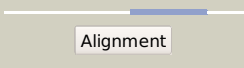
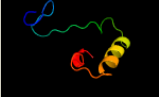
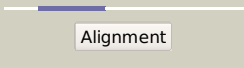

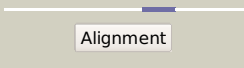

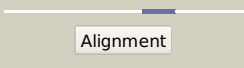

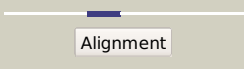

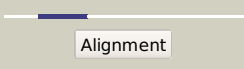

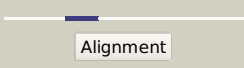
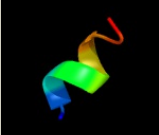
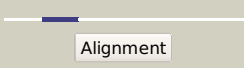

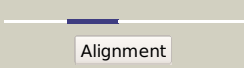
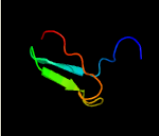


Phyre2

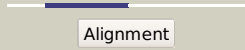
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Date	Wed Jul 31 22:05:06 BST 2019
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Detailed template information

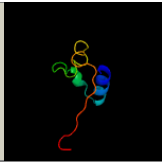
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2laiA_	 Alignment		26.0	29	PDB header: signaling protein Chain: A: PDB Molecule: avirulence protein atr13; PDBTitle: hyaloperonospora arabidopsidis effector protein atr13
2	c3qspB_	 Alignment		12.3	17	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
3	c2zjsE_	 Alignment		12.2	42	PDB header: protein transport/immune system Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of secye translocon from thermus thermophilus with a2 fab fragment
4	c2zqpE_	 Alignment		12.2	42	PDB header: protein transport Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of secye translocon from thermus2 thermophilus
5	c4narA_	 Alignment		6.9	45	PDB header: isomerase Chain: A: PDB Molecule: putative uronate isomerase; PDBTitle: crystal structure of the q9wys3 protein from thermotoga maritima.2 northeast structural genomics consortium target vr152
6	c2kbrA_	 Alignment		6.4	19	PDB header: structural protein/cell adhesion Chain: A: PDB Molecule: harmonin; PDBTitle: solution structure of harmonin n terminal domain in complex2 with a internal peptide of cadherin23
7	c4h62V_	 Alignment		6.2	78	PDB header: transcription Chain: V: PDB Molecule: mediator of rna polymerase ii transcription subunit 22; PDBTitle: structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c
8	d2atza1	 Alignment		5.7	35	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: HP0184-like
9	d1w36b1	 Alignment		5.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain

10

[d12asa_](#)



Alignment



5.2

37

Fold:Class II aaRS and biotin synthetases
Superfamily:Class II aaRS and biotin synthetases
Family:Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain