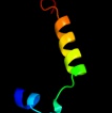
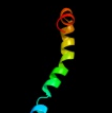
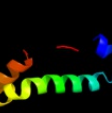
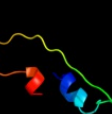


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y9mB_	 Alignment		55.6	16	PDB header: ligase/transport protein Chain: B: PDB Molecule: peroxisome assembly protein 22; PDBTitle: pex4p-pex22p structure
2	d2i5nh2	 Alignment		44.1	64	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
3	d1jdqa_	 Alignment		21.4	21	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
4	d1cola_	 Alignment		21.4	21	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
5	d1gjwa1	 Alignment		21.2	60	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
6	c3qqcA_	 Alignment		20.0	18	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit b, dna-directed rna PDBTitle: crystal structure of archaeal spt4/5 bound to the rnap clamp domain
7	d2etda1	 Alignment		19.5	22	Fold: Bromodomain-like Superfamily: LemA-like Family: LemA-like
8	d1ciia1	 Alignment		17.5	18	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
9	d1fkma2	 Alignment		17.5	27	Fold: Left-handed superhelix Superfamily: Ypt/Rab-GAP domain of gyp1p Family: Ypt/Rab-GAP domain of gyp1p
10	d1je3a_	 Alignment		17.4	21	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
11	d1rh1a2	 Alignment		14.9	15	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin

12	c1gj8A_	Alignment		10.6	63	PDB header: blood clotting, hydrolase Chain: A: PDB Molecule: urokinase-type plasminogen activator; PDBTitle: engineering inhibitors highly selective for the s1 sites of ser1902 trypsin-like serine protease drug targets
13	c1gjaA_	Alignment		10.6	63	PDB header: blood clotting, hydrolase Chain: A: PDB Molecule: urokinase-type plasminogen activator; PDBTitle: engineering inhibitors highly selective for the s1 sites of ser1902 trypsin-like serine protease drug targets
14	c1gjdA_	Alignment		10.6	63	PDB header: blood clotting, hydrolase Chain: A: PDB Molecule: urokinase-type plasminogen activator; PDBTitle: engineering inhibitors highly selective for the s1 sites of ser1902 trypsin-like serine protease drug targets
15	d1a87a_	Alignment		10.2	13	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
16	c1a87A_	Alignment		10.2	13	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
17	d1pava_	Alignment		9.5	15	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
18	c3fewX_	Alignment		9.4	19	PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
19	d1p9ga_	Alignment		9.2	57	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
20	d1dcja_	Alignment		8.9	12	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
21	c2kmcA_	Alignment	not modelled	8.0	30	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 1; PDBTitle: solution structure of the n-terminal domain of kindlin-1
22	c1rh1A_	Alignment	not modelled	8.0	16	PDB header: antibiotic Chain: A: PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
23	c3oq0D_	Alignment	not modelled	8.0	33	PDB header: cell cycle Chain: D: PDB Molecule: dbf4; PDBTitle: crystal structure of motif n of saccharomyces cerevisiae dbf4
24	c2lgaA_	Alignment	not modelled	8.0	37	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 2; PDBTitle: nmr structure for kindle-2 n-terminus
25	c3mlrP_	Alignment	not modelled	7.6	62	PDB header: immune system Chain: P: PDB Molecule: hiv-1 gp120 third variable region (v3) crown; PDBTitle: crystal structure of anti-hiv-1 v3 fab 2557 in complex with a ny5 v32 peptide
26	c3nohA_	Alignment	not modelled	7.3	16	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
27	c3qwlA_	Alignment	not modelled	7.2	17	PDB header: hydrolase activator Chain: A: PDB Molecule: tbc1 domain family member 7; PDBTitle: crystal structure of human tbc1 domain family member 7
28	c3lnoA_	Alignment	not modelled	7.1	54	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59

					from2 bacillus anthracis
29	c1agqB_	Alignment	not modelled	6.9	29 PDB header: growth factor Chain: B: PDB Molecule: glial cell-derived neurotrophic factor; PDBTitle: glial cell-derived neurotrophic factor from rat
30	c2i88A_	Alignment	not modelled	6.8	22 PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin2 e1
31	c2pijB_	Alignment	not modelled	6.6	25 PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
32	d1u3da2	Alignment	not modelled	6.4	21 Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
33	d1d1la_	Alignment	not modelled	6.2	25 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
34	c2diiA_	Alignment	not modelled	6.1	47 PDB header: transcription Chain: A: PDB Molecule: tftih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tftih basal2 transcription factor complex p62 subunit
35	d1uwda_	Alignment	not modelled	6.0	27 Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
36	d2ha2a1	Alignment	not modelled	5.6	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
37	d2diiA1	Alignment	not modelled	5.6	47 Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
38	d4croa_	Alignment	not modelled	5.6	25 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
39	d2cu6a1	Alignment	not modelled	5.2	23 Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
40	c2yy8B_	Alignment	not modelled	5.2	24 PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
41	d1dwua_	Alignment	not modelled	5.1	20 Fold: Ribosomal protein L1 Superfamily: Ribosomal protein L1 Family: Ribosomal protein L1