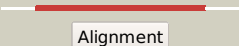



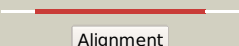


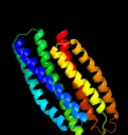


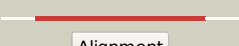




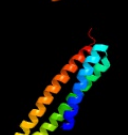

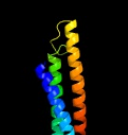






# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3301c\_(phoY1)\_3686909\_3687574  
 Date Thu Aug 8 16:20:51 BST 2019  
 Unique Job ID ca4c86c78c8838bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1sumb_</a>	 Alignment		100.0	17	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PhoU-like <b>Family:</b> PhoU-like
2	<a href="#">d1t72a_</a>	 Alignment		100.0	24	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PhoU-like <b>Family:</b> PhoU-like
3	<a href="#">d1xwma_</a>	 Alignment		100.0	29	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PhoU-like <b>Family:</b> PhoU-like
4	<a href="#">c4q25B_</a>	 Alignment		100.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate-specific transport system accessory protein phou <b>PDBTitle:</b> crystal structure of phou from pseudomonas aeruginosa
5	<a href="#">c2i0mA_</a>	 Alignment		100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transport system protein phou; <b>PDBTitle:</b> crystal structure of the phosphate transport system regulatory protein2 phou from streptococcus pneumoniae
6	<a href="#">c3i39A_</a>	 Alignment		99.8	9	<b>PDB header:</b> phosphate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phou-like phosphate regulatory protein; <b>PDBTitle:</b> crystal structure of putative phou-like phosphate regulatory protein2 (bt4638) from bacteroides thetaiotaomicron vpi-5482 at 1.93 a3 resolution
7	<a href="#">c2oltB_</a>	 Alignment		99.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
8	<a href="#">d1vcta1</a>	 Alignment		99.6	22	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PhoU-like <b>Family:</b> PhoU-like
9	<a href="#">c2bknA_</a>	 Alignment		99.3	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0236; <b>PDBTitle:</b> structure analysis of unknown function protein
10	<a href="#">c5vwwB_</a>	 Alignment		38.1	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-bh3 - cubic
11	<a href="#">c5vwwC_</a>	 Alignment		37.6	25	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-rt - tetragonal

12	<a href="#">c5vwwD_</a>	Alignment		34.5	25	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-rt - tetragonal
13	<a href="#">c1pq1B_</a>	Alignment		29.3	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2-like protein 11; <b>PDBTitle:</b> crystal structure of bcl-xl/bim
14	<a href="#">c3izcw_</a>	Alignment		28.2	16	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein rpl22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	<a href="#">c5ua4B_</a>	Alignment		27.4	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bh3-interacting domain death agonist; <b>PDBTitle:</b> crystal structure of a179l:bid bh3 complex
16	<a href="#">c5vmoB_</a>	Alignment		22.5	17	<b>PDB header:</b> viral protein/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2 interacting mediator of cell death; <b>PDBTitle:</b> crystal structure of grouper iridovirus giv66:bim complex
17	<a href="#">d1l0oc_</a>	Alignment		20.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
18	<a href="#">c1l0oC_</a>	Alignment		20.9	21	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
19	<a href="#">c2k7wB_</a>	Alignment		20.3	30	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bax activation is initiated at a novel interaction site
20	<a href="#">c4qvfb_</a>	Alignment		18.6	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> peptide from bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of bcl-xl in complex with bim bh3 domain
21	<a href="#">c5wosB_</a>	Alignment	not modelled	18.6	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
22	<a href="#">c4zieC_</a>	Alignment	not modelled	18.1	25	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of core/latch dimer of bax in complex with bim bh3
23	<a href="#">c4d2mB_</a>	Alignment	not modelled	18.1	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> vaccinia virus f1l bound to bim bh3
24	<a href="#">c4d2mD_</a>	Alignment	not modelled	18.0	25	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> vaccinia virus f1l bound to bim bh3
25	<a href="#">c2v6qB_</a>	Alignment	not modelled	17.9	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of a bhrf-1 : bim bh3 complex
26	<a href="#">c2wh6B_</a>	Alignment	not modelled	17.8	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of anti-apoptotic bhrf1 in complex with the bim bh32 domain
27	<a href="#">c2pqkB_</a>	Alignment	not modelled	17.7	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bim bh3 peptide; <b>PDBTitle:</b> x-ray crystal structure of human mcl-1 in complex with bim bh3
28	<a href="#">c2nl9B_</a>	Alignment	not modelled	17.5	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of the mcl-1:bim bh3 complex
						<b>PDB header:</b> apoptosis

29	<a href="#">c6qfiB_</a>	Alignment	not modelled	17.5	25	<b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> structure of human mcl-1 in complex with bim bh3 peptide
30	<a href="#">c3fdlB_</a>	Alignment	not modelled	17.2	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bim bh3 peptide in complex with bcl-xl
31	<a href="#">c3kj2B_</a>	Alignment	not modelled	17.1	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> mcl-1 in complex with bim bh3 mutant f4ae
32	<a href="#">c3ci9B_</a>	Alignment	not modelled	16.2	18	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
33	<a href="#">d1seta1</a>	Alignment	not modelled	14.6	17	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Seryl-tRNA synthetase (SerRS)
34	<a href="#">c3kz0C_</a>	Alignment	not modelled	12.6	17	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> mcl-1 specific peptide mb7; <b>PDBTitle:</b> mcl-1 complex with mcl-1-specific selected peptide
35	<a href="#">c3kz0D_</a>	Alignment	not modelled	12.6	17	<b>PDB header:</b> apoptosis <b>Chain:</b> D; <b>PDB Molecule:</b> mcl-1 specific peptide mb7; <b>PDBTitle:</b> mcl-1 complex with mcl-1-specific selected peptide
36	<a href="#">c5l33A_</a>	Alignment	not modelled	12.1	23	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> denovo ntf2; <b>PDBTitle:</b> crystal structure of a de novo designed protein with curved beta-sheet
37	<a href="#">d1uptb_</a>	Alignment	not modelled	11.6	3	<b>Fold:</b> GRIP domain <b>Superfamily:</b> GRIP domain <b>Family:</b> GRIP domain
38	<a href="#">c3d7vB_</a>	Alignment	not modelled	10.8	29	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of mcl-1 in complex with an mcl-1 selective bh32 ligand
39	<a href="#">d1eqzb_</a>	Alignment	not modelled	10.2	19	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
40	<a href="#">d1kx5d_</a>	Alignment	not modelled	10.1	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
41	<a href="#">d1s32d_</a>	Alignment	not modelled	10.1	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
42	<a href="#">c3io8D_</a>	Alignment	not modelled	10.0	30	<b>PDB header:</b> apoptosis <b>Chain:</b> D; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12f in complex with bcl-xl
43	<a href="#">d1nexa1</a>	Alignment	not modelled	9.7	15	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
44	<a href="#">c4j7oA_</a>	Alignment	not modelled	9.6	40	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> putative surface cell antigen sca2; <b>PDBTitle:</b> structure of the n-terminal repeat domain of rickettsia sca2
45	<a href="#">c1nfoA_</a>	Alignment	not modelled	9.4	11	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> apolipoprotein e2; <b>PDBTitle:</b> apolipoprotein e2 (apoe2, d154a mutation)
46	<a href="#">c3e6sD_</a>	Alignment	not modelled	9.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> crystal structure of ferritin soaked with iron from pseudonitzschia2 multiseris
47	<a href="#">c3axjB_</a>	Alignment	not modelled	9.1	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> translin associated factor x, isoform b; <b>PDBTitle:</b> high resolution crystal structure of c3po
48	<a href="#">d1jmsa1</a>	Alignment	not modelled	9.1	7	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
49	<a href="#">c4h63K_</a>	Alignment	not modelled	8.9	24	<b>PDB header:</b> transcription <b>Chain:</b> K; <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 11; <b>PDBTitle:</b> structure of the schizosaccharomyces pombe mediator head module
50	<a href="#">c3io8B_</a>	Alignment	not modelled	8.8	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12f in complex with bcl-xl
51	<a href="#">c6qeqD_</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> pcff; <b>PDBTitle:</b> pcff from enterococcus faecalis pcf10
52	<a href="#">c3kj0B_</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> mcl-1 in complex with bim bh3 mutant i2dy
53	<a href="#">d1fs1b1</a>	Alignment	not modelled	8.0	18	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
54	<a href="#">c3io9B_</a>	Alignment	not modelled	7.5	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12y in complex with mcl-1
55	<a href="#">c3kgkA_</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor arsd; <b>PDBTitle:</b> crystal structure of arsd <b>Fold:</b> Skp1 dimerisation domain-like

56	<a href="#">d1fs2b1</a>	Alignment	not modelled	7.3	18	<b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
57	<a href="#">c3kj1B</a>	Alignment	not modelled	7.1	17	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> mcl-1 in complex with bim bh3 mutant i2da
58	<a href="#">d2o02a1</a>	Alignment	not modelled	7.0	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> 14-3-3 protein <b>Family:</b> 14-3-3 protein
59	<a href="#">d1uptd</a>	Alignment	not modelled	7.0	4	<b>Fold:</b> GRIP domain <b>Superfamily:</b> GRIP domain <b>Family:</b> GRIP domain
60	<a href="#">c2k6sB</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> rab11fip2 protein; <b>PDBTitle:</b> structure of rab11-fip2 c-terminal coiled-coil domain
61	<a href="#">c3p8cF</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> abl interactor 2; <b>PDBTitle:</b> structure and control of the actin regulatory wave complex
62	<a href="#">d2coha1</a>	Alignment	not modelled	6.7	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
63	<a href="#">c3iz5w</a>	Alignment	not modelled	6.7	23	<b>PDB header:</b> ribosome <b>Chain:</b> W; <b>PDB Molecule:</b> 60s ribosomal protein l22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
64	<a href="#">c5jreC</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> neq131; <b>PDBTitle:</b> crystal structure of nec3po in complex with ssdna.
65	<a href="#">c3d1dC</a>	Alignment	not modelled	6.4	24	<b>PDB header:</b> nuclear protein <b>Chain:</b> C; <b>PDB Molecule:</b> rna-induced transcriptional silencing complex <b>PDBTitle:</b> hexagonal crystal structure of tas3 c-terminal alpha motif
66	<a href="#">c4dg7D</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> sgm27569p; <b>PDBTitle:</b> low resolution structure of drosophila translin
67	<a href="#">c3fmtF</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> replication inhibitor/dna <b>Chain:</b> F; <b>PDB Molecule:</b> protein seqa; <b>PDBTitle:</b> crystal structure of seqa bound to dna
68	<a href="#">d1ofcx1</a>	Alignment	not modelled	6.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
69	<a href="#">c3ktbD</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> D; <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor; <b>PDBTitle:</b> crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
70	<a href="#">d1t6ua</a>	Alignment	not modelled	5.9	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nickel-containing superoxide dismutase, NiSOD <b>Family:</b> Nickel-containing superoxide dismutase, NiSOD
71	<a href="#">d1rp3a1</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
72	<a href="#">d1q0ga</a>	Alignment	not modelled	5.7	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nickel-containing superoxide dismutase, NiSOD <b>Family:</b> Nickel-containing superoxide dismutase, NiSOD
73	<a href="#">d1tzyb</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
74	<a href="#">d1ku2a1</a>	Alignment	not modelled	5.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
75	<a href="#">d2ovra1</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
76	<a href="#">d1x92a</a>	Alignment	not modelled	5.4	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
77	<a href="#">c2xa0C</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> apoptosis regulator bax; <b>PDBTitle:</b> crystal structure of bcl-2 in complex with a bax bh32 peptide
78	<a href="#">c5toiB</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the marburg virus vp35 oligomerization domain2 p4222
79	<a href="#">c4d18l</a>	Alignment	not modelled	5.3	8	<b>PDB header:</b> signaling protein <b>Chain:</b> l; <b>PDB Molecule:</b> cop9 signalosome complex subunit 1; <b>PDBTitle:</b> crystal structure of the cop9 signalosome
80	<a href="#">c4khaA</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> chaperone/nuclear protein <b>Chain:</b> A; <b>PDB Molecule:</b> spt16m-histone h2b 1.1 chimera; <b>PDBTitle:</b> structural basis of histone h2a-h2b recognition by the essential2 chaperone fact
81	<a href="#">d1fpoa2</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> HSC20 (HSCB), C-terminal oligomerisation domain <b>Family:</b> HSC20 (HSCB), C-terminal oligomerisation domain
82	<a href="#">c5xauC</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> C; <b>PDB Molecule:</b> laminin subunit gamma-1; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511