








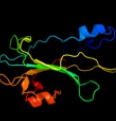









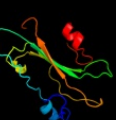


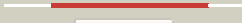

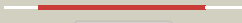
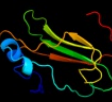



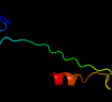



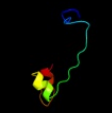



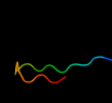
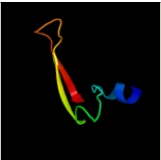


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fjja_	 Alignment		100.0	97	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
2	d1fuxa_	 Alignment		100.0	50	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
3	c3n08A_	 Alignment		100.0	33	PDB header: phosphatidylethanolamine-binding protein Chain: A: PDB Molecule: putative phosphatidylethanolamine-binding protein (pebp); PDBTitle: crystal structure of a putative phosphatidylethanolamine-binding2 protein (pebp) homolog ct736 from chlamydia trachomatis d/uv-3/cx
4	c2evvD_	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein hp0218; PDBTitle: crystal structure of the pebp-like protein of unknown function hp02182 from helicobacter pylori
5	d1wpxb1	 Alignment		99.8	26	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
6	c2r77A_	 Alignment		99.8	23	PDB header: lipid binding protein Chain: A: PDB Molecule: phosphatidylethanolamine-binding protein, putative; PDBTitle: crystal structure of phosphatidylethanolamine-binding protein,2 pfl0955c, from plasmodium falciparum
7	c2qzqA_	 Alignment		99.8	22	PDB header: lipid binding protein Chain: A: PDB Molecule: phosphatidylethanolamine-binding protein; PDBTitle: phosphatidylethanolamine-binding protein from plasmodium vivax
8	c2jyzA_	 Alignment		99.8	31	PDB header: unknown function Chain: A: PDB Molecule: cg7054-pa; PDBTitle: cg7054 solution structure
9	c1wkpA_	 Alignment		99.7	22	PDB header: signaling protein Chain: A: PDB Molecule: flowering locus t protein; PDBTitle: flowering locus t (ft) from arabidopsis thaliana
10	d1qoua_	 Alignment		99.6	21	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
11	d1kn3a_	 Alignment		99.6	30	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein

12	d1a44a_	 Alignment		99.6	31	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
13	d2qyqa1	 Alignment		99.6	33	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
14	c3ks7D_	 Alignment		35.7	24	PDB header: hydrolase Chain: D: PDB Molecule: putative putative pngase f; PDBTitle: crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
15	c3d7jD_	 Alignment		10.7	5	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein sco6650; PDBTitle: sco6650, a 6-pyruvoyltetrahydropterin synthase homolog from2 streptomyces coelicolor
16	c3pnrB_	 Alignment		9.2	29	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: pbi cp-c; PDBTitle: structure of pbi cp-c in complex with falcipain-2
17	c2dj6B_	 Alignment		8.9	13	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein ph0634; PDBTitle: crystal structure of 6-pyruvoyl tetrahydrobiopterin synthase from2 pyrococcus horikoshii ot3
18	c3kmlB_	 Alignment		6.9	44	PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: circular permutant of the tobacco mosaic virus
19	c1ljzB_	 Alignment		6.2	44	PDB header: receptor, toxin Chain: B: PDB Molecule: acetylcholine receptor protein; PDBTitle: nmr structure of anachr-peptide (torpedo californica,2 alpha-subunit residues 182-202) in complex with alpha-3 bungarotoxin

20 [dlqcsa1](#)

Alignment



5.6

16

Fold:Double psi beta-barrel
Superfamily:ADC-like
Family:Cdc48 N-terminal domain-like