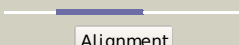
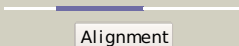
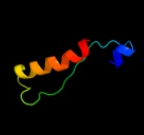
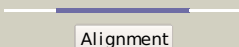
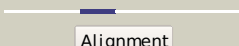
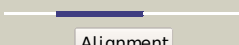
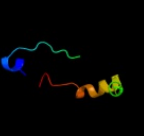
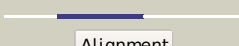
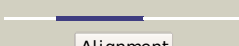
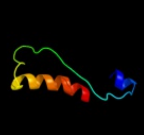
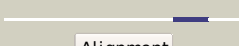
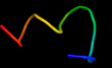
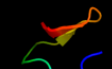
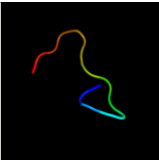


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlvkoa2	 Alignment		17.0	19	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
2	dlplja2	 Alignment		13.4	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
3	d2bgca1	 Alignment		10.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
4	dl1sisa_	 Alignment		9.5	46	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
5	dlvjpa2	 Alignment		9.0	14	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
6	c3cinA_	 Alignment		8.1	15	PDB header: isomerase Chain: A: PDB Molecule: myo-inositol-1-phosphate synthase-related protein; PDBTitle: crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
7	dlul1a2	 Alignment		7.8	31	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
8	c2pmzN_	 Alignment		7.1	50	PDB header: translation, transferase Chain: N: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
9	c2bgcA_	 Alignment		6.8	16	PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
10	c1vkoA_	 Alignment		6.8	20	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
11	dl1bwfi_	 Alignment		6.8	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10

12	d1chla_	Alignment		6.5	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
13	d1en2a2	Alignment		6.4	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
14	d1hqz1_	Alignment		6.4	19	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Cofilin-like
15	d1ehda2	Alignment		6.3	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
16	c3a1yF_	Alignment		6.2	50	PDB header: ribosomal protein Chain: F: PDB Molecule: 50s ribosomal protein p1 (l12p); PDBTitle: the structure of protein complex
17	d2hipa_	Alignment		5.8	32	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
18	d2a1ia1	Alignment		5.8	30	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XPB/Rad1/Mus81 nuclease

19 [dlhpia_](#)

Alignment



5.3

29

Fold:HIPIP (high potential iron protein)
Superfamily:HIPIP (high potential iron protein)
Family:HIPIP (high potential iron protein)