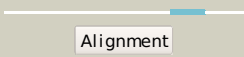

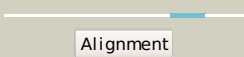

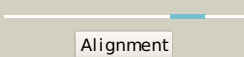

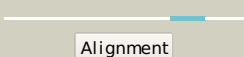

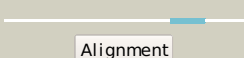



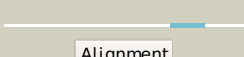

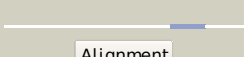



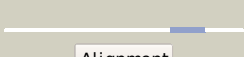

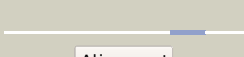



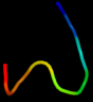





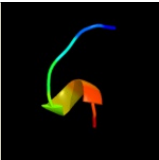


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p2oA_	 Alignment		36.3	20	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
2	c3l07B_	 Alignment		35.7	20	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
3	c2c2xB_	 Alignment		35.2	33	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
4	c3p2oB_	 Alignment		35.2	20	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
5	c4a26B_	 Alignment		34.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5, n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
6	c4a5oB_	 Alignment		34.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
7	c1b0aA_	 Alignment		34.0	20	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
8	d1b0aa1	 Alignment		27.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
9	c1a4iB_	 Alignment		25.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
10	c3nglA_	 Alignment		24.4	33	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
11	d1a4ia1	 Alignment		21.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain

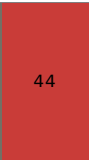
12	c3cwbT_	Alignment		18.4	27	PDB header: oxidoreductase Chain: T: PDB Molecule: mitochondrial ubiquinol-cytochrome c reductase ubiquinone- PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
13	d1ydha_	Alignment		17.6	44	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
14	c2q4dB_	Alignment		17.0	44	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
15	d1bccg_	Alignment		16.5	28	Fold: Single transmembrane helix Superfamily: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
16	d1t35a_	Alignment		16.3	44	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
17	d2q4oa1	Alignment		14.2	56	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
18	c2q4oA_	Alignment		14.2	56	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
19	c3quaA_	Alignment		6.2	22	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis

20 [dlweha_](#)

Alignment



5.3



44

Fold: MCP/YpsA-like
Superfamily: MCP/YpsA-like
Family: MoCo carrier protein-like