







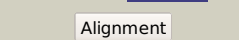



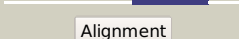
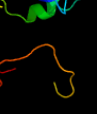
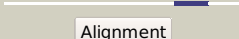
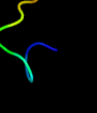
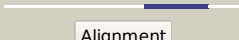

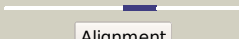

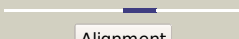


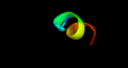


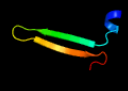
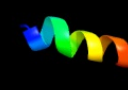
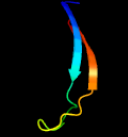


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1064c_(lpqV)_1186909_1187328
Date	Wed Jul 31 22:05:14 BST 2019
Unique Job ID	a305d77ca98bf8c8

Detailed template information

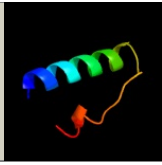
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3btpA_	 Alignment		22.2	89	PDB header: dna binding protein, chaperone Chain: A: PDB Molecule: single-strand dna-binding protein; PDBTitle: crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
2	c3ez0D_	 Alignment		12.3	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein with ferritin-like fold; PDBTitle: crystal structure of protein of unknown function with ferritin-like2 fold (yp_832262.1) from arthrobacter sp. fb24 at 2.33 a resolution
3	d2i09a2	 Alignment		11.5	33	Fold: DeoB insert domain-like Superfamily: DeoB insert domain-like Family: DeoB insert domain-like
4	c2hroA_	 Alignment		10.3	35	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus
5	c3sggA_	 Alignment		9.4	11	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical hydrolase; PDBTitle: crystal structure of a putative hydrolase (bt_2193) from bacteroides2 thetaiotaomicron vpi-5482 at 1.25 a resolution
6	c2rovA_	 Alignment		9.1	10	PDB header: transferase Chain: A: PDB Molecule: rho-associated protein kinase 2; PDBTitle: the split ph domain of rock ii
7	c4zv4C_	 Alignment		8.7	20	PDB header: translation Chain: C: PDB Molecule: tse6; PDBTitle: structure of tse6 in complex with ef-tu
8	c2dziA_	 Alignment		8.3	29	PDB header: sugar binding protein Chain: A: PDB Molecule: synaptic glycoprotein sc2; PDBTitle: 2dzj/solution structure of the n-terminal ubiquitin-like2 domain in human synaptic glycoprotein sc2
9	d1baka_	 Alignment		7.7	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
10	c2ffuA_	 Alignment		7.5	56	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalact-2 complexed with udp and ea2
11	c6iwqE_	 Alignment		7.5	22	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of gainc-t7 with mn2+

12	c2dhkA_	Alignment		6.5	22	PDB header: immune system Chain: A: PDB Molecule: tbc1 domain family member 2; PDBTitle: solution structure of the ph domain of tbc1 domain family2 member 2 protein from human
13	c2k47A_	Alignment		6.5	20	PDB header: replication Chain: A: PDB Molecule: phosphoprotein; PDBTitle: solution structure of the c-terminal n-rna binding domain2 of the vesicular stomatitis virus phosphoprotein
14	c2hwgA_	Alignment		6.4	35	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
15	c5us5B_	Alignment		6.2	17	PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
16	c5olaD_	Alignment		6.1	30	PDB header: transcription Chain: D: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of mitochondrial transcription elongation complex in complex2 with elongation factor tefm
17	c3ftqA_	Alignment		5.6	31	PDB header: cell cycle Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of septin 2 in complex with gppnhp and2 mg2+
18	c5mr1A_	Alignment		5.4	17	PDB header: signaling protein Chain: A: PDB Molecule: interactor protein for cytohesin exchange factors 1; PDBTitle: crystal structure of the pleckstrin homology domain of interactor2 protein for cytohesin exchange factors 1 (ipcef1)

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[c5ifgB_](#)

Alignment



5.3

23

PDB header:hydrolase/antitoxin

Chain: B: **PDB Molecule:**antitoxin higa;

PDBTitle: crystal structure of higa-highb complex from e. coli