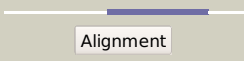
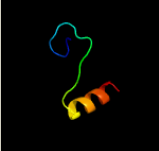
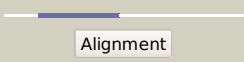
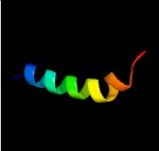
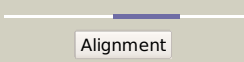
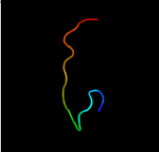
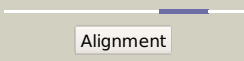

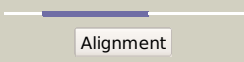
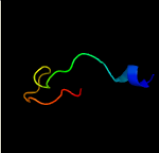
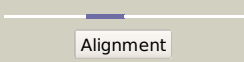

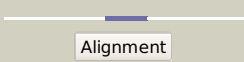

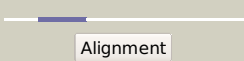
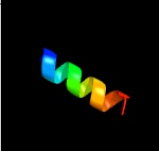
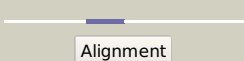

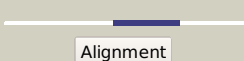

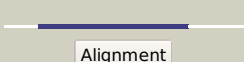
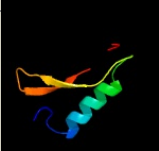


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2512A_(RVBD2512A)_2829964_2830149
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	a141ae65b0fa7b77

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3on1A_</a>	 Alignment		17.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> bh2414 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from bacillus2 halodurans c
2	<a href="#">c4lh9A_</a>	 Alignment		15.2	32	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the refolded hood domain (asp256-gly295) of hetr
3	<a href="#">c3v7qB_</a>	 Alignment		14.8	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> probable ribosomal protein ylxq; <b>PDBTitle:</b> crystal structure of b. subtilis ylxq at 1.55 a resolution
4	<a href="#">c3ci9B_</a>	 Alignment		13.1	57	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
5	<a href="#">c5c8sD_</a>	 Alignment		12.7	33	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> guanine-n7 methyltransferase; <b>PDBTitle:</b> crystal structure of the sars coronavirus nsp14-nsp10 complex with2 functional ligands sah and gpppa
6	<a href="#">c4x9zA_</a>	 Alignment		12.4	64	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> alphad-conotoxin gexxa from the venom of conus generalis; <b>PDBTitle:</b> dimeric conotoxin alphad-gexxa
7	<a href="#">c1qjlA_</a>	 Alignment		11.3	58	<b>PDB header:</b> metallothionein <b>Chain:</b> A; <b>PDB Molecule:</b> metallothionein; <b>PDBTitle:</b> metallothionein: mta from sea urchin (beta domain)
8	<a href="#">c6dkmB_</a>	 Alignment		11.2	57	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> dhd131_b; <b>PDBTitle:</b> dhd131
9	<a href="#">c4x9zB_</a>	 Alignment		10.4	78	<b>PDB header:</b> toxin <b>Chain:</b> B; <b>PDB Molecule:</b> alphad-conotoxin gexxa from the venom of conus generalis; <b>PDBTitle:</b> dimeric conotoxin alphad-gexxa
10	<a href="#">d2bo1a1</a>	 Alignment		8.6	33	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
11	<a href="#">c2gpcB_</a>	 Alignment		8.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> iron superoxide dismutase; <b>PDBTitle:</b> the crystal structure of the enzyme fe-superoxide dismutase2 from trypanosoma cruzi

12	<a href="#">c1jb0K_</a>	Alignment		7.9	73	<b>PDB header:</b> photosynthesis <b>Chain:</b> K; <b>PDB Molecule:</b> photosystem 1 reaction centre subunit x; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
13	<a href="#">d1jb0k_</a>	Alignment		7.9	73	<b>Fold:</b> Photosystem I reaction center subunit X, PsaK <b>Superfamily:</b> Photosystem I reaction center subunit X, PsaK <b>Family:</b> Photosystem I reaction center subunit X, PsaK
14	<a href="#">c5h63C_</a>	Alignment		7.2	35	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> transferase; <b>PDBTitle:</b> structure of transferase mutant-c23s,c199s
15	<a href="#">c4ynlB_</a>	Alignment		7.0	32	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the hood domain of anabaena hetr in complex with2 the hexapeptide ergsgr derived from pats
16	<a href="#">d2hrkb1</a>	Alignment		6.3	39	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Arc1p N-terminal domain-like
17	<a href="#">c5mjyF_</a>	Alignment		6.0	55	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 9; <b>PDBTitle:</b> crystal structure of the his domain protein tyrosine phosphatase (hd-2 ptp/ptpn23) bro1 domain (sara complex structure)
18	<a href="#">c5mjyE_</a>	Alignment		6.0	55	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 9; <b>PDBTitle:</b> crystal structure of the his domain protein tyrosine phosphatase (hd-2 ptp/ptpn23) bro1 domain (sara complex structure)
19	<a href="#">c2w5zA_</a>	Alignment		5.9	50	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histone-lysine n-methyltransferase hrx; <b>PDBTitle:</b> ternary complex of the mixed lineage leukaemia (mll1) set2 domain with the cofactor product s-adenosylhomocysteine3 and histone peptide.
20	<a href="#">c3p3dA_</a>	Alignment		5.7	27	<b>PDB header:</b> nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoporin 53; <b>PDBTitle:</b> crystal structure of the nup53 rrm domain from pichia guilliermondii
21	<a href="#">c5uazB_</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoporin nup53; <b>PDBTitle:</b> crystal structure of the yeast nucleoporin
22	<a href="#">c1f8vD_</a>	Alignment	not modelled	5.5	39	<b>PDB header:</b> virus/rna <b>Chain:</b> D; <b>PDB Molecule:</b> mature capsid protein gamma; <b>PDBTitle:</b> the structure of pariacoto virus reveals a dodecahedral cage of duplex2 rna
23	<a href="#">c3zf7g_</a>	Alignment	not modelled	5.3	41	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
24	<a href="#">d1p7ga2</a>	Alignment	not modelled	5.3	18	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain