

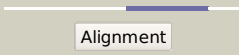

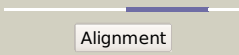

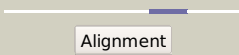

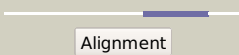

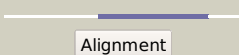

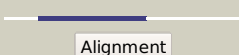



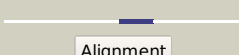
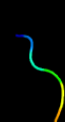
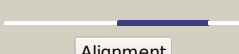

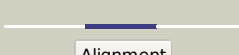



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1535_(-)_1735982_1736218
Date	Fri Aug 2 13:30:12 BST 2019
Unique Job ID	49cce67528d5e7ef

Detailed template information

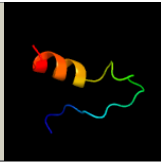
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ekoA_	 Alignment		16.2	56	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pfoi; PDBTitle: crystal structure of type iip restriction endonuclease pfoi with2 cognate dna
2	c2m8gX_	 Alignment		15.9	36	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
3	d1ntca_	 Alignment		13.3	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
4	c3kbyB_	 Alignment		12.4	50	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical protein from staphylococcus aureus
5	c4l5eA_	 Alignment		11.6	42	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
6	c4hkaA_	 Alignment		11.6	31	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of drosophila melanogaster tryptophan 2,3-2 dioxygenase in complex with heme
7	d1es6a1	 Alignment		7.7	29	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
8	c3umvB_	 Alignment		7.6	27	PDB header: lyase Chain: B: PDB Molecule: deoxyribodipyrimidine photo-lyase; PDBTitle: eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants
9	c5ebzF_	 Alignment		6.9	50	PDB header: transferase/transferase inhibitor Chain: F: PDB Molecule: inhibitor of nuclear factor kappa-b kinase subunit alpha; PDBTitle: crystal structure of human ikk1
10	c4o5pB_	 Alignment		6.6	27	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
11	d2gkeal	 Alignment		6.5	28	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: Diaminopimelate epimerase

12	d1etob_	Alignment		6.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c5m47A_	Alignment		6.2	16	PDB header: isomerase Chain: A: PDB Molecule: diaminopimelate epimerase; PDBTitle: crystal structure of dapf from corynebacterium glutamicum in complex2 with d,l-diaminopimelate
14	c3r45C_	Alignment		5.6	43	PDB header: nuclear protein Chain: C: PDB Molecule: holliday junction recognition protein; PDBTitle: structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp
15	d2d0ta1	Alignment		5.5	21	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
16	c2a5hC_	Alignment		5.4	38	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
17	c3e7ID_	Alignment		5.4	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	d1xqoa_	Alignment		5.4	47	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like

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[c2lf6A_](#)

Alignment



5.2

29

PDB header:signaling protein

Chain: A: **PDB Molecule:**effector protein hopab1;

PDBTitle: solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a