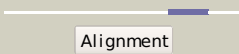
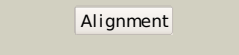
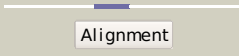
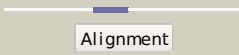
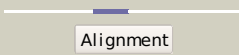
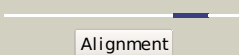
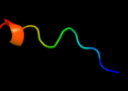
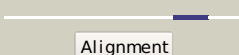
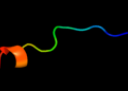


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2axtl	 Alignment		16.1	15	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, Psbl Family: Psbl-like
2	c3giaA	 Alignment		15.5	13	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
3	c2dyoB	 Alignment		12.8	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
4	c1bzgA	 Alignment		11.5	71	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
5	c3zrkY	 Alignment		11.2	67	PDB header: transferase/peptide Chain: Y: PDB Molecule: proto-oncogene frat1; PDBTitle: identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
6	c1gngX	 Alignment		10.7	67	PDB header: transferase Chain: X: PDB Molecule: frattide; PDBTitle: glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
7	d1lira	 Alignment		10.6	63	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
8	c1tqeY	 Alignment		8.7	7	PDB header: transcription/protein binding/dna Chain: Y: PDB Molecule: histone deacetylase 9; PDBTitle: mechanism of recruitment of class ii histone deacetylases2 by myocyte enhancer factor-2
9	c1tqeX	 Alignment		8.7	7	PDB header: transcription/protein binding/dna Chain: X: PDB Molecule: histone deacetylase 9; PDBTitle: mechanism of recruitment of class ii histone deacetylases2 by myocyte enhancer factor-2
10	c1zczA	 Alignment		8.5	25	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
11	d1jwya	 Alignment		8.4	17	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain

12	c3skdA_	Alignment		7.5	67	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein tthb187; PDBTitle: crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
13	d3bz7a1	Alignment		7.5	17	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
14	d2eyqa6	Alignment		7.2	9	Fold: TRCF domain-like Superfamily: TRCF domain-like Family: TRCF domain
15	c2ogiA_	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
16	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
17	c3ccgA_	Alignment		5.9	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
18	d2crda_	Alignment		5.8	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
19	c2qsrA_	Alignment		5.8	27	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
20	c4a1oB_	Alignment		5.7	16	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
21	c3rf1B_	Alignment	not modelled	5.6	17	PDB header: ligase Chain: B: PDB Molecule: glycyl-trna synthetase alpha subunit; PDBTitle: the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
22	c2l2ta_	Alignment	not modelled	5.5	19	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
23	c2levA_	Alignment	not modelled	5.5	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
24	c3a7oB_	Alignment	not modelled	5.3	29	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of the coiled-coil domain of2 saccharomyces cerevisiae atg16