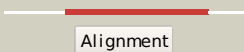
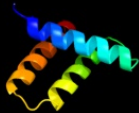
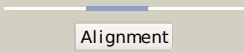
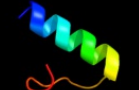

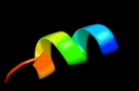
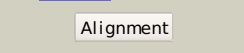



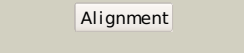
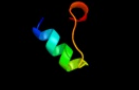
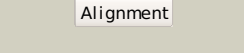

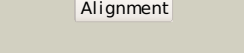



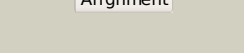
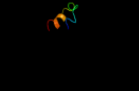
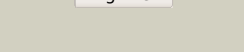








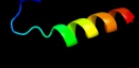



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oxlA_	 Alignment		99.9	98	PDB header: gene regulation Chain: A: PDB Molecule: hypothetical protein ymgb; PDBTitle: structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
2	c1stzB_	 Alignment		25.1	17	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
3	d1v92a_	 Alignment		15.5	42	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
4	c3ct5A_	 Alignment		13.4	19	PDB header: hydrolase Chain: A: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
5	c2bn5A_	 Alignment		11.2	37	PDB header: nuclear protein Chain: A: PDB Molecule: psi; PDBTitle: p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
6	d1stza1	 Alignment		10.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
7	c3gxvA_	 Alignment		10.3	20	PDB header: hydrolase/replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnaB2 helicase from helicobacter pylori and its interactions with3 primase
8	c2j8aA_	 Alignment		9.8	23	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: x-ray structure of the n-terminus rrm domain of set1
9	c3eyyA_	 Alignment		9.5	18	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
10	d1eiya1	 Alignment		8.9	22	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Phenylalanyl-tRNA synthetase (PheRS)
11	c2izpB_	 Alignment		8.9	16	PDB header: toxin Chain: B: PDB Molecule: putative membrane antigen; PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.

12	d2b3ya2	Alignment		8.6	29	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
13	d1ugpa_	Alignment		8.0	20	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
14	d1gotg_	Alignment		7.8	11	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
15	c3h8dE_	Alignment		7.7	45	PDB header: motor protein/signaling protein Chain: E: PDB Molecule: disabled homolog 2; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide
16	c3f1iH_	Alignment		7.6	20	PDB header: protein binding Chain: H: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: human escrt-0 core complex
17	d1acoa2	Alignment		7.3	29	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
18	c2dzlA_	Alignment		6.9	25	PDB header: structural genomics unknown function Chain: A: PDB Molecule: protein fam100b; PDBTitle: solution structure of the uba domain in human protein2 fam100b
19	d1q5za_	Alignment		6.8	38	Fold: Invasion protein A (SipA) , C-terminal actin binding domain Superfamily: Invasion protein A (SipA) , C-terminal actin binding domain Family: Invasion protein A (SipA) , C-terminal actin binding domain
20	c1q5zA_	Alignment		6.8	38	PDB header: cell invasion Chain: A: PDB Molecule: sipa; PDBTitle: crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa)
21	d2iy5a1	Alignment	not modelled	6.5	22	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Phenylalanyl-tRNA synthetase (PheRS)
22	d1mzba_	Alignment	not modelled	6.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
23	c2b3yB_	Alignment	not modelled	6.1	29	PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
24	c3csqC_	Alignment	not modelled	5.7	18	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
25	c2o8sA_	Alignment	not modelled	5.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_984p; PDBTitle: x-ray crystal structure of protein agr_c_984 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr120.
26	d1l5ja3	Alignment	not modelled	5.4	0	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
27	d2f76x1	Alignment	not modelled	5.2	17	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Mason-Pfizer monkey virus matrix protein