

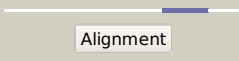

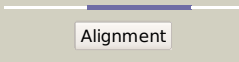

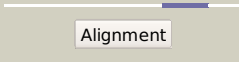

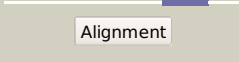

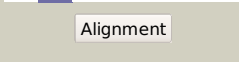
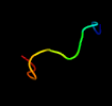
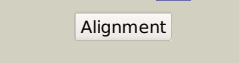
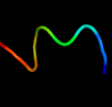
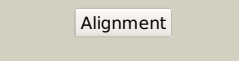

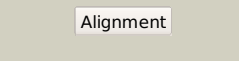
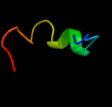
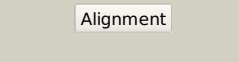

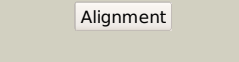



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1583c_(-)_1785919_1786317
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	cda8e74a583e8394

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g7rA_	 Alignment		19.3	23	PDB header: hydrolase Chain: A: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
2	c2m8gX_	 Alignment		13.8	25	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
3	c3gw6F_	 Alignment		12.8	21	PDB header: chaperone Chain: F: PDB Molecule: endo-n-acetylneuraminidase; PDBTitle: intramolecular chaperone
4	d1etob_	 Alignment		12.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
5	c4l5eA_	 Alignment		11.2	14	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
6	c2eqfA_	 Alignment		10.8	43	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: solution structure of the 7th a20-type zinc finger domain2 from human tumor necrosis factor, alpha-induced protein3
7	c2jp6A_	 Alignment		10.6	67	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 18.1; PDBTitle: structural and functional characterization of the2 recombinant form of the kv1.3 channel blocker tc32
8	c2lgzA_	 Alignment		9.8	25	PDB header: transferase, membrane protein Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: solution structure of stt3p
9	c4hikA_	 Alignment		9.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: protection of telomeres protein 1; PDBTitle: crystal structure of schizosaccharomyces pombe pot1pc bound to ssdna2 (ggttacggt)
10	c3vzaF_	 Alignment		9.5	50	PDB header: cell cycle Chain: F: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
11	c3vzaE_	 Alignment		9.5	50	PDB header: cell cycle Chain: E: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide

12	c3ushB_	Alignment		8.6	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
13	c4iohA_	Alignment		8.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tl11086 protein; PDBTitle: crystal structure of the tl11086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
14	d1fipa_	Alignment		7.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1ntca_	Alignment		7.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c1umqA_	Alignment		7.0	25	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
17	d1umqa_	Alignment		7.0	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	d1pu6a_	Alignment		6.3	11	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
19	d1vaja1	Alignment		6.1	37	Fold: AMMECR1-like Superfamily: AMMECR1-like Family: AMMECR1-like
20	c4nooA_	Alignment		5.8	11	PDB header: immune system Chain: A: PDB Molecule: vgrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
21	d1etxa_	Alignment	not modelled	5.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like