

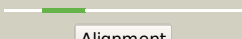

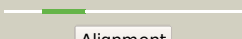




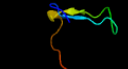


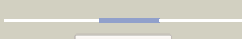
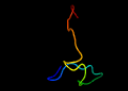

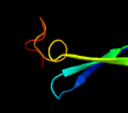





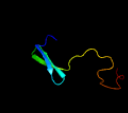

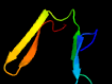
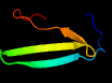
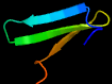

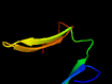
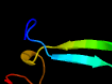

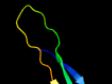


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3004\_cfp6\_3363358\_3363696  
 Date Thu Aug 8 16:20:17 BST 2019  
 Unique Job ID 5a714f9b5f79f431

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2na7A_</a>	 Alignment		60.8	37	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of human fas/cd95 death receptor
2	<a href="#">c2na7B_</a>	 Alignment		57.1	37	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of human fas/cd95 death receptor
3	<a href="#">c2na7C_</a>	 Alignment		57.1	37	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of human fas/cd95 death receptor
4	<a href="#">c3kifD_</a>	 Alignment		53.6	25	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> 5-bladed beta-propeller lectin; <b>PDBTitle:</b> the crystal structures of two fragments truncated from 5-bladed beta-2 propeller lectin, tachylectin-2 (lib1-b7-18 and lib2-d2-15)
5	<a href="#">d1e5wa2</a>	 Alignment		31.5	17	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
6	<a href="#">c4cvuA_</a>	 Alignment		29.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannosidase; <b>PDBTitle:</b> structure of fungal beta-mannosidase from glycoside hydrolase family 22 of trichoderma harzianum
7	<a href="#">d1j19a2</a>	 Alignment		25.7	17	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
8	<a href="#">c3k8rA_</a>	 Alignment		25.6	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
9	<a href="#">d1t12a_</a>	 Alignment		23.1	17	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Tachylectin-2 <b>Family:</b> Tachylectin-2
10	<a href="#">d1ef1a2</a>	 Alignment		22.9	15	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
11	<a href="#">c3kihC_</a>	 Alignment		22.7	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> 5-bladed beta-propeller lectin; <b>PDBTitle:</b> the crystal structures of two fragments truncated from 5-bladed beta-2 propeller lectin, tachylectin-2 (lib2-d2-15)

12	<a href="#">d1isna2</a>	Alignment		21.7	13	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
13	<a href="#">d1gg3a2</a>	Alignment		19.6	13	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
14	<a href="#">d2cx1a2</a>	Alignment		18.6	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Hypothetical protein APE0525, N-terminal domain
15	<a href="#">c5c2mA_</a>	Alignment		18.3	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
16	<a href="#">d2zpya2</a>	Alignment		18.1	15	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
17	<a href="#">d1h4ra2</a>	Alignment		16.4	11	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
18	<a href="#">c2x8nA_</a>	Alignment		9.1	17	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> cv0863; <b>PDBTitle:</b> solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. oosp target cv0863.
19	<a href="#">c2i1jA_</a>	Alignment		9.0	17	<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
20	<a href="#">c3nqnB_</a>	Alignment		8.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function. (dr_2006) from2 deinococcus radiodurans at 1.88 a resolution
21	<a href="#">c3osvC_</a>	Alignment	not modelled	8.4	28	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
22	<a href="#">c2i1kA_</a>	Alignment	not modelled	7.6	17	<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 at2 3.0 angstrom resolution
23	<a href="#">c4h7lB_</a>	Alignment	not modelled	7.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of plim_4148 protein from planctomyces limnophilus
24	<a href="#">c6d2qA_</a>	Alignment	not modelled	7.2	21	<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
25	<a href="#">c2lnzA_</a>	Alignment	not modelled	7.1	60	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein mdy2; <b>PDBTitle:</b> solution structure of the get5 carboxyl domain from s. cerevisiae
26	<a href="#">c3vejB_</a>	Alignment	not modelled	7.0	60	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein mdy2; <b>PDBTitle:</b> crystal structure of the get5 carboxyl domain from s. cerevisiae
27	<a href="#">c1e5wA_</a>	Alignment	not modelled	6.8	15	<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
28	<a href="#">d1hnga1</a>	Alignment	not modelled	6.6	37	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)

29	<a href="#">d1rl6a2</a>	Alignment	not modelled	6.1	57	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
30	<a href="#">d2zjre1</a>	Alignment	not modelled	6.0	43	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
31	<a href="#">d2diga1</a>	Alignment	not modelled	5.7	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> Tudor domain
32	<a href="#">d2j01h2</a>	Alignment	not modelled	5.6	43	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
33	<a href="#">c2yowB_</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rbam17540; <b>PDBTitle:</b> bacillus amyloliquefaciens cbm33
34	<a href="#">c2e6xD_</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ttha1281; <b>PDBTitle:</b> x-ray structure of tt1592 from thermus thermophilus hb8
35	<a href="#">c2diga_</a>	Alignment	not modelled	5.5	32	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lamin-b receptor; <b>PDBTitle:</b> solusion structure of the todor domain of human lamin-b2 receptor
36	<a href="#">c3c8B_</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ftsZ-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
37	<a href="#">c1u2pA_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine- <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
38	<a href="#">d1dg9a_</a>	Alignment	not modelled	5.4	18	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
39	<a href="#">d2qamg2</a>	Alignment	not modelled	5.2	57	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
40	<a href="#">c4a02A_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> chitin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin binding protein; <b>PDBTitle:</b> x-ray crystallographic structure of efcbm33a