

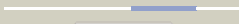
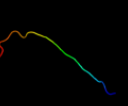

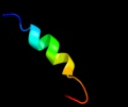

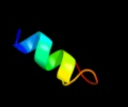














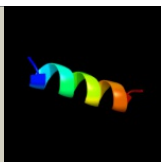


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2diiA_	 Alignment		28.2	47	PDB header: transcription Chain: A: PDB Molecule: tftih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tftih basal2 transcription factor complex p62 subunit
2	c3p9vA_	 Alignment		27.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197
3	d2diia1	 Alignment		24.7	47	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
4	d1zu1a1	 Alignment		23.4	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
5	c2qwub_	 Alignment		12.1	25	PDB header: cell invasion Chain: B: PDB Molecule: intracellular growth locus, subunit c; PDBTitle: crystal structure of f. tularensis pathogenicity island2 protein c
6	d1y3na1	 Alignment		11.5	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	d1k78a2	 Alignment		8.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
8	c2l76A_	 Alignment		7.4	6	PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
9	d1p42a1	 Alignment		6.5	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
10	c3i38B_	 Alignment		6.5	25	PDB header: chaperone Chain: B: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
11	d6paxa2	 Alignment		6.0	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain

12

[c2o7hF_](#)

Alignment



5.4

38

PDB header:transcription
Chain: F: **PDB Molecule:**general control protein gcn4;
PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper