



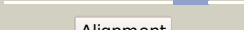
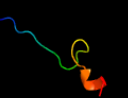






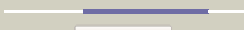
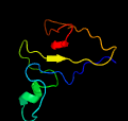
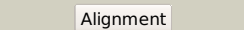

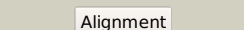

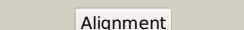
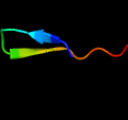
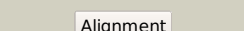

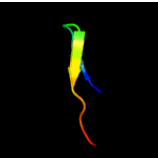
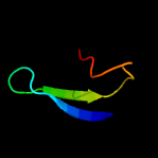
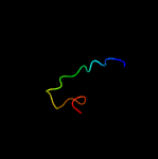
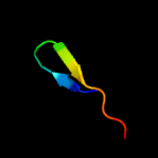
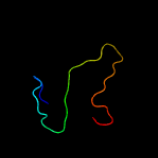
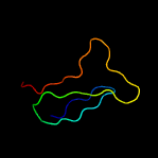
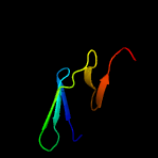

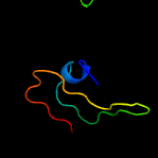


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0680c_(-)_780045_780419
Date	Fri Jul 26 01:50:25 BST 2019
Unique Job ID	5d83c36a5589565d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ljyA_</a>	 Alignment		40.1	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> putative adhesin; <b>PDBTitle:</b> crystal structure of putative adhesin (yp_001304413.1) from <i>Mycobacterium tuberculosis</i> H37Rv at 2.41 Å resolution
2	<a href="#">c3sula_</a>	 Alignment		29.5	29	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> cerato-platanin-like protein; <b>PDBTitle:</b> crystal structure of cerato-platanin 3 from <i>M. perniciosus</i> (mpcp3)
3	<a href="#">d1ckqa_</a>	 Alignment		26.1	30	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease EcoRI
4	<a href="#">c4tmdA_</a>	 Alignment		24.4	25	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray structure of putative uncharacterized protein (rv0999 ortholog)2 from <i>Mycobacterium smegmatis</i>
5	<a href="#">d1k4za_</a>	 Alignment		16.4	16	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> C-terminal domain of adenyllycyclase associated protein <b>Family:</b> C-terminal domain of adenyllycyclase associated protein
6	<a href="#">d1q7ha2</a>	 Alignment		16.1	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Hypothetical protein Ta1423, N-terminal domain
7	<a href="#">d1f00i2</a>	 Alignment		13.5	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
8	<a href="#">d1vqoe1</a>	 Alignment		13.0	9	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
9	<a href="#">c3sukB_</a>	 Alignment		11.6	30	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> cerato-platanin-like protein; <b>PDBTitle:</b> crystal structure of cerato-platanin 2 from <i>M. perniciosus</i> (mpcp2)
10	<a href="#">c1yn3A_</a>	 Alignment		11.5	43	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> truncated cell surface protein map-w; <b>PDBTitle:</b> crystal structures of eap domains from <i>Staphylococcus aureus</i> reveal an unexpected homology to bacterial superantigens
11	<a href="#">d1rl6a1</a>	 Alignment		11.4	23	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6

12	<a href="#">c1yn4A_</a>	Alignment		11.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> eaph1; <b>PDBTitle:</b> crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
13	<a href="#">c3sujA_</a>	Alignment		11.3	26	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> cerato-platanin 1; <b>PDBTitle:</b> crystal structure of cerato-platanin 1 from m. pernicioso (mpcp1)
14	<a href="#">c3hh1D_</a>	Alignment		11.1	30	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> tetrapyrrole methylase family protein; <b>PDBTitle:</b> the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
15	<a href="#">c1yn5B_</a>	Alignment		11.1	21	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> eaph2; <b>PDBTitle:</b> crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
16	<a href="#">c1e5uI_</a>	Alignment		8.1	21	<b>PDB header:</b> intimin <b>Chain:</b> I; <b>PDB Molecule:</b> intimin; <b>PDBTitle:</b> nmr representative structure of intimin-190 (int190) from2 enteropathogenic e. coli
17	<a href="#">d2z3qb1</a>	Alignment		7.6	19	<b>Fold:</b> Complement control module/SCR domain <b>Superfamily:</b> Complement control module/SCR domain <b>Family:</b> Complement control module/SCR domain
18	<a href="#">c3j21F_</a>	Alignment		7.4	11	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
19	<a href="#">c5g5oC_</a>	Alignment		7.3	15	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> lh3 hexon-interlacing capsid protein; <b>PDBTitle:</b> structure of the snake adenovirus 1 hexon-interlacing lh3 protein,2 native
20	<a href="#">c2vbeA_</a>	Alignment		7.0	29	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> tailspike-protein; <b>PDBTitle:</b> tailspike protein of bacteriophage sf6
21	<a href="#">c5hceD_</a>	Alignment	not modelled	6.9	39	<b>PDB header:</b> immune system <b>Chain:</b> D; <b>PDB Molecule:</b> rhhipcephalus appendiculatus raci1; <b>PDBTitle:</b> ternary complex of human complement c5 with ornithodoros moubata omc12 and rhhipcephalus appendiculatus raci1
22	<a href="#">c2n21A_</a>	Alignment	not modelled	6.8	83	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dhx36; <b>PDBTitle:</b> solution structure of complex between dna g-quadruplex and g-2 quadruplex recognition domain of rhau
23	<a href="#">c2n16A_</a>	Alignment	not modelled	6.8	83	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dhx36; <b>PDBTitle:</b> solution structure of g-quadruplex recognition domain of rhau
24	<a href="#">c2zwkA_</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> intimin; <b>PDBTitle:</b> crystal structure of intimin-tir90 complex
25	<a href="#">d2e1ba1</a>	Alignment	not modelled	6.6	37	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> AlaX-M N-terminal domain-like
26	<a href="#">c2xvsA_</a>	Alignment	not modelled	6.5	24	<b>PDB header:</b> antitumor protein <b>Chain:</b> A; <b>PDB Molecule:</b> tetratricopeptide repeat protein 5; <b>PDBTitle:</b> crystal structure of human ttc5 (strap) c-terminal ob2 domain
27	<a href="#">c2b0rB_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> possible adenyl cyclase-associated protein; <b>PDBTitle:</b> crystal structure of cyclase-associated protein from cryptosporidium2 parvum
28	<a href="#">c2z3rF_</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> cytokine/cytokine receptor <b>Chain:</b> F; <b>PDB Molecule:</b> interleukin-15 receptor alpha chain; <b>PDBTitle:</b> crystal structure of the il-15/il-15ra complex

29	<a href="#">c4p3xA_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate synthase a; <b>PDBTitle:</b> structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima
30	<a href="#">c1qfnB_</a>	Alignment	not modelled	6.1	55	<b>PDB header:</b> electron transport/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (ribonucleoside-diphosphate reductase 1); <b>PDBTitle:</b> glutaredoxin-1-ribonucleotide reductase b1 mixed disulfide2 bond
31	<a href="#">d1wzua1</a>	Alignment	not modelled	5.6	38	<b>Fold:</b> NadA-like <b>Superfamily:</b> NadA-like <b>Family:</b> NadA-like
32	<a href="#">c3j3wJ_</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
33	<a href="#">c6az5A_</a>	Alignment	not modelled	5.2	28	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k