










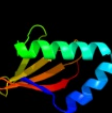



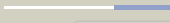
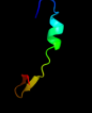





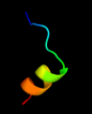







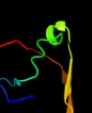










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2a6sa1</a>	 Alignment		100.0	100	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> YoeB/Txe-like
2	<a href="#">c3oeiH_</a>	 Alignment		100.0	46	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> relk (toxin rv3358); <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
3	<a href="#">dlz8ma1</a>	 Alignment		99.8	19	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> RelE-like
4	<a href="#">c2otrA_</a>	 Alignment		99.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hp0892; <b>PDBTitle:</b> solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
5	<a href="#">c2kheA_</a>	 Alignment		99.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> toxin-like protein; <b>PDBTitle:</b> solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
6	<a href="#">c3bpgD_</a>	 Alignment		99.3	13	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> toxin rele3; <b>PDBTitle:</b> crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
7	<a href="#">c3g5oC_</a>	 Alignment		99.3	25	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein rv2866; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
8	<a href="#">dlwmia1</a>	 Alignment		99.3	14	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> RelE-like
9	<a href="#">c3kixy_</a>	 Alignment		98.6	15	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)
10	<a href="#">c3kxeB_</a>	 Alignment		97.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> toxin protein pare-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
11	<a href="#">d2p2ea1</a>	 Alignment		32.3	7	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain <b>Family:</b> HesB-like domain

12	<a href="#">c2qgoA</a>	 Alignment		31.9	7	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative fe-s biosynthesis protein; <b>PDBTitle:</b> crystal structure of a putative fe-s biosynthesis protein from <i>Lactobacillus acidophilus</i>
13	<a href="#">d3bb9a1</a>	 Alignment		24.1	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
14	<a href="#">d2qn6a2</a>	 Alignment		22.0	36	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
15	<a href="#">d1s0ua2</a>	 Alignment		21.9	45	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
16	<a href="#">c2l09A</a>	 Alignment		20.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> asr4154 protein; <b>PDBTitle:</b> solution nmr structure of protein asr4154 from <i>Nostoc sp. pcc71202</i> northeast structural genomics consortium target id nsr143
17	<a href="#">d1kk1a2</a>	 Alignment		20.5	45	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
18	<a href="#">d3e9va1</a>	 Alignment		17.7	15	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
19	<a href="#">c1wmvA</a>	 Alignment		16.2	18	<b>PDB header:</b> oxidoreductase, apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> ww domain containing oxidoreductase; <b>PDBTitle:</b> solution structure of the second ww domain of wwox
20	<a href="#">c2dogA</a>	 Alignment		14.5	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable 16s rRNA-processing protein rimm; <b>PDBTitle:</b> solution structure of the n-terminal domain of rimm from <i>Thermus2 thermophilus</i> hb8
21	<a href="#">d2ux0a1</a>	 Alignment	not modelled	13.6	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
22	<a href="#">c2kruA</a>	 Alignment	not modelled	13.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> solution nmr structure of the pcpr_red domain of light-2 independent protochlorophyllide reductase subunit b from <i>Chlorobium tepidum</i> northeast structural genomics4 consortium target ctr69a (casp target)
23	<a href="#">c2apnA</a>	 Alignment	not modelled	13.1	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hi1723; <b>PDBTitle:</b> hi1723 solution structure
24	<a href="#">d1khba2</a>	 Alignment	not modelled	13.0	28	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
25	<a href="#">d2z15a1</a>	 Alignment	not modelled	11.5	29	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
26	<a href="#">c3sjaG</a>	 Alignment	not modelled	10.3	16	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> golgi to er traffic protein 1; <b>PDBTitle:</b> crystal structure of <i>S. cerevisiae</i> get3 in the open state in complex2 with get1 cytosolic domain
27	<a href="#">d2f86b1</a>	 Alignment	not modelled	8.6	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
28	<a href="#">d1hkva</a>	 Alignment	not modelled	8.5	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like

28	<a href="#">d1tkaa_</a>	Alignment	not modelled	8.3	42	<b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
29	<a href="#">c2l4ja_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yes-associated protein 2 (yap2); <b>PDBTitle:</b> yap ww2
30	<a href="#">c3hx8a_</a>	Alignment	not modelled	8.4	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase2 (np_103587.1) from mesorhizobium loti at 1.45 a resolution
31	<a href="#">d1jtma_</a>	Alignment	not modelled	8.2	13	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage Lysozyme
32	<a href="#">c3sjbC_</a>	Alignment	not modelled	8.1	14	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> golgi to er traffic protein 1; <b>PDBTitle:</b> crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
33	<a href="#">d1p5ca_</a>	Alignment	not modelled	7.8	11	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage Lysozyme
34	<a href="#">c3q9cF_</a>	Alignment	not modelled	7.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> acetyl polyamine amidohydrolase; <b>PDBTitle:</b> crystal structure of h159a apah complexed with n8-acetylspermidine
35	<a href="#">c3robC_</a>	Alignment	not modelled	7.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from plantomyces2 limnophilus dsm 3776
36	<a href="#">c2qeyA_</a>	Alignment	not modelled	6.5	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase, cytosolic [gtp]; <b>PDBTitle:</b> rat cytosolic pepck in complex with gtp
37	<a href="#">d1nwba_</a>	Alignment	not modelled	5.7	0	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain <b>Family:</b> HesB-like domain
38	<a href="#">c2fh0A_</a>	Alignment	not modelled	5.6	6	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 16.0 kda protein in abf2-chl12 <b>PDBTitle:</b> nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
39	<a href="#">d2jb0b1</a>	Alignment	not modelled	5.2	11	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
40	<a href="#">d1eiia_</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Double-stranded DNA-binding domain <b>Family:</b> Double-stranded DNA-binding domain
41	<a href="#">d1tbga_</a>	Alignment	not modelled	5.2	12	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
42	<a href="#">c2awyB_</a>	Alignment	not modelled	5.1	30	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> B: <b>PDB Molecule:</b> hemerythrin-like domain protein dcrh; <b>PDBTitle:</b> met-dcrh-hr