


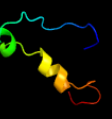
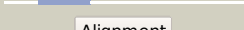
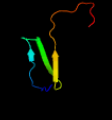
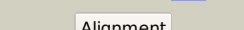


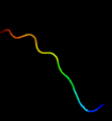

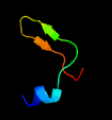

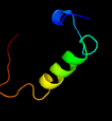
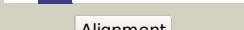
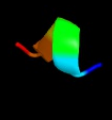


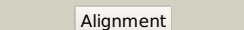


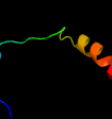

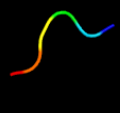


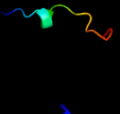



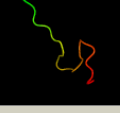


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2828c_(-)_3135798_3136343
Date	Wed Aug 7 12:50:49 BST 2019
Unique Job ID	485e19dd26ec73f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2dp9a1	 Alignment		43.0	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical protein TTHA0113
2	c5hkjA	 Alignment		36.8	32	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	c3c4nB	 Alignment		27.5	30	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
4	c4v19Q	 Alignment		24.1	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	d1dcja	 Alignment		13.8	42	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
6	c3sb1B	 Alignment		12.4	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hydrogenase expression protein; PDBTitle: hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
7	c6q64A	 Alignment		11.4	13	PDB header: hydrolase Chain: A: PDB Molecule: endoglycosidase; PDBTitle: bt1044semet e190q
8	d1dq3a2	 Alignment		8.9	67	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: PI-Pfui intein middle domain
9	d3bnea2	 Alignment		8.6	80	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
10	c2kjaA	 Alignment		8.3	24	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
11	c4dncD	 Alignment		8.3	21	PDB header: transcription Chain: D: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of human mof in complex with msl1

12	d1rrha2	Alignment		8.1	60	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
13	d1pk6a_	Alignment		7.9	67	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
14	c3lr4A_	Alignment		7.7	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
15	c2knpA_	Alignment		7.4	67	PDB header: unknown function Chain: A: PDB Molecule: mcocc-1; PDBTitle: isolation and characterization of peptides from momordica2 cochinchinensis seeds.
16	d2proc1	Alignment		7.1	20	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
17	c4xb6E_	Alignment		5.9	24	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
18	c3fqdA_	Alignment		5.8	71	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: 5'-3' exoribonuclease 2; PDBTitle: crystal structure of the s. pombe rat1-rai1 complex
19	d1g64b_	Alignment		5.7	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
20	c5k9hA_	Alignment		5.6	9	PDB header: hydrolase Chain: A: PDB Molecule: 0940_gh29; PDBTitle: crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium
21	c1k09B_	Alignment	not modelled	5.6	100	PDB header: de novo protein Chain: B: PDB Molecule: core module ii; PDBTitle: solution structure of betacore, a designed water soluble2 four-stranded antiparallel b-sheet protein
22	c4kisA_	Alignment	not modelled	5.5	16	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
23	d1c1da2	Alignment	not modelled	5.3	24	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
24	d1tdza1	Alignment	not modelled	5.1	12	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins