


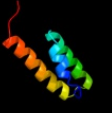

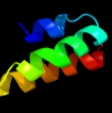
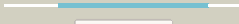
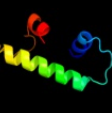




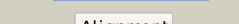

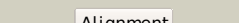

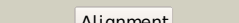



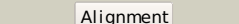



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dljw2a_</a>	 Alignment		100.0	40	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Hemolysin expression modulating protein HHA <b>Family:</b> Hemolysin expression modulating protein HHA
2	<a href="#">c2jqta_</a>	 Alignment		99.9	100	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> h-ns/stpa-binding protein 2; <b>PDBTitle:</b> structure of the bacterial replication origin-associated2 protein cnu
3	<a href="#">c2jpnA_</a>	 Alignment		36.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase uvsw; <b>PDBTitle:</b> solution structure of t4 bacteriophage helicase uvsw.1
4	<a href="#">c3jvoA_</a>	 Alignment		31.9	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp6; <b>PDBTitle:</b> crystal structure of bacteriophage hk97 gp6
5	<a href="#">d1lr1a_</a>	 Alignment		28.0	25	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
6	<a href="#">c3ke4B_</a>	 Alignment		25.2	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical cytosolic protein; <b>PDBTitle:</b> crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus
7	<a href="#">c2idxA_</a>	 Alignment		23.6	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cob(i)yrinic acid a,c-diamide <b>PDBTitle:</b> structure of human atp:cobalamin adenosyltransferase bound2 to atp.
8	<a href="#">d1trra_</a>	 Alignment		23.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
9	<a href="#">d1ej2a_</a>	 Alignment		21.8	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
10	<a href="#">d1jhga_</a>	 Alignment		12.8	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
11	<a href="#">c3cvfA_</a>	 Alignment		11.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> homer protein homolog 3; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer3

12	<a href="#">c3d0jA_</a>	Alignment		10.6	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ca_c3497; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
13	<a href="#">c2g2dA_</a>	Alignment		10.3	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp:cobalamin adenosyltransferase; <b>PDBTitle:</b> crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
14	<a href="#">c3cm8A_</a>	Alignment		9.8	18	<b>PDB header:</b> rna binding protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase acidic protein; <b>PDBTitle:</b> a rna polymerase subunit structure from virus
15	<a href="#">d1t07a_</a>	Alignment		9.7	19	<b>Fold:</b> YggX-like <b>Superfamily:</b> YggX-like <b>Family:</b> YggX-like
16	<a href="#">d1xs8a_</a>	Alignment		9.4	38	<b>Fold:</b> YggX-like <b>Superfamily:</b> YggX-like <b>Family:</b> YggX-like
17	<a href="#">c3i5qA_</a>	Alignment		9.3	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin nup170; <b>PDBTitle:</b> nup170(aa1253-1502) at 2.2 a, s.cerevisiae
18	<a href="#">c2rbgB_</a>	Alignment		8.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein st0493; <b>PDBTitle:</b> crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
19	<a href="#">c1nybA_</a>	Alignment		8.5	42	<b>PDB header:</b> transcription/rna <b>Chain:</b> A: <b>PDB Molecule:</b> probable regulatory protein n; <b>PDBTitle:</b> solution structure of the bacteriophage phi21 n peptide-boxb2 rna complex
20	<a href="#">d1dd4c_</a>	Alignment		8.4	26	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
21	<a href="#">d1od6a_</a>	Alignment	not modelled	8.2	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyllyltransferase
22	<a href="#">c2nt8A_</a>	Alignment	not modelled	7.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin adenosyltransferase; <b>PDBTitle:</b> atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
23	<a href="#">c2zhzC_</a>	Alignment	not modelled	7.7	31	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> atp:cob(i)alamin adenosyltransferase, putative; <b>PDBTitle:</b> crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
24	<a href="#">c3nd5D_</a>	Alignment	not modelled	7.5	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphopantetheine adenyllyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenyllyltransferase (ppat)2 from enterococcus faecalis
25	<a href="#">d1vlha_</a>	Alignment	not modelled	7.5	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyllyltransferase
26	<a href="#">d1ni8a_</a>	Alignment	not modelled	7.2	21	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
27	<a href="#">d1uhra_</a>	Alignment	not modelled	7.1	21	<b>Fold:</b> SWIB/MDM2 domain <b>Superfamily:</b> SWIB/MDM2 domain <b>Family:</b> SWIB/MDM2 domain
28	<a href="#">c2h29A_</a>	Alignment	not modelled	7.0	60	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenyllyltransferase from staphylococcus aureus: product3 bound

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29	<a href="#">c3frwF_</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trp protein from ruminococcus obeum
30	<a href="#">d1f3ua_</a>	Alignment	not modelled	6.7	40	<b>Fold:</b> triple barrel <b>Superfamily:</b> Rap30/74 interaction domains <b>Family:</b> Rap30/74 interaction domains
31	<a href="#">d1tfua_</a>	Alignment	not modelled	6.4	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyl transferase
32	<a href="#">d1i27a_</a>	Alignment	not modelled	6.1	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of the rap74 subunit of TFIIIF
33	<a href="#">d1v31a_</a>	Alignment	not modelled	5.9	21	<b>Fold:</b> SWIB/MDM2 domain <b>Superfamily:</b> SWIB/MDM2 domain <b>Family:</b> SWIB/MDM2 domain
34	<a href="#">c1dd3D_</a>	Alignment	not modelled	5.9	26	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> crystal structure of ribosomal protein l12 from thermotoga maritima
35	<a href="#">c1dd3C_</a>	Alignment	not modelled	5.9	26	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> crystal structure of ribosomal protein l12 from thermotoga maritima
36	<a href="#">c3f3mA_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenyl transferase; <b>PDBTitle:</b> six crystal structures of two phosphopantetheine2 adenyl transferases reveal an alternative ligand binding3 mode and an associated structural change
37	<a href="#">d1o6ba_</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyl transferase
38	<a href="#">c2l3lA_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin-specific chaperone c; <b>PDBTitle:</b> the solution structure of the n-terminal domain of human tubulin2 binding cofactor c reveals a platform for the interaction with ab-3 tubulin
39	<a href="#">c1zawV_</a>	Alignment	not modelled	5.5	26	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
40	<a href="#">c2kngA_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> solution structure of c-domain of lsr2
41	<a href="#">c3korD_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
42	<a href="#">d1qjca_</a>	Alignment	not modelled	5.3	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyl transferase
43	<a href="#">c1zawW_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
44	<a href="#">c1zawU_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
45	<a href="#">c1xhmB_</a>	Alignment	not modelled	5.2	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-binding protein g(i)/g(s) <b>PDBTitle:</b> the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
46	<a href="#">c1zaxV_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
47	<a href="#">c1zavV_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
48	<a href="#">c1zaxY_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
49	<a href="#">c1zavW_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
50	<a href="#">c1zaxW_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
51	<a href="#">c1zavX_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> structural protein <b>Chain:</b> X: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21