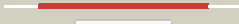

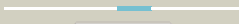




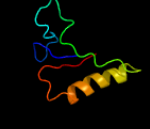

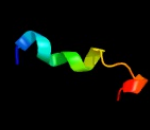





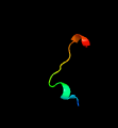

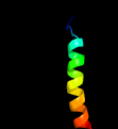

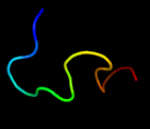

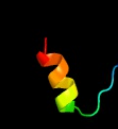
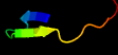
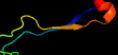
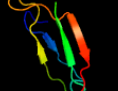


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	4a602634223ba44a

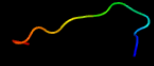
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4esqA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine protein kinase; <b>PDBTitle:</b> crystal structure of the extracellular domain of pknh from2 mycobacterium tuberculosis
2	<a href="#">c3lo3E_</a>	 Alignment		39.7	24	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> E; <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
3	<a href="#">d2fiua1</a>	 Alignment		39.2	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Atu0297-like
4	<a href="#">c2mheB_</a>	 Alignment		28.2	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein np_419126.1 from caulobacter crescentus
5	<a href="#">c2b3gB_</a>	 Alignment		26.5	12	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> p53n (fragment 33-60) bound to rpa70n
6	<a href="#">c3i08D_</a>	 Alignment		23.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> D; <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
7	<a href="#">c5hb8B_</a>	 Alignment		13.1	37	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoporin nup53; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum nup53 rrm (space group2 p3121)
8	<a href="#">c2i14B_</a>	 Alignment		12.5	12	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
9	<a href="#">c4dwlA_</a>	 Alignment		11.4	31	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> bbp7; <b>PDBTitle:</b> avd molecule from bordetella bacteriophage dgr
10	<a href="#">c2ly4B_</a>	 Alignment		11.3	12	<b>PDB header:</b> nuclear protein/antitumour protein <b>Chain:</b> B; <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> hmgb1-facilitated p53 dna binding occurs via hmgb1/p532 transactivation domain interaction and is regulated by the acidic3 tail
11	<a href="#">c5uz5C_</a>	 Alignment		8.9	32	<b>PDB header:</b> nuclear protein/rna <b>Chain:</b> C; <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein a,tap tag; <b>PDBTitle:</b> s. cerevisiae u1 snrnp

12	<a href="#">d2pp6a1</a>	Alignment		7.8	10	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> gpFII-like
13	<a href="#">c3dcaC_</a>	Alignment		7.2	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
14	<a href="#">c2kerA_</a>	Alignment		6.6	15	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-amylase inhibitor z-2685; <b>PDBTitle:</b> alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus

15 [dlg94a1](#)

Alignment



6.1

29

**Fold:** Glycosyl hydrolase domain  
**Superfamily:** Glycosyl hydrolase domain  
**Family:** alpha-Amylases, C-terminal beta-sheet domain