
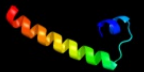


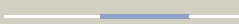

















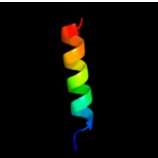

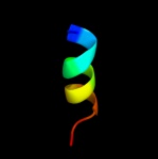

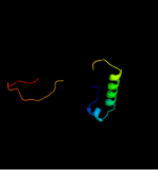


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bhpA_</a>	 Alignment		40.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynz; <b>PDBTitle:</b> crystal structure of upf0291 protein ynz from bacillus subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
2	<a href="#">d1t08b_</a>	 Alignment		32.0	36	<b>Fold:</b> beta-catenin-interacting protein ICAT <b>Superfamily:</b> beta-catenin-interacting protein ICAT <b>Family:</b> beta-catenin-interacting protein ICAT
3	<a href="#">d1m1eb_</a>	 Alignment		25.8	33	<b>Fold:</b> beta-catenin-interacting protein ICAT <b>Superfamily:</b> beta-catenin-interacting protein ICAT <b>Family:</b> beta-catenin-interacting protein ICAT
4	<a href="#">d1st6a5</a>	 Alignment		18.4	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
5	<a href="#">d1lujb_</a>	 Alignment		18.2	36	<b>Fold:</b> beta-catenin-interacting protein ICAT <b>Superfamily:</b> beta-catenin-interacting protein ICAT <b>Family:</b> beta-catenin-interacting protein ICAT
6	<a href="#">c2vn2B_</a>	 Alignment		13.8	40	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dna protein2 from geobacillus kaustophilus hta426
7	<a href="#">c1uixA_</a>	 Alignment		13.4	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rho-associated kinase; <b>PDBTitle:</b> coiled-coil structure of the rho-binding domain in rho-2 kinase
8	<a href="#">c3layF_</a>	 Alignment		13.1	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> zinc resistance-associated protein; <b>PDBTitle:</b> alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. It2
9	<a href="#">c2jvdA_</a>	 Alignment		11.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynz; <b>PDBTitle:</b> solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynz from bacillus subtilis. northeast3 structural genomics target sr384-1-46
10	<a href="#">d2fupa1</a>	 Alignment		10.9	13	<b>Fold:</b> STAT-like <b>Superfamily:</b> FlgN-like <b>Family:</b> FlgN-like
11	<a href="#">c2fupA_</a>	 Alignment		10.9	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa3352; <b>PDBTitle:</b> crystal structure of a putative flagella synthesis protein flgn2 (pa3352) from pseudomonas aeruginosa at 1.48 a resolution

12	<a href="#">c1rh4A_</a>	Alignment		7.8	56	<b>PDB header:</b> coiled coil <b>Chain:</b> A: <b>PDB Molecule:</b> right-handed coiled coil tetramer; <b>PDBTitle:</b> rh4 designed right-handed coiled coil tetramer
13	<a href="#">c3qsqA_</a>	Alignment		7.0	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid polyprotein; <b>PDBTitle:</b> crystal structure of the projection domain of the human astrovirus2 capsid protein
14	<a href="#">c1hbwA_</a>	Alignment		7.0	46	<b>PDB header:</b> transcriptional activator <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein gal4; <b>PDBTitle:</b> solution nmr structure of the dimerization domain of the2 yeast transcriptional activator gal4 (residues 50-106)
15	<a href="#">c1s1hO_</a>	Alignment		6.9	16	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 40s ribosomal protein s13; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
16	<a href="#">d1nb4a_</a>	Alignment		5.7	24	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase

17	<a href="#">c3aapA</a>	Alignment		5.5	26	<p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>ectonucleoside triphosphate diphosphohydrolase i;</p> <p><b>PDBTitle:</b> crystal structure of Ip1ntpdase from legionella pneumophila</p>
----	------------------------	-----------	--	-----	----	--