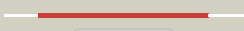
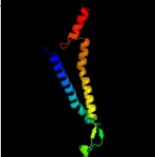
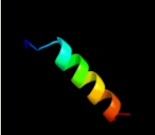
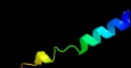
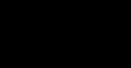
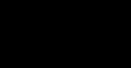


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oarA_	 Alignment		100.0	36	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
2	d2oara1	 Alignment		100.0	33	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
3	c3hzqA_	 Alignment		100.0	50	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscl in an expanded intermediate2 state
4	c3qngD_	 Alignment		82.2	14	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
5	d1q1va_	 Alignment		35.3	28	Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain
6	c1vdfB_	 Alignment		25.8	38	PDB header: extracellular matrix protein Chain: B: PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: assembly domain of cartilage oligomeric matrix protein
7	c3t98A_	 Alignment		18.9	41	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
8	d1lm8v_	 Alignment		17.8	38	Fold: Prealbumin-like Superfamily: VHL Family: VHL
9	c3n53B_	 Alignment		13.9	35	PDB header: transcription Chain: B: PDB Molecule: response regulator receiver modulated diguanylate cyclase; PDBTitle: crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
10	d1sh0a_	 Alignment		12.6	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
11	c2uutA_	 Alignment		11.5	29	PDB header: hydrolase Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: the 2.4 angstrom resolution structure of the d346g mutant2 of the sapporo virus rdrp polymerase

12	c2qzjC_	Alignment		11.4	23	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
13	c3snxB_	Alignment		10.7	16	PDB header: sugar binding protein Chain: B: PDB Molecule: putative susd-like carbohydrate binding protein; PDBTitle: crystal structure of a putative susd-like carbohydrate binding protein2 (bt_1439) from bacteroides thetaiotaomicron vpi-5482 at 1.88 a3 resolution
14	c1eysH_	Alignment		10.6	19	PDB header: electron transport Chain: H: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
15	c2b43D_	Alignment		10.5	12	PDB header: viral protein Chain: D: PDB Molecule: non-structural polyprotein; PDBTitle: crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
16	c2rddB_	Alignment		9.8	6	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
17	d1khva_	Alignment		9.1	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
18	c2l35B_	Alignment		8.4	15	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
19	c2l34B_	Alignment		8.0	15	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
20	c2l34A_	Alignment		8.0	15	PDB header: protein binding Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
21	c3p5nA_	Alignment	not modelled	7.4	18	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
22	c2jo1A_	Alignment	not modelled	6.6	26	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
23	c3nahC_	Alignment	not modelled	6.5	24	PDB header: transferase Chain: C: PDB Molecule: rna dependent rna polymerase; PDBTitle: crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
24	c2jp3A_	Alignment	not modelled	6.4	16	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
25	d1xr6a_	Alignment	not modelled	6.2	24	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
26	c1c94B_	Alignment	not modelled	6.1	36	PDB header: gene regulation Chain: B: PDB Molecule: retro-gcn4 leucine zipper; PDBTitle: reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
27	d2b3wa1	Alignment	not modelled	6.0	38	Fold: YbiA-like Superfamily: YbiA-like Family: YbiA-like
28	d1u09a_	Alignment	not modelled	5.8	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase

29	c3si5X_	Alignment	not modelled	5.8	38	PDB header: cell cycle Chain: X: PDB Molecule: protein casc5; PDBTitle: kinetochore-bubr1 kinase complex
30	c2ijjd1_	Alignment	not modelled	5.6	24	PDB header: hydrolase, transferase Chain: 1: PDB Molecule: picornain 3c, rna-directed rna polymerase; PDBTitle: crystal structure of the poliovirus precursor protein 3cd
31	d1xdpa1	Alignment	not modelled	5.5	14	Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like