























Phyre2

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 Description: RVBD2875_(mpt70)_3187040_3187621
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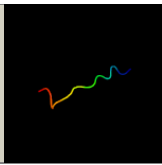
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nyoa_	 Alignment		100.0	100	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
2	c5nv6A_	 Alignment		100.0	32	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_	 Alignment		100.0	30	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_	 Alignment		100.0	22	PDB header: cell adhesion Chain: A: PDB Molecule: periostin; PDBTitle: structural insights into periostin functions
5	c5wt7A_	 Alignment		100.0	22	PDB header: cell adhesion Chain: A: PDB Molecule: periostin; PDBTitle: fas1-iv domain of human periostin
6	c1w7eA_	 Alignment		100.0	43	PDB header: cell adhesion Chain: A: PDB Molecule: beta-ig-h3/fasciclin; PDBTitle: nmr ensemble of fasciclin-like protein from rhodobacter sphaeroides
7	c2mxaA_	 Alignment		100.0	40	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	 Alignment		100.0	18	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
9	c5n86A_	 Alignment		100.0	23	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	 Alignment		99.9	23	Fold: FAS1 domain Superfamily: FAS1 domain Family: FAS1 domain
11	c1o70A_	 Alignment		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		19.0	42	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)-(16) amide with a triazole
13	c1u9fA_	Alignment		10.8	42	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))(16)
14	c1u9fC_	Alignment		10.2	42	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))(16)
15	c1u9fB_	Alignment		10.2	42	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))(16)
16	c1u9fD_	Alignment		10.0	42	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))(16)
17	c4v19P_	Alignment		7.5	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

18 [c2kwrA](#)

Alignment



7.5

25

PDB header:transferase

Chain: A: **PDB Molecule:**putative uncharacterized protein;

PDBTitle: solution nmr structure of the apoform of nare (nmb1343)