



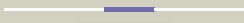
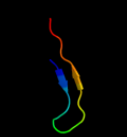

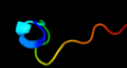



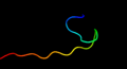

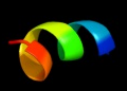



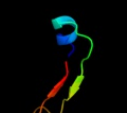



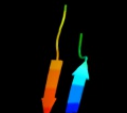

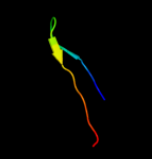
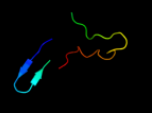



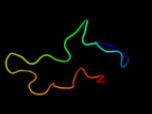
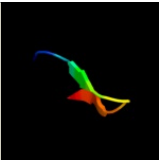


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2hja1</a>	 Alignment		100.0	57	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain <b>Family:</b> YkfF-like
2	<a href="#">c2hja_</a>	 Alignment		100.0	57	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ykff; <b>PDBTitle:</b> solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
3	<a href="#">c1xs3A_</a>	 Alignment		13.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein xc975; <b>PDBTitle:</b> solution structure analysis of the xc975 protein
4	<a href="#">dl1ioa_</a>	 Alignment		12.9	33	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> Hypothetical protein MTH865 <b>Family:</b> Hypothetical protein MTH865
5	<a href="#">c3isyA_</a>	 Alignment		11.7	35	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor; <b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
6	<a href="#">c3tr3A_</a>	 Alignment		11.0	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bola; <b>PDBTitle:</b> structure of a bola protein homologue from coxiella burnetii
7	<a href="#">c1yewF_</a>	 Alignment		9.5	33	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> particulate methane monooxygenase, a subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
8	<a href="#">dlr1ga_</a>	 Alignment		9.1	13	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
9	<a href="#">c2dhmA_</a>	 Alignment		9.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein bola; <b>PDBTitle:</b> solution structure of the bola protein from escherichia coli
10	<a href="#">c2zt9F_</a>	 Alignment		8.1	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
11	<a href="#">c3o2eA_</a>	 Alignment		8.1	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein; <b>PDBTitle:</b> crystal structure of a bol-like protein from babesia bovis

12	<a href="#">c2kdnA_</a>	Alignment		7.6	27	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein pfe0790c; <b>PDBTitle:</b> solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
13	<a href="#">c2q2eB_</a>	Alignment		7.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazel
14	<a href="#">dlrwha3</a>	Alignment		7.2	23	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain
15	<a href="#">c3chxF_</a>	Alignment		7.0	33	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> pmoa; <b>PDBTitle:</b> crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
16	<a href="#">dlk1sa1</a>	Alignment		6.6	16	<b>Fold:</b> Lesion bypass DNA polymerase (Y-family), little finger domain <b>Superfamily:</b> Lesion bypass DNA polymerase (Y-family), little finger domain <b>Family:</b> Lesion bypass DNA polymerase (Y-family), little finger domain
17	<a href="#">dlv9ja_</a>	Alignment		5.3	40	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> BolA-like <b>Family:</b> BolA-like
18	<a href="#">dlf1sa4</a>	Alignment		5.2	20	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain

19 [d2zgwa1](#)

Alignment



5.2

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**Fold:**SH3-like barrel  
**Superfamily:**C-terminal domain of transcriptional repressors  
**Family:**Biotin repressor (BirA)