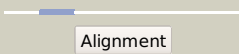

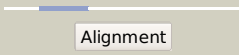
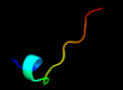
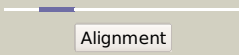

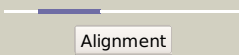

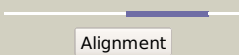

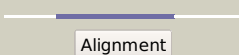

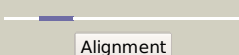


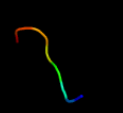
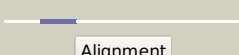

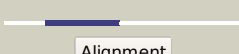
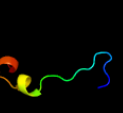
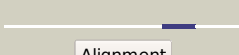



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2307A (-) _2579238_2579429
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	a429d6a082bbee09

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hlwB_</a>	 Alignment		24.7	60	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
2	<a href="#">c6hmvB_</a>	 Alignment		22.2	29	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, Ivvy mutant)
3	<a href="#">c6hltD_</a>	 Alignment		19.4	40	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
4	<a href="#">c5jhfA_</a>	 Alignment		18.7	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> klth0d11660p; <b>PDBTitle:</b> crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
5	<a href="#">d1x9ba_</a>	 Alignment		18.2	24	<b>Fold:</b> Protozoan pheromone-like <b>Superfamily:</b> Hypothetical membrane protein Ta0354, soluble domain <b>Family:</b> Hypothetical membrane protein Ta0354, soluble domain
6	<a href="#">d2fx0a2</a>	 Alignment		14.2	16	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
7	<a href="#">c5I20A_</a>	 Alignment		12.5	56	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> clostripain-related protein; <b>PDBTitle:</b> crystal structure of a clostripain (bt_0727) from bacteroides2 thetaiotaomicron atcc 29148 in complex with peptide inhibitor btn-3 vltk-aomk
8	<a href="#">c3uwsA_</a>	 Alignment		11.6	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a clostripain (parmer_00083) from parabacteroides2 merdae atcc 43184 at 1.70 a resolution
9	<a href="#">c5dynA_</a>	 Alignment		11.5	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> b. fragilis cysteine protease
10	<a href="#">c3rlcA_</a>	 Alignment		9.2	43	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> a1 protein; <b>PDBTitle:</b> crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form
11	<a href="#">d2bmta_</a>	 Alignment		8.6	71	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins

12	<a href="#">c2zoeA_</a>			7.9	53	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin components ha3; <b>PDBTitle:</b> ha3 subcomponent of clostridium botulinum type c progenitor2 toxin, complex with n-acetylneuramic acid
13	<a href="#">d2gmga1</a>			7.3	43	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like
14	<a href="#">c2bh1Y_</a>			6.7	71	<b>PDB header:</b> transport protein <b>Chain:</b> Y: <b>PDB Molecule:</b> general secretion pathway protein e.; <b>PDBTitle:</b> x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
15	<a href="#">d2bh1x1</a>			6.7	71	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> EspE N-terminal domain-like <b>Family:</b> GSPiI protein E N-terminal domain-like
16	<a href="#">c2i02B_</a>			6.6	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
17	<a href="#">c3rmsA_</a>			6.3	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
18	<a href="#">c2i01A_</a>			6.2	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
19	<a href="#">c5ubkA_</a>			6.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-homoserine lactone acylase pvdq; <b>PDBTitle:</b> inactive s1a/m269d-cppvdq mutant in complex with the pyoverdine2 precursor pvdq reveals a specific binding pocket for the d-tyr of3 this substrate
20	<a href="#">d1lira_</a>			5.9	71	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
21	<a href="#">c2d7dB_</a>		not modelled	5.8	67	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
22	<a href="#">c3am2A_</a>		not modelled	5.8	54	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> heat-labile enterotoxin b chain; <b>PDBTitle:</b> clostridium perfringens enterotoxin
23	<a href="#">c2m9IA_</a>		not modelled	5.7	50	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> beta-theraphotoxin-tp1a; <b>PDBTitle:</b> solution structure of protoxin-1
24	<a href="#">d1ei5a2</a>		not modelled	5.7	60	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
25	<a href="#">c1q2iA_</a>		not modelled	5.6	63	<b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> pnc27; <b>PDBTitle:</b> nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
26	<a href="#">d2f1da1</a>		not modelled	5.5	27	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
27	<a href="#">c6gcsc_</a>		not modelled	5.3	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 49-kda protein (nucm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica