
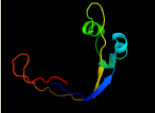







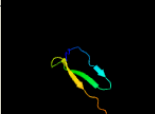



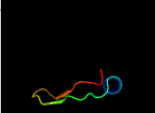








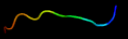

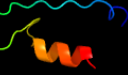
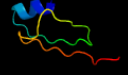
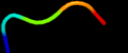
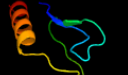





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2825c_(-)_3132902_3133549
Date	Wed Aug 7 12:50:49 BST 2019
Unique Job ID	760ed52aaae926b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2dp9a1	 Alignment		78.5	27	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical protein TTHA0113
2	c5hkJA_	 Alignment		48.4	26	PDB header: signaling protein Chain: A: PDB Molecule: complement c1q subcomponent subunit a,complement c1q PDBTitle: single chain recombinant globular head of the complement system2 protein c1q
3	c3ne9B_	 Alignment		24.3	17	PDB header: transferase Chain: B: PDB Molecule: phosphopantetheine protein transferase, ppt1p; PDBTitle: chronobacterium ammoiniagenes apo-acps strucutre
4	c4v19Q_	 Alignment		22.8	13	PDB header: ribosome Chain: Q: PDB Molecule: mitoribosomal protein ul16m, mrp16; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
5	c3c4nB_	 Alignment		22.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein dr_0571; PDBTitle: crystal structure of dr_0571 protein from deinococcus radiodurans in2 complex with adp. northeast structural genomics consortium target3 drr125
6	c5vbxB_	 Alignment		20.8	41	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 escherichia coli
7	c3sb1B_	 Alignment		19.2	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hydrogenase expression protein; PDBTitle: hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
8	c5cmoB_	 Alignment		16.1	32	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 neisseria meningitidis
9	c2kIwA_	 Alignment		15.5	24	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
10	c6q64A_	 Alignment		15.1	13	PDB header: hydrolase Chain: A: PDB Molecule: endoglycosidase; PDBTitle: bt1044semet e190q
11	d2a6aa2	 Alignment		14.5	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like

12	d1dcja_	Alignment		13.8	42	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
13	d3bnea2	Alignment		13.6	80	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
14	d1qasa3	Alignment		13.5	21	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
15	d1g64b_	Alignment		13.2	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
16	d1rrha2	Alignment		12.8	60	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
17	c4mzpC_	Alignment		10.8	12	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
18	d1dq3a2	Alignment		10.8	67	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: PI-Pfui intein middle domain
19	c3o6xC_	Alignment		10.1	18	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
20	d1ftha_	Alignment		9.9	19	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
21	c5xumA_	Alignment	not modelled	9.4	29	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)
22	c3h88A_	Alignment	not modelled	8.2	32	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor
23	c3ohmB_	Alignment	not modelled	7.9	33	PDB header: signaling protein / hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase PDBTitle: crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
24	d1f7la_	Alignment	not modelled	7.8	23	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
25	d1pk6a_	Alignment	not modelled	7.2	67	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
26	d1tdza1	Alignment	not modelled	6.7	12	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
27	c2ci6A_	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: A: PDB Molecule: ng, ng-dimethylarginine dimethylaminohydrolase 1; PDBTitle: crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph
28	c6cgaB_	Alignment	not modelled	6.2	29	PDB header: hydrolase Chain: B: PDB Molecule: polycomb protein asx; PDBTitle: structure of the pr-dub complex

29	c4n4uA_	Alignment	not modelled	6.1	20	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter periplasmic solute-binding PDBTitle: crystal structure of abc transporter solute binding protein bb07192 from bordetella bronchiseptica rb50, target efi-510049
30	c2lqtA_	Alignment	not modelled	5.9	22	PDB header: unknown function Chain: A: PDB Molecule: coiled-coil-helix-coiled-coil-helix domain-containing PDBTitle: solution structure of chcd7
31	c4xb6E_	Alignment	not modelled	5.8	21	PDB header: transferase Chain: E: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-triphosphate synthase PDBTitle: structure of the e. coli c-p lyase core complex
32	c1x31A_	Alignment	not modelled	5.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of the streptomyces coelicolor holo-2 from2 corynebacterium sp. u-96
33	c2jbzA_	Alignment	not modelled	5.8	27	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
34	d1ub4a_	Alignment	not modelled	5.6	17	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
35	d2zkmx4	Alignment	not modelled	5.5	24	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
36	c2knpA_	Alignment	not modelled	5.5	67	PDB header: unknown function Chain: A: PDB Molecule: mcocc-1; PDBTitle: isolation and characterization of peptides from momordica2 cochinchinensis seeds.
37	c3hqjA_	Alignment	not modelled	5.3	32	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
38	c1om8A_	Alignment	not modelled	5.1	11	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
39	d1g5ta_	Alignment	not modelled	5.1	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)