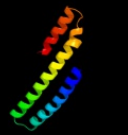
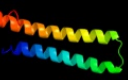
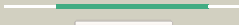
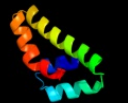
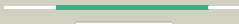
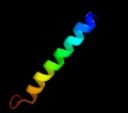
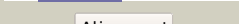
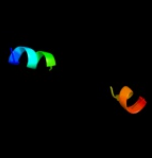
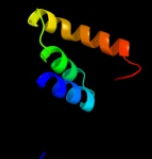
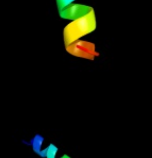
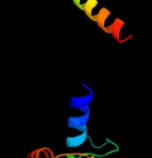
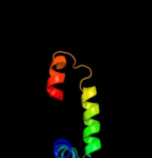
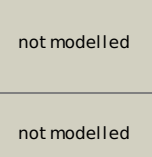
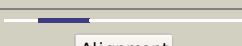
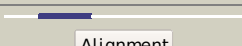
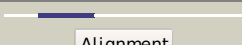
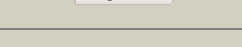
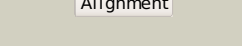


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hh7A_	 Alignment		99.9	26	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
2	c3aaiB_	 Alignment		99.9	22	PDB header: transcription Chain: B: PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
3	c1paqA_	 Alignment		41.5	14	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
4	d1paqa_	 Alignment		41.5	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
5	c2p5tA_	 Alignment		32.3	44	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator peza; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
6	c3juiA_	 Alignment		28.5	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
7	d1obba2	 Alignment		22.7	20	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
8	d1ivsa1	 Alignment		19.9	13	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
9	c3nepX_	 Alignment		19.4	18	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
10	c3frwF_	 Alignment		19.4	13	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trp protein from ruminococcus obeum
11	c2nv2U_	 Alignment		19.1	18	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis

12	c3zs9D_	Alignment		17.6	44	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
13	d1up7a2	Alignment		17.6	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
14	c2qycA_	Alignment		16.5	23	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
15	d1ev0a_	Alignment		14.1	25	Fold: Cell division protein MinE topological specificity domain Superfamily: Cell division protein MinE topological specificity domain Family: Cell division protein MinE topological specificity domain
16	c3cveC_	Alignment		11.8	25	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
17	c3korD_	Alignment		11.1	16	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
18	c2gtlO_	Alignment		10.2	19	PDB header: oxygen storage/transport Chain: O: PDB Molecule: extracellular hemoglobin linker l3 subunit; PDBTitle: lumbricus erythrocrurorin at 3.5a resolution
19	c4a1qB_	Alignment		9.8	16	PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
20	c3femB_	Alignment		9.0	24	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
21	c3ku7B_	Alignment	not modelled	8.3	25	PDB header: cell cycle Chain: B: PDB Molecule: cell division topological specificity factor; PDBTitle: crystal structure of helicobacter pylori mine, a cell division2 topological specificity factor
22	c1obbB_	Alignment	not modelled	8.0	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
23	d2hyec2	Alignment	not modelled	7.8	15	Fold: alpha-alpha superhelix Superfamily: Cullin repeat-like Family: Cullin repeat
24	d1tr0a_	Alignment	not modelled	7.8	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
25	d1q4ra_	Alignment	not modelled	7.8	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
26	d1sxjd1	Alignment	not modelled	7.6	5	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
27	d1qnaa2	Alignment	not modelled	7.2	7	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
28	c1up6F_	Alignment	not modelled	7.1	10	PDB header: hydrolase Chain: F: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate

29	d1cdwa2	 Alignment	not modelled	6.3	7	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
30	d1c2ya	 Alignment	not modelled	6.2	14	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
31	c2ovcA	 Alignment	not modelled	6.2	25	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
32	d1josa	 Alignment	not modelled	5.8	5	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
33	d1kkgA	 Alignment	not modelled	5.6	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
34	c2xa0C	 Alignment	not modelled	5.5	35	PDB header: apoptosis Chain: C: PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
35	c3bdeA	 Alignment	not modelled	5.2	25	PDB header: unknown function Chain: A: PDB Molecule: ml15499 protein; PDBTitle: crystal structure of a dabb family protein with a ferredoxin-like fold2 (ml15499) from mesorhizobium loti maff303099 at 1.79 a resolution
36	c3fajA	 Alignment	not modelled	5.2	5	PDB header: structural protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)
37	c3hugl	 Alignment	not modelled	5.1	23	PDB header: transcription/membrane protein Chain: J: PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
38	c2kxoA	 Alignment	not modelled	5.0	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae