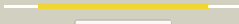

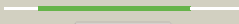
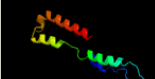





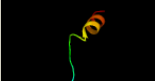














# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0025 (-) _29245_29607
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	64c6bee548746364

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4p40A_</a>	 Alignment		70.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> copn; <b>PDBTitle:</b> chlamydia pneumoniae copn
2	<a href="#">c2jswA_</a>	 Alignment		57.6	15	<b>PDB header:</b> actin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> nmr structure of the talin c-terminal actin binding site
3	<a href="#">c3tu3A_</a>	 Alignment		30.7	39	<b>PDB header:</b> toxin/toxin chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> exou chaperone; <b>PDBTitle:</b> 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
4	<a href="#">c4akxA_</a>	 Alignment		30.7	39	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> spcu; <b>PDBTitle:</b> structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
5	<a href="#">c5a29A_</a>	 Alignment		17.5	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolygalacturonate lyase; <b>PDBTitle:</b> family 2 pectate lyase from vibrio vulnificus
6	<a href="#">c2v8kA_</a>	 Alignment		16.7	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pectate lyase; <b>PDBTitle:</b> structure of a family 2 pectate lyase in complex with trigalacturonic2 acid
7	<a href="#">d1eera_</a>	 Alignment		15.2	33	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
8	<a href="#">c1tqeX_</a>	 Alignment		11.0	40	<b>PDB header:</b> transcription/protein binding/dna <b>Chain:</b> X: <b>PDB Molecule:</b> histone deacetylase 9; <b>PDBTitle:</b> mechanism of recruitment of class ii histone deacetylases by myocyte2 enhancer factor-2
9	<a href="#">c1tqeY_</a>	 Alignment		11.0	40	<b>PDB header:</b> transcription/protein binding/dna <b>Chain:</b> Y: <b>PDB Molecule:</b> histone deacetylase 9; <b>PDBTitle:</b> mechanism of recruitment of class ii histone deacetylases by myocyte2 enhancer factor-2
10	<a href="#">c6cfzG_</a>	 Alignment		10.5	33	<b>PDB header:</b> nuclear protein <b>Chain:</b> G: <b>PDB Molecule:</b> hsk3; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
11	<a href="#">c5fv8B_</a>	 Alignment		9.7	44	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.

12	<a href="#">c6ohzA_</a>	Alignment		9.6	24	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of an uncharacterized protein from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
13	<a href="#">c3t4aG_</a>	Alignment		9.6	21	<b>PDB header:</b> immune system <b>Chain:</b> G; <b>PDB Molecule:</b> fibrinogen-binding protein; <b>PDBTitle:</b> structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
14	<a href="#">c5fv8A_</a>	Alignment		9.5	44	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
15	<a href="#">c5frgA_</a>	Alignment		9.4	29	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
16	<a href="#">c6ao3B_</a>	Alignment		9.2	16	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> gasdermin-d; <b>PDBTitle:</b> crystal structure of the murine gasdermin d c-terminal domain
17	<a href="#">c1d7mA_</a>	Alignment		8.8	24	<b>PDB header:</b> contractile protein <b>Chain:</b> A; <b>PDB Molecule:</b> cortexillin i; <b>PDBTitle:</b> coiled-coil dimerization domain from cortexillin i
18	<a href="#">d1v7mv_</a>	Alignment		8.8	42	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
19	<a href="#">c4qkvB_</a>	Alignment		8.7	27	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> polymerase i and transcript release factor; <b>PDBTitle:</b> crystal structure of the mouse cavin1 hr1 domain
20	<a href="#">d2k0bx1</a>	Alignment		8.1	25	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
21	<a href="#">c5nh1A_</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> gasdermin-d; <b>PDBTitle:</b> structure of the c-terminal domain of human gasdermin d
22	<a href="#">c1y66D_</a>	Alignment	not modelled	8.0	24	<b>PDB header:</b> de novo protein <b>Chain:</b> D; <b>PDB Molecule:</b> engrailed homeodomain; <b>PDBTitle:</b> dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
23	<a href="#">c4qkwB_</a>	Alignment	not modelled	7.9	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> muscle-related coiled-coil protein; <b>PDBTitle:</b> crystal structure of the zebrafish cavin4a hr1 domain
24	<a href="#">c1usdA_</a>	Alignment	not modelled	7.6	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> vasodilator-stimulated phosphoprotein; <b>PDBTitle:</b> human vasp tetramerisation domain I352m
25	<a href="#">d1ldda_</a>	Alignment	not modelled	7.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> SCF ubiquitin ligase complex WHB domain
26	<a href="#">c2rmgA_</a>	Alignment	not modelled	7.3	50	<b>PDB header:</b> hormone <b>Chain:</b> A; <b>PDB Molecule:</b> urocortin-2; <b>PDBTitle:</b> human urocortin 2
27	<a href="#">c2lrmB_</a>	Alignment	not modelled	7.2	34	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein ymgd; <b>PDBTitle:</b> assignment and structure of e coli periplasmic protein ymgd
28	<a href="#">c3cvgD_</a>	Alignment	not modelled	7.0	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> putative metal binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic putative metal binding protein
						<b>Fold:</b> Cell division protein ZapA-like

29	<a href="#">d1t3ua_</a>	Alignment	not modelled	7.0	30	<b>Superfamily:</b> Cell division protein ZapA-like <b>Family:</b> Cell division protein ZapA-like
30	<a href="#">c6cn0B_</a>	Alignment	not modelled	6.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 16s rrna (guanine(1405)-n(7))-methyltransferase; <b>PDBTitle:</b> 2.95 angstrom crystal structure of 16s rrna methylase from proteus2 mirabilis
31	<a href="#">c2kztA_</a>	Alignment	not modelled	6.4	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> structure of the tandem ma-3 region of pdcd4
32	<a href="#">d2fp1a1</a>	Alignment	not modelled	6.1	15	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Secreted chorismate mutase-like
33	<a href="#">c5nj1A_</a>	Alignment	not modelled	6.0	36	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein (putative s-layer protein); <b>PDBTitle:</b> cwp2 from clostridium difficile
34	<a href="#">c2jy8A_</a>	Alignment	not modelled	5.9	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-binding protein p62; <b>PDBTitle:</b> nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
35	<a href="#">d1grja1</a>	Alignment	not modelled	5.9	34	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
36	<a href="#">c4kd5A_</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type transport system, molybdenum-specific <b>PDBTitle:</b> substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
37	<a href="#">c2qkdA_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> signaling protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein zpr1; <b>PDBTitle:</b> crystal structure of tandem zpr1 domains
38	<a href="#">c1n6jG_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> G: <b>PDB Molecule:</b> calcineurin-binding protein cabin 1; <b>PDBTitle:</b> structural basis of sequence-specific recruitment of histone2 deacetylases by myocyte enhancer factor-2