

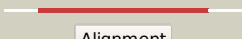
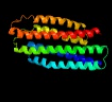
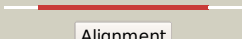


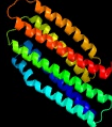
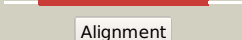
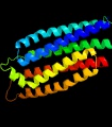

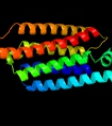
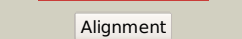

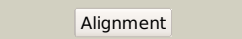

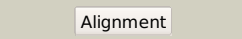
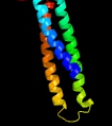
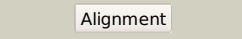

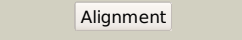









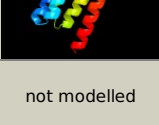


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0821c_(phoY2)_913561_914202
 Date Fri Jul 26 01:50:40 BST 2019
 Unique Job ID 5b4b6b754e578696

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sumb_	 Alignment		100.0	18	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
2	d1t72a_	 Alignment		100.0	28	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
3	c4q25B_	 Alignment		100.0	24	PDB header: unknown function Chain: B: PDB Molecule: phosphate-specific transport system accessory protein phou PDBTitle: crystal structure of phou from pseudomonas aeruginosa
4	d1xwma_	 Alignment		100.0	30	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
5	c2i0mA_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphate transport system protein phou; PDBTitle: crystal structure of the phosphate transport system regulatory protein2 phou from streptococcus pneumoniae
6	c3i39A_	 Alignment		99.8	9	PDB header: phosphate-binding protein Chain: A: PDB Molecule: putative phou-like phosphate regulatory protein; PDBTitle: crystal structure of putative phou-like phosphate regulatory protein2 (bt4638) from bacteroides thetaiotaomicron vpi-5482 at 1.93 a3 resolution
7	c2oltB_	 Alignment		99.8	17	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
8	d1vcta1	 Alignment		99.6	22	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
9	c2bknA_	 Alignment		99.3	22	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein ph0236; PDBTitle: structure analysis of unknown function protein
10	c5vwwB_	 Alignment		34.5	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-bh3 - cubic
11	c5vwwC_	 Alignment		33.9	25	PDB header: apoptosis Chain: C: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-rt - tetragonal

12	c3izcw_	Alignment		32.8	11	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (I22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
13	c5vwwD_	Alignment		31.1	25	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-rt - tetragonal
14	c2qrxA_	Alignment		27.9	15	PDB header: dna binding protein Chain: A: PDB Molecule: gm27569p; PDBTitle: crystal structure of drosophila melanogaster translin protein
15	c1pq1B_	Alignment		25.2	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl2-like protein 11; PDBTitle: crystal structure of bcl-xl/bim
16	dlseta1	Alignment		23.9	17	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Seryl-tRNA synthetase (SerRS)
17	c5z1nA_	Alignment		22.2	11	PDB header: protein binding Chain: A: PDB Molecule: g-protein interacting protein 1; PDBTitle: crystal structure of c terminal region of g-protein interacting2 protein 1 (gip1) from dictyostelium discoideum
18	c1nfoA_	Alignment		21.1	10	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoE2, d154a mutation)
19	c5ua4B_	Alignment		21.0	20	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of a179l:bid bh3 complex
20	c3e6sD_	Alignment		18.6	10	PDB header: oxidoreductase Chain: D: PDB Molecule: ferritin; PDBTitle: crystal structure of ferritin soaked with iron from pseudo-nitzschia2 multiseris
21	c2k7wB_	Alignment	not modelled	16.7	20	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bax activation is initiated at a novel interaction site
22	c4qvfB_	Alignment	not modelled	15.9	25	PDB header: apoptosis Chain: B: PDB Molecule: peptide from bcl-2-like protein 11; PDBTitle: crystal structure of bcl-xl in complex with bim bh3 domain
23	c5wosB_	Alignment	not modelled	15.9	25	PDB header: viral protein Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
24	c4d2mB_	Alignment	not modelled	15.4	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: vaccinia virus f1l bound to bim bh3
25	c4zieC_	Alignment	not modelled	15.4	25	PDB header: apoptosis Chain: C: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of core/latch dimer of bax in complex with bim bh3
26	c4d2mD_	Alignment	not modelled	15.3	25	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: vaccinia virus f1l bound to bim bh3
27	c2v6qB_	Alignment	not modelled	15.3	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of a bhrf-1 : bim bh3 complex
28	c2pqkB_	Alignment	not modelled	15.1	25	PDB header: apoptosis Chain: B: PDB Molecule: bim bh3 peptide; PDBTitle: x-ray crystal structure of human mcl-1 in complex with bim bh3
29	c2wh6B_	Alignment	not modelled	15.1	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of anti-apoptotic bhrf1 in complex with

						the bim bh32 domain
30	c6qfiB_	Alignment	not modelled	14.9	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: structure of human mcl-1 in complex with bim bh3 peptide
31	c2nl9B_	Alignment	not modelled	14.9	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of the mcl-1:bim bh3 complex
32	c3fdlB_	Alignment	not modelled	14.7	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bim bh3 peptide in complex with bcl-xl
33	c3kj2B_	Alignment	not modelled	14.5	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim bh3 mutant f4ae
34	d2o02a1	Alignment	not modelled	14.4	15	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
35	c2uv1B_	Alignment	not modelled	14.3	18	PDB header: inhibitor Chain: B: PDB Molecule: host-nuclease inhibitor protein gam; PDBTitle: hexagonal crystal form of gams from bacteriophage lambda.
36	c3fmtF_	Alignment	not modelled	12.7	7	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
37	c6qeqD_	Alignment	not modelled	11.3	16	PDB header: dna binding protein Chain: D: PDB Molecule: pcff; PDBTitle: pcff from enterococcus faecalis pcf10
38	c3kz0D_	Alignment	not modelled	10.8	33	PDB header: apoptosis Chain: D: PDB Molecule: mcl-1 specific peptide mb7; PDBTitle: mcl-1 complex with mcl-1-specific selected peptide
39	c3kz0C_	Alignment	not modelled	10.8	33	PDB header: apoptosis Chain: C: PDB Molecule: mcl-1 specific peptide mb7; PDBTitle: mcl-1 complex with mcl-1-specific selected peptide
40	c3iz5w_	Alignment	not modelled	10.5	20	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
41	c5vmoB_	Alignment	not modelled	9.8	12	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66:bim complex
42	c3io8D_	Alignment	not modelled	8.9	20	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: biml12f in complex with bcl-xl
43	c5toiB_	Alignment	not modelled	8.7	9	PDB header: viral protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the marburg virus vp35 oligomerization domain2 p4222
44	c1oxzA_	Alignment	not modelled	8.2	11	PDB header: membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1_gat domain
45	d1oxza_	Alignment	not modelled	8.2	11	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
46	c3io8B_	Alignment	not modelled	8.2	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: biml12f in complex with bcl-xl
47	c3ci9B_	Alignment	not modelled	8.0	16	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
48	c4v1ai_	Alignment	not modelled	7.6	11	PDB header: ribosome Chain: I: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
49	c3d7vB_	Alignment	not modelled	7.5	27	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of mcl-1 in complex with an mcl-1 selective bh32 ligand
50	c5jreC_	Alignment	not modelled	7.1	12	PDB header: dna binding protein Chain: C: PDB Molecule: neq131; PDBTitle: crystal structure of nec3po in complex with ssdna.
51	c3hr0A_	Alignment	not modelled	6.9	15	PDB header: transport protein Chain: A: PDB Molecule: cog4; PDBTitle: crystal structure of homo sapiens conserved oligomeric golgi subunit 4
52	c3he4A_	Alignment	not modelled	6.8	18	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
53	c3kj0B_	Alignment	not modelled	6.8	22	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim bh3 mutant i2dy
54	d2za7a1	Alignment	not modelled	6.7	7	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
55	d2coha1	Alignment	not modelled	6.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
56	c5fz5M_	Alignment	not modelled	6.3	10	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna

						opening (cc)
57	c6h9xA_	Alignment	not modelled	6.3	22	PDB header: ligase Chain: A: PDB Molecule: serine--trna ligase; PDBTitle: klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
58	c1wvtA_	Alignment	not modelled	6.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st2180; PDBTitle: crystal structure of uncharacterized protein st2180 from sulfobolbus2 tokodaii
59	c4h63K_	Alignment	not modelled	6.3	22	PDB header: transcription Chain: K: PDB Molecule: mediator of rna polymerase ii transcription subunit 11; PDBTitle: structure of the schizosaccharomyces pombe mediator head module
60	d1nf4a_	Alignment	not modelled	6.1	9	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
61	c3io9B_	Alignment	not modelled	6.0	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bim112y in complex with mcl-1
62	c2gzdC_	Alignment	not modelled	6.0	20	PDB header: protein transport Chain: C: PDB Molecule: rab11 family-interacting protein 2; PDBTitle: crystal structure of rab11 in complex with rab11-fip2
63	d1o3xa_	Alignment	not modelled	6.0	10	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
64	c3kj1B_	Alignment	not modelled	6.0	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim bh3 mutant i2da
65	d1uptb_	Alignment	not modelled	5.6	6	Fold: GRIP domain Superfamily: GRIP domain Family: GRIP domain
66	c5zwnY_	Alignment	not modelled	5.6	8	PDB header: splicing Chain: Y: PDB Molecule: protein luc7; PDBTitle: cryo-em structure of the yeast pre-b complex at an average resolution2 of 3.3 angstrom (part ii: u1 snrnp region)
67	c5xauC_	Alignment	not modelled	5.4	11	PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511
68	c6dlmA_	Alignment	not modelled	5.4	18	PDB header: de novo protein Chain: A: PDB Molecule: dhd127_a; PDBTitle: dhd127
69	d1jgca_	Alignment	not modelled	5.2	12	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
70	c5i33A_	Alignment	not modelled	5.2	30	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
71	c2w1oA_	Alignment	not modelled	5.2	20	PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
72	d1eqzb_	Alignment	not modelled	5.2	14	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
73	d3d19a1	Alignment	not modelled	5.1	12	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like Family: Bacillus cereus metalloprotein-like
74	c3kyiA_	Alignment	not modelled	5.1	3	PDB header: transferase Chain: A: PDB Molecule: putative histidine protein kinase; PDBTitle: crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
75	c3dzuD_	Alignment	not modelled	5.1	9	PDB header: transcription/dna Chain: D: PDB Molecule: peroxisome proliferator-activated receptor gamma; PDBTitle: intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
76	c1sryB_	Alignment	not modelled	5.0	17	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution