Phyre^2

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Description	P0AC19
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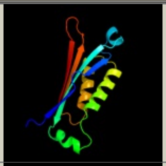
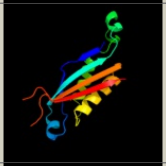
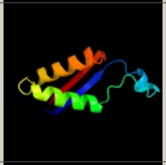
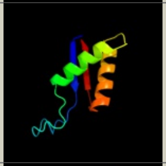
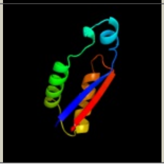
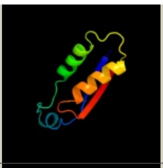
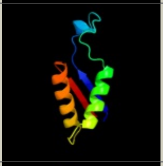
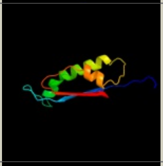
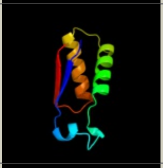
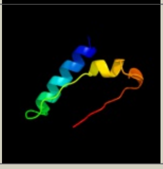
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b9la_	Alignment		100.0	100	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
2	c1sqlN_	Alignment		100.0	20	**PDB header:**lyase **Chain:** N: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
3	c2o90A_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** atomic resolution crystal structure of e.coli2 dihydroneopterin aldolase in complex with neopterin
4	d1sqla_	Alignment		100.0	20	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
5	d1nbua_	Alignment		100.0	23	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
6	d1dhna_	Alignment		100.0	20	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
7	c2cg8B_	Alignment		100.0	19	**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
8	d2ibaa1	Alignment		91.7	14	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
9	d2yzca1	Alignment		88.7	14	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
10	d1j2ga1	Alignment		87.8	9	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
11	c1r56H_	Alignment		85.9	14	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**uricase; **PDBTitle:** uncomplexed urate oxidase from aspergillus flavus

12	c2yzbA_	Alignment		83.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uricase; **PDBTitle:** crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
13	c1j2gC_	Alignment		77.0	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**uricase; **PDBTitle:** crystal structure of urate oxidase from bacillus sp. tb-90 co-2 crystallized with 8-azaxanthine
14	d1y13a_	Alignment		53.4	13	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
15	c2dj6B_	Alignment		45.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein ph0634; **PDBTitle:** crystal structure of 6-pyruvoyl tetrahydrobiopterin synthase from2 pyrococcus horikoshii ot3
16	d2a0sa1	Alignment		41.0	13	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
17	c2r5rA_	Alignment		33.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0343 protein ne1163; **PDBTitle:** the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718
18	d1j2ga2	Alignment		27.0	7	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
19	c3d2oB_	Alignment		20.3	19	**PDB header:**hydrolase, biosynthetic protein **Chain:** B: **PDB Molecule:**upf0343 protein ngo0387; **PDBTitle:** crystal structure of manganese-metallated gtp cyclohydrolase2 type ib
20	d1ghha_	Alignment		14.5	10	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
21	d2ieca1	Alignment	not modelled	12.1	23	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
22	d1oaoc_	Alignment	not modelled	11.9	14	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
23	d1ru3a_	Alignment	not modelled	11.1	19	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
24	c2obaE_	Alignment	not modelled	9.4	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**probable 6-pyruvoyl tetrahydrobiopterin synthase; **PDBTitle:** pseudomonas aeruginosa 6-pyruvoyl tetrahydrobiopterin synthase
25	d1a04a2	Alignment	not modelled	8.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	d1wpla_	Alignment	not modelled	7.3	17	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
27	c1is7F_	Alignment	not modelled	7.3	17	**PDB header:**hydrolase/protein binding **Chain:** F: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex
28	d2i52a1	Alignment	not modelled	7.3	7	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
						Fold:T-fold

29	d2yzca2	Alignment	not modelled	7.2	11	**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
30	c2zw2B_	Alignment	not modelled	7.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
31	c2i44A_	Alignment	not modelled	7.0	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine-threonine phosphatase 2c; **PDBTitle:** crystal structure of serine-threonine phosphatase 2c from2 toxoplasma gondii
32	d1a8ra_	Alignment	not modelled	6.7	21	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
33	c2ogfD_	Alignment	not modelled	6.6	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
34	d1gpma3	Alignment	not modelled	5.8	10	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**GMP synthetase C-terminal dimerisation domain **Family:**GMP synthetase C-terminal dimerisation domain
35	d1a6qa2	Alignment	not modelled	5.7	16	**Fold:**PP2C-like **Superfamily:**PP2C-like **Family:**PP2C-like
36	d1b66a_	Alignment	not modelled	5.6	15	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase