


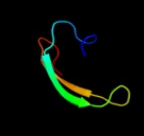

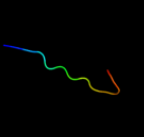

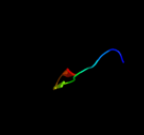

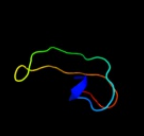

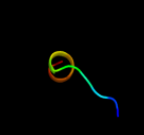





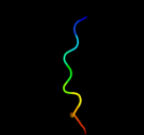



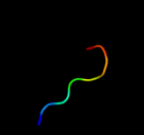


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sknp_	 Alignment		27.3	43	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
2	c3izcn_	 Alignment		24.1	38	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein rpl14 (l14e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
3	c2kd2A_	 Alignment		19.1	36	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of fain-ctd
4	c4a18P_	 Alignment		17.6	53	PDB header: ribosome Chain: P: PDB Molecule: rpl38; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
5	c3iz5n_	 Alignment		17.4	31	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l14 (l14e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
6	c2wfuA_	 Alignment		11.7	55	PDB header: signaling protein Chain: A: PDB Molecule: probable insulin-like peptide 5 a chain; PDBTitle: crystal structure of dilp5 variant db
7	c2wfvA_	 Alignment		11.7	55	PDB header: signaling protein Chain: A: PDB Molecule: probable insulin-like peptide 5 a chain; PDBTitle: crystal structure of dilp5 variant c4
8	c2kz5A_	 Alignment		11.1	48	PDB header: transcription Chain: A: PDB Molecule: transcription factor nf-e2 45 kda subunit; PDBTitle: solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
9	c2v1lA_	 Alignment		8.4	27	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
10	c1o7dD_	 Alignment		7.8	56	PDB header: hydrolase Chain: D: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
11	d1qz8a_	 Alignment		7.6	63	Fold: Replicase NSP9 Superfamily: Replicase NSP9 Family: Replicase NSP9

12	c2w56B_	Alignment		7.6	27	PDB header: unknown function Chain: B: PDB Molecule: vc0508; PDBTitle: structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
13	c2j98A_	Alignment		7.2	50	PDB header: rna-binding protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: human coronavirus 229e non structural protein 9 cys69ala2 mutant (nsp9)
14	c1uw7A_	Alignment		7.2	63	PDB header: replicase protein Chain: A: PDB Molecule: nsp9; PDBTitle: nsp9 protein from sars-coronavirus.
15	d2j7ja3	Alignment		6.6	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
16	c2dzqA_	Alignment		6.3	44	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
17	c3kz0D_	Alignment		6.2	70	PDB header: apoptosis Chain: D: PDB Molecule: mcl-1 specific peptide mb7; PDBTitle: mcl-1 complex with mcl-1-specific selected peptide
18	c3kz0C_	Alignment		6.2	70	PDB header: apoptosis Chain: C: PDB Molecule: mcl-1 specific peptide mb7; PDBTitle: mcl-1 complex with mcl-1-specific selected peptide
19	c2dn5A_	Alignment		6.1	56	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
20	c4a18A_	Alignment		6.1	39	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein l37; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of molecule 1
21	d1q60a_	Alignment	not modelled	5.8	44	Fold: GTF2I-like repeat Superfamily: GTF2I-like repeat Family: GTF2I-like repeat
22	c2ed2A_	Alignment	not modelled	5.8	44	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
23	c2dn4A_	Alignment	not modelled	5.7	44	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
24	c2d99A_	Alignment	not modelled	5.4	44	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna