
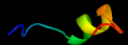



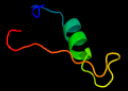

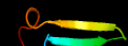



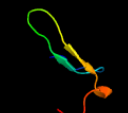



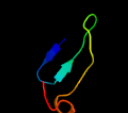

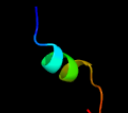




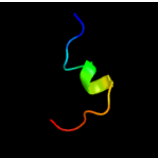

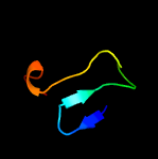
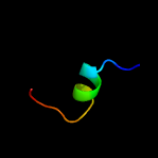
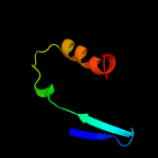
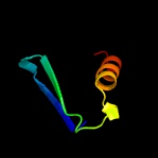

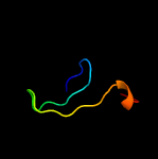



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0010c (- )_13133_13558
Date	Tue Jul 23 14:50:03 BST 2019
Unique Job ID	649c6cbdcdeca1a9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1mpga2</a>	 Alignment		60.5	39	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> DNA repair glycosylase, N-terminal domain
2	<a href="#">d1gg3a2</a>	 Alignment		44.1	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
3	<a href="#">c3tu3A_</a>	 Alignment		37.6	22	<b>PDB header:</b> toxin/toxin chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> exou chaperone; <b>PDBTitle:</b> 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
4	<a href="#">d1e5wa2</a>	 Alignment		37.2	30	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
5	<a href="#">c4akxA_</a>	 Alignment		34.6	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> spcu; <b>PDBTitle:</b> structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
6	<a href="#">d1isna2</a>	 Alignment		31.9	26	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
7	<a href="#">d1j19a2</a>	 Alignment		27.8	26	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
8	<a href="#">d1lef1a2</a>	 Alignment		24.9	26	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
9	<a href="#">d1lef4a_</a>	 Alignment		24.5	50	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> RNA polymerase subunit RPB10 <b>Family:</b> RNA polymerase subunit RPB10
10	<a href="#">c2mc5A_</a>	 Alignment		21.6	38	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> 45I; <b>PDBTitle:</b> a bacteriophage transcription regulator inhibits bacterial2 transcription initiation by -factor displacement
11	<a href="#">d1ywyv1</a>	 Alignment		18.6	26	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PA2021-like <b>Family:</b> PA2021-like

12	<a href="#">c4qiwV_</a>	Alignment		18.3	50	<b>PDB header:</b> transcription <b>Chain:</b> V: <b>PDB Molecule:</b> dna-directed rna polymerase subunit n; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
13	<a href="#">d2zpya2</a>	Alignment		17.0	15	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
14	<a href="#">c1e5wA_</a>	Alignment		16.7	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> structure of isolated ferm domain and first long helix of moesin
15	<a href="#">c2pmzN_</a>	Alignment		13.0	44	<b>PDB header:</b> translation, transferase <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit n; <b>PDBTitle:</b> archaeal rna polymerase from sulfolobus solfataricus
16	<a href="#">c4g6tA_</a>	Alignment		12.7	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> type iii chaperone protein shca; <b>PDBTitle:</b> structure of the hopa1-scha chaperone-effector complex
17	<a href="#">d1qupa2</a>	Alignment		10.7	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
18	<a href="#">c6d2kA_</a>	Alignment		9.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferm, arhgef and pleckstrin domain-containing protein 2; <b>PDBTitle:</b> crystal structure of the ferm domain of mouse farp2
19	<a href="#">c2i1kA_</a>	Alignment		9.6	22	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda reveals the coiled-coil domain at 2.3 angstrom resolution
20	<a href="#">c4rm9A_</a>	Alignment		9.0	22	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ezrin; <b>PDBTitle:</b> crystal structure of human ezrin in space group c2221
21	<a href="#">d1mxaa3</a>	Alignment	not modelled	8.7	13	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
22	<a href="#">c2i88A_</a>	Alignment	not modelled	8.4	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin-e1; <b>PDBTitle:</b> crystal structure of the channel-forming domain of colicin e1
23	<a href="#">d2p02a3</a>	Alignment	not modelled	8.1	19	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
24	<a href="#">d2jxta1</a>	Alignment	not modelled	7.3	26	<b>Fold:</b> RplX-like <b>Superfamily:</b> RplX-like <b>Family:</b> RplX-like
25	<a href="#">d1fe0a_</a>	Alignment	not modelled	7.2	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
26	<a href="#">d1twfj_</a>	Alignment	not modelled	7.2	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> RNA polymerase subunit RPB10 <b>Family:</b> RNA polymerase subunit RPB10
27	<a href="#">d2pb9a1</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> AraD/HMP-PK domain-like <b>Superfamily:</b> AraD/HMP-PK domain-like <b>Family:</b> Phosphomethylpyrimidine kinase C-terminal domain-like
28	<a href="#">d1ib8a1</a>	Alignment	not modelled	6.9	24	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> YhbC-like, C-terminal domain <b>Family:</b> YhbC-like, C-terminal domain
29	<a href="#">d2phpa1</a>	Alignment	not modelled	6.8	33	<b>Fold:</b> AraD/HMP-PK domain-like <b>Superfamily:</b> AraD/HMP-PK domain-like

					<b>Family:</b> Phosphomethylpyrimidine kinase C-terminal domain-like
30	<a href="#">d1h4ra2</a>	Alignment	not modelled	6.7	13 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
31	<a href="#">c2i1jA</a>	Alignment	not modelled	6.2	26 <b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda at 2.1 angstroms resolution
32	<a href="#">c3j21l</a>	Alignment	not modelled	6.0	21 <b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 50s ribosomal protein l15p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
33	<a href="#">c5lc5F</a>	Alignment	not modelled	6.0	33 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nahd dehydrogenase [ubiquinone] flavoprotein 1, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
34	<a href="#">d1qm4a3</a>	Alignment	not modelled	5.8	19 <b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
35	<a href="#">c6d2qA</a>	Alignment	not modelled	5.7	22 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferm, rhogef (arhgef) and pleckstrin domain protein 1 <b>PDBTitle:</b> crystal structure of the ferm domain of zebrafish farp1
36	<a href="#">d2arza1</a>	Alignment	not modelled	5.6	17 <b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
37	<a href="#">c1gg3A</a>	Alignment	not modelled	5.5	16 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> erythroid membrane protein 4.1r; <b>PDBTitle:</b> crystal structure of the protein 4.1r membrane binding2 domain
38	<a href="#">d1cia1</a>	Alignment	not modelled	5.5	16 <b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
39	<a href="#">d1tz7a1</a>	Alignment	not modelled	5.4	30 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
40	<a href="#">c4a19X</a>	Alignment	not modelled	5.4	23 <b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> rpl18a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
41	<a href="#">d1eswa</a>	Alignment	not modelled	5.3	35 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
42	<a href="#">c1rg9D</a>	Alignment	not modelled	5.3	13 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> s-adenosylmethionine synthetase complexed with sam and pnp