Phyre2

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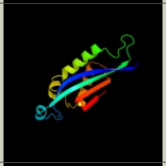
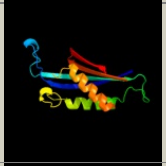
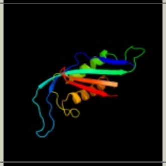
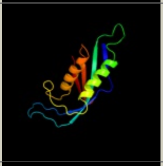
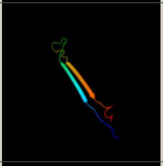
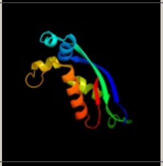
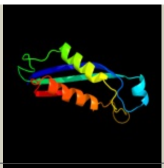
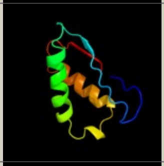
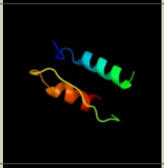
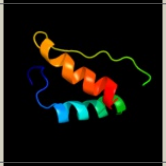
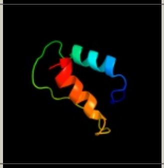
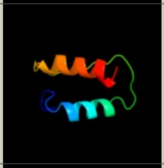
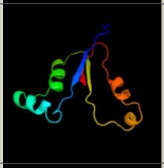
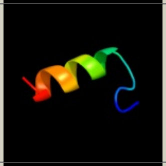
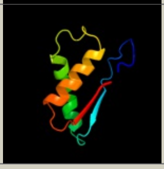
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2obaE_	Alignment		100.0	75	**PDB header:**lyase **Chain:** E: **PDB Molecule:**probable 6-pyruvoyl tetrahydrobiopterin synthase; **PDBTitle:** pseudomonas aeruginosa 6-pyruvoyl tetrahydrobiopterin synthase
2	d2g64a1	Alignment		100.0	32	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
3	d1b66a_	Alignment		100.0	33	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
4	c3jygB_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein ws1659 from2 wolinella succinogenes
5	c3d7jD_	Alignment		100.0	21	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein sco6650; **PDBTitle:** sco6650, a 6-pyruvoyltetrahydropterin synthase homolog from2 streptomyces coelicolor
6	c2dj6B_	Alignment		100.0	34	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein ph0634; **PDBTitle:** crystal structure of 6-pyruvoyl tetrahydrobiopterin synthase from2 pyrococcus horikoshii ot3
7	d2a0sa1	Alignment		100.0	28	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
8	d1y13a_	Alignment		100.0	28	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
9	c2l7eA_	Alignment		58.6	4	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid subunit 14; **PDBTitle:** the structure of a domain from yeast
10	c2o90A_	Alignment		48.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** atomic resolution crystal structure of e.coli2 dihydroneopterin aldolase in complex with neopterin
11	d1dhna_	Alignment		48.1	18	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase

12	c2cg8B_	Alignment		45.9	20	**PDB header:**lyase/transferase **Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8- **PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
13	d1oaoc_	Alignment		31.3	24	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
14	d1yaga1	Alignment		29.4	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	d1k8ka1	Alignment		21.1	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
16	d2hf3a1	Alignment		20.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	d2fxua1	Alignment		20.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
18	c3rhfB_	Alignment		19.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
19	c2ju2A_	Alignment		19.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase; **PDBTitle:** minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
20	c3gitA_	Alignment		18.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
21	c3czpA_	Alignment	not modelled	15.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
22	d1c0fa1	Alignment	not modelled	14.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
23	c2fvgA_	Alignment	not modelled	14.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
24	d1aoza3	Alignment	not modelled	13.7	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
25	d1kyaa3	Alignment	not modelled	13.5	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
26	c1sqlN_	Alignment	not modelled	12.6	20	**PDB header:**lyase **Chain:** N: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
27	d2q9oa3	Alignment	not modelled	11.1	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
28	d1b9la_	Alignment	not modelled	10.8	9	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
						Fold: Prismane protein-like

29	d1ru3a_	Alignment	not modelled	10.3	25	**Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
30	d1hfua3	Alignment	not modelled	9.7	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
31	c3qb0C_	Alignment	not modelled	9.4	10	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin-related protein 4; **PDBTitle:** crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
32	d1jjca_	Alignment	not modelled	9.2	22	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
33	c2pe3A_	Alignment	not modelled	9.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**354aa long hypothetical operon protein frv; **PDBTitle:** crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
34	d1td6a_	Alignment	not modelled	9.0	19	**Fold:**Hypothetical protein MPN330 **Superfamily:**Hypothetical protein MPN330 **Family:**Hypothetical protein MPN330
35	d2h1ta1	Alignment	not modelled	9.0	33	**Fold:**Spiral beta-roll **Superfamily:**PA1994-like **Family:**PA1994-like
36	d1sqla_	Alignment	not modelled	8.6	20	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
37	d1gyca3	Alignment	not modelled	8.1	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
38	c3czqA_	Alignment	not modelled	7.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
39	c3sqgF_	Alignment	not modelled	7.5	33	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methyl-coenzyme m reductase, gamma subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
40	c2afdA_	Alignment	not modelled	7.4	31	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**protein asl1650; **PDBTitle:** solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
41	d1nbua_	Alignment	not modelled	6.9	18	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
42	d1hbnc_	Alignment	not modelled	6.9	39	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
43	d2gdwa1	Alignment	not modelled	6.5	31	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
44	c1zpuE_	Alignment	not modelled	6.5	56	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3; **PDBTitle:** crystal structure of fet3p, a multicopper oxidase that functions in2 iron import
45	c1zvbC_	Alignment	not modelled	6.2	24	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
46	d1e6yc_	Alignment	not modelled	6.0	39	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
47	c2gejA_	Alignment	not modelled	5.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
48	c1b70A_	Alignment	not modelled	5.6	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
49	c2ihr1_	Alignment	not modelled	5.5	29	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
50	d1v10a3	Alignment	not modelled	5.3	67	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
51	d1e6vc_	Alignment	not modelled	5.3	28	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
52	c3abgA_	Alignment	not modelled	5.2	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bilirubin oxidase; **PDBTitle:** x-ray crystal analysis of bilirubin oxidase from myrothecium2 verrucaria at 2.3 angstrom resolution using a twin crystal