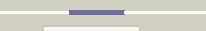
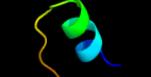
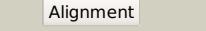
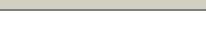


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD2873_(mpt83)_3183915_3184577
Date	Wed Aug 7 12:50:54 BST 2019
Unique Job ID	3cf727967d07242f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nyoa			100.0	74	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
2	c5nv6A			100.0	34	PDB header: structural protein Chain: A: PDB Molecule: transforming growth factor-beta-induced protein ig-h3; PDBTitle: structure of human transforming growth factor beta-induced protein2 (tgfbip).
3	c1x3bA			100.0	33	PDB header: cell adhesion Chain: A: PDB Molecule: transforming growth factor-beta induced protein PDBTitle: solution structure of the fas1 domain of human transforming2 growth factor-beta induced protein ig-h3
4	c5yjhA			100.0	26	PDB header: cell adhesion Chain: A: PDB Molecule: periostin; PDBTitle: structural insights into periostin functions
5	c5wt7A			100.0	26	PDB header: cell adhesion Chain: A: PDB Molecule: periostin; PDBTitle: fas1-iv domain of human periostin
6	c1w7eA			100.0	39	PDB header: cell adhesion Chain: A: PDB Molecule: beta-ig-h3/fasciclin; PDBTitle: nmr ensemble of fasciclin-like protein from rhodobacter sphaeroides
7	c2mxAA			100.0	36	PDB header: membrane protein Chain: A: PDB Molecule: ndh-1 complex sensory subunit cups; PDBTitle: solution structure of the ndh-1 complex subunit cups from2 thermosynechococcus elongatus
8	d1o70a2			100.0	17	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
9	c5n86A			100.0	17	PDB header: cell adhesion Chain: A: PDB Molecule: stabilin-2; PDBTitle: crystal structure of fas1 domain of hyaluronic acid receptor stabilin-2 2
10	d1o70a1			99.9	25	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
11	c1o70A			99.9	26	PDB header: cell adhesion Chain: A: PDB Molecule: fasciclin i; PDBTitle: novel fold revealed by the structure of a fas1 domain pair2 from the insect cell adhesion molecule fasciclin i

12	c2ag3A_		Alignment		22.0	45	PDB header: de novo protein Chain: A: PDB Molecule: gcn4-pli; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: substitution of the k(15)-l(16) amide with a triazole
13	c1u9fA_		Alignment		13.3	45	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
14	d1j5ya2		Alignment		12.7	16	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
15	c1u9fB_		Alignment		12.6	45	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
16	c1u9fC_		Alignment		12.6	45	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
17	c1u9fD_		Alignment		12.4	45	PDB header: transcription Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
18	c4v19P_		Alignment		8.2	23	PDB header: ribosome Chain: P: PDB Molecule: mitoribosomal protein ul15m, mrpl15; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
19	d1q42a_		Alignment		6.6	24	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
20	d1gsoa2		Alignment		6.3	33	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
21	c2kwrA_		Alignment	not modelled	6.3	25	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution nmr structure of the apoform of nare (nmb1343)
22	c6hv9B_		Alignment	not modelled	5.9	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon subunit b; PDBTitle: s. cerevisiae cmg-pol epsilon-dna