

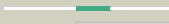






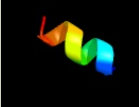





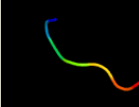

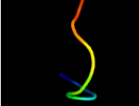

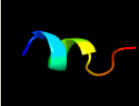

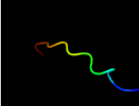











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2661c (-) _2981197_2981586
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	e73a471bb00384c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pd0D_	 Alignment		45.1	55	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: protein cgd2_2020 from cryptosporidium parvum
2	c4fbdB_	 Alignment		44.5	73	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 2.35 angstrom crystal structure of conserved hypothetical protein from2 toxoplasma gondii me49.
3	c5ue0A_	 Alignment		25.5	45	PDB header: protein binding Chain: A: PDB Molecule: ct622 protein; PDBTitle: 1.90 a resolution structure of ct622 c-terminal domain from chlamydia2 trachomatis
4	c4mubA_	 Alignment		15.3	32	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: schistosoma mansoni (blood fluke) sulfotransferase/oxamniquin complex
5	c1or7C_	 Alignment		12.6	40	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
6	d1or7c_	 Alignment		12.6	40	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
7	c6in7A_	 Alignment		10.9	33	PDB header: transcription Chain: A: PDB Molecule: sigma factor algu negative regulatory protein; PDBTitle: crystal structure of algu in complex with muca(cyto)
8	c2n3pA_	 Alignment		10.3	71	PDB header: toxin Chain: A: PDB Molecule: asteropsin_g; PDBTitle: solution nmr structure of asteropsin g from marine sponge asteropus
9	c3hi2C_	 Alignment		8.7	56	PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqa(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqa2 (ygit/b3021) in complex with the e. coli toxin mqs (yglu/b3022)
10	c1s5rA_	 Alignment		8.7	73	PDB header: transcription Chain: A: PDB Molecule: high mobility group box transcription factor 1; PDBTitle: solution structure of hbp1 sid-msin3a pah2 complex
11	d1pcea_	 Alignment		7.5	50	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like

12	c2q82A_	Alignment		7.5	30	PDB header: structural protein Chain: A; PDB Molecule: core protein p7; PDBTitle: crystal structure of core protein p7 from pseudomonas phage phi12.2 northeast structural genomics target oc1
13	c3piwA_	Alignment		7.4	67	PDB header: cytokine Chain: A; PDB Molecule: type i interferon 2; PDBTitle: zebrafish interferon 2
14	d1rh2a_	Alignment		7.2	67	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
15	d2dy1a3	Alignment		6.6	45	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
16	d1au1a_	Alignment		6.6	67	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
17	d1b5la_	Alignment		6.5	67	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
18	d1wu3i_	Alignment		6.3	56	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
19	d2bv3a3	Alignment		6.2	45	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
20	d1lr7a2	Alignment		6.2	46	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
21	c3oq3A_	Alignment	not modelled	5.9	67	PDB header: cytokine/viral protein Chain: A; PDB Molecule: interferon alpha-5; PDBTitle: structural basis of type-i interferon sequestration by a poxvirus2 decoy receptor
22	c2ihr1_	Alignment	not modelled	5.9	56	PDB header: translation Chain: 1; PDB Molecule: peptide chain release factor 2; PDBTitle: rf2 of thermus thermophilus
23	c3se4B_	Alignment	not modelled	5.8	67	PDB header: immune system receptor Chain: B; PDB Molecule: interferon omega-1; PDBTitle: human ifnw-ifnar ternary complex
24	c2llyA_	Alignment	not modelled	5.7	56	PDB header: metal binding protein Chain: A; PDB Molecule: protein e6; PDBTitle: haddock model structure of the n-terminal domain dimer of hpv16 e6
25	d3ovoa_	Alignment	not modelled	5.6	46	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
26	c2mw0A_	Alignment	not modelled	5.5	44	PDB header: protein binding Chain: A; PDB Molecule: kalata b7; PDBTitle: kalata b7 ser mutant
27	c2gkvA_	Alignment	not modelled	5.4	38	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: ovomucoid; PDBTitle: crystal structure of the sgpb:p14'-ala32 omtky3-del(1-5)2 complex
28	c2gkvB_	Alignment	not modelled	5.4	38	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: ovomucoid; PDBTitle: crystal structure of the sgpb:p14'-ala32 omtky3-del(1-5)2 complex
						PDB header: hydrolase inhibitor

29	c2gktl_	Alignment	not modelled	5.4	38	Chain: I; PDB Molecule: ovomucoid; PDBTitle: crystal structure of the p14'-ala32 variant of the n-2 terminally truncated omtky3-del(1-5)
30	c1iy5A_	Alignment	not modelled	5.3	38	PDB header: hydrolase Chain: A; PDB Molecule: omsvp3; PDBTitle: solution structure of wild type omsvp3
31	c2ptfB_	Alignment	not modelled	5.2	18	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein mth_863; PDBTitle: crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn