



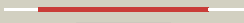








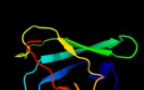






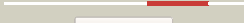



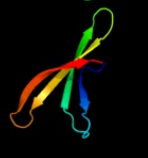

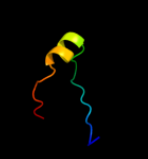
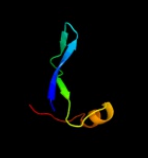
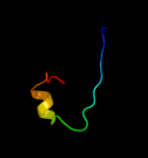
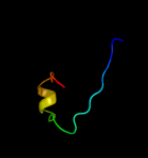



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h9nA_</a>	 Alignment		100.0	66	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome maturation factor rimm; <b>PDBTitle:</b> crystal structure of the ribosome maturation factor rimm2 (hi0203) from h.influenzae. northeast structural genomics3 consortium target ir66.
2	<a href="#">c2f1lA_</a>	 Alignment		100.0	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rRNA processing protein; <b>PDBTitle:</b> crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
3	<a href="#">c2qggA_</a>	 Alignment		100.0	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rRNA-processing protein rimm; <b>PDBTitle:</b> x-ray structure of the protein q6f7i0 from acinetobacter2 calcoaceticus amms 248. northeast structural genomics3 consortium target asr73.
4	<a href="#">c2dyiA_</a>	 Alignment		100.0	30	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> probable 16s rRNA-processing protein rimm; <b>PDBTitle:</b> crystal structure of 16s ribosomal rna processing protein rimm from2 thermus thermophilus hb8
5	<a href="#">d2f1la2</a>	 Alignment		100.0	39	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> RimM N-terminal domain-like
6	<a href="#">c2dogA_</a>	 Alignment		99.9	21	<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 thermus2 thermophilus hb8
7	<a href="#">d2f1la1</a>	 Alignment		99.9	39	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> RimM C-terminal domain-like
8	<a href="#">c3htrB_</a>	 Alignment		97.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized prc-barrel domain protein; <b>PDBTitle:</b> crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris
9	<a href="#">d1eysh1</a>	 Alignment		97.4	27	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
10	<a href="#">c1eysH_</a>	 Alignment		97.4	27	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
11	<a href="#">d1rzhh1</a>	 Alignment		96.9	27	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain

12	<a href="#">c1k6nH_</a>	Alignment		96.8	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center h subunit; <b>PDBTitle:</b> e(l1212)a,d(l1213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
13	<a href="#">d2i5nh1</a>	Alignment		96.8	24	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
14	<a href="#">c2i5nH_</a>	Alignment		96.7	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
15	<a href="#">d1pm3a_</a>	Alignment		94.4	22	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> MTH1895
16	<a href="#">d1sqra_</a>	Alignment		81.4	36	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Ribosomal protein L35ae
17	<a href="#">c4a1dH_</a>	Alignment		80.5	10	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> rpl35a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of3 molecule 4.
18	<a href="#">c3izcj_</a>	Alignment		72.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein rpl12 (l11p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
19	<a href="#">c3iz5j_</a>	Alignment		70.9	11	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l12 (l11p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
20	<a href="#">c2hvyB_</a>	Alignment		68.6	18	<b>PDB header:</b> isomerase/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> small nucleolar rnp similar to gar1; <b>PDBTitle:</b> crystal structure of an h/aca box rnp from pyrococcus furiosus
21	<a href="#">d2ey4c1</a>	Alignment	not modelled	63.4	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Gar1-like SnoRNP
22	<a href="#">c3uaiC_</a>	Alignment	not modelled	60.5	13	<b>PDB header:</b> isomerase/chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 1; <b>PDBTitle:</b> structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
23	<a href="#">c2ro0A_</a>	Alignment	not modelled	53.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase esa1; <b>PDBTitle:</b> solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
24	<a href="#">c2kk4A_</a>	Alignment	not modelled	40.2	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af_2094; <b>PDBTitle:</b> solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consortium (nesg)3 target gt2
25	<a href="#">c2eqnA_</a>	Alignment	not modelled	22.4	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein loc92345; <b>PDBTitle:</b> solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]
26	<a href="#">d1wb1a2</a>	Alignment	not modelled	15.2	36	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
27	<a href="#">d1fxkc_</a>	Alignment	not modelled	13.8	27	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
28	<a href="#">d1qhka_</a>	Alignment	not modelled	11.7	13	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> L9 N-domain-like <b>Family:</b> N-terminal domain of RNase HI

29	<a href="#">c3h9wA_</a>	Alignment	not modelled	11.6	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase with pas/pac sensor; <b>PDBTitle:</b> crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
30	<a href="#">d2b78a1</a>	Alignment	not modelled	10.4	21	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
31	<a href="#">c2rnzA_</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase esa1; <b>PDBTitle:</b> solution structure of the presumed chromodomain of the2 yeast histone acetyltransferase, esa1
32	<a href="#">c2pdtD_</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> circadian clock protein <b>Chain:</b> D: <b>PDB Molecule:</b> vivid pas protein vvd; <b>PDBTitle:</b> 2.3 angstrom structure of phosphodiesterase treated vivid
33	<a href="#">c2v3mF_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> ribosomal protein <b>Chain:</b> F: <b>PDB Molecule:</b> naf1; <b>PDBTitle:</b> structure of the gar1 domain of naf1
34	<a href="#">c3ml6D_</a>	Alignment	not modelled	8.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> chimeric complex between protein dishevelled2 homolog dvl-2 <b>PDBTitle:</b> a complex between dishevelled2 and clathrin adaptor ap-2
35	<a href="#">d1bywa_</a>	Alignment	not modelled	7.3	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
36	<a href="#">c2l4rA_</a>	Alignment	not modelled	7.2	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> nmr solution structure of the n-terminal pas domain of herg
37	<a href="#">c3ewkA_</a>	Alignment	not modelled	7.0	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
38	<a href="#">c2gj3A_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen fixation regulatory protein; <b>PDBTitle:</b> crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.
39	<a href="#">c3mxqC_</a>	Alignment	not modelled	6.1	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
40	<a href="#">d1n9la_</a>	Alignment	not modelled	5.8	21	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
41	<a href="#">c3kxrA_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transporter, putative; <b>PDBTitle:</b> structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
42	<a href="#">d2f5ka1</a>	Alignment	not modelled	5.6	4	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo barrel domain
43	<a href="#">c3gbyA_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ct1051; <b>PDBTitle:</b> crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
44	<a href="#">c2w7aA_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> line-1 orf1p; <b>PDBTitle:</b> structure of the human line-1 orf1p central domain
45	<a href="#">c3luqC_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a
46	<a href="#">c2zdiC_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> prefoldin subunit alpha; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
47	<a href="#">c3l3lB_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable manganase-dependent inorganic <b>PDBTitle:</b> crystal structure of the cbs and drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
48	<a href="#">c3oi8B_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58