






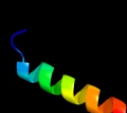

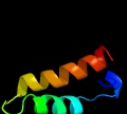









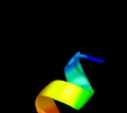

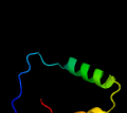











# Phyre2

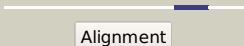
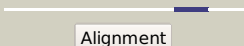

Email	mdejesus@rockefeller.edu
Description	RVBD3899c_(-)_4384325_4385557
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	dc6e9a80ccc5eec3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5imuA_</a>	 Alignment		100.0	100	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tat (twin-arginine translocation) pathway signal sequence <b>PDBTitle:</b> a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis
2	<a href="#">c6r24D_</a>	 Alignment		74.1	6	<b>PDB header:</b> virus like particle <b>Chain:</b> D: <b>PDB Molecule:</b> transposon ty3-i gag-pol polyprotein; <b>PDBTitle:</b> the structure of a ty3 retrotransposon icosahedral capsid
3	<a href="#">c1wyoA_</a>	 Alignment		55.2	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule-associated protein rp/eb family <b>PDBTitle:</b> solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
4	<a href="#">c1q0wA_</a>	 Alignment		48.5	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein <b>PDBTitle:</b> solution structure of vps27 amino-terminal uim-ubiquitin2 complex
5	<a href="#">d1q1va_</a>	 Alignment		46.3	23	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> DEK C-terminal domain <b>Family:</b> DEK C-terminal domain
6	<a href="#">c4dx8H_</a>	 Alignment		27.5	18	<b>PDB header:</b> protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> krev interaction trapped protein 1; <b>PDBTitle:</b> icap1 in complex with krit1 n-terminus
7	<a href="#">d1wh4a_</a>	 Alignment		23.6	19	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
8	<a href="#">c2konA_</a>	 Alignment		21.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
9	<a href="#">d1v5ka_</a>	 Alignment		20.5	18	<b>Fold:</b> CH domain-like <b>Superfamily:</b> Calponin-homology domain, CH-domain <b>Family:</b> Calponin-homology domain, CH-domain
10	<a href="#">c5aj3h_</a>	 Alignment		20.3	25	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
11	<a href="#">c1itkB_</a>	 Alignment		17.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase-peroxidase; <b>PDBTitle:</b> crystal structure of catalase-peroxidase from haloarcula2 marismortui

12	<a href="#">c5i82A_</a>	Alignment		17.3	40	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> enterococcin k1; <b>PDBTitle:</b> nmr structure of enterocin k1 in 50%/50% tfe/water
13	<a href="#">c3rx6A_</a>	Alignment		16.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> polarity suppression protein; <b>PDBTitle:</b> crystal structure of polarity suppression protein from enterobacteria2 phage p4
14	<a href="#">d2qjza1</a>	Alignment		16.2	14	<b>Fold:</b> CH domain-like <b>Superfamily:</b> Calponin-homology domain, CH-domain <b>Family:</b> Calponin-homology domain, CH-domain
15	<a href="#">c2kneB_</a>	Alignment		16.2	22	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, ca++ transporting, plasma membrane 4; <b>PDBTitle:</b> calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
16	<a href="#">d2pofa1</a>	Alignment		15.1	17	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> CDH-like
17	<a href="#">d1joga_</a>	Alignment		14.6	27	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nucleotidyltransferase substrate binding subunit/domain <b>Family:</b> Family 1 bi-partite nucleotidyltransferase subunit
18	<a href="#">c3vlmB_</a>	Alignment		13.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase-peroxidase 2; <b>PDBTitle:</b> crystal structure analysis of the met244ala variant of katg from2 haloarcula marismortui
19	<a href="#">c5f5uB_</a>	Alignment		13.0	25	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
20	<a href="#">d1i2la_</a>	Alignment		11.9	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
21	<a href="#">d1prtF_</a>	Alignment	not modelled	11.9	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
22	<a href="#">c2p0tA_</a>	Alignment	not modelled	11.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0307 protein pspto_4464; <b>PDBTitle:</b> structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
23	<a href="#">d2p0ta1</a>	Alignment	not modelled	11.7	12	<b>Fold:</b> PSPTO4464-like <b>Superfamily:</b> PSPTO4464-like <b>Family:</b> PSPTO4464-like
24	<a href="#">c6gseA_</a>	Alignment	not modelled	11.7	5	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> activity-regulated cytoskeleton-associated protein; <b>PDBTitle:</b> solution structure of the capsid domain from the activity-regulated2 cytoskeleton-associated protein, arc
25	<a href="#">d1wtya_</a>	Alignment	not modelled	11.6	19	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nucleotidyltransferase substrate binding subunit/domain <b>Family:</b> Family 1 bi-partite nucleotidyltransferase subunit
26	<a href="#">c6od7D_</a>	Alignment	not modelled	10.8	17	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> portal protein; <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) pul6 portal protein, dodecameric2 complex
27	<a href="#">c2rqpa_</a>	Alignment	not modelled	10.8	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> heterochromatin protein 1-binding protein 3; <b>PDBTitle:</b> the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
28	<a href="#">c5f5uH_</a>	Alignment	not modelled	10.5	25	<b>PDB header:</b> splicing <b>Chain:</b> H: <b>PDB Molecule:</b> putative uncharacterized protein;

28	<a href="#">c19du1</a>	Alignment	not modelled	10.3	29	<b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum <b>PDB header:</b> transferase
29	<a href="#">c4hl7A</a>	Alignment	not modelled	10.0	18	<b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
30	<a href="#">d1w0ba</a>	Alignment	not modelled	10.0	47	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Alpha-hemoglobin stabilizing protein AHSP <b>Family:</b> Alpha-hemoglobin stabilizing protein AHSP
31	<a href="#">d1vcva1</a>	Alignment	not modelled	9.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
32	<a href="#">d1mp1a</a>	Alignment	not modelled	9.5	21	<b>Fold:</b> PWI domain <b>Superfamily:</b> PWI domain <b>Family:</b> PWI domain
33	<a href="#">d1yl7a1</a>	Alignment	not modelled	9.1	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	<a href="#">c5ed9A</a>	Alignment	not modelled	8.5	33	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sun domain-containing protein 2; <b>PDBTitle:</b> crystal structure of cc1 of mouse sun2
35	<a href="#">c3ut2B</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase-peroxidase 2; <b>PDBTitle:</b> crystal structure of fungal magkatg2
36	<a href="#">d1b8xa1</a>	Alignment	not modelled	7.8	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
37	<a href="#">d1z8ua1</a>	Alignment	not modelled	7.8	47	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Alpha-hemoglobin stabilizing protein AHSP <b>Family:</b> Alpha-hemoglobin stabilizing protein AHSP
38	<a href="#">d1usta</a>	Alignment	not modelled	7.6	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Linker histone H1/H5
39	<a href="#">d1ybea1</a>	Alignment	not modelled	7.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase C-terminal domain
40	<a href="#">d1yqaa1</a>	Alignment	not modelled	7.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Linker histone H1/H5
41	<a href="#">d2qeec1</a>	Alignment	not modelled	7.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Uronate isomerase-like
42	<a href="#">d2ccaa1</a>	Alignment	not modelled	6.8	15	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
43	<a href="#">c5ldwg</a>	Alignment	not modelled	6.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
44	<a href="#">d1duga1</a>	Alignment	not modelled	6.4	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
45	<a href="#">c6dg6F</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> neoleukin-2/15; <b>PDBTitle:</b> structure of a de novo designed interleukin-2/interleukin-15 mimetic
46	<a href="#">c1cffB</a>	Alignment	not modelled	6.0	29	<b>PDB header:</b> calmodulin <b>Chain:</b> B: <b>PDB Molecule:</b> calcium pump; <b>PDBTitle:</b> nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
47	<a href="#">c5f5tD</a>	Alignment	not modelled	5.9	25	<b>PDB header:</b> splicing <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum
48	<a href="#">c2bbzC</a>	Alignment	not modelled	5.9	16	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
49	<a href="#">c5dggB</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
50	<a href="#">c2qjxA</a>	Alignment	not modelled	5.6	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein bim1; <b>PDBTitle:</b> structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1
51	<a href="#">d2o8ra3</a>	Alignment	not modelled	5.6	16	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
52	<a href="#">d1ifla2</a>	Alignment	not modelled	5.4	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
53	<a href="#">c2kscA</a>	Alignment	not modelled	5.4	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cyanoglobin; <b>PDBTitle:</b> solution structure of synechococcus sp. pcc 7002 hemoglobin
54	<a href="#">c6fzoC</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> fluorescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> smurfp; <b>PDBTitle:</b> smurfp-y56f mutant

55	<a href="#">c6fhgB_</a>	 Alignment	not modelled	5.1	18	<p><b>PDB header:</b>antimicrobial protein  <b>Chain:</b> B: <b>PDB Molecule:</b>lyst endolysin;  <b>PDBTitle:</b> crystal structure of the ts2631 endolysin from thermus scotoductus2 phage with the unique n-terminal moiety responsible for peptidoglycan3 anchoring</p>
56	<a href="#">c2mniA_</a>	 Alignment	not modelled	5.1	27	<p><b>PDB header:</b>unknown function  <b>Chain:</b> A: <b>PDB Molecule:</b>hp_q4d059;  <b>PDBTitle:</b> chemical shift assignments and structure of q4d059, a hypothetical2 protein from trypanosoma cruzi</p>
57	<a href="#">c5lcwS_</a>	 Alignment	not modelled	5.0	15	<p><b>PDB header:</b>cell cycle  <b>Chain:</b> S: <b>PDB Molecule:</b>mitotic checkpoint serine/threonine-protein kinase bub1  <b>PDBTitle:</b> cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 angstrom resolution</p>