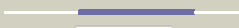
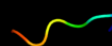
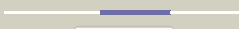
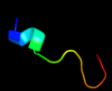
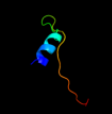
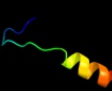
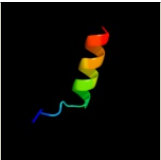


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lujb_	 Alignment		15.1	21	Fold: beta-catenin-interacting protein ICAT Superfamily: beta-catenin-interacting protein ICAT Family: beta-catenin-interacting protein ICAT
2	d3bzka2	 Alignment		12.4	63	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
3	d2paga1	 Alignment		10.7	26	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
4	d1yuaa2	 Alignment		10.3	53	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
5	c2qyxB_	 Alignment		9.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein mj0159; PDBTitle: crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
6	c3pzdB_	 Alignment		9.8	33	PDB header: motor protein/apoptosis Chain: B: PDB Molecule: netrin receptor dcc; PDBTitle: structure of the myosin x myth4-ferm/dcc complex
7	c3mx3B_	 Alignment		8.6	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: susd homolog; PDBTitle: crystal structure of a susd homolog (bf0972) from bacteroides fragilis2 nctc 9343 at 2.00 a resolution
8	c3f1jA_	 Alignment		8.3	42	PDB header: viral protein Chain: A: PDB Molecule: matrix protein; PDBTitle: crystal structure of the borna disease virus matrix protein2 (bdv-m) reveals rna binding properties
9	d1lg4a_	 Alignment		7.9	25	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
10	c2ip6A_	 Alignment		7.7	29	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
11	c2r26C_	 Alignment		7.7	23	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum

12	c3l4gl_	Alignment		7.4	28	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
13	cljqsB_	Alignment		7.3	44	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
14	d3cgha1	Alignment		7.2	21	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: SusD-like
15	d1dp3a_	Alignment		7.1	19	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: DNA-binding domain (fragment?) of the TraM protein
16	d1zs3a1	Alignment		6.5	9	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
17	d1ty0a2	Alignment		6.2	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: Superantigen toxins, C-terminal domain Family: Superantigen toxins, C-terminal domain
18	d1vl2a2	Alignment		5.8	33	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
19	c2dymE_	Alignment		5.4	29	PDB header: protein turnover/protein turnover Chain: E: PDB Molecule: autophagy protein 5; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex

20 [d3ejna1](#)

Alignment



5.1

16

Fold:alpha-alpha superhelix
Superfamily:TPR-like
Family:SusD-like