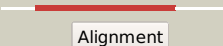



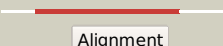

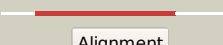

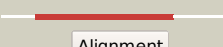

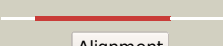




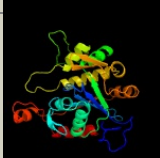

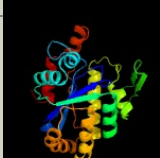

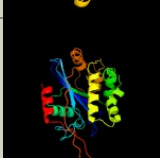

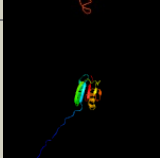

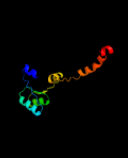
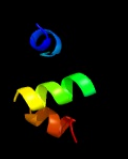
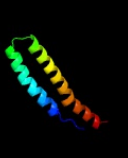
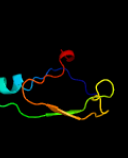


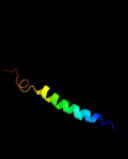



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3267 (-) _3647882_3649378
Date	Thu Aug 8 16:20:47 BST 2019
Unique Job ID	5fd62ec8339b6fc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pe5B_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein a7vv38_9clot from clostridium2 leptum dsm 753, northeast structural genomics consortium target3 qlr103
2	c4de8A_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: cps2a; PDBTitle: lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
3	c3okzB_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein gbs0355; PDBTitle: crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
4	c5v8cA_	 Alignment		100.0	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: lytr-csp2a-psr enzyme from actinomyces oris
5	c3qfiA_	 Alignment		100.0	29	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190
6	c3owqB_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin1025 protein; PDBTitle: x-ray structure of lin1025 protein from listeria innocua, northeast2 structural genomics consortium target lkr164
7	c3nroA_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo1026 protein; PDBTitle: crystal structure of putative transcriptional factor lmo1026 from2 listeria monocytogenes (fragment 52-321), northeast structural3 genomics consortium target lmr194
8	c3mejA_	 Alignment		100.0	28	PDB header: transcriptional regulator Chain: A: PDB Molecule: transcriptional regulator ywtf; PDBTitle: crystal structure of putative transcriptional regulator ywtf from2 bacillus subtilis, northeast structural genomics consortium target3 sr736
9	c4obmA_	 Alignment		100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative transcription regulator (eubsir_01389)2 from eubacterium siraeum dsm 15702 at 2.15 a resolution
10	c3nxhA_	 Alignment		100.0	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator yvhj; PDBTitle: crystal structure of the transcriptional regulator yvhj from bacillus2 subtilis. northeast structural genomics consortium target sr735.
11	c2m5yA_	 Alignment		99.5	22	PDB header: unknown function Chain: A: PDB Molecule: putative tuberculin related peptide; PDBTitle: solution structure of the c-terminal domain of rv0431

12	c6dfdB_	Alignment		43.7	31	PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm3; PDBTitle: crystal structure of cnm3 cyclic nucleotide-binding homology domain
13	c2pjuD_	Alignment		40.9	16	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
14	c5j5vC_	Alignment		40.7	36	PDB header: toxin Chain: C: PDB Molecule: immunity protein cdii; PDBTitle: cdia-ct from uropathogenic escherichia coli in complex with cognate2 immunity protein and cysk
15	c3txsC_	Alignment		26.5	13	PDB header: viral protein Chain: C: PDB Molecule: terminase dna packaging enzyme small subunit; PDBTitle: crystal structure of phage 44rr small terminase gp16
16	c6dj3B_	Alignment		23.5	33	PDB header: transport protein Chain: B: PDB Molecule: metal transporter cnm2; PDBTitle: crystal structure of cnm2 cyclic nucleotide-binding homology domain
17	d1ny8a_	Alignment		10.9	29	Fold: Alpha-lytic protease prodomain-like Superfamily: BolA-like Family: BolA-like
18	c2liyA_	Alignment		10.1	31	PDB header: hormone Chain: A: PDB Molecule: epidermal patterning factor-like protein 9; PDBTitle: plant peptide hormone regulating stomatal density
19	c6f0kA_	Alignment		9.6	13	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
20	d1r2ja1	Alignment		9.3	11	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
21	c3tr3A_	Alignment	not modelled	9.3	26	PDB header: unknown function Chain: A: PDB Molecule: bola; PDBTitle: structure of a bola protein homologue from coxiella burnetii
22	d1g4yb_	Alignment	not modelled	9.2	10	Fold: Small-conductance potassium channel Superfamily: Small-conductance potassium channel Family: Small-conductance potassium channel
23	c4ddpA_	Alignment	not modelled	8.9	31	PDB header: membrane protein Chain: A: PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd)
24	c2xznT_	Alignment	not modelled	8.8	13	PDB header: ribosome Chain: T: PDB Molecule: rps19e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
25	c6az1X_	Alignment	not modelled	8.2	7	PDB header: ribosome/antibiotic Chain: X: PDB Molecule: ribosomal protein s19e; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
26	c4fw9A_	Alignment	not modelled	8.1	18	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the lon-like protease mtalonc
27	c2o8sA_	Alignment	not modelled	8.1	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_984p; PDBTitle: x-ray crystal structure of protein agr_c_984 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr120.
28	c4b96A_	Alignment	not modelled	8.0	20	PDB header: sugar binding protein Chain: A: PDB Molecule: cellulose binding domain-containing protein;

						PDBTitle: family 3b carbohydrate-binding module from the biomass2 sensing system of clostridium clariflavum
29	d1gsoa2	Alignment	not modelled	8.0	27	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
30	d3etja2	Alignment	not modelled	7.7	43	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
31	c5e24D	Alignment	not modelled	7.3	17	PDB header: transport/dna binding/dna Chain: D: PDB Molecule: protein hairless; PDBTitle: structure of the su(h)-hairless-dna repressor complex
32	c4hynA	Alignment	not modelled	7.2	13	PDB header: signaling protein Chain: A: PDB Molecule: chec, inhibitor of mcp methylation / flin fusion protein; PDBTitle: x-ray crystal structure of thermotoga maritima fly
33	d1xjca	Alignment	not modelled	7.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
34	c4ymkA	Alignment	not modelled	6.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
35	d2o8sa1	Alignment	not modelled	6.7	30	Fold: AGR C 984p-like Superfamily: AGR C 984p-like Family: AGR C 984p-like
36	c5z5bA	Alignment	not modelled	6.7	25	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase; PDBTitle: crystal structure of tk-ptp in the g95a mutant form
37	d1tf4a2	Alignment	not modelled	6.6	40	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: type 3a cellulose-binding domain protein; PDBTitle: biomass sensing modules from putative rsgi-like proteins2 of clostridium thermocellum resemble family 3 carbohydrate-3 binding module of cellulosome
38	c4b9cA	Alignment	not modelled	6.3	30	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III PDB header: transport protein Chain: A: PDB Molecule: coiled-coil and c2 domain-containing protein 1-like, PDBTitle: crystal structure of lgd-shrub complex, single chain fusion
39	d1nbca	Alignment	not modelled	6.2	50	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III PDB header: transport protein Chain: A: PDB Molecule: coiled-coil and c2 domain-containing protein 1-like, PDBTitle: crystal structure of lgd-shrub complex, single chain fusion
40	c5vo5A	Alignment	not modelled	6.1	12	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
41	d1vkza2	Alignment	not modelled	6.1	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
42	d2zjrwl	Alignment	not modelled	6.1	13	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
43	c3o2eA	Alignment	not modelled	6.0	28	PDB header: unknown function Chain: A: PDB Molecule: bola-like protein; PDBTitle: crystal structure of a bol-like protein from babesia bovis
44	c4puiA	Alignment	not modelled	5.8	22	PDB header: protein binding Chain: A: PDB Molecule: sufe-like protein, chloroplastic; PDBTitle: bola domain of sufe1 from arabidopsis thaliana
45	d1j6ra	Alignment	not modelled	5.7	16	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Hypothetical protein TM0269
46	d1vh4a	Alignment	not modelled	5.5	14	Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD Family: Stabilizer of iron transporter SufD
47	c2l8aA	Alignment	not modelled	5.5	40	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: structure of a novel cbm3 lacking the calcium-binding site
48	d1gwyA	Alignment	not modelled	5.3	15	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Anemone pore-forming cytolysin
49	c5dfzD	Alignment	not modelled	5.3	26	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
50	c2nclA	Alignment	not modelled	5.2	28	PDB header: protein binding Chain: A: PDB Molecule: bola-like protein 3; PDBTitle: solution structure of bola3 from homo sapiens
51	c1t0fC	Alignment	not modelled	5.2	22	PDB header: dna binding protein Chain: C: PDB Molecule: transposon tn7 transposition protein tncs; PDBTitle: crystal structure of the tnsa/tncs(504-555) complex