
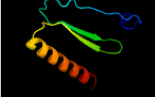





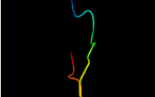



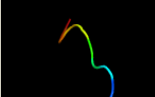

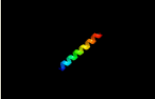








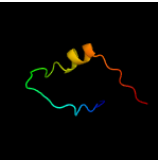

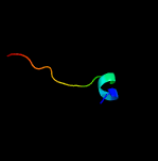
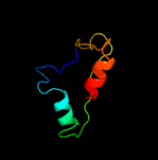
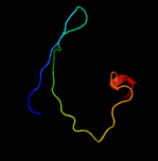
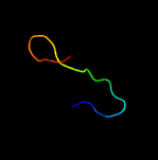
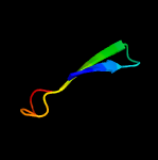
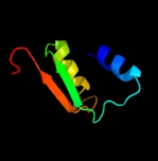
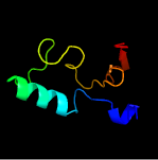


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1528c\_papA4\_1728959\_1729456  
 Date Fri Aug 2 13:30:11 BST 2019  
 Unique Job ID 8281f30fa56ee08d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6aefB_</a>	 Alignment		98.3	36	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
2	<a href="#">c6ehrF_</a>	 Alignment		70.9	7	<b>PDB header:</b> signaling protein <b>Chain:</b> F; <b>PDB Molecule:</b> ras-related gtp-binding protein a; <b>PDBTitle:</b> the crystal structure of the human lamtor-raga ctd-ragc ctd complex
3	<a href="#">c2w91A_</a>	 Alignment		36.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase d; <b>PDBTitle:</b> structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
4	<a href="#">c3gdbA_</a>	 Alignment		34.9	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein spr0440; <b>PDBTitle:</b> crystal structure of spr0440 glycoside hydrolase domain,2 endo-d from streptococcus pneumoniae r6
5	<a href="#">d3e9va1</a>	 Alignment		20.5	18	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
6	<a href="#">c3fhaD_</a>	 Alignment		17.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> structure of endo-beta-n-acetylglucosaminidase a
7	<a href="#">c5y88V_</a>	 Alignment		16.9	23	<b>PDB header:</b> splicing <b>Chain:</b> V; <b>PDB Molecule:</b> pre-mrna-splicing factor ntr2; <b>PDBTitle:</b> cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
8	<a href="#">c4gu4B_</a>	 Alignment		16.3	17	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t11 reovirus attachment protein sigma1 in2 complex with alpha-2,3-sialyllactose
9	<a href="#">c5dijA_</a>	 Alignment		16.3	6	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
10	<a href="#">c3rlcA_</a>	 Alignment		13.8	23	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> a1 protein; <b>PDBTitle:</b> crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form
11	<a href="#">c5t3eA_</a>	 Alignment		12.9	9	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.

12	<a href="#">d1kke2</a>	Alignment		11.7	30	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Reovirus attachment protein sigma 1 head domain
13	<a href="#">d2z15a1</a>	Alignment		10.9	21	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
14	<a href="#">c4chjA_</a>	Alignment		10.6	29	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> imc sub-compartment protein isp3; <b>PDBTitle:</b> structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
15	<a href="#">d1r46a2</a>	Alignment		10.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
16	<a href="#">c4cu9A_</a>	Alignment		9.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> unravelling the multiple functions of the architecturally2 intricate streptococcus pneumoniae beta-galactosidase, bgaa
17	<a href="#">c2n8kA_</a>	Alignment		9.6	26	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> u33-theraphotoxin-cg1b; <b>PDBTitle:</b> chemical shift assignments and structure determination for spider2 toxin, u33-theraphotoxin-cg1c
18	<a href="#">c3kwrA_</a>	Alignment		8.6	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative rna-binding protein; <b>PDBTitle:</b> crystal structure of putative rna-binding protein (np_785364.1) from2 lactobacillus plantarum at 1.45 a resolution
19	<a href="#">d1a4ia1</a>	Alignment		8.6	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
20	<a href="#">c5td6A_</a>	Alignment		8.5	9	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fog-3 protein; <b>PDBTitle:</b> c. elegans fog-3 btg/tob domain - h47n, c117a
21	<a href="#">c1kkeA_</a>	Alignment	not modelled	8.2	30	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> sigma 1 protein; <b>PDBTitle:</b> crystal structure of reovirus attachment protein sigma12 trimer
22	<a href="#">c6av8A_</a>	Alignment	not modelled	7.8	80	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> u5-theraphotoxin-hs1b 1; <b>PDBTitle:</b> exploring cystine dense peptide space to open a unique molecular2 toolbox
23	<a href="#">c2aapA_</a>	Alignment	not modelled	7.5	80	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> jingzhaotoxin-vii; <b>PDBTitle:</b> solution structure of jingzhaotoxin-vii
24	<a href="#">c3qm1C_</a>	Alignment	not modelled	7.5	26	<b>PDB header:</b> chaperone/protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nucleotide exchange factor sil1; <b>PDBTitle:</b> the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor
25	<a href="#">c3ushB_</a>	Alignment	not modelled	7.2	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
26	<a href="#">c4chmB_</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> imc sub-compartment protein isp1; <b>PDBTitle:</b> structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
27	<a href="#">c3i07B_</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
28	<a href="#">c3s6xA_</a>	Alignment	not modelled	6.3	30	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> structure of reovirus attachment protein sigma1 in

						complex with alpha-2,3-sialyllactose
29	<a href="#">c1a4iB_</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
30	<a href="#">c5oltA_</a>	Alignment	not modelled	6.0	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose biosynthesis protein bcsG; <b>PDBTitle:</b> crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsG from salmonella typhimurium
31	<a href="#">d1a6qa1</a>	Alignment	not modelled	5.9	38	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> Protein serine/threonine phosphatase 2C, C-terminal domain <b>Family:</b> Protein serine/threonine phosphatase 2C, C-terminal domain
32	<a href="#">c2lq3A_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of syc0711_d from synechococcus sp., northeast2 structural genomics consortium (nesg) target snr212
33	<a href="#">c3e2sA_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure reduced puta86-630 mutant y540s complexed with l-2 proline
34	<a href="#">c5yvua_</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structures of unlinked full length ns3 from dengue virus2 provide insights into dynamics of protease domain
35	<a href="#">d1p42a1</a>	Alignment	not modelled	5.3	28	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
36	<a href="#">c2n59A_</a>	Alignment	not modelled	5.3	67	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein csgh; <b>PDBTitle:</b> solution structure of r. palustris csgh
37	<a href="#">c4iohA_</a>	Alignment	not modelled	5.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tl11086 protein; <b>PDBTitle:</b> crystal structure of the tl1086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
38	<a href="#">c5i8iD_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> urea amidolyase; <b>PDBTitle:</b> crystal structure of the k. lactis urea amidolyase
39	<a href="#">d1o5wa2</a>	Alignment	not modelled	5.0	13	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> L-aminoacid/polyamine oxidase
40	<a href="#">c2k1kA_</a>	Alignment	not modelled	5.0	100	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
41	<a href="#">c2k1kB_</a>	Alignment	not modelled	5.0	100	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
42	<a href="#">c2k1lA_</a>	Alignment	not modelled	5.0	100	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3