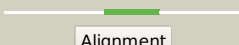
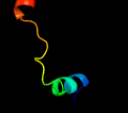
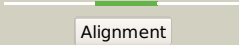
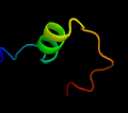
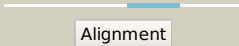

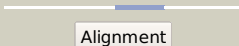
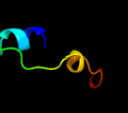




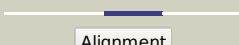

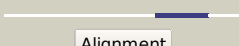
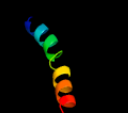
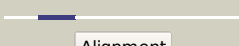
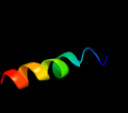






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2044c (-) _2289290_2289607
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	7de02a556d7d79fe

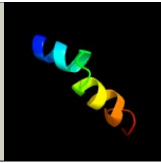
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5un7B_	 Alignment		53.2	8	PDB header: protein binding Chain: B; PDB Molecule: adrenocortical dysplasia protein homolog; PDBTitle: structure of the human pot1-tpp1 telomeric complex
2	c2z6vA_	 Alignment		53.2	17	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium
3	c3pmiC_	 Alignment		31.7	21	PDB header: protein binding Chain: C; PDB Molecule: pwwp domain-containing protein mum1; PDBTitle: pwwp domain of human mutated melanoma-associated antigen 1
4	c6ckgA_	 Alignment		25.3	17	PDB header: transferase Chain: A; PDB Molecule: d-glycerate 3-kinase; PDBTitle: d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
5	d2ozka2	 Alignment		10.1	33	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
6	d1h8ba_	 Alignment		9.9	15	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
7	d2h85a2	 Alignment		9.5	33	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
8	c2lowA_	 Alignment		9.0	22	PDB header: membrane protein Chain: A; PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
9	c1w8xP_	 Alignment		7.5	33	PDB header: virus Chain: P; PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
10	c1p1hD_	 Alignment		7.0	20	PDB header: isomerase Chain: D; PDB Molecule: inositol-3-phosphate synthase; PDBTitle: crystal structure of the 1l-myo-inositol/nad+ complex
11	c3sqiA_	 Alignment		6.3	17	PDB header: dna binding protein/dna Chain: A; PDB Molecule: klla0e03807p; PDBTitle: dna binding domain of ndc10

12	c3t79A_	Alignment		6.3	17	<p>PDB header: dna binding protein/dna Chain: A: PDB Molecule: klla0e03807p; PDBTitle: ndc10: a platform for inner kinetochore assembly in budding yeast</p>
13	c2najA_	Alignment		6.1	67	<p>PDB header: toxin Chain: A: PDB Molecule: tau-theraphotoxin-hs1a; PDBTitle: solution structure of k2 lobe of double-knot toxin</p>
14	d1cb8a1	Alignment		5.9	8	<p>Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Hyaluronate lyase-like catalytic, N-terminal domain</p>
15	c2lnuA_	Alignment		5.7	31	<p>PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the uncharacterized protein from gene locus2 rrnac0354 of haloarcula marismortui, northeast structural genomics3 consortium target hmr11</p>
16	c4xb6C_	Alignment		5.7	33	<p>PDB header: transferase Chain: C: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-triphosphate synthase PDBTitle: structure of the e. coli c-p lyase core complex</p>
17	c5zcnA_	Alignment		5.5	23	<p>PDB header: unknown function Chain: A: PDB Molecule: brevunsin; PDBTitle: solution nmr structure of a new lasso peptide brevunsin</p>

18 [c3a16C_](#)

Alignment



5.3

20

PDB header:lyase
Chain: C: **PDB Molecule:**aldoxime dehydratase;
PDBTitle: crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime