


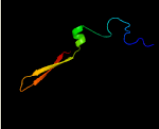

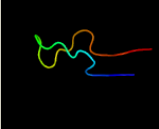
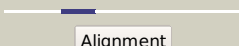

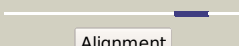
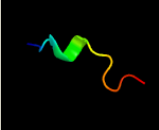
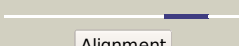
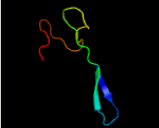
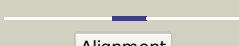
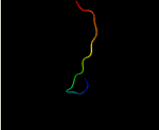

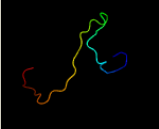

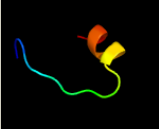

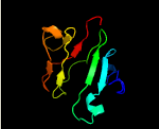

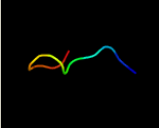

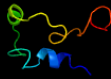


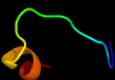






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1958c_(-)_2203025_2203639
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	222213db2a7f71db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qaza_	 Alignment		22.3	48	Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Alginate lyase A1-III
2	d1p30a1	 Alignment		19.4	43	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
3	c4l4dxB_	 Alignment		11.6	32	PDB header: transcription/dna Chain: B: PDB Molecule: auxin response factor 1; PDBTitle: crystal structure of the dna binding domain of arabidopsis thaliana2 auxin response factor 1 (arf1) in complex with protomor-like sequence3 er7
4	c3q7cA_	 Alignment		9.9	50	PDB header: hydrolase Chain: A: PDB Molecule: nucleoprotein; PDBTitle: exonuclease domain of lassa virus nucleoprotein bound to manganese
5	c2vakF_	 Alignment		9.5	54	PDB header: viral protein Chain: F: PDB Molecule: sigma a; PDBTitle: crystal structure of the avian reovirus inner capsid protein sigmaa
6	c3x0uB_	 Alignment		8.9	29	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pirb
7	d2vdfa1	 Alignment		7.5	38	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
8	c3n6yA_	 Alignment		7.4	28	PDB header: unknown function Chain: A: PDB Molecule: immunoglobulin-like protein; PDBTitle: crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
9	c4gveA_	 Alignment		7.1	44	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: tacaribe nucleoprotein structure
10	c3i7dB_	 Alignment		7.0	21	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase; PDBTitle: crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution
11	c3bboX_	 Alignment		7.0	42	PDB header: ribosome Chain: X: PDB Molecule: ribosomal protein I27; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome

12	d2gycu1	Alignment		6.8	42	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
13	c4l54A	Alignment		6.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: terminal olefin-forming fatty acid decarboxylase; PDBTitle: structure of cytochrome p450 olet, ligand-free
14	c4o6hA	Alignment		6.6	50	PDB header: hydrolase Chain: A: PDB Molecule: nucleoprotein; PDBTitle: 2.8a crystal structure of lymphocytic choriomeningitis virus2 nucleoprotein c-terminal domain
15	c2ftcO	Alignment		6.4	42	PDB header: ribosome Chain: O: PDB Molecule: mitochondrial 39s ribosomal protein l27; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
16	c4k7eA	Alignment		6.2	33	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of junin virus nucleoprotein
17	c6dzkB	Alignment		6.1	67	PDB header: ribosome Chain: B: PDB Molecule: conserved domain protein; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
18	c5zeuu	Alignment		6.1	67	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: m. smegmatis p/p state 30s ribosomal subunit
19	c5o5jB	Alignment		6.1	67	PDB header: ribosome Chain: B: PDB Molecule: conserved domain protein; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
20	c1vw4R	Alignment		6.0	54	PDB header: ribosome Chain: R: PDB Molecule: 54s ribosomal protein l2, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
21	c2wx3A	Alignment	not modelled	5.9	63	PDB header: structural protein Chain: A: PDB Molecule: mrna-decapping enzyme 1a; PDBTitle: asymmetric trimer of the human dcp1a c-terminal domain
22	d1jmxg	Alignment	not modelled	5.8	38	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Quinohemoprotein amine dehydrogenase C chain Family: Quinohemoprotein amine dehydrogenase C chain
23	c5nodA	Alignment	not modelled	5.6	61	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase stkp; PDBTitle: pasta subunit 4 of streptococcus pneumoniae stkp crystallized with peg2 and succinate
24	d1pbyc	Alignment	not modelled	5.5	35	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Quinohemoprotein amine dehydrogenase C chain Family: Quinohemoprotein amine dehydrogenase C chain
25	c5kx6A	Alignment	not modelled	5.4	30	PDB header: cell adhesion Chain: A: PDB Molecule: galactoside 2-alpha-l-fucosyltransferase; PDBTitle: the structure of arabidopsis thaliana fut1 mutant r284k in complex2 with gdp