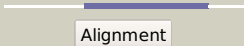
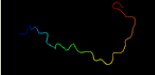

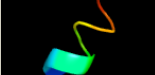
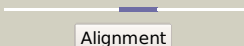

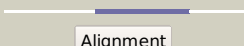
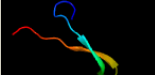
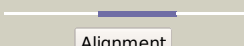

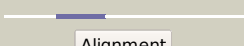
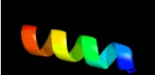
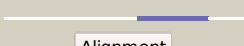
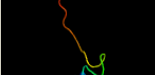







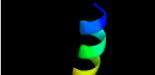

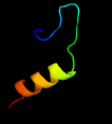
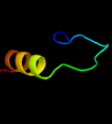

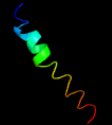
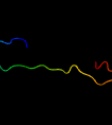

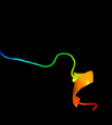
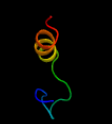


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0078B_(RVBD0078B)_87795_88001
 Date Tue Jul 23 14:50:11 BST 2019
 Unique Job ID a627de62acd66210

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mz6B_	 Alignment		19.6	37	PDB header: cell cycle Chain: B; PDB Molecule: interactor of fizzy protein; PDBTitle: cryo-em structure of a separase-securin complex from caenorhabditis2 elegans at 3.8 a resolution
2	c2f9jP_	 Alignment		18.0	55	PDB header: rna binding protein Chain: P; PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
3	d2dk8a1	 Alignment		16.8	67	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RPO3F domain-like
4	c3bmzA_	 Alignment		16.5	32	PDB header: biosynthetic protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: violacein biosynthetic enzyme vioe
5	c3kevA_	 Alignment		14.4	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: galleria sulfuraria dcun1 domain-containing protein; PDBTitle: x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria
6	c6gu1B_	 Alignment		13.9	47	PDB header: unknown function Chain: B; PDB Molecule: secreted rxlr effector peptide protein, putative; PDBTitle: sfi3 effector protein from the oomycete plant pathogen phytophthora2 infestans
7	c5ewnA_	 Alignment		13.0	29	PDB header: viral protein Chain: A; PDB Molecule: structural protein; PDBTitle: crystal structure of the human astrovirus 1 capsid protein core domain2 at 2.6 a resolution
8	c3b1sC_	 Alignment		12.0	35	PDB header: protein transport Chain: C; PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus
9	d2hg6a1	 Alignment		11.7	67	Fold: PA1123-like Superfamily: PA1123-like Family: PA1123-like
10	c3b1sA_	 Alignment		11.4	35	PDB header: protein transport Chain: A; PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus
11	c3b1sE_	 Alignment		10.9	35	PDB header: protein transport Chain: E; PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus

12	c5v89A_	Alignment		10.8	18	PDB header: ligase / protein binding Chain: A: PDB Molecule: dcn1-like protein 4; PDBTitle: structure of dcn4 pony domain bound to cul1 whb
13	c3bq3A_	Alignment		9.9	19	PDB header: cell cycle, ligase Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
14	c4gaoA_	Alignment		9.5	19	PDB header: ligase/peptide Chain: A: PDB Molecule: dcn1-like protein 2; PDBTitle: dcnl complex with n-terminally acetylated nedd8 e2 peptide
15	c6g90O_	Alignment		9.0	24	PDB header: splicing Chain: Q: PDB Molecule: cold sensitive u2 snrna suppressor 1; PDBTitle: prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
16	c2z5hT_	Alignment		8.1	37	PDB header: contractile protein Chain: T: PDB Molecule: troponin t, fast skeletal muscle isoforms; PDBTitle: crystal structure of the head-to-tail junction of tropomyosin2 complexed with a fragment of tnt
17	c5gneA_	Alignment		7.5	33	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of lapb from legionella pneumophila
18	d1s4ka_	Alignment		7.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Ydil-like
19	c3qliO_	Alignment		6.6	47	PDB header: transferase/dna Chain: O: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: crystal structure of the e. coli clamp loader bound to primer-template2 dna and psi peptide
20	c2is9A_	Alignment		6.6	19	PDB header: transcription Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
21	c3gliP_	Alignment	not modelled	6.5	47	PDB header: transferase/dna Chain: P: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: crystal structure of the e. coli clamp loader bound to primer-template2 dna and psi peptide
22	c4gbaA_	Alignment	not modelled	6.4	22	PDB header: ligase/peptide Chain: A: PDB Molecule: dcn1-like protein 3; PDBTitle: dcnl complex with n-terminally acetylated nedd8 e2 peptide
23	c6esiB_	Alignment	not modelled	6.1	30	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
24	d2c2la2	Alignment	not modelled	5.9	24	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
25	c6qfmB_	Alignment	not modelled	5.6	56	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of human mcl-1 in complex with puma bh3 peptide
26	c6k4eB_	Alignment	not modelled	5.5	16	PDB header: signaling protein Chain: B: PDB Molecule: hamp domain-containing protein; PDBTitle: siaa-pp2c domain of pseudomonas aeruginosa
27	c4hnjC_	Alignment	not modelled	5.4	56	PDB header: apoptosis/protein binding Chain: C: PDB Molecule: bcl-2-binding component 3; PDBTitle: crystallographic structure of bcl-xl domain-swapped dimer in complex2 with puma bh3 peptide at 2.9a resolution
28	c6qg8B_	Alignment	not modelled	5.2	56	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of human bcl-2 in complex with puma bh3 peptide