling complex
55	d1jkxa_	Alignment	not modelled	7.1	60	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
56	c5ujhA_	Alignment	not modelled	7.0	83	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin; **PDBTitle:** ov-grn12-34
57	c5jsdB_	Alignment	not modelled	7.0	50	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**phiab6 tailspike; **PDBTitle:** crystal structure of phiab6 tailspike in complex with five-repeated2 oligosaccharides of acinetobacter baumannii surface polysaccharide
58	d3proc1	Alignment	not modelled	6.9	54	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
59	c5ujgA_	Alignment	not modelled	6.7	83	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin; **PDBTitle:** ovgrn12-35_3s
60	c3q0iA_	Alignment	not modelled	6.6	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
61	d2c4fl3	Alignment	not modelled	6.5	73	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
62	c4nv1D_	Alignment	not modelled	6.5	50	**PDB header:**transferase **Chain:** D: **PDB Molecule:**formyltransferase; **PDBTitle:** crystal structure of a 4-n formyltransferase from francisella2 tularensis
63	c5al6A_	Alignment	not modelled	6.4	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**anastral spindle 2; **PDBTitle:** central coiled-coil domain (cccd) of drosophila melanogaster ana2. a2 natural, parallel, tetrameric coiled-coil bundle.
64	c3et4A_	Alignment	not modelled	6.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**outer membrane protein p4, nadp phosphatase; **PDBTitle:** structure of recombinant haemophilus influenzae e(p4) acid phosphatase
65	d1cyoa_	Alignment	not modelled	6.3	24	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
66	c4b8nC_	Alignment	not modelled	6.3	25	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**cytochrome b5-host origin; **PDBTitle:** cytochrome b5 of ostreococcus tauri virus 2
67	c4pzuF_	Alignment	not modelled	6.1	50	**PDB header:**transferase **Chain:** F: **PDB Molecule:**uncharacterized protein rv3404c/mt3512; **PDBTitle:** crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
68	c3tdqB_	Alignment	not modelled	6.0	24	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
69	c6gmaA_	Alignment	not modelled	5.9	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**rb1-inducible coiled-coil protein 1; **PDBTitle:** crystal structure of the fip200 c-terminal region
70	c3p9xB_	Alignment	not modelled	5.8	56	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
71	d1rgoa2	Alignment	not modelled	5.8	64	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger
72	c3hrdF_	Alignment	not modelled	5.8	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
73	c2kc8B_	Alignment	not modelled	5.7	64	**PDB header:**toxin/toxin repressor **Chain:** B: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
74	c2ywrA_	Alignment	not modelled	5.7	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex aeolicus
75	c3o1lB_	Alignment	not modelled	5.7	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
76	c4lzxB_	Alignment	not modelled	5.5	38	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**iq domain-containing protein g; **PDBTitle:** complex of iqcg and ca2+-free cam
77	d1meoa_	Alignment	not modelled	5.5	70	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase

78	d1axib1	Alignment	not modelled	5.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
79	c2i34B_	Alignment	not modelled	5.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound