

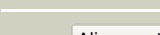
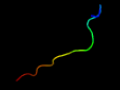






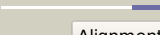

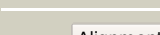
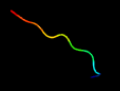
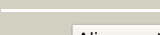
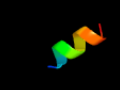



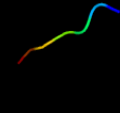




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2532c (-) _2857863_2858264
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	3f6ca0c82c5ff5cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w0cT_	 Alignment		40.5	45	PDB header: virus Chain: T: PDB Molecule: protein p6; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
2	d1pyla_	 Alignment		13.9	27	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Bacterial ribonucleases
3	c6dnmA_	 Alignment		13.4	22	PDB header: chaperone Chain: A: PDB Molecule: export chaperone sats; PDBTitle: the crystal structure of sats c-terminal domain
4	d1v8ha1	 Alignment		11.7	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: SoxZ-like
5	c2kq5A_	 Alignment		10.6	44	PDB header: unknown function Chain: A: PDB Molecule: avirulence protein; PDBTitle: solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
6	c2n2aA_	 Alignment		10.4	29	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the presence of cytoplasmic juxtamembrane domains
7	c1zgxB_	 Alignment		8.7	40	PDB header: hydrolase Chain: B: PDB Molecule: guanyl-specific ribonuclease sa; PDBTitle: crystal structure of ribonuclease mutant
8	c3h3pT_	 Alignment		8.2	45	PDB header: immune system Chain: T: PDB Molecule: 4e10_s0_1tjlc_004_n; PDBTitle: crystal structure of hiv epitope-scaffold 4e10 fv complex
9	d1s9ca2	 Alignment		8.1	54	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
10	d1gyca3	 Alignment		7.8	43	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
11	d1kyaa3	 Alignment		7.6	43	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins

12	c3d0fA_	Alignment		7.4	38	PDB header: transferase Chain: A; PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
13	d1v10a3	Alignment		7.3	43	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
14	d1hfua3	Alignment		6.5	43	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
15	d2idba1	Alignment		6.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: UbiD middle domain-like
16	d1mgra_	Alignment		6.3	33	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Bacterial ribonucleases
17	d1uyra1	Alignment		6.2	44	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
18	c2yxwB_	Alignment		6.1	22	PDB header: oxidoreductase Chain: B; PDB Molecule: blue copper oxidase cueo; PDBTitle: the deletion mutant of multicopper oxidase cueo
19	c3zfnA_	Alignment		6.1	45	PDB header: hydrolase Chain: A; PDB Molecule: n-terminal protease npro; PDBTitle: crystal structure of product-like, processed n-terminal protease npro
20	d1pn2a1	Alignment		6.1	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
21	d2q9oa3	Alignment	not modelled	6.0	71	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
22	c3gliP_	Alignment	not modelled	5.9	36	PDB header: transferase/dna Chain: P; PDB Molecule: dna polymerase iii subunit psi; PDBTitle: crystal structure of the e. coli clamp loader bound to primer-template2 dna and psi peptide
23	d1pj5a3	Alignment	not modelled	5.4	50	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
24	d1ku7a_	Alignment	not modelled	5.4	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
25	c6fhsH_	Alignment	not modelled	5.2	50	PDB header: dna binding protein Chain: H; PDB Molecule: les2; PDBTitle: cryoem structure of ino80core
26	c2uxtA_	Alignment	not modelled	5.1	0	PDB header: oxidoreductase Chain: A; PDB Molecule: protein sufi; PDBTitle: sufi protein from escherichia coli