
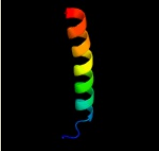



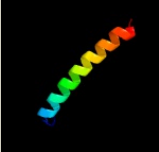





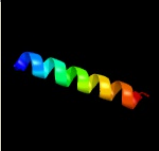







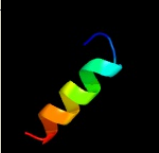


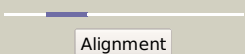



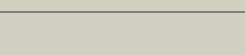

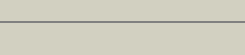
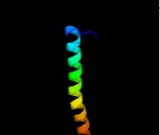

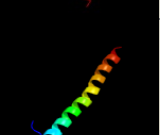
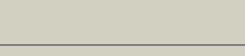
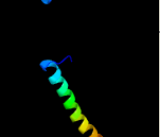
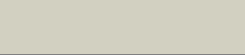

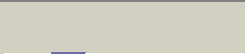


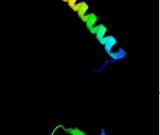
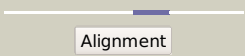

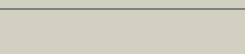
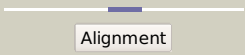


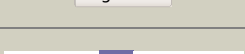
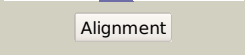



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0347 (- )_417304_418290
Date	Tue Jul 23 14:50:41 BST 2019
Unique Job ID	91003ec948881db9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1f4nb_</a>	 Alignment		75.9	27	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
2	<a href="#">d1f4na_</a>	 Alignment		74.9	27	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
3	<a href="#">c1yo7A_</a>	 Alignment		73.7	29	<b>PDB header:</b> replication regulator <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein rop; <b>PDBTitle:</b> re-engineering topology of the homodimeric rop protein into a single-2 chain 4-helix bundle
4	<a href="#">d2ijka1</a>	 Alignment		70.3	28	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
5	<a href="#">d1gtoa_</a>	 Alignment		65.0	24	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
6	<a href="#">d1qx8a_</a>	 Alignment		45.9	23	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
7	<a href="#">d1nkda_</a>	 Alignment		35.0	26	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
8	<a href="#">c2lttA_</a>	 Alignment		31.7	9	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein, mitochondrial; <b>PDBTitle:</b> solution nmr structure of nifu-like protein from saccharomyces2 cerevisiae, northeast structural genomics consortium (nesg) target3 yr313a
9	<a href="#">c4xtrG_</a>	 Alignment		27.1	54	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> pep12p; <b>PDBTitle:</b> structure of get3 bound to the transmembrane domain of pep12
10	<a href="#">d1e8oa_</a>	 Alignment		22.0	35	<b>Fold:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14 <b>Superfamily:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14 <b>Family:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14
11	<a href="#">c2mbtA_</a>	 Alignment		20.5	21	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> top7 fold protein top7m13; <b>PDBTitle:</b> solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33

12	<a href="#">c3tj1A_</a>		Alignment		19.2	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase i-specific transcription initiation factor <b>PDBTitle:</b> crystal structure of rna polymerase i transcription initiation factor2 rrn3
13	<a href="#">c2k1hA_</a>		Alignment		18.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ser13; <b>PDBTitle:</b> solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
14	<a href="#">d2ffma1</a>		Alignment		17.2	15	<b>Fold:</b> Hypothetical protein SAV1430 <b>Superfamily:</b> Hypothetical protein SAV1430 <b>Family:</b> Hypothetical protein SAV1430
15	<a href="#">c5ldxp_</a>		Alignment		16.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.
16	<a href="#">c5ldwp_</a>		Alignment		16.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
17	<a href="#">c5lc5p_</a>		Alignment		16.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
18	<a href="#">c5o31p_</a>		Alignment		16.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> mitochondrial complex i in the deactive state
19	<a href="#">c4uzmA_</a>		Alignment		15.6	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein igaa homolog; <b>PDBTitle:</b> shotgun proteolysis: a practical application
20	<a href="#">d1q1oa_</a>		Alignment		15.5	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
21	<a href="#">c5m32j_</a>		Alignment	not modelled	13.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> proteasome subunit beta type-2; <b>PDBTitle:</b> human 26s proteasome in complex with oprozomib
22	<a href="#">c1914A_</a>		Alignment	not modelled	13.5	24	<b>PDB header:</b> alu domain <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 9/14 fusion protein; <b>PDBTitle:</b> signal recognition particle alu rna binding heterodimer, srp9/14
23	<a href="#">c2k48A_</a>		Alignment	not modelled	12.2	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
24	<a href="#">c6a9wA_</a>		Alignment	not modelled	11.7	17	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> primase; <b>PDBTitle:</b> structure of the bifunctional dna primase-polymerase from phage nrs-1
25	<a href="#">d2p12a1</a>		Alignment	not modelled	11.6	14	<b>Fold:</b> FomD barrel-like <b>Superfamily:</b> FomD-like <b>Family:</b> FomD-like
26	<a href="#">d2gu2a1</a>		Alignment	not modelled	11.5	12	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> AstE/AspA-like
27	<a href="#">c3zeyT_</a>		Alignment	not modelled	11.2	12	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
28	<a href="#">d1wmha_</a>		Alignment	not modelled	11.1	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
							<b>Fold:</b> Nuclease A inhibitor (NuIA)

29	<a href="#">d2o3bb1</a>	Alignment	not modelled	10.6	16	<b>Superfamily:</b> Nuclease A inhibitor (NuiA) <b>Family:</b> Nuclease A inhibitor (NuiA)
30	<a href="#">d1ip9a_</a>	Alignment	not modelled	10.2	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
31	<a href="#">c3iz6U_</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 40s ribosomal protein s24 (s24e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
32	<a href="#">d1914a1</a>	Alignment	not modelled	9.7	29	<b>Fold:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14 <b>Superfamily:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14 <b>Family:</b> Signal recognition particle alu RNA binding heterodimer, SRP9/14
33	<a href="#">c2kssA_</a>	Alignment	not modelled	9.4	62	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> carotenogenesis protein cars; <b>PDBTitle:</b> nmr structure of myxococcus xanthus antirepressor cars1
34	<a href="#">c5eikA_</a>	Alignment	not modelled	9.3	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein y57a10a.28; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
35	<a href="#">c5egiB_</a>	Alignment	not modelled	9.0	35	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein y57a10a.10; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
36	<a href="#">c6iz0A_</a>	Alignment	not modelled	9.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> trimeric intracellular cation channel type a; <b>PDBTitle:</b> crystal structure analysis of a eukaryotic membrane protein
37	<a href="#">d1qzza1</a>	Alignment	not modelled	8.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
38	<a href="#">c6iz4G_</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> trimeric intracellular cation channel type b-b; <b>PDBTitle:</b> crystal structure analysis of tric counter-ion channels in calcium2 release
39	<a href="#">d1qkra_</a>	Alignment	not modelled	8.4	19	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
40	<a href="#">d1x1ma1</a>	Alignment	not modelled	8.3	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
41	<a href="#">c4p94A_</a>	Alignment	not modelled	8.1	28	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved flagellar protein f; <b>PDBTitle:</b> the crystal structure of the soluble domain of sulfolobus2 acidocaldarius flaf (residues 35-164)
42	<a href="#">c1jleB_</a>	Alignment	not modelled	8.0	29	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> troponin t; <b>PDBTitle:</b> crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
43	<a href="#">c6cddB_</a>	Alignment	not modelled	7.8	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> np14 zinc finger; <b>PDBTitle:</b> np14 zinc finger and mpn domains (chaetomium thermophilum)
44	<a href="#">c3tr7A_</a>	Alignment	not modelled	7.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of a uracil-dna glycosylase (ung) from coxiella burnetii
45	<a href="#">c4ptbA_</a>	Alignment	not modelled	7.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear autoantigen sp-100; <b>PDBTitle:</b> crystal structure of human sp100 phd-bromodomain in the free state
46	<a href="#">c5lxyH_</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc finger cchc domain-containing protein 8; <b>PDBTitle:</b> structure of the minimal rbm7 - zcch8 complex
47	<a href="#">d1ef1a3</a>	Alignment	not modelled	6.8	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> First domain of FERM
48	<a href="#">c5xxuY_</a>	Alignment	not modelled	6.7	15	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> ribosomal protein es24; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
49	<a href="#">c1jldF_</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> contractile protein <b>Chain:</b> F: <b>PDB Molecule:</b> troponin i; <b>PDBTitle:</b> crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
50	<a href="#">d2cqna1</a>	Alignment	not modelled	6.3	20	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> FF domain <b>Family:</b> FF domain
51	<a href="#">d1wglA_</a>	Alignment	not modelled	6.3	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
52	<a href="#">d2b7oa1</a>	Alignment	not modelled	6.3	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class-II DAHP synthetase
53	<a href="#">c2xzmP_</a>	Alignment	not modelled	6.2	18	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> rps24e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
54	<a href="#">c3cymA_</a>	Alignment	not modelled	6.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase;

54	<a href="#">c3c811A</a>	Alignment	not modelled	6.2	13	<b>PDBTitle:</b> leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil <b>PDB header:</b> contractile protein
55	<a href="#">c1j1eC</a>	Alignment	not modelled	6.0	17	<b>Chain:</b> C; <b>PDB Molecule:</b> troponin i; <b>PDBTitle:</b> crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
56	<a href="#">d2zpya3</a>	Alignment	not modelled	5.8	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> First domain of FERM
57	<a href="#">d1w2za2</a>	Alignment	not modelled	5.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
58	<a href="#">c4uukE</a>	Alignment	not modelled	5.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> human dynamin 1 k44a superconstricted polymer stabilized with gtp2 strand 2
59	<a href="#">c2rp4C</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> transcription factor p53; <b>PDBTitle:</b> solution structure of the oligomerization domain in dmp53
60	<a href="#">c3k44D</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> purine-rich binding protein-alpha, isoform b; <b>PDBTitle:</b> crystal structure of drosophila melanogaster pur-alpha
61	<a href="#">d1gg3a3</a>	Alignment	not modelled	5.3	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> First domain of FERM