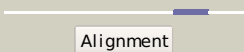
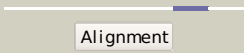
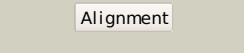
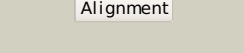
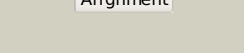


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hja1	 Alignment		16.4	19	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: Ykff-like
2	c2hja_	 Alignment		16.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ykff; PDBTitle: solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
3	c2vqlD_	 Alignment		11.1	75	PDB header: membrane protein Chain: D: PDB Molecule: uncharacterized protein cgl0972; PDBTitle: crystal structure of porb from corynebacterium glutamicum (2 crystal form iii)
4	c2rbdB_	 Alignment		6.3	31	PDB header: structural protein Chain: B: PDB Molecule: bh2358 protein; PDBTitle: crystal structure of a putative spore coat protein (bh2358) from2 bacillus halodurans c-125 at 1.54 a resolution
5	c1af7A_	 Alignment		6.3	13	PDB header: methyltransferase Chain: A: PDB Molecule: chemotaxis receptor methyltransferase cher; PDBTitle: cher from salmonella typhimurium
6	d2ijra1	 Alignment		5.8	50	Fold: Api92-like Superfamily: Api92-like Family: Api92-like
7	d2c9wc1	 Alignment		5.7	18	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
8	c2ii8F_	 Alignment		5.5	19	PDB header: signaling protein Chain: F: PDB Molecule: anabaena sensory rhodopsin transducer protein; PDBTitle: anabaena sensory rhodopsin transducer
9	d1f7ua3	 Alignment		5.4	9	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain Family: Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
10	c2bjgB_	 Alignment		5.4	14	PDB header: hydrolase Chain: B: PDB Molecule: choloylglycine hydrolase; PDBTitle: crystal structure of conjugated bile acid hydrolase from2 clostridium perfringens in complex with reaction products3 taurine and deoxycholate

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[c1kn7A](#)

Alignment



5.2

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PDB header:membrane protein
Chain: A: **PDB Molecule:**voltage-gated potassium channel protein kv1.4;
PDBTitle: solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)