



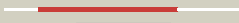














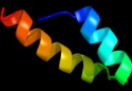




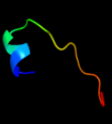
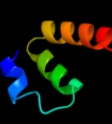
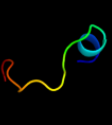
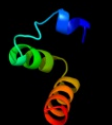





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2o9xa1</a>	 Alignment		100.0	24	<b>Fold:</b> TorD-like <b>Superfamily:</b> TorD-like <b>Family:</b> TorD-like
2	<a href="#">c2o9xA</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> reductase, assembly protein; <b>PDBTitle:</b> crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
3	<a href="#">d1n1ca</a>	 Alignment		99.9	22	<b>Fold:</b> TorD-like <b>Superfamily:</b> TorD-like <b>Family:</b> TorD-like
4	<a href="#">d1s9ua</a>	 Alignment		99.9	17	<b>Fold:</b> TorD-like <b>Superfamily:</b> TorD-like <b>Family:</b> TorD-like
5	<a href="#">d2idga1</a>	 Alignment		98.6	23	<b>Fold:</b> TorD-like <b>Superfamily:</b> TorD-like <b>Family:</b> TorD-like
6	<a href="#">d1lvaa3</a>	 Alignment		28.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
7	<a href="#">c3ol4B</a>	 Alignment		17.2	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
8	<a href="#">c2di4B</a>	 Alignment		14.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh homolog; <b>PDBTitle:</b> crystal structure of the ftsh protease domain
9	<a href="#">d2ce7a1</a>	 Alignment		11.1	15	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
10	<a href="#">d2ejna2</a>	 Alignment		8.2	22	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
11	<a href="#">d2d6fc2</a>	 Alignment		7.9	27	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain

12	<a href="#">c2kvcA_</a>	Alignment		7.6	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
13	<a href="#">d2g3aa1</a>	Alignment		7.5	28	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
14	<a href="#">d1ghea_</a>	Alignment		7.3	28	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
15	<a href="#">c3ka1A_</a>	Alignment		7.1	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rbcx protein; <b>PDBTitle:</b> crystal structure of rbcx from thermosynechococcus elongatus
16	<a href="#">d1yx0a1</a>	Alignment		6.9	28	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
17	<a href="#">c2penE_</a>	Alignment		6.6	18	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> orf134; <b>PDBTitle:</b> crystal structure of rbcx, crystal form i
18	<a href="#">d2peqa1</a>	Alignment		6.5	18	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like
19	<a href="#">c2g9mB_</a>	Alignment		6.5	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> phycoerythrin; <b>PDBTitle:</b> crystal structure of the pigment protein phycoerythrin from2 cyanobacterium at 2.6a resolution
20	<a href="#">c2lkyA_</a>	Alignment		5.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msme_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
21	<a href="#">d2py8a1</a>	Alignment	not modelled	5.9	18	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like
22	<a href="#">c3n4sC_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> monopolin complex subunit csm1; <b>PDBTitle:</b> structure of csm1 c-terminal domain, p21212 form
23	<a href="#">c3lisB_</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> csp231i c protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
24	<a href="#">c2r7hA_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative d-alanine n-acetyltransferase of gnat family; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution
25	<a href="#">c2py8B_</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rbxc; <b>PDBTitle:</b> rbxc
26	<a href="#">d1qaza_</a>	Alignment	not modelled	5.3	29	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Chondroitin AC/alginate lyase <b>Family:</b> Alginate lyase A1-III