
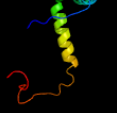



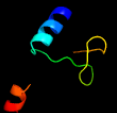

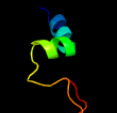







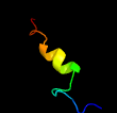



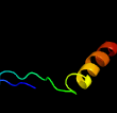



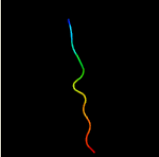

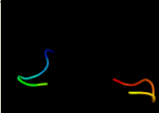


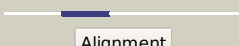

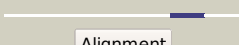

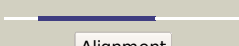


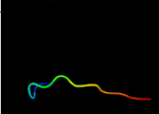





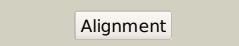


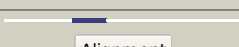


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1943c_(-)_2194977_2195354
Date	Mon Aug 5 13:25:03 BST 2019
Unique Job ID	dd378ce0a41ab4e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k5jB_</a>	 Alignment		45.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	<a href="#">c2rt4A_</a>	 Alignment		31.3	70	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> af.2a1; <b>PDBTitle:</b> nmr structure of designed protein, af.2a1, (ensembles)
3	<a href="#">c1xb4C_</a>	 Alignment		21.0	21	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical 23.6 kda protein in yuh1-ura8 intergenic <b>PDBTitle:</b> crystal structure of subunit vps25 of the endosomal trafficking2 complex escrt-ii
4	<a href="#">c3dmoD_</a>	 Alignment		20.5	48	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
5	<a href="#">c3zbeA_</a>	 Alignment		19.1	39	<b>PDB header:</b> toxin-antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> paaa2; <b>PDBTitle:</b> e. coli o157 pare2-associated antitoxin 2 (paaa2)
6	<a href="#">c5tw9D_</a>	 Alignment		16.3	35	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> iron uptake system component efeo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
7	<a href="#">c6a7vU_</a>	 Alignment		14.8	26	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
8	<a href="#">c5e8jC_</a>	 Alignment		13.2	33	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> rnmt-activating mini protein; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
9	<a href="#">c2n2sA_</a>	 Alignment		9.9	63	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> pheromone ep-1; <b>PDBTitle:</b> nmr solution structure of the pheromone ep-1 from euplotes petzi
10	<a href="#">c3lg8B_</a>	 Alignment		8.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> a-type atp synthase subunit e; <b>PDBTitle:</b> crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
11	<a href="#">c6gw6A_</a>	 Alignment		8.8	32	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> res toxin; <b>PDBTitle:</b> structure of the pseudomonas putida res-xre toxin-antitoxin complex

12	<a href="#">c3bbo3_</a>	 Alignment		8.5	42	<b>PDB header:</b> ribosome <b>Chain:</b> 3: <b>PDB Molecule:</b> ribosomal protein l33; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
13	<a href="#">c3le4A_</a>	 Alignment		8.5	46	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> crystal structure of the dgcr8 dimerization domain
14	<a href="#">d1x9ba_</a>	 Alignment		8.3	50	<b>Fold:</b> Protozoan pheromone-like <b>Superfamily:</b> Hypothetical membrane protein Ta0354, soluble domain <b>Family:</b> Hypothetical membrane protein Ta0354, soluble domain
15	<a href="#">d1dy2a_</a>	 Alignment		8.0	35	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Endostatin
16	<a href="#">d1jw2a_</a>	 Alignment		7.3	50	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Hemolysin expression modulating protein HHA <b>Family:</b> Hemolysin expression modulating protein HHA
17	<a href="#">c3qoyA_</a>	 Alignment		6.7	9	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of ribosomal protein l1 from aquifex aeolicus
18	<a href="#">d2qtva2</a>	 Alignment		6.7	75	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> beta-sandwich domain of Sec23/24 <b>Family:</b> beta-sandwich domain of Sec23/24
19	<a href="#">c6d0hA_</a>	 Alignment		6.4	23	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> part: cog5654 (res domain) toxin; <b>PDBTitle:</b> part: prs adp-ribosylating toxin bound to cognate antitoxin pars
20	<a href="#">c3vepC_</a>	 Alignment		6.2	42	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein rv3413c/mt3522; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
21	<a href="#">c3vepX_</a>	 Alignment	not modelled	6.2	42	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein rv3413c/mt3522; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
22	<a href="#">d1xsqa_</a>	 Alignment	not modelled	6.1	43	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Ureidoglycolate hydrolase AIIA
23	<a href="#">d1zbsa2</a>	 Alignment	not modelled	5.6	33	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
24	<a href="#">d1exqa_</a>	 Alignment	not modelled	5.3	50	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
25	<a href="#">d2bdra1</a>	 Alignment	not modelled	5.1	57	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Ureidoglycolate hydrolase AIIA