


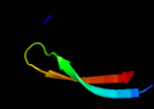
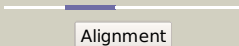

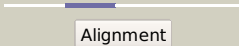



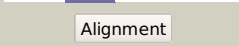
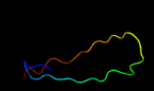
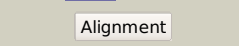
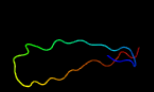
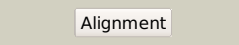



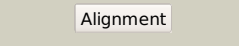

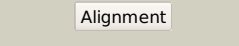

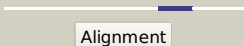
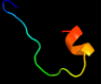
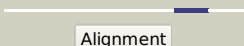
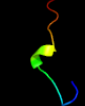
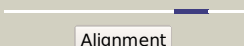

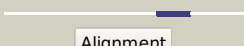

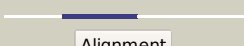

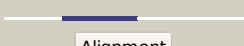






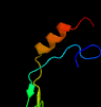



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2081c (-) _2338073_2338513
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	f99b28dcd8f0a0a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cu9a1	 Alignment		18.5	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
2	c4q6uA	 Alignment		16.9	42	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
3	d1roca	 Alignment		13.4	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
4	c6a6yA	 Alignment		12.7	15	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone asf1, putative; PDBTitle: crystal structure of asf1 from plasmodium falciparum
5	c2idcA	 Alignment		11.3	33	PDB header: replication/chaperone Chain: A: PDB Molecule: anti-silencing protein 1 and histone h3 chimera; PDBTitle: structure of the histone h3-asf1 chaperone interaction
6	c2i32A	 Alignment		11.2	36	PDB header: replication chaperone Chain: A: PDB Molecule: anti-silencing factor 1 paraloga; PDBTitle: structure of a human asf1a-hira complex and insights into specificity2 of histone chaperone complex assembly
7	d2i32a1	 Alignment		11.2	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
8	c5lnkb	 Alignment		9.0	78	PDB header: oxidoreductase Chain: B: PDB Molecule: PDBTitle: entire ovine respiratory complex i
9	c5lc5R	 Alignment		8.8	78	PDB header: oxidoreductase Chain: R: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 6, PDBTitle: structure of mammalian respiratory complex i, class2
10	c5ldxR	 Alignment		8.7	78	PDB header: oxidoreductase Chain: R: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 6, PDBTitle: structure of mammalian respiratory complex i, class3.
11	c5ldwR	 Alignment		8.7	78	PDB header: oxidoreductase Chain: R: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 6, PDBTitle: structure of mammalian respiratory complex i, class1

12	d1xm3a_	 Alignment		7.6	35	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
13	c6deiC_	 Alignment		6.9	60	PDB header: protein binding/cell cycle Chain: C: PDB Molecule: protein dse3; PDBTitle: structure of dse3-csm1 complex
14	c3htrB_	 Alignment		6.8	41	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
15	c2jvmA_	 Alignment		6.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95
16	d1oi2a_	 Alignment		6.0	19	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
17	c2iu6B_	 Alignment		6.0	35	PDB header: transferase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis
18	c5t76A_	 Alignment		5.3	30	PDB header: translation Chain: A: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: a fragment of a human trna synthetase
19	c2lrfA_	 Alignment		5.2	46	PDB header: antimicrobial protein Chain: A: PDB Molecule: anti-lipopolysaccharide factor; PDBTitle: nmr structure of the scylla serrata anti lipopolysaccharide factor-242 (ssalf-24) peptide
20	d1un8a4	 Alignment		5.1	29	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
21	c3ct4B_	 Alignment	not modelled	5.1	30	PDB header: transferase Chain: B: PDB Molecule: pts-dependent dihydroxyacetone kinase, dihydroxyacetone- PDBTitle: structure of dha-kinase subunit dhak from l. lactis