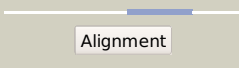
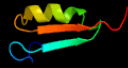
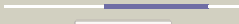
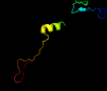







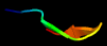



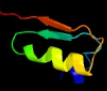

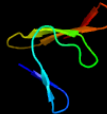



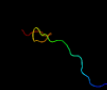
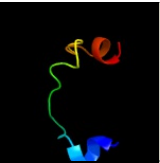

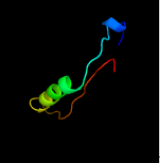
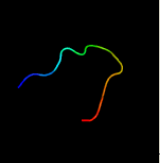
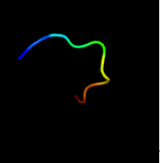


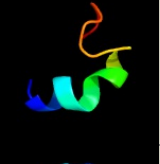




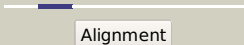
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1946c_(lppG)_2197515_2197967
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	91bb0ab5100adf10

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lqdB_	 Alignment		22.4	26	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
2	d1w79a1	 Alignment		13.5	30	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
3	c2lojA_	 Alignment		12.6	46	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of tstm1273 from salmonella typhimurium lt2,2 nesg target stt322, csqid target idp01027 and ocp target tstm1273
4	c2rhfA_	 Alignment		12.4	38	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase recq; PDBTitle: d. radiodurans recq hrdc domain 3
5	c3izcR_	 Alignment		11.2	31	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein rpl18 (l18e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
6	c2jraB_	 Alignment		10.8	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
7	c2lmdA_	 Alignment		9.1	37	PDB header: transcription Chain: A: PDB Molecule: prospero homeobox protein 1; PDBTitle: minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
8	c3t5tA_	 Alignment		8.9	24	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
9	c4wfwA_	 Alignment		8.0	32	PDB header: structural protein Chain: A: PDB Molecule: general secretion pathway protein b; PDBTitle: the crystal structure of dickeya dadantii gspb from the type 22 secretion system
10	c5ow4A_	 Alignment		7.9	35	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protease-resistant fragment of the trypanosoma2 cruzi gamete fusion protein hap2 ectodomain
11	c4wkyB_	 Alignment		7.9	50	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2

12	d2hgaa1	Alignment		7.8	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: MTH1368 C-terminal domain-like
13	c3ogiC	Alignment		7.5	47	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
14	c3zf7l	Alignment		7.3	28	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein I18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
15	c2kt5B	Alignment		7.2	60	PDB header: rna binding protein / viral protein Chain: B: PDB Molecule: icp27; PDBTitle: rrm domain of mrna export adaptor ref2-i bound to hsv-1 icp27 peptide
16	d2c4fl3	Alignment		7.1	60	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
17	d1danl3	Alignment		6.9	60	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
18	d1xr4a2	Alignment		6.9	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
19	c4gzrA	Alignment		6.8	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxop2 (rv2346c-rv2347c) complex in space group c2221
20	c2qipA	Alignment		6.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
21	c2p5xB	Alignment	not modelled	6.7	27	PDB header: cell cycle Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
22	c3j3bQ	Alignment	not modelled	6.6	20	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein I18; PDBTitle: structure of the human 60s ribosomal proteins
23	c4df1B	Alignment	not modelled	6.4	36	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 thermoproteus neutrophilus complexed with inhibitor bmp
24	c5dxfA	Alignment	not modelled	6.3	35	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
25	c4wxxY	Alignment	not modelled	6.2	67	PDB header: hydrolase, ligase Chain: Y: PDB Molecule: v(d)j recombination-activating protein 2; PDBTitle: crystal structure of the core rag1/2 recombinase
26	d2fnea1	Alignment	not modelled	6.1	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
27	d2o3bb1	Alignment	not modelled	6.1	50	Fold: Nuclease A inhibitor (NuiA) Superfamily: Nuclease A inhibitor (NuiA) Family: Nuclease A inhibitor (NuiA)
28	d1mfga	Alignment	not modelled	5.7	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

29	c3i18A_	 Alignment	not modelled	5.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
30	c2nswA_	 Alignment	not modelled	5.7	42	PDB header: signaling protein Chain: A: PDB Molecule: mating pheromone en-2; PDBTitle: nmr solution structure of the pheromone en-2