



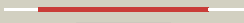






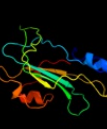












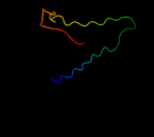

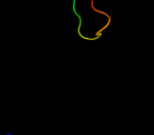



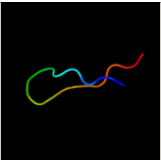
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fuxa_	 Alignment		100.0	99	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
2	d1fjja_	 Alignment		100.0	51	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
3	c3n08A_	 Alignment		100.0	36	PDB header: phosphatidylethanolamine-binding protein Chain: A: PDB Molecule: putative phosphatidylethanolamine-binding protein (pebp); PDBTitle: crystal structure of a putative phosphatidylethanolamine-binding 2 protein (pebp) homolog ct736 from chlamydia trachomatis d/uv-3/cx
4	c2evvD_	 Alignment		100.0	27	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	c2r77A_	 Alignment		99.8	24	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
6	d1wpxb1	 Alignment		99.8	22	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
7	c2qzqA_	 Alignment		99.8	23	PDB header: lipid binding protein Chain: A: PDB Molecule: phosphatidylethanolamine-binding protein; PDBTitle: phosphatidylethanolamine-binding protein from plasmodium vivax
8	c2jyzA_	 Alignment		99.8	30	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	d1kn3a_	 Alignment		99.7	28	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
11	d2qyqa1	 Alignment		99.7	29	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein

12	d1a44a_	Alignment		99.7	26	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
13	d1qoua_	Alignment		99.7	20	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
14	c3ks7D_	Alignment		45.6	26	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	d1qcsa1	Alignment		11.1	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
16	c1ljzB_	Alignment		10.7	33	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
17	c3pnrB_	Alignment		9.9	24	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: pbi-cp-c; PDBTitle: structure of pbi-cp-c in complex with falcipain-2

18 [c3kmlB_](#)

Alignment



7.2

38

PDB header:viral protein
Chain: B: **PDB Molecule:**coat protein;
PDBTitle: circular permutant of the tobacco mosaic virus