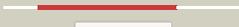
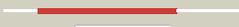


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1975 (- )_2218060_2218725
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	daa9940d9fb144b2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ifaA_</a>	 Alignment		100.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular protein containing a scp domain; <b>PDBTitle:</b> 1.5 angstrom resolution crystal structure of an extracellular protein2 containing a scp domain from bacillus anthracis str. ames
2	<a href="#">c4h0aB_</a>	 Alignment		100.0	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a cysteine-rich secretory protein (sav1118) from2 staphylococcus aureus subsp. aureus mu50 at 1.90 a resolution
3	<a href="#">c4d53A_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> bb0689; <b>PDBTitle:</b> outer surface protein bb0689 from borrelia burgdorferi
4	<a href="#">d1cfea_</a>	 Alignment		99.4	15	<b>Fold:</b> PR-1-like <b>Superfamily:</b> PR-1-like <b>Family:</b> PR-1-like
5	<a href="#">d1smba_</a>	 Alignment		99.1	23	<b>Fold:</b> PR-1-like <b>Superfamily:</b> PR-1-like <b>Family:</b> PR-1-like
6	<a href="#">c5jysA_</a>	 Alignment		99.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein pry1; <b>PDBTitle:</b> pry1 cap domain
7	<a href="#">c5v51B_</a>	 Alignment		98.9	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pr-1 protein; <b>PDBTitle:</b> crystal structure of mppr-1i soaked with selenourea for 10 min
8	<a href="#">d1qnxa_</a>	 Alignment		98.4	19	<b>Fold:</b> PR-1-like <b>Superfamily:</b> PR-1-like <b>Family:</b> PR-1-like
9	<a href="#">c3nt8A_</a>	 Alignment		98.4	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ancylostoma secreted protein 1; <b>PDBTitle:</b> crystal structure of na-asp-1
10	<a href="#">c2vznA_</a>	 Alignment		98.4	20	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> venom allergen 3; <b>PDBTitle:</b> crystal structure of the major allergen from fire ant venom, sol i 3
11	<a href="#">c5weeD_</a>	 Alignment		98.3	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> venom allergen like protein 4; <b>PDBTitle:</b> crystal structure of hpval4

12	<a href="#">c1u53A_</a>	Alignment		98.3	10	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protein asp-2; <b>PDBTitle:</b> novel x-ray structure of na-asp-2, a pr-1 protein from the nematode2 parasite necator americanus and a vaccine antigen for human hookworm3 infection
13	<a href="#">c1xx5B_</a>	Alignment		98.2	16	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> natrin 1; <b>PDBTitle:</b> crystal structure of natrin from naja atra snake venom
14	<a href="#">c2epfD_</a>	Alignment		98.2	15	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> pseudecin; <b>PDBTitle:</b> crystal structure of zinc-bound pseudocin from pseudechis porphyriacus
15	<a href="#">c4tpvA_</a>	Alignment		98.1	17	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> platelet inhibitor; <b>PDBTitle:</b> crystal structure of hookworm platelet inhibitor
16	<a href="#">c3s6sB_</a>	Alignment		98.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ac-asp-7; <b>PDBTitle:</b> ancylostoma-secreted protein ac-asp-7
17	<a href="#">c6anyA_</a>	Alignment		98.0	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> bm4233, isoform b; <b>PDBTitle:</b> structure of bmval-1
18	<a href="#">c4p27A_</a>	Alignment		98.0	14	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> venom allergen-like (val) 4 protein; <b>PDBTitle:</b> structure of schistosoma mansoni venom allergen-like protein 42 (smval4)
19	<a href="#">d1rc9a1</a>	Alignment		98.0	15	<b>Fold:</b> PR-1-like <b>Superfamily:</b> PR-1-like <b>Family:</b> PR-1-like
20	<a href="#">c3u3uC_</a>	Alignment		97.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> tablysin 15; <b>PDBTitle:</b> crystal structure of the tablysin-15-leukotriene e4 complex
21	<a href="#">c4g2uA_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ancylostoma-secreted protein-like protein; <b>PDBTitle:</b> crystal structure analysis of ostertagia ostertagi asp-1
22	<a href="#">d2bzea1</a>	Alignment	not modelled	37.8	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Plus3-like <b>Family:</b> Plus3
23	<a href="#">c3dgsA_</a>	Alignment	not modelled	29.1	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> coat protein a; <b>PDBTitle:</b> changing the determinants of protein stability from covalent to non-2 covalent interactions by in-vitro evolution: a structural and3 energetic analysis
24	<a href="#">c4a42B_</a>	Alignment	not modelled	27.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-n-acetylglucosaminidase family protein; <b>PDBTitle:</b> cpgh89cbm32-6 produced by clostridium perfringens
25	<a href="#">c3do8B_</a>	Alignment	not modelled	19.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 archaeoglobus fulgidus
26	<a href="#">c4zgfA_</a>	Alignment	not modelled	13.7	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4847 family protein (bvu_2626) from2 bacteroides vulgatus atcc 8482 at 1.00 a resolution
27	<a href="#">d1w5fa2</a>	Alignment	not modelled	9.4	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
28	<a href="#">d1rq2a2</a>	Alignment	not modelled	8.5	27	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
						<b>PDB header:</b> viral protein/immune system <b>Chain:</b> G: <b>PDB Molecule:</b> outer domain of hiv-1 gp120 (ker2018)

29	<a href="#">c4i3rG_</a>	Alignment	not modelled	7.6	31	od4.2.2); <b>PDBTitle:</b> crystal structure of the outer domain of hiv-1 gp120 in complex with2 vrc-pg04 space group p3221
30	<a href="#">c2kjmA_</a>	Alignment	not modelled	7.6	36	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone rna hairpin-binding protein; <b>PDBTitle:</b> solution structure of slbp rna binding domain fragment
31	<a href="#">d1ofua2</a>	Alignment	not modelled	7.0	23	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
32	<a href="#">d1bdsa_</a>	Alignment	not modelled	5.6	75	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
33	<a href="#">c1bdsA_</a>	Alignment	not modelled	5.6	75	<b>PDB header:</b> anti-hypertensive, anti-viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> bds-i; <b>PDBTitle:</b> determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
34	<a href="#">c2hgca_</a>	Alignment	not modelled	5.5	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yjcq protein; <b>PDBTitle:</b> solution nmr structure of the yjcq protein from bacillus2 subtilis. northeast structural genomics target sr346.
35	<a href="#">d2hgca1</a>	Alignment	not modelled	5.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> YjcQ-like
36	<a href="#">c3lo3E_</a>	Alignment	not modelled	5.2	26	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.