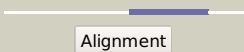
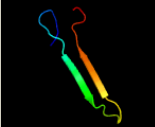
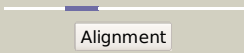


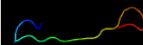
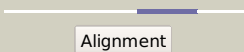
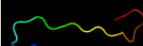
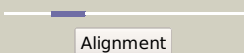
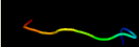

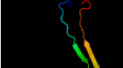


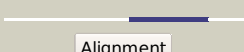
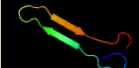
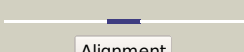

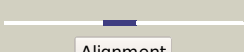
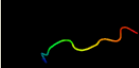

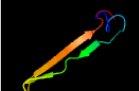






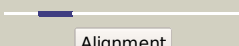

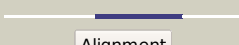

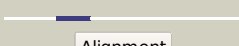

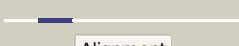







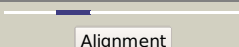


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3566A (-)_4008346_4008612
Date	Fri Aug 9 18:20:24 BST 2019
Unique Job ID	b66a2b89020f1eee

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2q49B	 Alignment		13.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
2	c2n6uA	 Alignment		11.9	100	PDB header: unknown function Chain: A: PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4
3	d2cvoa2	 Alignment		10.8	29	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
4	d2q49a2	 Alignment		10.4	23	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
5	c6niiA	 Alignment		10.3	64	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ravid; PDBTitle: crystal structure of ravid (residues 1-200) from legionella pneumophila2 (strain corby)
6	c2i3aD	 Alignment		9.6	23	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (rv1652) from mycobacterium tuberculosis
7	d2otma1	 Alignment		9.3	22	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
8	c2ozpA	 Alignment		9.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
9	c1y96C	 Alignment		8.6	25	PDB header: rna binding protein Chain: C: PDB Molecule: gem-associated protein 6; PDBTitle: crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
10	c2vxeA	 Alignment		7.9	58	PDB header: transcription Chain: A: PDB Molecule: cg10686-pa; PDBTitle: solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch)
11	d2hjsa2	 Alignment		7.5	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like

12	c2r28D_	 Alignment		7.3	75	PDB header: metal binding protein/hydrolase Chain: D: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: the complex structure of calmodulin bound to a calcineurin2 peptide
13	d2vxfa1	 Alignment		7.2	50	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: LSM14 N-terminal domain-like
14	c3d01G_	 Alignment		7.2	19	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
15	c2r28C_	 Alignment		7.1	75	PDB header: metal binding protein/hydrolase Chain: C: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: the complex structure of calmodulin bound to a calcineurin2 peptide
16	c4e04B_	 Alignment		6.9	27	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: rpbphp2 chromophore-binding domain crystallized by homologue-directed2 mutagenesis.
17	c2kppA_	 Alignment		6.4	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0431 protein; PDBTitle: solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
18	c2jziB_	 Alignment		6.2	75	PDB header: metal binding protein Chain: B: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
19	c4q5uC_	 Alignment		6.2	75	PDB header: calcium binding protein/protein binding Chain: C: PDB Molecule: serine/threonine-protein phosphatase 2b catalytic subunit PDBTitle: structure of calmodulin bound to its recognition site from calcineurin
20	c4obiA_	 Alignment		5.9	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1312 family protein (ef3258) from2 enterococcus faecalis v583 at 1.73 a resolution
21	c2hbpA_	 Alignment	not modelled	5.8	40	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
22	d1vkna2	 Alignment	not modelled	5.8	36	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
23	c2n6vA_	 Alignment	not modelled	5.8	67	PDB header: unknown function Chain: A: PDB Molecule: astexin3; PDBTitle: solution study of astexin3