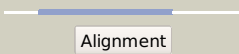
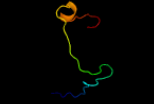
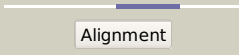

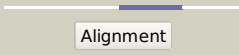

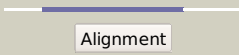
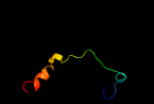

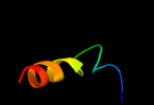
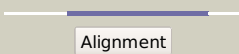

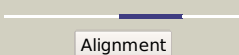

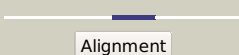

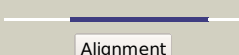

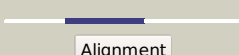
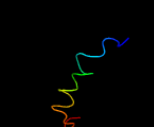
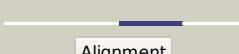
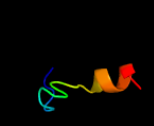





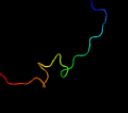
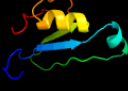
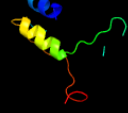
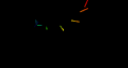


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0609A (-) _703833_704060
Date	Fri Jul 26 01:50:17 BST 2019
Unique Job ID	9b5f13c6e5d4098d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4k7gD_	 Alignment		26.1	29	PDB header: isomerase Chain: D: PDB Molecule: 3-hydroxyproline dehydratse; PDBTitle: crystal structure of a 3-hydroxyproline dehydratse from agrobacterium2 vitis, target efi-506470, with bound pyrrole 2-carboxylate, ordered3 active site
2	c4lb0B_	 Alignment		12.4	35	PDB header: isomerase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hydroxyproline epimerase from agrobacterium2 vitis, target efi-506420, with bound trans-4-oh-l-proline
3	c6ijoG_	 Alignment		11.6	44	PDB header: photosynthesis Chain: G: PDB Molecule: psag; PDBTitle: photosystem i of chlamydomonas reinhardtii
4	c2wsfG_	 Alignment		11.3	28	PDB header: photosynthesis Chain: G: PDB Molecule: photosystem i reaction center subunit v, chloroplastic; PDBTitle: improved model of plant photosystem i
5	c3lw5K_	 Alignment		11.0	39	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x psak; PDBTitle: improved model of plant photosystem i
6	d1f07a_	 Alignment		10.4	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
7	c2wscK_	 Alignment		9.8	39	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit psak, chloroplastic; PDBTitle: improved model of plant photosystem i
8	c5zjiO_	 Alignment		9.4	33	PDB header: membrane protein Chain: O: PDB Molecule: 16kda membrane protein; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
9	d1rhca_	 Alignment		9.2	25	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
10	c2o01F_	 Alignment		9.2	48	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
11	c6ijjK_	 Alignment		9.0	44	PDB header: membrane protein Chain: K: PDB Molecule: psak; PDBTitle: photosystem i of chlamydomonas reinhardtii

12	d1kqfb2	Alignment		8.0	46	Fold: Single transmembrane helix Superfamily: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor Family: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
13	c2wsfF_	Alignment		7.8	48	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, chloroplastic; PDBTitle: improved model of plant photosystem i
14	c2nv2U_	Alignment		6.7	38	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
15	c1z69D_	Alignment		6.7	15	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
16	c6igzK_	Alignment		6.5	39	PDB header: plant protein Chain: K: PDB Molecule: psak; PDBTitle: structure of psi-lhci
17	c5w9pl_	Alignment		6.4	30	PDB header: viral protein Chain: I: PDB Molecule: spike glycoprotein; PDBTitle: mers s ectodomain trimer in complex with variable domain of2 neutralizing antibody g4
18	d2nsfa2	Alignment		6.3	28	Fold: SCP-like Superfamily: SCP-like Family: Micothiol-dependent maleylpyruvate isomerase C-terminal domain-like
19	c3c8nB_	Alignment		6.2	26	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
20	c1cagC_	Alignment		6.0	53	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
21	c1cagA_	Alignment	not modelled	6.0	53	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
22	c5kzoA_	Alignment	not modelled	5.4	53	PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment
23	c4l67B_	Alignment	not modelled	5.3	75	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: crystal structure of catalytic domain of pak4
24	c2hw2A_	Alignment	not modelled	5.2	47	PDB header: transferase Chain: A: PDB Molecule: rifampin adp-ribosyl transferase; PDBTitle: crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
25	c1cgdB_	Alignment	not modelled	5.1	56	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
26	c1cagB_	Alignment	not modelled	5.1	56	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
27	c1cgdC_	Alignment	not modelled	5.1	56	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide