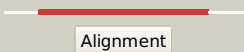

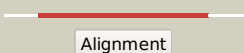

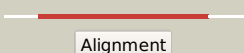
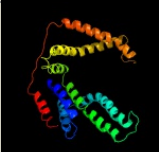
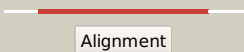

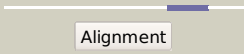
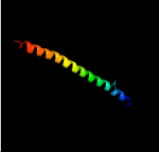
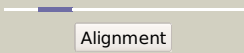
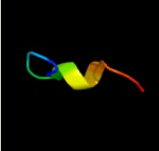
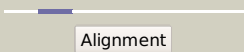
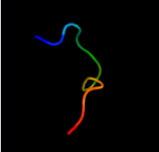
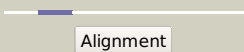
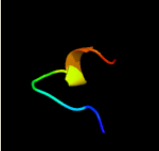
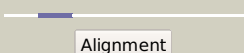
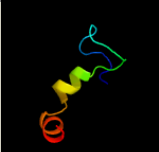




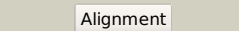


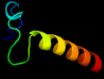



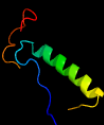
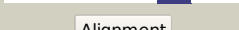





Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2325c (-) _2597019_2597867 |
| Date | Mon Aug 5 13:25:47 BST 2019 |
| Unique Job ID | 6ec5738ddef5bc3d |

Detailed template information

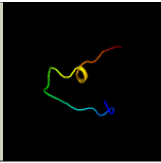
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| 1 | c5d7tH_ |  Alignment |  | 100.0 | 18 | PDB header: transport protein Chain: H: PDB Molecule: energy-coupling factor transporter transmembrane protein PDBTitle: folate ecf transporter: apo state |
| 2 | c4huqT_ |  Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: T: PDB Molecule: energy-coupling factor transporter transmembrane protein PDBTitle: crystal structure of a transporter |
| 3 | c4rfsT_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase, transport protein Chain: T: PDB Molecule: energy-coupling factor transporter transmembrane protein PDBTitle: structure of a pantothenate energy coupling factor transporter |
| 4 | c5x3xq_ |  Alignment |  | 100.0 | 20 | PDB header: transport protein Chain: Q: PDB Molecule: uncharacterized protein cbiq; PDBTitle: 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo |
| 5 | c3hd7A_ |  Alignment |  | 17.9 | 12 | PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1 |
| 6 | c2xzmL_ |  Alignment |  | 17.5 | 23 | PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s12; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 7 | c1s1hL_ |  Alignment |  | 17.3 | 15 | PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s23; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i. |
| 8 | c3u5qX_ |  Alignment |  | 14.6 | 17 | PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b |
| 9 | d1k4ta2 |  Alignment |  | 13.5 | 20 | Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core |
| 10 | c3j20N_ |  Alignment |  | 12.9 | 25 | PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal protein s12p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 11 | c2zkqL_ |  Alignment |  | 12.2 | 15 | PDB header: ribosomal protein/rna Chain: L: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c3zeyS_ |  Alignment |  | 10.8 | 25 | PDB header: ribosome Chain: S; PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 13 | c2mv6A_ |  Alignment |  | 10.3 | 29 | PDB header: membrane protein Chain: A; PDB Molecule: erythropoietin receptor; PDBTitle: solution structure of the transmembrane domain and the juxta-membrane2 domain of the erythropoietin receptor in micelles |
| 14 | c5xyiX_ |  Alignment |  | 8.7 | 17 | PDB header: ribosome Chain: X; PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 15 | c5jx6C_ |  Alignment |  | 6.1 | 20 | PDB header: hydrolase Chain: C; PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme |
| 16 | c3skqA_ |  Alignment |  | 5.9 | 19 | PDB header: metal transport Chain: A; PDB Molecule: mitochondrial distribution and morphology protein 38; PDBTitle: mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane |
| 17 | c2lsmA_ |  Alignment |  | 5.7 | 20 | PDB header: chaperone Chain: A; PDB Molecule: dna-packaging protein fi; PDBTitle: solution structure of gpfi c-terminal domain |

18

[c3oi0C_](#)

Alignment



5.3

27

PDB header:de novo protein

Chain: C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which

PDBTitle: crystal structure of monofold-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly