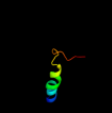
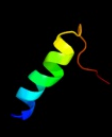
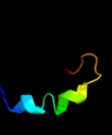
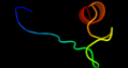
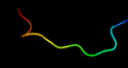
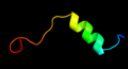
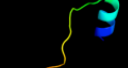
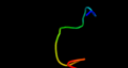
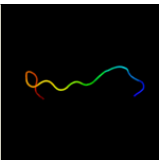


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pa8A_	 Alignment		25.7	20	PDB header: toxin/peptide inhibitor Chain: A: PDB Molecule: toxin b; PDBTitle: structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
2	d2zjrk1	 Alignment		16.6	18	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
3	d2cqma1	 Alignment		14.6	41	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
4	d1tifa_	 Alignment		12.8	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
5	d1bnla_	 Alignment		10.6	32	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Endostatin
6	d1gd8a_	 Alignment		9.6	23	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
7	c2jyaA_	 Alignment		9.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
8	d1m9sa3	 Alignment		8.2	18	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: GW domain
9	c3bboP_	 Alignment		8.2	25	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein l17; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
10	d1koea_	 Alignment		8.1	35	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Endostatin
11	d2qamn1	 Alignment		7.3	18	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17

12	d1hd2a_	Alignment		7.0	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
13	d1ztxe1	Alignment		6.6	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
14	d2bh1a1	Alignment		6.1	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Cyto-EpsL domain
15	d2q79a1	Alignment		6.1	27	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
16	d2j01s1	Alignment		5.9	40	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11

17	c2jz8A	Alignment		5.3	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
----	------------------------	-----------	--	-----	----	--