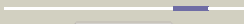
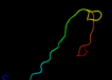
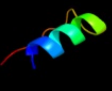
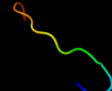
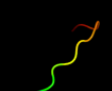


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nr1A_	 Alignment		18.1	80	PDB header: receptor Chain: A: PDB Molecule: nr1 m2; PDBTitle: transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
2	d1ffgb_	 Alignment		17.9	57	Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA
3	c1a0oH_	 Alignment		17.7	57	PDB header: chemotaxis Chain: H: PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey
4	c2ysrA_	 Alignment		13.4	20	PDB header: signaling protein Chain: A: PDB Molecule: dep domain-containing protein 1; PDBTitle: solution structure of the dep domain from human dep domain-2 containing protein 1
5	c2ld7A_	 Alignment		11.6	47	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap30; PDBTitle: solution structure of the msin3a pah3-sap30 sid complex
6	c3mqpB_	 Alignment		11.5	73	PDB header: apoptosis Chain: B: PDB Molecule: phorbol-12-myristate-13-acetate-induced protein 1; PDBTitle: crystal structure of human bfl-1 in complex with noxa bh3 peptide,2 northeast structural genomics consortium target hr2930
7	c3kzwD_	 Alignment		8.1	22	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
8	c2eqoA_	 Alignment		8.0	63	PDB header: transcription Chain: A: PDB Molecule: tnf receptor-associated factor 3-interacting PDBTitle: solution structure of the tnfr3ip1_nd domain of interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
9	d1sg1x2	 Alignment		8.0	63	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
10	d1j3ba2	 Alignment		7.0	21	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
11	c3im0A_	 Alignment		6.3	19	PDB header: lyase Chain: A: PDB Molecule: val-1; PDBTitle: crystal structure of chlorella virus val-1 soaked in 200mm d-2 glucuronic acid, 10% peg-3350, and 200mm glycine-naoh (ph 10.0)

12	c2iifA_	Alignment		6.0	40	PDB header: recombination/dna Chain: A: PDB Molecule: integration host factor; PDBTitle: single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
13	dlw4ma_	Alignment		5.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
14	d2csoa1	Alignment		5.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
15	c3hluA_	Alignment		5.6	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein duf2179; PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
16	c1lanA_	Alignment		5.6	19	PDB header: hydrolase (alpha-aminoacylpeptide) Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal
17	dlkjsa_	Alignment		5.6	33	Fold: Anaphylotoxins (complement system) Superfamily: Anaphylotoxins (complement system) Family: Anaphylotoxins (complement system)
18	dlgxie_	Alignment		5.5	60	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Photosystem I accessory protein E (PsaE)
19	dlpsea_	Alignment		5.4	60	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Photosystem I accessory protein E (PsaE)
20	dlk8rb_	Alignment		5.4	64	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
21	d2o0qa1	Alignment	not modelled	5.4	40	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: CC0527-like
22	dlevsA_	Alignment	not modelled	5.3	24	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines