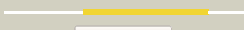






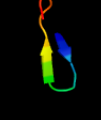



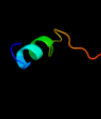

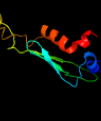







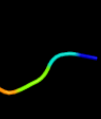
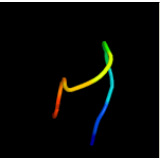
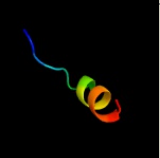
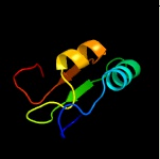
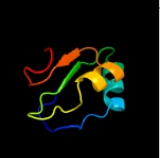
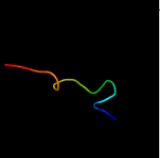
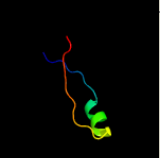
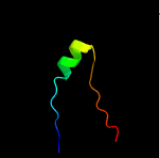
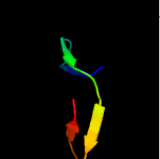
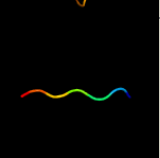


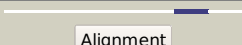
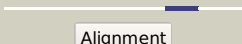
# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1418\_(lprH)\_1592645\_1593331  
 Date Wed Jul 31 22:05:52 BST 2019  
 Unique Job ID 23daa73830187c57

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4esqA_</a>	 Alignment		72.6	15	<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="#">c4b9cA_</a>	 Alignment		14.0	23	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type 3a cellulose-binding domain protein; <b>PDBTitle:</b> biomass sensing modules from putative rsgi-like proteins2 of clostridium thermocellum resemble family 3 carbohydrate-3 binding module of cellulosome
3	<a href="#">d1d1da1</a>	 Alignment		13.8	32	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Retrovirus capsid dimerization domain-like <b>Family:</b> Retrovirus capsid protein C-terminal domain
4	<a href="#">c5n60Q_</a>	 Alignment		12.5	46	<b>PDB header:</b> transferase <b>Chain:</b> Q: <b>PDB Molecule:</b> rna polymerase i-specific transcription initiation factor <b>PDBTitle:</b> cryo-em structure of rna polymerase i in complex with rrn3 and core2 factor (orientation i)
5	<a href="#">c5dudB_</a>	 Alignment		12.3	60	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ybgj; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
6	<a href="#">c6dexB_</a>	 Alignment		11.4	25	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> suppressor of hydroxyurea sensitivity protein 2; <b>PDBTitle:</b> structure of eremothecium gossypii shu1:shu2 complex
7	<a href="#">c4e6nB_</a>	 Alignment		11.4	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure of bacterial pnkp-c/hen1-n heterodimer
8	<a href="#">c2zp2B_</a>	 Alignment		10.3	55	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> c-terminal domain of kipi from bacillus subtilis
9	<a href="#">c3pntA_</a>	 Alignment		10.2	55	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> nad+-glycohydrolase; <b>PDBTitle:</b> crystal structure of the streptococcus pyogenes nad+ glycohydrolase2 spn in complex with ifs, the immunity factor for spn
10	<a href="#">c3sumA_</a>	 Alignment		9.9	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cerato-platanin-like protein; <b>PDBTitle:</b> crystal structure of cerato-platanin 5 from m. perniciosa (mpcp5)
11	<a href="#">d1iyca_</a>	 Alignment		9.8	100	<b>Fold:</b> Invertebrate chitin-binding proteins <b>Superfamily:</b> Invertebrate chitin-binding proteins <b>Family:</b> Antifungal peptide scarabaecin

12	<a href="#">c3mm1D_</a>	Alignment		9.5	60	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> allophanate hydrolase subunit 1; <b>PDBTitle:</b> allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
13	<a href="#">c6nd1D_</a>	Alignment		8.7	47	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> protein transport protein sbh1; <b>PDBTitle:</b> cryoem structure of the sec complex from yeast
14	<a href="#">c1vl6C_</a>	Alignment		8.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
15	<a href="#">d1vl6a1</a>	Alignment		8.3	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
16	<a href="#">c3dgsA_</a>	Alignment		8.2	60	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> coat protein a; <b>PDBTitle:</b> changing the determinants of protein stability from covalent to non-2 covalent interactions by in-vitro evolution: a structural and3 energetic analysis
17	<a href="#">c4b9pA_</a>	Alignment		8.2	43	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type 3a cellulose-binding domain protein; <b>PDBTitle:</b> biomass sensing module from putative rsg12 protein of2 clostridium thermocellum resemble family 3 carbohydrate-3 binding module of cellulosome
18	<a href="#">c2y1kD_</a>	Alignment		7.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> carbohydrate-binding module cbm3b from the cellulosomal2 cellobiohydrolase 9a from clostridium thermocellum
19	<a href="#">c2kk4A_</a>	Alignment		7.7	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af_2094; <b>PDBTitle:</b> solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consotium (nesg)3 target gt2
20	<a href="#">d2vrda1</a>	Alignment		7.6	57	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
21	<a href="#">c2wwbC_</a>	Alignment	not modelled	7.2	53	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> protein transport protein sec61 subunit beta; <b>PDBTitle:</b> cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
22	<a href="#">c2rmhA_</a>	Alignment	not modelled	7.1	43	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> urocortin-3; <b>PDBTitle:</b> human urocortin 3
23	<a href="#">c2phcB_</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ph0987; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
24	<a href="#">c2cosA_</a>	Alignment	not modelled	6.8	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine protein kinase lats2; <b>PDBTitle:</b> solution structure of rsg1 ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
25	<a href="#">c2outA_</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mu-like prophage flumu protein gp35, protein <b>PDBTitle:</b> solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
26	<a href="#">d1c1ka_</a>	Alignment	not modelled	6.4	25	<b>Fold:</b> gene 59 helicase assembly protein <b>Superfamily:</b> gene 59 helicase assembly protein <b>Family:</b> gene 59 helicase assembly protein
27	<a href="#">c3s3zA_</a>	Alignment	not modelled	6.0	32	<b>PDB header:</b> antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tandem cyanovirin-n dimer cvn2i10; <b>PDBTitle:</b> crystal structure an tandem cyanovirin-n dimer, cvn2i10
28	<a href="#">c4lqeA_</a>	Alignment	not modelled	6.0	39	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mepb; <b>PDBTitle:</b> crystal structure of mepb

29	<a href="#">d2phcb1</a>	 Alignment	not modelled	5.9	63	<b>Fold:</b> Cyclophilin-like <b>Superfamily:</b> Cyclophilin-like <b>Family:</b> PH0987 C-terminal domain-like
30	<a href="#">c5xynD</a>	 Alignment	not modelled	5.4	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> suppressor of hydroxyurea sensitivity protein 2; <b>PDBTitle:</b> the crystal structure of csm2-psy3-shu1-shu2 complex from budding2 yeast