


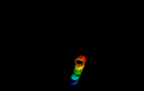


















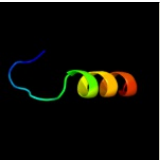


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v29a_	 Alignment		23.7	31	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
2	c3mp7B_	 Alignment		23.5	38	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase subunit sece; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
3	d2f93b1	 Alignment		15.0	50	Fold: Transmembrane helix hairpin Superfamily: Htr2 transmembrane domain-like Family: Htr2 transmembrane domain-like
4	c2f93B_	 Alignment		15.0	50	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: k intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
5	c2f95B_	 Alignment		13.8	50	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: m intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
6	d1h2sb_	 Alignment		11.6	50	Fold: Transmembrane helix hairpin Superfamily: Htr2 transmembrane domain-like Family: Htr2 transmembrane domain-like
7	c1h2sB_	 Alignment		11.6	50	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: molecular basis of transmembrane signalling by sensory2 rhodopsin ii-transducer complex
8	d2ftxb1	 Alignment		7.9	30	Fold: Kinetochore globular domain-like Superfamily: Kinetochore globular domain Family: Spc24-like
9	c2fv4B_	 Alignment		7.8	30	PDB header: structural protein, protein binding Chain: B: PDB Molecule: hypothetical 24.6 kda protein in ilv2-ade17 PDBTitle: nmr solution structure of the yeast kinetochore spc24/spc252 globular domain
10	c2k1aA_	 Alignment		5.8	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
11	d1rzhh2	 Alignment		5.3	47	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region

12 [d2p41a1](#)

Alignment



5.3

25

Fold:S-adenosyl-L-methionine-dependent methyltransferases
Superfamily:S-adenosyl-L-methionine-dependent methyltransferases
Family:mRNA cap methylase