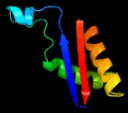










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3607c_folB_4048923_4049324
Date	Fri Aug 9 18:20:29 BST 2019
Unique Job ID	969ee3d5a635e4ef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dhna_	Alignment		100.0	33	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
2	d1nbua_	Alignment		100.0	100	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
3	c5f3mA_	Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: 7,8-dihydroneopterin aldolase; PDBTitle: crystal structure of dihydroneopterin aldolase from bacillus anthracis2 complexed with l-neopterin at 1.5 angstroms resolution .
4	c1sqlN_	Alignment		100.0	42	PDB header: lyase Chain: N: PDB Molecule: dihydroneopterin aldolase; PDBTitle: crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
5	d1sqLA_	Alignment		100.0	42	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
6	c2o90A_	Alignment		100.0	32	PDB header: lyase Chain: A: PDB Molecule: dihydroneopterin aldolase; PDBTitle: atomic resolution crystal structure of e.coli dihydroneopterin2 aldolase in complex with neopterin
7	d1b9la_	Alignment		100.0	23	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
8	c2cg8B_	Alignment		100.0	24	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
9	c3v9oA_	Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: dihydroneopterin aldolase; PDBTitle: crystal structure of dihydroneopterin aldolase (bth_i0291) from2 burkholderia thailendensis bound to guanine.
10	c4aeyA_	Alignment		100.0	25	PDB header: isomerase Chain: A: PDB Molecule: d-erythro-7,8-dihydroneopterin triphosphate epimerase; PDBTitle: crystal structure of folx from pseudomonas aeruginosa
11	d2ibaa1	Alignment		90.9	13	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)

12	c5m98H_	Alignment		89.3	16	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: crystal structure of urate oxidase from zebrafish
13	d2yzca1	Alignment		87.6	12	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
14	d1j2ga1	Alignment		86.7	10	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
15	c1r56H_	Alignment		83.7	13	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: uncomplexed urate oxidase from aspergillus flavus
16	c2yzbA_	Alignment		82.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: uricase; PDBTitle: crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
17	c1j2gC_	Alignment		76.1	10	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
18	c4r99B_	Alignment		74.8	10	PDB header: hydrolase Chain: B: PDB Molecule: uricase; PDBTitle: crystal structure of a uricase from bacillus fastidiosus
19	c2dj6B_	Alignment		62.9	23	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein ph0634; PDBTitle: crystal structure of 6-pyruvoyl tetrahydrobiopterin synthase from2 pyrococcus horikoshii ot3
20	c3d2oB_	Alignment		58.0	15	PDB header: hydrolase, biosynthetic protein Chain: B: PDB Molecule: upf0343 protein ngo0387; PDBTitle: crystal structure of manganese-metallated gtp cyclohydrolase type ib
21	c2r5rA_	Alignment	not modelled	55.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0343 protein ne1163; PDBTitle: the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718
22	c5jyxB_	Alignment	not modelled	49.6	15	PDB header: transferase Chain: B: PDB Molecule: archaeosine synthase quef-like; PDBTitle: crystal structure of the covalent thioimide intermediate of the2 archaeosine synthase quef-like
23	c4jndA_	Alignment	not modelled	44.2	14	PDB header: hydrolase Chain: A: PDB Molecule: ca(2+)/calmodulin-dependent protein kinase phosphatase; PDBTitle: structure of a c.elegans sex determining protein
24	c2mraA_	Alignment	not modelled	37.7	20	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein or459; PDBTitle: solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or459
25	d1y13a_	Alignment	not modelled	30.6	25	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
26	d1j2ga2	Alignment	not modelled	18.2	7	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
27	d2a0sa1	Alignment	not modelled	16.9	19	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
28	c2i44A_	Alignment	not modelled	14.6	12	PDB header: hydrolase Chain: A: PDB Molecule: serine-threonine phosphatase 2c; PDBTitle: crystal structure of serine-threonine phosphatase 2c from2 toxoplasma gondii
						Fold: PP2C-like

29	d1a6qa2	Alignment	not modelled	12.0	14	Superfamily: PP2C-like Family: PP2C-like
30	c2qnkA	Alignment	not modelled	9.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
31	c6a4mA	Alignment	not modelled	9.3	9	PDB header: hydrolase Chain: A: PDB Molecule: uric acid degradation bifunctional protein pucl; PDBTitle: structure of urate oxidase from bacillus subtilis 168
32	c4e9iB	Alignment	not modelled	9.1	25	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
33	c3gdzA	Alignment	not modelled	8.5	5	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
34	c1is7F	Alignment	not modelled	8.5	17	PDB header: hydrolase/protein binding Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/gfrp stimulatory complex
35	d1wpla	Alignment	not modelled	8.5	17	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
36	d1a04a2	Alignment	not modelled	8.4	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
37	c4uqfB	Alignment	not modelled	8.3	19	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
38	d2ieca1	Alignment	not modelled	8.2	19	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
39	c5i8iA	Alignment	not modelled	8.1	20	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of the full-length cell wall-binding module of cpl72 mutant r223a
40	d1a8ra	Alignment	not modelled	8.0	10	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
41	c2zw2B	Alignment	not modelled	7.9	16	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
42	c4yzhA	Alignment	not modelled	7.5	13	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: protein phosphatase 2c 57; PDBTitle: structure of the arabidopsis tap38/pph1 in complex with plhcb12 phosphopeptide substrate
43	d1b66a	Alignment	not modelled	6.5	20	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
44	c1a6qA	Alignment	not modelled	6.3	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase 2c; PDBTitle: crystal structure of the protein serine/threonine phosphatase 2c at 22 a resolution
45	d1yfua1	Alignment	not modelled	6.1	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
46	c1qkiE	Alignment	not modelled	6.0	25	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
47	c5i82A	Alignment	not modelled	6.0	57	PDB header: antibiotic Chain: A: PDB Molecule: enterococin k1; PDBTitle: nmr structure of enterocin k1 in 50%/50% tfe/water
48	c6fkfd	Alignment	not modelled	5.6	11	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 1
49	d2apla1	Alignment	not modelled	5.2	18	Fold: PG0816-like Superfamily: PG0816-like Family: PG0816-like
50	d1nt2b	Alignment	not modelled	5.1	14	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
51	d2yzca2	Alignment	not modelled	5.1	9	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)