
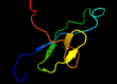

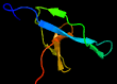

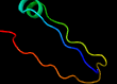
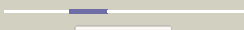

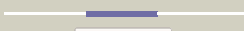




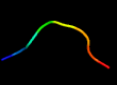





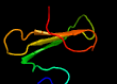

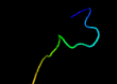
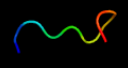
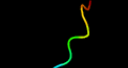
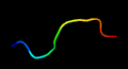
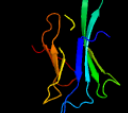

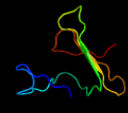

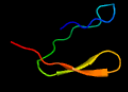



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1352_(-)_1518769_1519140
Date	Wed Jul 31 22:05:45 BST 2019
Unique Job ID	6fd453f8b0f51cc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wlga_	 Alignment		18.5	16	Fold: Flagellar hook protein flgE Superfamily: Flagellar hook protein flgE Family: Flagellar hook protein flgE
2	c5az4A_	 Alignment		17.8	18	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook subunit protein; PDBTitle: crystal structure of a 79kda fragment of flge, the hook protein from2 campylobacter jejuni
3	c4kh9B_	 Alignment		14.5	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4785 family protein (lpg0956) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 2.003 a resolution
4	c3k0bA_	 Alignment		13.9	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted n6-adenine-specific dna methylase; PDBTitle: crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
5	d1ht6a1	 Alignment		12.8	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
6	d1o9ga_	 Alignment		12.7	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
7	c3be3A_	 Alignment		11.7	63	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
8	c5npyA_	 Alignment		11.2	8	PDB header: motor protein Chain: A: PDB Molecule: flagellar basal body protein; PDBTitle: crystal structure of helicobacter pylori flagellar hook protein flge2
9	c4js0B_	 Alignment		10.1	29	PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: complex of cdc42 with the crib-pr domain of irsp53
10	c3a0fA_	 Alignment		9.6	17	PDB header: hydrolase Chain: A: PDB Molecule: xyloglucanase; PDBTitle: the crystal structure of geotrichum sp. m128 xyloglucanase
11	c3v8vB_	 Alignment		9.2	43	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase I; PDBTitle: crystal structure of bifunctional methyltransferase ycbY (rlmlk) from2 escherichia coli, sam binding

12	c2mwrA_	Alignment		9.1	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: acidocin b; PDBTitle: solution structure of acidocin b, a circular bacteriocin from <i>Lactobacillus acidophilus</i> m46
13	d1zdva1	Alignment		9.1	60	Fold: FimD N-terminal domain-like Superfamily: FimD N-terminal domain-like Family: Usher N-domain
14	d1zdxa1	Alignment		8.9	60	Fold: FimD N-terminal domain-like Superfamily: FimD N-terminal domain-like Family: Usher N-domain
15	c2cn2C_	Alignment		8.4	10	PDB header: hydrolase Chain: C: PDB Molecule: beta-1,4-xyloglucan hydrolase; PDBTitle: crystal structures of <i>Clostridium thermocellum</i> 2 xyloglucanase
16	d2jdid2	Alignment		8.4	41	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
17	c2ebsB_	Alignment		8.4	14	PDB header: hydrolase Chain: B: PDB Molecule: oligoxyloglucan reducing end-specific PDBTitle: crystal structure analysis of oligoxyloglucan reducing-end-2 specific cellobiohydrolase (oxg-rcbh) d465n mutant 3 complexed with a xyloglucan heptasaccharide
18	c3nrqB_	Alignment		8.3	31	PDB header: transport protein Chain: B: PDB Molecule: periplasmic protein-probably involved in high-affinity Fe ²⁺ PDBTitle: crystal structure of copper-reconstituted Fetp from uropathogenic <i>Escherichia coli</i> strain f11
19	c5a6wC_	Alignment		8.3	30	PDB header: antiviral protein Chain: C: PDB Molecule: avr-pik protein; PDBTitle: complex of rice blast (<i>Magnaporthe oryzae</i>) effector protein avr-pikd2 with the hma domain of pikp1 from rice (<i>Oryza sativa</i>)
20	c4parC_	Alignment		7.9	8	PDB header: dna binding protein/dna Chain: C: PDB Molecule: uncharacterized protein abasi; PDBTitle: the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a 2 complex with product-like dna
21	d1pe4a_	Alignment	not modelled	7.5	20	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
22	d1avaa1	Alignment	not modelled	7.1	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
23	d2nn6h2	Alignment	not modelled	6.9	22	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
24	d1q42a_	Alignment	not modelled	6.8	56	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
25	c6ffyA_	Alignment	not modelled	6.8	9	PDB header: apoptosis Chain: A: PDB Molecule: vps10 domain-containing receptor sorcs2; PDBTitle: structure of the mouse sorcs2-ngf complex
26	c2xtlB_	Alignment	not modelled	6.6	33	PDB header: structural protein Chain: B: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the major pilus backbone protein from <i>Streptococcus 2 agalactiae</i>
27	c3rpka_	Alignment	not modelled	6.5	40	PDB header: cell adhesion Chain: A: PDB Molecule: backbone pilus subunit; PDBTitle: structure of the full-length major pilin rrgb from <i>Streptococcus 2 pneumoniae</i>
28	c6f0kD_	Alignment	not modelled	6.3	15	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
29	d2ba0a2	Alignment	not modelled	6.2	26	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like

						Family: ECR1 N-terminal domain-like
30	d2adza1	Alignment	not modelled	6.1	15	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
31	c2k9uB_	Alignment	not modelled	6.0	75	PDB header: structural protein Chain: B; PDB Molecule: filamin-binding lim protein 1; PDBTitle: solution nmr structure of the filamin-migfilin complex
32	c6ftkA_	Alignment	not modelled	5.9	9	PDB header: viral protein Chain: A; PDB Molecule: envelope protein; PDBTitle: gp36-mper
33	c3rlcA_	Alignment	not modelled	5.9	25	PDB header: structural protein Chain: A; PDB Molecule: a1 protein; PDBTitle: crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form
34	c1ikqA_	Alignment	not modelled	5.8	18	PDB header: transferase Chain: A; PDB Molecule: exotoxin a; PDBTitle: pseudomonas aeruginosa exotoxin a, wild type
35	d1z0mb1	Alignment	not modelled	5.8	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
36	c2qeyA_	Alignment	not modelled	5.7	34	PDB header: lyase Chain: A; PDB Molecule: phosphoenolpyruvate carboxykinase, cytosolic [gtp]; PDBTitle: rat cytosolic pepck in complex with gtp
37	c1q40C_	Alignment	not modelled	5.7	56	PDB header: translation Chain: C; PDB Molecule: mrna transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
38	c3q8jA_	Alignment	not modelled	5.4	33	PDB header: toxin Chain: A; PDB Molecule: asteropsin a; PDBTitle: crystal structure of asteropsin a from marine sponge asteropus sp.
39	d3bwud1	Alignment	not modelled	5.3	54	Fold: FimD N-terminal domain-like Superfamily: FimD N-terminal domain-like Family: Usher N-domain