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Comparative modeling of the N-terminal domain of the 67 kDa laminin-binding protein: implications for putative ribosomal function

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Abstract

Laminin-binding protein/p40 (LBP/p40) precursor appears to be involved in two seemingly unrelated activities—cell adhesion and ribosomal biogenesis. Analysis of primary structure revealed a two-domain organization of the LBP/p40. The N-terminal portion of LBP is similar to the S2 family of prokaryotic ribosomal proteins, while the C-terminus is unique for *Metazoa* and is involved in extraribosomal functions. To gain insight into putative ribosomal functions of LBP we performed comparative modeling of the N-terminal domain using crystal structures of S2p from *Thermus thermophilus*. The LBP model assumes an α–β sandwich fold similar to that of S2. Modeling revealed the loss of a significant portion of ribosomal RNA (rRNA) interaction domain, lack of conservation of many residues involved in interactions with rRNA, and a major shift in surface charge distribution (compared to the S2 protein). The overall stability of the fold argues against a proposed transmembrane domain in the central part of the protein. Partial overlap in S2 and laminin-binding domains suggests that ribosomal and surface receptor functions would be mutually exclusive. The possible biological role of LBP/p40 bifunctionality is discussed.

Keywords: Translation; Structure prediction; Laminin; Receptor; Cancer; Ribosome; Ribosomal proteins

Multifunctional proteins engaged in different, often unrelated activities, facilitate coordinated responses to biological events across cellular compartments. A specific environment in various cellular compartments often triggers a switch between alternative functions [1]. Many ribosomal proteins are involved in various extraribosomal activities such as replication, transcription, RNA processing, and DNA repair [2]. Ribosomal protein p40/laminin-binding protein (LBP/p40) provides a striking example of such a functional diversity. Cell surface-expressed LBP, presumably a homodimer of 32 kDa subunits [3], referred to as 67 kDa LBP, mediates interactions of the cell with laminin-1, a protein of the extracellular matrix [4–6]. Intracellular LBP in the monomeric form and its homologues have been found in the small ribosomal subunit and polysomes [7,8]. Thus, LBP/p40 appears to be engaged in two seemingly unrelated activities—cell adhesion and ribosomal assembly and maintenance.

The likely dual function of the LBP has been debated for many years. Previous biochemical studies and phylogenetic analysis have ascribed these functions to non-overlapping domains of LBP [9]. All documented laminin-1 interaction sites reside in the C-terminal one-third (residues 161–295), which is unique for *Metazoa* and is involved in extracellular functions [3,5,10], while the N-terminal portion of the protein (residues 13–161), which is the region that is characteristic of the S2/Sae family of ribosomal proteins (PFAM family F00318), is presumably involved in ribosomal function. Dissecting the structural basis of LBP action has been the focus of research of several groups [5,11] yet no 3-dimensional structure of this molecule is available.

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Using a 3-dimensional structure for the ribosomal protein S2 from *Thermus thermophilus* [12,13] as a template, we performed comparative modeling of the N-terminal domain of LBP/p40. While the overall fold is conserved between the prototype and the model, a significant portion of the rRNA-binding domain is missing in the modeled LBP/p40. Partial overlap of the S2 homology domain and the region required for laminin binding suggests that these functions are likely to be mutually exclusive. However, we were not able to model the laminin-binding C-terminal domain of LBP/p40 and, therefore, are not able to infer into mechanisms of interaction with laminin or dimerization.

Materials and methods

Alignment. Multiple alignments were built using ClustalW [14] and ClustalX [15–17] software using the Gonnet 250 weight matrix. The alignment was further refined by removing N- and C-terminal parts of sequences that do not show high similarity to all other sequences in the set, and realigning the central parts using the Gonnet 250 weight matrix. Gaps, whenever possible, were manually moved to positions outside the elements of secondary structure in *T. thermophilus* S2 (1FJF, [18]).

Modeling. The satisfaction of spatial restraints procedure implemented in the program MODELLER 4 [19] has been used to predict a 3-dimensional structure of the N-terminal two-thirds of human LBP/p40. The X-ray coordinates for the ribosomal protein S2p from *T. thermophilus* resolved at 3.05 Å were used as a template. The quality of the predicted fold was evaluated by calculating Z scores for each out of 20 generated models using Prosa II software [20]. The lowest scoring model was selected for further analysis. Superposition of protein backbones using a combinatorial extension method [21] yielded the RMSD equal to 0.6 Å, indicating a good match of the overall fold between the modeled protein and the template. Similar results were obtained using the DALI server (RMSD 0.8 Å) [22]. The resulting structure was then energy minimized using the Insight II Discover software (MSI) using the steepest descent algorithm (2200 iterations). The model structure was then hydrated and additional energy minimization was performed, using first the steepest descent algorithm (2000 iterations), and then conjugate gradient algorithm (5000 iterations). Following energy minimization, the water sheath was removed and the model was visualized and manipulated using the Insight (MSI) and SwissPDB Viewer [23] software packages. Models were built based on both 1FJF [18] and 1FJG [13]. For evaluation of possible interactions of LBP/p40 within the ribosome, backbones of the LBP/p40 model and the S2p template were superimposed in the context of the 30S subunit.

Results and discussion

Sequence analysis and multiple alignment

Multiple alignment of S2p/SAe proteins from *Bacteria*, *Archea*, *Protozoa*, *Fungi*, *Viridiplantae*, and *Metazoa* species revealed several clusters of conserved residues that are involved in stabilization of a protein fold, protein–protein and protein–RNA contacts in ribosomal protein S2p (Fig. 1). The regions of highest similarity include α-helices 1, 2, and 4, and hydrophobic residues of β-strands 2, 3, 5, 6, and 7. A loop between β-strands 4 and 5 that contains several RNA-contacting residues is almost identical across all S2 family members. α-Helix 5 is highly hydrophobic in all analyzed proteins. In *Metazoa*, the region corresponding to α-helix 5 contains the palindromic motif LMWWML implicated in interaction with the laminin-1 [5]. Interestingly, the region encompassing α-helixes 3′ and 3″ in prokaryotic proteins is missing from all eukaryotic and most archaebacterial homologues. In S2 from *T. thermophilus*, this region forms extensive contacts with 16S RNA [25]. This suggests that in eukaryotic ribosomes LBP/p40 could not interact with 16S RNA in the same manner as S2p does in prokaryotic ribosomes, and that the strength of putative LBP/p40–RNA interactions would be reduced compared to prokaryotic S2. A relatively high similarity between S2 and LBP (29.7% identity in the modeled region) and conservation of the elements of secondary structure predicted for LBP/p40 with respect to that of S2p makes the comparative modeling of eukaryotic LBP feasible.

Molecular modeling

Predicted LBP/p40 fold contains 5 parallel β strands "sandwiched" between two α-helical sub-domains composed of α-helices 1, 2, 4, and 5 (Figs. 1B and 2A). Both surfaces of the central β-sheet are enriched with aliphatic and hydrophobic residues that together with aliphatic residues of α-helical sub-domains form the hydrophobic core of LBP/p40. Most of the hydrophobic amino-acid residues conserved among S2 family members that stabilize the hydrophobic core of the *T. thermophilus* S2p are found in similar positions in the LBP model (Fig. 1, marked by black circles). However, distribution of charged residues in S2 and LBP is markedly different. In S2 positively charged residues are primarily distributed along the surface that faces the rRNA, while in the LBP/p40 model, positively charged residues are clustered more around the N-terminal portion of the S2-like domain. These differences may influence protein–protein and/or protein–RNA interactions of LBP/p40 within the ribosome as compared to its S2p template.

The apparent stability of the core structure in the LBP model argues against a putative transmembrane domain placed by Castronovo et al. [5] between amino-acid residues 86–101. In the LBP/p40 model presented here this region encompasses part of α-helix 2 and β-strand 4 that contains several conserved residues from the hydrophobic core of the molecule. Therefore, major structural rearrangements would be required to disrupt the protein core to attain an extended membrane-spanning conformation. The energy expenditure involved in such a process suggests that the presence of transmembrane domain in this region is highly unlikely. Therefore, failure of the mutant LBP protein with deletion of

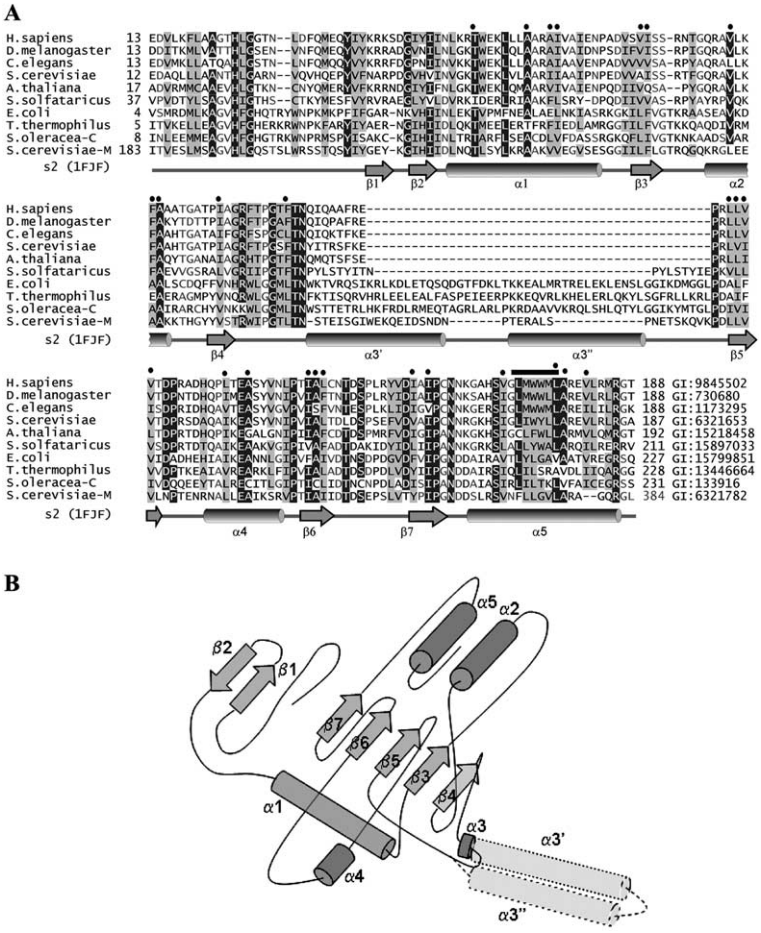

Fig. 1. (A) Sequence similarity of the N-terminal region of LBP/rpSAE to prokaryotic ribosomal proteins S2p. The N-terminal part of LBP/rpSAE is similar to bacterial ribosomal proteins S2p. Clustal [14] alignment (Gonnet 250 similarity matrix) of representative sequences from all kingdoms is shown. Black letters on light gray background represent conserved hydrophobic amino acids (ACFGHILMTVWY). Positionally conserved amino acids with the frequency greater than 80% are shown in white on black background. Secondary structure of *T. thermophilus* S2p as described in [18] is shown on the bottom of the alignment with gray rectangles representing α-helices and gray arrows representing β-strands. The region involved in interaction with laminin is marked on the top of the alignment. (B) Schematic representation of the structure of the modeled LBP domain and enumeration of the elements of secondary structure as referred to in text. Protruding two-helix domain of S2p, missing in LBP model, is shown with dashed lines and pale gray color.

the proposed transmembrane domain to associate with cell membrane [26] is likely the result of the incorrect folding of this mutant of LBP that interferes with normal localization.

Protein–RNA contacts

The structure of yeast 40S subunit contains the yeast homologue of LBP, rpS0A, in a location very similar to that occupied by S2p in the ribosome of *T. thermophilus* [27], which indicates that this is a potential-binding site for other LBP/p40 homologues. Three regions are involved in protein–rRNA contact in *T. thermophilus* S2p, including the N-terminal region and the residues in the first β-strand, α-helix 4, and several residues in the α-helices 3′ and 3″ and the adjacent region (Fig. 2B) [25]. The N-terminal residues involved in rRNA-binding in S2p (Lys 22, Trp 24, and Lys 27) are not conserved in LBP/p40. Superposition of LBP onto S2p in the context of *T. thermophilus* 30S subunit structure suggests that the relative flexibility of this region could allow for the formation of an alternative set of contacts involving Asn 29, Met 34, Ser 43 and basic residues between β-strands 1 and 2. The most notable difference between LBP/p40 and S2p is the absence of the protruding two-helix domain (α-helices 3′ and 3″) that forms multiple contacts with 16S RNA in *T. thermophilus*. A long loop between β-strands 4 and 5 of LBP/p40 contains a group of potential RNA-binding residues (Arg 102, Thr 109, and Asn 110) that are conserved in the S2 family (Figs. 1A and 2B). When placed in the context of 30S subunit, spatial arrangements of these residues are similar to those of their prokaryotic counterparts, suggesting that in LBP/p40 they could be involved in rRNA-binding. Additional RNA-contacts in LBP/p40 could be formed by Thr 104 and Gln 112. These residues are conserved

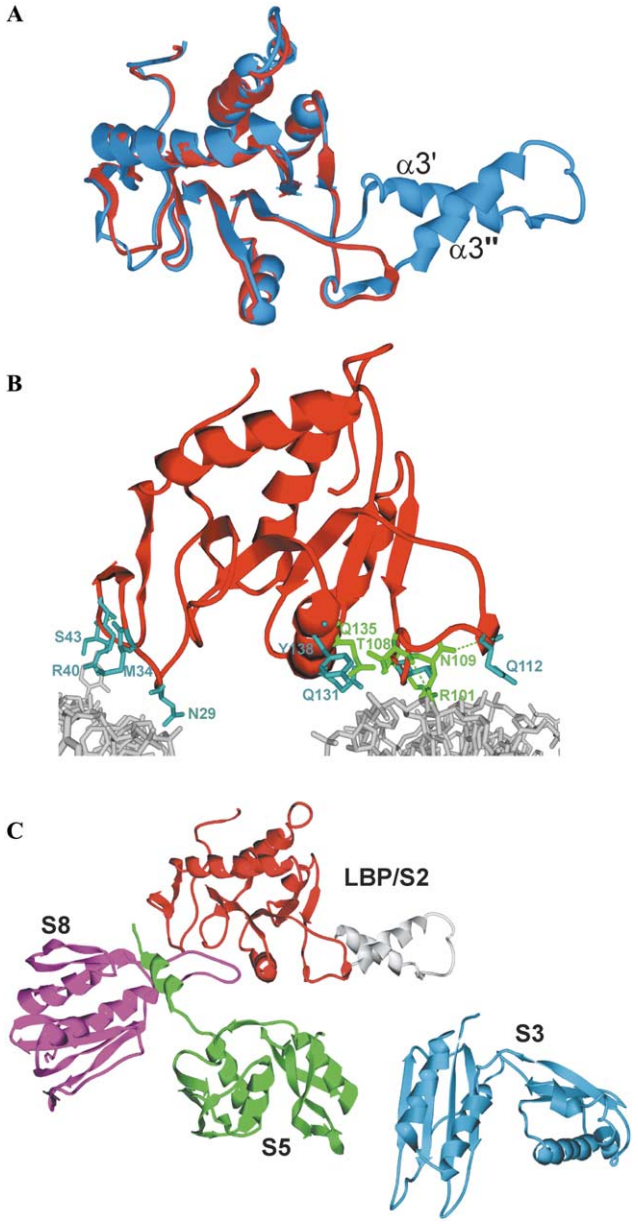

Fig. 2. Superposition of ribosomal protein S2 from *T. thermophilus* (A) and putative protein–RNA (B) and protein–protein (C) contacts formed by LBP/p40 in ribosomal context. (A) Protein backbones of ribosomal protein S2 (blue) and modeled LBP/p40 (red) have been superimposed using combinatorial extension method. α-Helixes 3 and 4 of S2p involved in interactions with 16S RNA are labeled. (B) LBP and S2p have been superimposed in the context of *T. thermophilus* 30S subunit. The residues in LBP positioned in close proximity to 16S RNA are shown in cyan. The residues involved in RNA binding by S2p and conserved across the whole S2/SAe family are shown in green. The 16S RNA is shown in gray. Amino-acid residues are labeled according to the position in human LBP. (C) LBP and S2p have been superimposed in the context of *T. thermophilus* 30S subunit. LBP is shown in red, S3p in blue, S5 in purple, and S8 in green. The two-helical protruding domain of S2p absent from LBP is shown in gray.

only among eukaryotic members of LBP/p40 family and, in the context of 30S subunit, are positioned close to rRNA. Additional protein–rRNA contact formed by non-conserved residues could partially compensate for the loss of the two-helix protruding domain in eukaryotic proteins. Despite the lower reliability of the model in this region due to the lack of proper template coordinates, the fact that conserved rRNA-binding residues are similarly positioned both in the model and the template is reassuring. However, the suggested interactions of LBP/p40 with rRNA in this region would require considerable experimental testing before their likelihood could be evaluated.

The only non-hydrophobic residue in α-helix 4 conserved across the S2 family is Glu 136 (Glu 176 in *T. thermophilus*). This residue interacts with the sugar–phosphate backbone of 16S RNA in *T. thermophilus* and is similarly positioned in the LBP model. In eukaryotic LBP-related proteins, additional protein–RNA contacts could be formed by polar residues in amphipathic α-helix 4 (Gln 132 and Tyr 139).

It should be noted that while helices 36 and 37 of 16/18S rRNA are structurally conserved between species, H26 is a site of an expansion segment, and the length of this helix, as well as stem-and-loop features, may differ from specie to specie [25,27,28]. It is difficult to predict how the interactions between LBP/p40 and rRNA could be affected by the variability of rRNA structure at this site.

Protein–protein interactions

Localization of the S2p protein close to the 30S/50S intersubunit interface results in an extensive network of protein–protein interactions. These involve proteins from both small and large subunits of the ribosome. Chemical cross-linking experiments put S2p into proximity of S1p, S3p, S5p, and S8p from the 30S subunits and L1 and L7/L12 from the 50S subunit of the ribosome [29–31]. In the crystal structure of *T. thermophilus* 30S ribosome, S2p contacts S8p and is favorably positioned to also form contacts with ribosomal proteins S3p and S5p. S3p interacts with residues in the loop connecting helices in the protruding two-helix domain that is absent in all LBP proteins, suggesting that direct interactions between LBP/p40 and S3e are unlikely.

The backbone carbonyl group of Asp 195 and side chains of Asp 198 and Arg 178 of S2p form hydrogen bonds with the side chain of Arg 68 and the backbone carbonyl groups of Gly 71 of S8 [12,25]. However, the interstrand loop in S8, which is involved in interactions with S2p in *T. thermophilus*, is shorter in other species, suggesting that S2–S8 interactions are species-specific.

The C-terminal region of the LBP/p40 α-helix 4, that in S2p contains positively charged residues, appears to be in proximity to the ribosomal protein S5 in the superimposed model. Similarly, Tyr 139, conserved in LBP/p40, could be positioned in close proximity to Arg

64 in S5 when LBP and S2p have been superimposed in the context of *T. thermophilus* 30S subunit. Since the residues in the central part of S2p are involved in protein–RNA contact, it is possible that in LBP/p40 α-helix 5 forms a continuous protein–RNA/protein–protein interface.

Several other LBP/p40 interaction partners have been identified in yeast two-hybrid screening and cross-linking experiments, including ribosomal protein S21e, midkine, and laminin-1 [4,32–34]. Deletion analysis demonstrated that the N-terminal region of LBP/p40 is required for interactions with S21e, however, detailed structural information is lacking [33].

The interaction interface(s) with laminin-1 encompass the C-terminal portion of LBP/p40 and partially overlaps S2 domain (α-helix 5). In all metazoan proteins this helix contains a palindromic motif LMWWML that is involved in interaction with laminin-1 both in vitro and in vivo [5,10]. The appearance of a unique C-terminal extension and the LMWWML palindromic motif in S2 proteins correlates with the advent of *Metazoa* and evolution of extracellular matrix [9,35]. Conceivably, functional duality of LBP/p40 proteins developed as an adaptation to multicellularity. Interestingly, LMWWML motif has been found in several parasitic *Protista* including *Entamoeba histolytica* (Chinenov, unpublished observations). Matrix attachment is a crucial step in *Entamoeba* infection, suggesting that the fixation of this sequence in non-*Metazoa* could be the result of host-parasite co-evolution and that the sequence may have evolved independently in species where the interaction with the host extracellular matrix is required during the life cycle.

Competition between laminin-1 and midkine for LBP binding in vitro [34] suggests that these proteins interact with the same region on the C-terminus of LBP. Thus, interaction with midkine, and possibly other ligands, can disrupt interactions between LBP and extracellular matrix, leading to relocalization of LBP away from the membrane compartment. Since eukaryotic LBP/p40 is involved in ribosomal assembly and subunit recycling [7,36], it is possible that rapid increase in cytoplasmic/nuclear concentrations of this protein results in enhanced translation in response to midkine stimulation and, possibly, other extracellular stimuli. Thus, metazoan LBP/p40 might function as a membrane receptor for molecules such as midkine that activates translation upon internalization. Recently demonstrated ligand-dependent nuclear translocation of LBP [34] lends support to this hypothesis. Increased cytoplasmic concentration of LBP/p40 may lead to increased ribosome binding, hence more rapid subunit turnover. Expression of a number of other ribosomal proteins is increased in cancer [38–44], which probably plays similar role, stimulating protein synthesis to satisfy the needs of the rapidly dividing cells.

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References

[1] C.J. Jeffery, Moonlighting proteins, Trends Biochem. Sci. 24 (1999) 8–11.
[2] I.G. Wool, Extraribosomal functions of ribosomal proteins, Trends Biochem. Sci. 21 (1996) 164–165.
[3] T.H. Landowski, S. Uthayakumar, J.R. Starkey, Control pathways of the 67 kDa laminin binding protein: surface expression and activity of a new ligand binding domain, Clin. Exp. Metastasis 13 (1995) 357–372.
[4] H.K. Yow, J.M. Wong, H.S. Chen, C.G. Lee, S. Davis, G.D. Steele Jr., L.B. Chen, Increased mRNA expression of a laminin-binding protein in human colon carcinoma: complete sequence of a full-length cDNA encoding the protein, Proc. Natl. Acad. Sci. USA 85 (1988) 6394–6398.
[5] V. Castronovo, G. Taraboletti, M.E. Sobel, Functional domains of the 67-kDa laminin receptor precursor, J. Biol. Chem. 266 (1991) 20440–20446.
[6] V. Castronovo, G. Taraboletti, M.E. Sobel, Laminin receptor complementary DNA-deduced synthetic peptide inhibits cancer cell attachment to endothelium, Cancer Res. 51 (1991) 5672–5678.
[7] D. Auth, G. Brawerman, A 33-kDa polypeptide with homology to the laminin receptor: component of translation machinery, Proc. Natl. Acad. Sci. USA 89 (1992) 4368–4372.
[8] S.C. Davis, A. Tzagoloff, S.R. Ellis, Characterization of a yeast mitochondrial ribosomal protein structurally related to the mammalian 68-kDa high affinity laminin receptor, J. Biol. Chem. 267 (1992) 5508–5514.
[9] E. Ardini, G. Pesole, E. Tagliabue, A. Magnifico, V. Castronovo, M.E. Sobel, M.I. Colnaghi, S. Menard, The 67-kDa laminin receptor originated from a ribosomal protein that acquired a dual function during evolution, Mol. Biol. Evol. 15 (1998) 1017–1025.
[10] D.A. Kazmin, T.R. Hoyt, L. Taubner, M. Teintze, J.R. Starkey, Phage display mapping for peptide 11 sensitive sequences binding to laminin-1, J. Mol. Biol. 298 (2000) 431–445.
[11] A.V. Sorokin, A.M. Mikhailov, A.V. Kachko, E.V. Protopopova, S.N. Konovalova, M.E. Andrianova, S.V. Netesov, A.N. Kornev, V.B. Loktev, Human recombinant laminin-binding protein: isolation, purification, and crystallization, Biochemistry (Moscow) 65 (2000) 546–553.
[12] D.E. Brodersen, W.M. Clemons Jr., A.P. Carter, R.J. Morgan-Warren, B.T. Wimberly, V. Ramakrishnan, The structural basis for the action of the antibiotics tetracycline, pactamycin, and hygromycin B on the 30S ribosomal subunit, Cell 103 (2000) 1143–1154.
[13] A.P. Carter, W.M. Clemons, D.E. Brodersen, R.J. Morgan-Warren, B.T. Wimberly, V. Ramakrishnan, Functional insights from the structure of the 30S ribosomal subunit and its interactions with antibiotics, Nature 407 (2000) 340–348.
[14] J.D. Thompson, D.G. Higgins, T.J. Gibson, CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice, Nucleic Acids Res. 22 (1994) 4673–4680.
[15] J.D. Thompson, T.J. Gibson, F. Plewniak, F. Jeanmougin, D.G. Higgins, The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools, Nucleic Acids Res. 25 (1997) 4876–4882.

[16] D.G. Higgins, P.M. Sharp, CLUSTAL: a package for performing multiple sequence alignment on a microcomputer, Gene 73 (1988) 237–244.
[17] F. Jeanmougin, J.D. Thompson, M. Gouy, D.G. Higgins, T.J. Gibson, Multiple sequence alignment with Clustal X, Trends Biochem. Sci. 23 (1998) 403–405.
[18] B.T. Wimberly, D.E. Brodersen, W.M. Clemons Jr., R.J. Morgan-Warren, A.P. Carter, C. Vonhrein, T. Hartsch, V. Ramakrishnan, Structure of the 30S ribosomal subunit, Nature 407 (2000) 327–339.
[19] A. Sali, T.L. Blundell, Comparative protein modeling by satisfaction of spatial restraints, J. Mol. Biol. 234 (1993) 779–815.
[20] M.J. Sippl, Recognition of errors in three-dimensional structures of proteins, Proteins 17 (1993) 355–362.
[21] A. Godzik, The structural alignment between two proteins: is there a unique answer?, Protein Sci. 5 (1996) 1325–1338.
[22] L. Holm, C. Sander, Protein structure comparison by alignment of distance matrices, J. Mol. Biol. 233 (1993) 123–138.
[23] N. Guex, M.C. Peitsch, SWISS-MODEL and the Swiss-Pdb-Viewer: an environment for comparative protein modeling, Electrophoresis 18 (1997) 2714–2723.
[24] Deleted in proof.
[25] D.E. Brodersen, W.M. Clemons, A.P. Carter, B.T. Wimberly, V. Ramakrishnan, Crystal structure of the 30S ribosomal subunit from *Thermus thermophilus*: structure of the proteins and their interactions with 16S RNA, J. Mol. Biol. 316 (2002) 725–768.
[26] S. Gauczynski, J.M. Peyrin, S. Haik, C. Leucht, C. Hundt, R. Rieger, S. Krasemann, J.P. Deslys, D. Dormont, C.I. Lasmezas, S. Weiss, The 37-kDa/67-kDa laminin receptor acts as the cell-surface receptor for the cellular prion protein, EMBO J. 20 (2001) 5863–5875.
[27] C.M. Spahn, R. Beckmann, N. Eswar, P.A. Penczek, A. Sali, G. Blobel, J. Frank, Structure of the 80S ribosome from saccharomyces cerevisiae–tRNA–ribosome and subunit–subunit interactions, Cell 107 (2001) 373–386.
[28] S.A. Gerbi, Expansion segments: regions of variable size that interrupt the universal core secondary structure of ribosomal RNA, in: R.A. Zimmermann, A.E. Dahlberg (Eds.), Ribosomal RNA: Structure, Evolution, Processing and Function in Protein Synthesis, CRC Press, New York, 1996, pp. 71–87.
[29] D. Dey, D.E. Bochkariov, G.G. Jokhadze, R.R. Traut, Cross-linking of selected residues in the N- and C-terminal domains of *Escherichia coli* protein L7/L12 to other ribosomal proteins and the effect of elongation factor Tu, J. Biol. Chem. 273 (1998) 1670–1676.
[30] J.M. Lambert, G. Boileau, J.A. Cover, R.R. Traut, Cross-links between ribosomal proteins of 30S subunits in 70S tight couples and in 30S subunits, Biochem. 22 (1983) 3913–3920.
[31] G. Boileau, A. Sommer, R.R. Traut, Identification of proteins at the binding site for protein S1 in 70S ribosomes and 30S subunits by cross-linking with 2-iminothiolane, J. Biol. Chem. 256 (1981) 8222–8227.
[32] I. Torok, D. Herrmann-Horle, I. Kiss, G. Tick, G. Speer, R. Schmitt, B.M. Mechler, Down-regulation of RpS21, a putative translation initiation factor interacting with P40, produces viable minute images and larval lethality with overgrown hematopoietic organs and imaginal discs, Mol. Cell. Biol. 19 (1999) 2308–2321.
[33] M. Sato, Y. Saeki, K. Tanaka, Y. Kaneda, Ribosome-associated protein LBP/p40 binds to S21 protein of 40S ribosome: analysis using a yeast two-hybrid system, Biochem. Biophys. Res. Commun. 256 (1999) 385–390.
[34] R.H. Salama, H. Muramatsu, K. Zou, T. Inui, T. Kimura, T. Muramatsu, Midkine binds to 37-kDa laminin binding protein precursor, leading to nuclear transport of the complex, Exp. Cell. Res. 270 (2001) 13–20.
[35] W.E. Muller, Review: how was metazoan threshold crossed? The hypothetical Urmetazoa, Comp. Biochem. Physiol.: A. Mol. Integr. Physiol. 129 (2001) 433–460.
[36] C.L. Ford, L. Randal-Whitis, S.R. Ellis, Yeast proteins related to the p40/laminin receptor precursor are required for 20S ribosomal RNA processing and the maturation of 40S ribosomal subunits, Cancer Res. 59 (1999) 704–710.
[37] Deleted in proof.
[38] K. Pogue-Geile, J.R. Geiser, M. Shu, C. Miller, I.G. Wool, A.I. Meisler, J.M. Pipas, Ribosomal protein genes are overexpressed in colorectal cancer: isolation of a cDNA clone encoding the human S3 ribosomal protein, Mol. Cell. Biol. 11 (1991) 3842–3849.
[39] N. Kondoh, C.W. Schweinfest, K.W. Henderson, T.S. Papas, Differential expression of S19 ribosomal protein, laminin-binding protein, and human lymphocyte antigen class I messenger RNAs associated with colon carcinoma progression and differentiation, Cancer Res. 52 (1992) 791–796.
[40] J.L. Henry, D.L. Coggin, C.R. King, High-level expression of the ribosomal protein L19 in human breast tumors that overexpress erbB-2, Cancer Res. 53 (1993) 1403–1408.
[41] K.A. Chester, L. Robson, R.H. Begent, I.C. Talbot, J.H. Pringle, L. Primrose, A.J. Macpherson, G. Boxer, P. Southall, A.D. Malcolm, Identification of a human ribosomal protein mRNA with increased expression in colorectal tumours, Biochim. Biophys. Acta 1009 (1989) 297–300.
[42] W.T. Loging, D. Reisman, Elevated expression of ribosomal protein genes L37, RPP-1, and S2 in the presence of mutant p53, Cancer Epidemiol. Biomarkers Prev. 8 (1999) 1011–1016.
[43] P.J. Chiao, D.M. Shin, P.G. Sacks, W.K. Hong, M.A. Tainsky, Elevated expression of the ribosomal protein S2 gene in human tumors, Mol. Carcinog. 5 (1992) 219–231.
[44] D. Karan, D.L. Kelly, A. Rizzino, M.F. Lin, S.K. Batra, Expression profile of differentially-regulated genes during progression of androgen-independent growth in human prostate cancer cells, Carcinogenesis 23 (2002) 967–975.