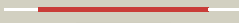
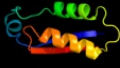
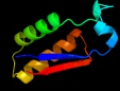


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o90A_	 Alignment		100.0	100	PDB header: lyase Chain: A; PDB Molecule: dihydroneopterin aldolase; PDBTitle: atomic resolution crystal structure of e.coli2 dihydroneopterin aldolase in complex with neopterin
2	clsq1N_	 Alignment		100.0	34	PDB header: lyase Chain: N; PDB Molecule: dihydroneopterin aldolase; PDBTitle: crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
3	dlb9la_	 Alignment		100.0	24	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
4	dlsqla_	 Alignment		100.0	34	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
5	dlnbua_	 Alignment		100.0	31	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
6	dl dhna_	 Alignment		100.0	26	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
7	c2cg8B_	 Alignment		100.0	23	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		94.9	7	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
9	dlj2ga1	 Alignment		93.8	11	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
10	d2yzca1	 Alignment		93.8	17	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
11	c1r56H_	 Alignment		92.7	7	PDB header: oxidoreductase Chain: H; PDB Molecule: uricase; PDBTitle: uncomplexed urate oxidase from aspergillus flavus

12	c2yzbA_	Alignment		92.0	17	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		90.1	11	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	d2a0sa1	Alignment		76.3	15	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
15	c2r5rA_	Alignment		69.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0343 protein ne1163; PDBTitle: the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718
16	d1y13a_	Alignment		55.6	18	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
17	c3d2oB_	Alignment		53.5	24	PDB header: hydrolase, biosynthetic protein Chain: B: PDB Molecule: upf0343 protein ngo0387; PDBTitle: crystal structure of manganese-metallated gtp cyclohydrolase2 type ib
18	c2dj6B_	Alignment		32.7	12	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein ph0634; PDBTitle: crystal structure of 6-pyruvoyl tetrahydrobiopterin synthase from2 pyrococcus horikoshii ot3
19	d1j2ga2	Alignment		25.6	12	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
20	d1a6qa2	Alignment		21.7	19	Fold: PP2C-like Superfamily: PP2C-like Family: PP2C-like
21	c3gdzA_	Alignment	not modelled	15.6	11	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
22	c2i44A_	Alignment	not modelled	13.8	16	PDB header: hydrolase Chain: A: PDB Molecule: serine-threonine phosphatase 2c; PDBTitle: crystal structure of serine-threonine phosphatase 2c from2 toxoplasma gondii
23	d1ghha_	Alignment	not modelled	10.6	21	Fold: DNA damage-inducible protein DinI Superfamily: DNA damage-inducible protein DinI Family: DNA damage-inducible protein DinI
24	d1a04a2	Alignment	not modelled	9.8	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
25	d2yzca2	Alignment	not modelled	9.2	9	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
26	d1wura1	Alignment	not modelled	8.3	20	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
27	c1wm9D_	Alignment	not modelled	8.3	20	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
28	d1wpla_	Alignment	not modelled	7.6	13	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
						PDB header: hydrolase/protein binding

29	c1is7F_	Alignment	not modelled	7.6	13	Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/grfp stimulatory complex
30	d2ibaa2	Alignment	not modelled	7.5	25	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
31	d1a8ra_	Alignment	not modelled	6.9	15	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
32	c2zw2B_	Alignment	not modelled	6.7	12	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)