

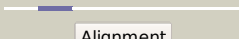

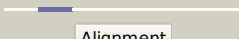









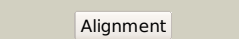

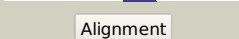

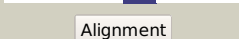





Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3078_(hab)_3441350_3441751
 Date Thu Aug 8 16:20:25 BST 2019
 Unique Job ID 1c4b8ea4c9a38305

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5yixA_	 Alignment		14.2	57	PDB header: dna binding protein Chain: A; PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
2	c6hwhM_	 Alignment		12.4	23	PDB header: electron transport Chain: M; PDB Molecule: cytochrome bc1 complex cytochrome c subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
3	c6hwhK_	 Alignment		10.5	23	PDB header: electron transport Chain: K; PDB Molecule: cytochrome bc1 complex cytochrome c subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
4	c1emzA_	 Alignment		8.4	27	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein e1; PDBTitle: solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
5	c3if4C_	 Alignment		7.5	54	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm sewage outfall:2 integron cassette protein hfx_cass5
6	d1siga_	 Alignment		7.3	57	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
7	c3uc8C_	 Alignment		6.1	86	PDB header: de novo protein Chain: C; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
8	c2ii5A_	 Alignment		6.1	86	PDB header: de novo protein Chain: A; PDB Molecule: cyclo-tc1; PDBTitle: cyclo-tc1 trp-cage
9	c3uc8B_	 Alignment		6.1	86	PDB header: de novo protein Chain: B; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
10	c3uc7E_	 Alignment		6.1	86	PDB header: de novo protein Chain: E; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
11	c3uc7D_	 Alignment		6.1	86	PDB header: de novo protein Chain: D; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form

12	c3uc8A_	Alignment		6.1	86	PDB header: de novo protein Chain: A: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
13	c3uc7F_	Alignment		6.1	86	PDB header: de novo protein Chain: F: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
14	c3uc7A_	Alignment		6.1	86	PDB header: de novo protein Chain: A: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
15	c3uc7B_	Alignment		6.1	86	PDB header: de novo protein Chain: B: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
16	c3uc7C_	Alignment		6.1	86	PDB header: de novo protein Chain: C: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
17	c5wdaL_	Alignment		6.0	29	PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
18	c5zlgA_	Alignment		5.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
19	c6hwhQ_	Alignment		5.6	18	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
20	c2l4uA_	Alignment		5.3	15	PDB header: signaling protein Chain: A: PDB Molecule: 24mer peptide from protein ste5; PDBTitle: solution structure of ste5pm24 in the presence of sds micelle
21	d2bcqa2	Alignment	not modelled	5.2	54	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
22	c4xpuA_	Alignment	not modelled	5.1	38	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: the crystal structure of endov from e.coli