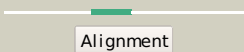

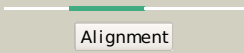

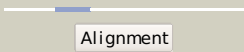

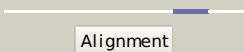

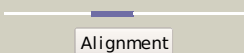





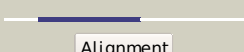
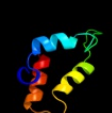
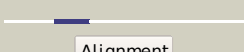

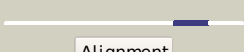

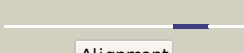

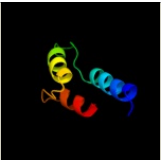


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c9pA_	 Alignment		45.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sp1917; PDBTitle: crystal structure of uncharacterized protein sp1917
2	c1a92B_	 Alignment		40.9	13	PDB header: leucine zipper Chain: B: PDB Molecule: delta antigen; PDBTitle: oligomerization domain of hepatitis delta antigen
3	d1k8ia2	 Alignment		23.2	31	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
4	d2bs2a1	 Alignment		13.4	38	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
5	d2fug61	 Alignment		10.5	9	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nqo6-like
6	c2jtvA_	 Alignment		10.4	20	PDB header: structural genomics Chain: A: PDB Molecule: protein of unknown function; PDBTitle: solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
7	c3izcH_	 Alignment		9.7	12	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein rp18 (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
8	c2vvyC_	 Alignment		9.4	16	PDB header: viral protein Chain: C: PDB Molecule: protein b15; PDBTitle: structure of vaccinia virus protein b14
9	d1hdma2	 Alignment		9.0	42	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
10	c1xkmC_	 Alignment		8.8	43	PDB header: antibiotic Chain: C: PDB Molecule: distinctin chain a; PDBTitle: nmr structure of antimicrobial peptide distinctin in water
11	c1xkmA_	 Alignment		8.7	43	PDB header: antibiotic Chain: A: PDB Molecule: distinctin chain a; PDBTitle: nmr structure of antimicrobial peptide distinctin in water

12	c2bpbB_	Alignment		7.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
13	d2glia5	Alignment		7.2	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
14	c2d35A_	Alignment		6.6	56	PDB header: cell cycle Chain: A: PDB Molecule: cell division activator ceda; PDBTitle: solution structure of cell division reactivation factor,2 ceda
15	c2bn8A_	Alignment		6.2	56	PDB header: cell cycle protein Chain: A: PDB Molecule: cell division activator ceda; PDBTitle: solution structure and interactions of the e.coli cell12 division activator protein ceda
16	c3e0zB_	Alignment		5.9	15	PDB header: unknown function Chain: B: PDB Molecule: protein of unknown function; PDBTitle: crystal structure of a putative imidazole glycerol phosphate synthase2 homolog (eubrec_1070) from eubacterium rectale at 1.75 a resolution
17	d1nsaa2	Alignment		5.6	12	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
18	c3rysA_	Alignment		5.5	8	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
19	c2y92A_	Alignment		5.3	11	PDB header: immune system Chain: A: PDB Molecule: toll/interleukin-1 receptor domain-containing adapter PDBTitle: crystal structure of mal adaptor protein



PDB header:transport protein
Chain: A: **PDB Molecule:**d7 protein;
PDBTitle: crystal structure of anst-d7I1