


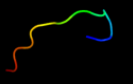







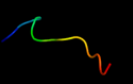


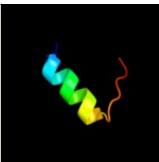
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l42A_	 Alignment		12.7	33	PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rap1; PDBTitle: the solution structure of rap1 brct domain from saccharomyces2 cerevisiae
2	d2bbkl_	 Alignment		9.1	23	Fold: Methylamine dehydrogenase, L chain Superfamily: Methylamine dehydrogenase, L chain Family: Methylamine dehydrogenase, L chain
3	c3c75L_	 Alignment		8.9	23	PDB header: oxidoreductase Chain: L: PDB Molecule: methylamine dehydrogenase light chain; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
4	c2iurD_	 Alignment		8.8	23	PDB header: oxidoreductase Chain: D: PDB Molecule: aromatic amine dehydrogenase beta subunit; PDBTitle: crystal structure of n-quinol form of aromatic amine2 dehydrogenase (aadh) from alcaligenes faecalis, form a3 cocrystal
5	d2di0a1	 Alignment		8.6	22	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
6	c1fi8F_	 Alignment		6.7	38	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: ecotin; PDBTitle: rat granzyme b [n66q] complexed to ecotin [81-84 iepd]

7

c2xvCA

Alignment



5.2

20

PDB header:cell cycle
Chain: A: **PDB Molecule:**escrt-iii;
PDBTitle: molecular and structural basis of escrt-iii recruitment to2 membranes during archaeal cell division