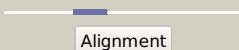


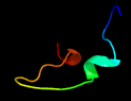


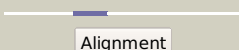


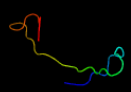
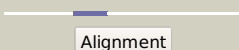
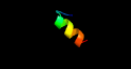
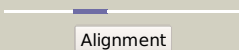

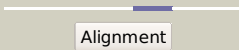



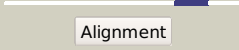
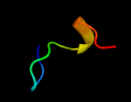

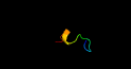


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2023c_(-)_2267757_2268116
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	c734c57186ada645

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5e9fD_	 Alignment		18.1	44	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
2	c2r7mA_	 Alignment		14.9	50	PDB header: ligase Chain: A: PDB Molecule: 5-formaminoimidazole-4-carboxamide-1-(beta)-d-ribofuranosyl PDBTitle: crystal structure of faicr synthetase (purp) from m. jannaschii2 complexed with amp
3	c5d5oE_	 Alignment		13.4	67	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein mj0489; PDBTitle: hgc from methanocaldococcus jannaschii
4	d1dqua_	 Alignment		13.0	44	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
5	d3bnea2	 Alignment		12.2	21	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
6	d1f61a_	 Alignment		11.9	44	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
7	d1igwa_	 Alignment		11.6	31	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
8	c3j81j_	 Alignment		11.5	24	PDB header: ribosome Chain: J: PDB Molecule: us4; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
9	c5o4jC_	 Alignment		10.5	67	PDB header: transferase Chain: C: PDB Molecule: hgcg; PDBTitle: hgcg from methanococcus maripaludis cocrystallized with sah and2 pyridinol
10	d2j01d1	 Alignment		9.3	47	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
11	d2qamc1	 Alignment		8.8	33	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2

12	c2gyaA_	Alignment		7.9	38	PDB header: ribosome Chain: A; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
13	d2zjra1	Alignment		7.8	50	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
14	c1q46A_	Alignment		7.2	23	PDB header: translation Chain: A; PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
15	c3e5bB_	Alignment		6.8	25	PDB header: lyase Chain: B; PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
16	c3i4eA_	Alignment		6.4	31	PDB header: lyase Chain: A; PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
17	d1inza_	Alignment		6.3	33	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: ENTH domain
18	c3d5bD_	Alignment		6.3	47	PDB header: ribosome Chain: D; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
19	c2z4lC_	Alignment		5.9	38	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l2; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with paromomycin and ribosome recycling factor (rrf). this3 file contains the 50s subunit of the first 70s ribosome, with4 paromomycin and rrf bound. the entire crystal structure contains two5 70s ribosomes and is described in remark 400.
20	c4owfG_	Alignment		5.8	83	PDB header: transcription/protein binding Chain: G; PDB Molecule: e3 ubiquitin-protein ligase rnf31; PDBTitle: crystal structure of the nemo cozi in complex with hoip nzf1 domain
21	d6paxa1	Alignment	not modelled	5.5	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain