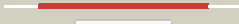
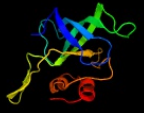


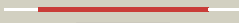














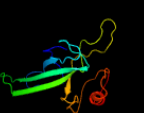

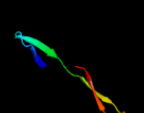


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0714 (rplN)_811376_811744
Date	Fri Jul 26 01:50:28 BST 2019
Unique Job ID	484d8a8c2cafede2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1whia_</a>	 Alignment		100.0	78	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
2	<a href="#">d2j01o1</a>	 Alignment		100.0	71	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
3	<a href="#">d2zjrhl</a>	 Alignment		100.0	70	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
4	<a href="#">c3bboM</a>	 Alignment		100.0	60	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein l14; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
5	<a href="#">d2gycl1</a>	 Alignment		100.0	66	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
6	<a href="#">c1vw4l</a>	 Alignment		100.0	44	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 54s ribosomal protein l38, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
7	<a href="#">c3j21j</a>	 Alignment		100.0	50	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l14p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
8	<a href="#">d1vqok1</a>	 Alignment		100.0	45	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
9	<a href="#">c2zkrk</a>	 Alignment		100.0	40	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> K: <b>PDB Molecule:</b> rna expansion segment es19; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
10	<a href="#">c4ce40</a>	 Alignment		100.0	32	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> mrpl14; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
11	<a href="#">d1oj5a</a>	 Alignment		37.1	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> PAS domain of steroid receptor coactivator 1A, NCo-A1

12	<a href="#">c5iu1A_</a>	Alignment		26.6	18	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> ctr1-like protein; <b>PDBTitle:</b> n-terminal pas domain homodimer of ppanr map3k from physcomitrella2 patens.
13	<a href="#">c3icyB_</a>	Alignment		25.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of sensory box histidine kinase/response2 regulator domain from chlorobium tepidum t1s
14	<a href="#">c3ewkA_</a>	Alignment		21.9	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
15	<a href="#">d1zv9a1</a>	Alignment		21.3	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
16	<a href="#">d1tyja1</a>	Alignment		20.7	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
17	<a href="#">c3ghpA_</a>	Alignment		19.0	47	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulosomal scaffoldin adaptor protein b; <b>PDBTitle:</b> structure of the second type ii cohesin module from the adaptor scaa2 scaffoldin of acetivibrio cellulolyticus (including long c-terminal3 linker)
18	<a href="#">d2bm3a1</a>	Alignment		18.2	33	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
19	<a href="#">c2b59A_</a>	Alignment		18.2	33	<b>PDB header:</b> hydrolase/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cog1196: chromosome segregation atpases; <b>PDBTitle:</b> the type ii cohesin dockerin complex
20	<a href="#">c5mu7B_</a>	Alignment		17.8	26	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit delta-like protein; <b>PDBTitle:</b> crystal structure of the beta/delta-copi core complex
21	<a href="#">c3fnkA_</a>	Alignment	not modelled	17.6	47	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulosomal scaffoldin adaptor protein b; <b>PDBTitle:</b> crystal structure of the second type ii cohesin module from the2 cellulosomal adaptor scaa scaffoldin of acetivibrio cellulolyticus
22	<a href="#">c4wn5A_</a>	Alignment	not modelled	16.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxia-inducible factor 3-alpha; <b>PDBTitle:</b> crystal structure of the c-terminal per-arnt-sim (pasb) of human hif-2 3alpha9 bound to 18:1-1-monoacylglycerol
23	<a href="#">c6dslB_</a>	Alignment	not modelled	13.5	24	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> consensus engineered intein catc; <b>PDBTitle:</b> consensus engineered intein (cat) with atypical split site
24	<a href="#">c5vaeH_</a>	Alignment	not modelled	13.0	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> H: <b>PDB Molecule:</b> accessory sec system protein asp3; <b>PDBTitle:</b> crystal structure of accessory secretion protein 1 and 3
25	<a href="#">c5f6aA_</a>	Alignment	not modelled	11.3	22	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein cycle; <b>PDBTitle:</b> drosophila melanogaster cycle w398a pas-b with empty pocket
26	<a href="#">c2kdkA_</a>	Alignment	not modelled	11.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> aryl hydrocarbon receptor nuclear translocator-like protein <b>PDBTitle:</b> structure of human circadian clock protein bmal2 c-terminal pas domain
27	<a href="#">c5nwmA_</a>	Alignment	not modelled	10.6	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear receptor coactivator 1; <b>PDBTitle:</b> insight into the molecular recognition mechanism of the coactivator2 ncoa1 by stat6
28	<a href="#">c5a1vP_</a>	Alignment	not modelled	9.3	22	<b>PDB header:</b> transport protein <b>Chain:</b> P: <b>PDB Molecule:</b> coatomer subunit delta; <b>PDBTitle:</b> the structure of the cop1 coat linkage i

29	<a href="#">c2xk0A_</a>	Alignment	not modelled	8.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> polycomb protein pcl; <b>PDBTitle:</b> solution structure of the tudor domain from drosophila2 polycomblike (pcl)
30	<a href="#">c6cw2D_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> histone acetyltransferase gcn5; <b>PDBTitle:</b> crystal structure of a yeast saga transcriptional coactivator2 ada2/gcn5 hat subcomplex, crystal form 1
31	<a href="#">c2pdtD_</a>	Alignment	not modelled	8.5	9	<b>PDB header:</b> circadian clock protein <b>Chain:</b> D: <b>PDB Molecule:</b> vidvid pas protein vvd; <b>PDBTitle:</b> 2.3 angstrom structure of phosphodiesterase treated vidvid
32	<a href="#">d2do3a1</a>	Alignment	not modelled	8.1	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
33	<a href="#">d1v74a_</a>	Alignment	not modelled	6.9	28	<b>Fold:</b> Colicin D/E5 nuclease domain <b>Superfamily:</b> Colicin D/E5 nuclease domain <b>Family:</b> Colicin D nuclease domain
34	<a href="#">c2eqjA_</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metal-response element-binding transcription <b>PDBTitle:</b> solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
35	<a href="#">c4zprB_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> protein transport/transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxia-inducible factor 1-alpha; <b>PDBTitle:</b> crystal structure of the heterodimeric hif-1a:arnt complex with hre2 dna
36	<a href="#">c2l3bA_</a>	Alignment	not modelled	6.6	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein found in conjugate transposon; <b>PDBTitle:</b> solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
37	<a href="#">c3lhnB_</a>	Alignment	not modelled	6.5	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution
38	<a href="#">c2cwpA_</a>	Alignment	not modelled	6.4	30	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> metrs related protein; <b>PDBTitle:</b> crystal structure of metrs related protein from pyrococcus horikoshii
39	<a href="#">c1xnil_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> cell cycle <b>Chain:</b> I: <b>PDB Molecule:</b> tumor suppressor p53-binding protein 1; <b>PDBTitle:</b> tandem tudor domain of 53bp1
40	<a href="#">c4wujB_</a>	Alignment	not modelled	6.3	6	<b>PDB header:</b> circadian clock protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 15, cellulose signaling <b>PDBTitle:</b> structural biochemistry of a fungal lov domain photoreceptor reveals2 an evolutionarily conserved pathway integrating blue-light and3 oxidative stress
41	<a href="#">d1ijdb_</a>	Alignment	not modelled	6.1	44	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
42	<a href="#">c2pnyA_</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 2; <b>PDBTitle:</b> structure of human isopentenyl-diphosphate delta-isomerase 2
43	<a href="#">c1vw4M_</a>	Alignment	not modelled	5.7	15	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 54s ribosomal protein img1, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
44	<a href="#">c5znmB_</a>	Alignment	not modelled	5.6	26	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> colicin-d; <b>PDBTitle:</b> colicin d central domain and c-terminal trnase domain
45	<a href="#">c2xdpA_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 4c; <b>PDBTitle:</b> crystal structure of the tudor domain of human jmj2c
46	<a href="#">c3h9wA_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase with pas/pac sensor; <b>PDBTitle:</b> crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
47	<a href="#">c6h2bC_</a>	Alignment	not modelled	5.4	33	<b>PDB header:</b> virus like particle <b>Chain:</b> C: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> structure of the macrobrachium rosenbergii nodavirus
48	<a href="#">c5x3eA_</a>	Alignment	not modelled	5.4	28	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein; <b>PDBTitle:</b> kinesin 6
49	<a href="#">c3k2yD_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein lp_0118; <b>PDBTitle:</b> crystal structure of protein lp_0118 from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr91b
50	<a href="#">c6fm0A_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> deoxyguanylosuccinate synthase (dgss) and atp structure at 1.72 angstrom resolution
51	<a href="#">c2xkjE_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> topoisomerase iv; <b>PDBTitle:</b> crystal structure of catalytic core of a. baumannii topo iv (pare-2 parc fusion truncate)
52	<a href="#">c2m0oA_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> the solution structure of human phf1 in complex with h3k36me3

53	<a href="#">dlt3ta4</a>	Alignment	not modelled	5.2	40	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
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