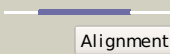
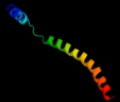
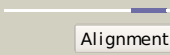
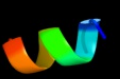
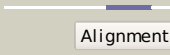

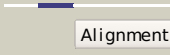




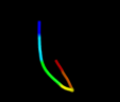




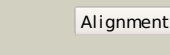

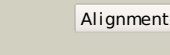
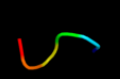
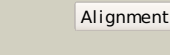
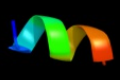


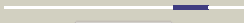
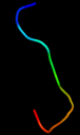






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rh5b_	 Alignment		12.1	15	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
2	c2dyoB_	 Alignment		11.2	40	PDB header: protein turnover/protein turnover Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
3	c2l2tA_	 Alignment		10.7	21	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
4	d2f22a1	 Alignment		9.6	37	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
5	c1bzgA_	 Alignment		8.9	57	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
6	c1zczA_	 Alignment		8.8	50	PDB header: transferase/hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
7	c3skdA_	 Alignment		8.6	50	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein thb187; PDBTitle: crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
8	c2lkjA_	 Alignment		7.6	50	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-m; PDBTitle: structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
9	d1lira_	 Alignment		6.8	63	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
10	c2oqiA_	 Alignment		6.7	50	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein sag1661; PDBTitle: crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
11	c3zrkY_	 Alignment		6.4	40	PDB header: transferase/peptide Chain: Y: PDB Molecule: proto-oncogene frat1; PDBTitle: identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors

12	c2o08B_	Alignment			6.3	33	PDB header: hydrolase Chain: B: PDB Molecule: bh1327 protein; PDBTitle: crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
13	c2rf9D_	Alignment			6.0	50	PDB header: transferase Chain: D: PDB Molecule: erbb receptor feedback inhibitor 1; PDBTitle: crystal structure of the complex between the egfr kinase2 domain and a mig6 peptide
14	c3ccgA_	Alignment			5.8	33	PDB header: hydrolase Chain: A: PDB Molecule: hd superfamily hydrolase; PDBTitle: crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
15	c1gngX_	Alignment			5.7	40	PDB header: transferase Chain: X: PDB Molecule: frattide; PDBTitle: glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide

16

[c1thzA_](#)

Alignment

5

5.6

40

PDB header:transferase, hydrolase
Chain: A: **PDB Molecule:**bifunctional purine biosynthesis protein purh;
PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening