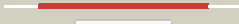
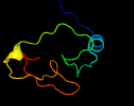


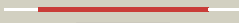
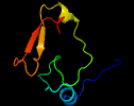

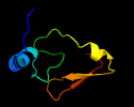

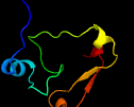









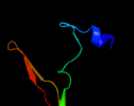

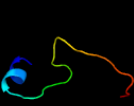
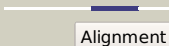

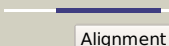

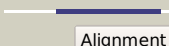

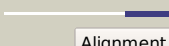
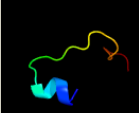
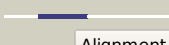
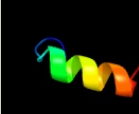
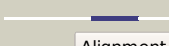
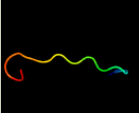
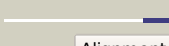

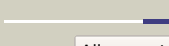


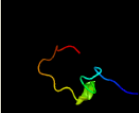
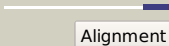
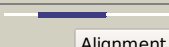


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3224B (-)_3600798_3601016
Date	Thu Aug 8 16:20:42 BST 2019
Unique Job ID	bdd68ab0a97ab1bd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dbxa_	 Alignment		99.6	42	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
2	d1wdva_	 Alignment		99.6	25	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
3	c2dxaA_	 Alignment		99.5	34	PDB header: translation Chain: A: PDB Molecule: protein ybak; PDBTitle: crystal structure of trans editing enzyme prox from e.coli
4	c2cx5B_	 Alignment		99.5	27	PDB header: translation Chain: B: PDB Molecule: a putative trans-editing enzyme; PDBTitle: crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
5	d1vkia_	 Alignment		99.5	17	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
6	d1vjfa_	 Alignment		99.4	19	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
7	c3memA_	 Alignment		99.4	10	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein; PDBTitle: crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
8	c3op6B_	 Alignment		99.3	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution
9	c4d2iB_	 Alignment		50.0	15	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfobolus solfataricus bound to amp-pnp
10	c3uepB_	 Alignment		8.6	17	PDB header: protein transport Chain: B: PDB Molecule: yscq-c, type iii secretion protein; PDBTitle: crystal structure of yscq-c from yersinia pseudotuberculosis
11	d1xi8a3	 Alignment		8.6	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like

12	c5jpdq_	 Alignment		8.3	19	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
13	c3bqhA_	 Alignment		7.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb; PDBTitle: structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
14	c2j89A_	 Alignment		6.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
15	d2nqra3	 Alignment		6.4	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
16	c2hbpA_	 Alignment		6.4	29	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
17	c4mj7B_	 Alignment		6.2	25	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
18	d1spia_	 Alignment		6.1	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
19	c5oezA_	 Alignment		5.7	14	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
20	d1bk4a_	 Alignment		5.5	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
21	d1nuwa_	 Alignment	not modelled	5.3	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	c2m86A_	 Alignment	not modelled	5.1	29	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: mco-pmi; PDBTitle: solution structure of hdm2 with engineered cyclotide