

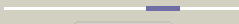






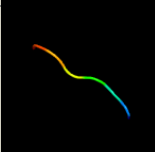

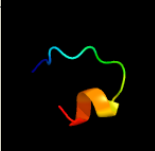



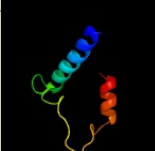




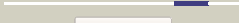

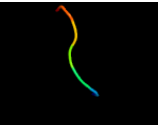

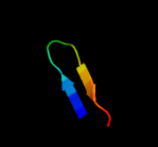


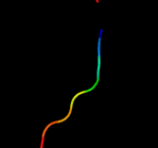





# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2964B\_(RVBD2964B)\_3318111\_3318296  
 Date Thu Aug 8 16:20:12 BST 2019  
 Unique Job ID 5766ff8ba7ce43a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1hgvA_</a>	 Alignment		21.3	59	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> ph75 inovirus major coat protein; <b>PDBTitle:</b> filamentous bacteriophage ph75
2	<a href="#">c5jyxB_</a>	 Alignment		19.8	0	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> archaeosine synthase quef-like; <b>PDBTitle:</b> crystal structure of the covalent thioimide intermediate of the2 archaeosine synthase quef-like
3	<a href="#">c1hgzA_</a>	 Alignment		15.8	59	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> ph75 inovirus major coat protein; <b>PDBTitle:</b> filamentous bacteriophage ph75
4	<a href="#">c3zheC_</a>	 Alignment		13.4	75	<b>PDB header:</b> mrna-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> nonsense-mediated mrna decay protein; <b>PDBTitle:</b> structure of the c. elegans smg5-smg7 complex
5	<a href="#">d1xmwa1</a>	 Alignment		11.6	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
6	<a href="#">d1c55a_</a>	 Alignment		9.7	50	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
7	<a href="#">c3oaiB_</a>	 Alignment		8.8	40	<b>PDB header:</b> membrane protein, cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, myelin protein p0; <b>PDBTitle:</b> crystal structure of the extra-cellular domain of human myelin protein2 zero
8	<a href="#">c6idvB_</a>	 Alignment		8.2	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide asparaginyl ligases; <b>PDBTitle:</b> peptide asparaginyl ligases from viola yedoensis
9	<a href="#">c3bp1A_</a>	 Alignment		7.6	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-dependent 7-cyano-7-deazaguanine reductase; <b>PDBTitle:</b> crystal structure of putative 7-cyano-7-deazaguanine reductase quef2 from vibrio cholerae o1 biovar eltor
10	<a href="#">d1wwbx_</a>	 Alignment		7.6	43	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
11	<a href="#">c1ki8B_</a>	 Alignment		7.5	71	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> neuronal acetylcholine receptor protein, alpha-7 <b>PDBTitle:</b> nmr structural analysis of the complex formed between alpha-2 bungarotoxin and the principal alpha-neurotoxin binding3 sequence on the alpha7 subunit of a neuronal nicotinic4 acetylcholine receptor
						<b>PDB header:</b> toxin

12	<a href="#">c1kc4B_</a>	Alignment		7.5	71	<b>Chain:</b> B; <b>PDB Molecule:</b> neuronal acetylcholine receptor protein, alpha-7 <b>PDBTitle:</b> nmr structural analysis of the complex formed between alpha-2 bungarotoxin and the principal alpha-neurotoxin binding3 sequence on the alpha7 subunit of a neuronal nicotinic4 acetylcholine receptor
13	<a href="#">c5h0iB_</a>	Alignment		7.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> asparaginyl endopeptidase; <b>PDBTitle:</b> name to be released when published
14	<a href="#">d1xiwb_</a>	Alignment		6.8	36	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
15	<a href="#">c2vraD_</a>	Alignment		6.0	43	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> roundabout 1; <b>PDBTitle:</b> drosophila robo ig1-2 (monoclinic form)
16	<a href="#">c4f8bE_</a>	Alignment		6.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> nadph-dependent 7-cyano-7-deazaguanine reductase; <b>PDBTitle:</b> crystal structure of the covalent thioimide intermediate of unimodular2 nitrile reductase quef
17	<a href="#">d1m4ka2</a>	Alignment		5.9	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
18	<a href="#">d1olla2</a>	Alignment		5.6	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
19	<a href="#">d1f97a1</a>	Alignment		5.5	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
20	<a href="#">c1cdhA_</a>	Alignment		5.3	57	<b>PDB header:</b> t-cell surface glycoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> t cell surface glycoprotein cd4; <b>PDBTitle:</b> structures of an hiv and mhc binding fragment from human cd4 as2 refined in two crystal lattices
21	<a href="#">c3bp6B_</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> programmed cell death 1 ligand 2; <b>PDBTitle:</b> crystal structure of the mouse pd-1 mutant and pd-l2 complex
22	<a href="#">d1tnna_</a>	Alignment	not modelled	5.2	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
23	<a href="#">c3vh8H_</a>	Alignment	not modelled	5.2	36	<b>PDB header:</b> immune system <b>Chain:</b> H; <b>PDB Molecule:</b> killer cell immunoglobulin-like receptor 3d11; <b>PDBTitle:</b> kir3d11 in complex with hla-b*5701
24	<a href="#">d1mvka_</a>	Alignment	not modelled	5.2	75	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
25	<a href="#">c3rbgB_</a>	Alignment	not modelled	5.2	43	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> cytotoxic and regulatory t-cell molecule; <b>PDBTitle:</b> crystal structure analysis of class-i mhc restricted t-cell associated2 molecule
26	<a href="#">c4nikB_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> oncoprotein/immune system <b>Chain:</b> B; <b>PDB Molecule:</b> single-chain fv fragment antibody; <b>PDBTitle:</b> structure of human gankyrin in complex to the single chain antibody f5
27	<a href="#">d1nkra2</a>	Alignment	not modelled	5.1	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
28	<a href="#">d1ry7b1</a>	Alignment	not modelled	5.1	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
29	<a href="#">c2a38A_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> titin; <b>PDBTitle:</b> crystal structure of the n-terminus of titin

30 [c6onbB](#)

Alignment

not modelled

5.0

38

**PDB header:**cell adhesion  
**Chain:** B: **PDB Molecule:**neuronal igcam-5;  
**PDBTitle:** crystal structure of the zig-8-rig-5 ig1-ig1 heterodimer, monoclinic2 form