

## 6 Literaturverzeichnis

- Adams, P.D., Grosse-Kunstleve, R.W., Hung, L.W., Ioerger, T.R., McCoy, A.J., Moriarty, N.W., Read, R.J., Sacchettini, J.C., Sauter, N.K. and Terwilliger, T.C. (2002) PHENIX: building new software for automated crystallographic structure determination. *Acta Crystallogr D Biol Crystallogr*, **58**, 1948-1954.
- Addlagatta, A., Quillin, M.L., Omotoso, O., Liu, J.O. and Matthews, B.W. (2005) Identification of an SH3-binding motif in a new class of methionine aminopeptidases from Mycobacterium tuberculosis suggests a mode of interaction with the ribosome. *Biochemistry*, **44**, 7166-7174.
- Agashe, V.R., Guha, S., Chang, H.C., Genevaux, P., Hayer-Hartl, M., Stemp, M., Georgopoulos, C., Hartl, F.U. and Barral, J.M. (2004) Function of trigger factor and DnaK in multidomain protein folding: increase in yield at the expense of folding speed. *Cell*, **117**, 199-209.
- Amit, M., Berisio, R., Baram, D., Harms, J., Bashan, A. and Yonath, A. (2005) A crevice adjoining the ribosome tunnel: hints for cotranslational folding. *FEBS Lett*, **579**, 3207-3213.
- Andrade, M.A., Chacon, P., Merelo, J.J. and Moran, F. (1993) Evaluation of secondary structure of proteins from UV circular dichroism spectra using an unsupervised learning neural network. *Protein Eng*, **6**, 383-390.
- Arcus, V. (2002) OB-fold domains: a snapshot of the evolution of sequence, structure and function. *Curr Opin Struct Biol*, **12**, 794-801.
- Ban, N., Nissen, P., Hansen, J., Moore, P.B. and Steitz, T.A. (2000) The complete atomic structure of the large ribosomal subunit at 2.4 Å resolution. *Science*, **289**, 905-920.
- Baram, D., Pyetan, E., Sittner, A., Auerbach-Nevo, T., Bashan, A. and Yonath, A. (2005) Structure of trigger factor binding domain in biologically homologous complex with eubacterial ribosome reveals its chaperone action. *Proc Natl Acad Sci U S A*, **102**, 12017-12022.
- Beatrix, B., Sakai, H. and Wiedmann, M. (2000) The alpha and beta subunit of the nascent polypeptide-associated complex have distinct functions. *J Biol Chem*, **275**, 37838-37845.
- Bergfors, T. (2003) Seeds to crystals. *J Struct Biol*, **142**, 66-76.
- Bloss, T.A., Witze, E.S. and Rothman, J.H. (2003) Suppression of CED-3-independent apoptosis by mitochondrial betaNAC in *Caenorhabditis elegans*. *Nature*, **424**, 1066-1071.
- Bradford, M.M. (1976) A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal Biochem*, **72**, 248-254.
- Brunger, A.T., Adams, P.D., Clore, G.M., DeLano, W.L., Gros, P., Grosse-Kunstleve, R.W., Jiang, J.S., Kuszewski, J., Nilges, M., Pannu, N.S., Read, R.J., Rice, L.M., Simonson, T. and Warren, G.L. (1998) Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr D Biol Crystallogr*, **54** ( Pt 5), 905-921.
- BSA. Definition der buried surface area (BSA):  $BSA = [ASA(\text{DimerAB}) - ASA(\text{Monomer A}) - ASA(\text{monomer B})]/2$ . Die accessible surface area (ASA) wurde mit dem Programm AREAIMOL des CCP4 Programm Pakets berechnet.
- Buchner, J. (1996) Supervising the fold: functional principles of molecular chaperones. *Faseb J*, **10**, 10-19.

- Budisa, N., Steipe, B., Demange, P., Eckerskorn, C., Kellermann, J. and Huber, R. (1995) High-level biosynthetic substitution of methionine in proteins by its analogs 2-aminohexanoic acid, selenomethionine, telluromethionine and ethionine in *Escherichia coli*. *Eur J Biochem*, **230**, 788-796.
- Bukau, B. (2005) Ribosomes catch Hsp70s. *Nat Struct Mol Biol*, **12**, 472-473.
- Bukau, B., Deuerling, E., Pfund, C. and Craig, E.A. (2000) Getting newly synthesized proteins into shape. *Cell*, **101**, 119-122.
- Cate, J.H. (2005) The ins and outs of protein synthesis. *Structure (Camb)*, **13**, 1584-1585.
- CCP4. (1994) Collaborative Computational Project, Number 4; The CCP4 Suite: Programs for Protein Crystallography. *Acta Crystallogr D Biol Crystallogr*, **D50**, 760-763.
- Chang, H.C., Kaiser, C.M., Hartl, F.U. and Barral, J.M. (2005) De novo folding of GFP fusion proteins: high efficiency in eukaryotes but not in bacteria. *J Mol Biol*, **353**, 397-409.
- Crooke, E. and Wickner, W. (1987) Trigger factor: a soluble protein that folds pro-OmpA into a membrane-assembly-competent form. *Proc Natl Acad Sci U S A*, **84**, 5216-5220.
- D'Arcy, A. (1994) Crystallizing proteins - a rational approach? *Acta Crystallogr D Biol Crystallogr*, **50**, 469-471.
- Deng, J.M. and Behringer, R.R. (1995) An insertional mutation in the BTF3 transcription factor gene leads to an early postimplantation lethality in mice. *Transgenic Res*, **4**, 264-269.
- Deuerling, E., Schulze-Specking, A., Tomoyasu, T., Mogk, A. and Bukau, B. (1999) Trigger factor and DnaK cooperate in folding of newly synthesized proteins. *Nature*, **400**, 693-696.
- Diaconu, M., Kothe, U., Schlunzen, F., Fischer, N., Harms, J.M., Tonevitsky, A.G., Stark, H., Rodnina, M.V. and Wahl, M.C. (2005) Structural basis for the function of the ribosomal L7/12 stalk in factor binding and GTPase activation. *Cell*, **121**, 991-1004.
- Dobson, C.M. and Karplus, M. (1999) The fundamentals of protein folding: bringing together theory and experiment. *Curr Opin Struct Biol*, **9**, 92-101.
- Dunker, A.K., Brown, C.J., Lawson, J.D., Iakoucheva, L.M. and Obradovic, Z. (2002) Intrinsic disorder and protein function. *Biochemistry*, **41**, 6573-6582.
- Dunker, A.K., Lawson, J.D., Brown, C.J., Williams, R.M., Romero, P., Oh, J.S., Oldfield, C.J., Campen, A.M., Ratliff, C.M., Hipps, K.W., Ausio, J., Nissen, M.S., Reeves, R., Kang, C., Kissinger, C.R., Bailey, R.W., Griswold, M.D., Chiu, W., Garner, E.C. and Obradovic, Z. (2001) Intrinsically disordered protein. *J Mol Graph Model*, **19**, 26-59.
- Dyson, H.J. and Wright, P.E. (2005) Intrinsically unstructured proteins and their functions. *Nat Rev Mol Cell Biol*, **6**, 197-208.
- Egea, P.F., Stroud, R.M. and Walter, P. (2005) Targeting proteins to membranes: structure of the signal recognition particle. *Curr Opin Struct Biol*, **15**, 213-220.
- Eiler, S., Dock-Bregeon, A., Moulinier, L., Thierry, J.C. and Moras, D. (1999) Synthesis of aspartyl-tRNA(Asp) in *Escherichia coli*--a snapshot of the second step. *Embo J*, **18**, 6532-6541.
- Ellis, R.J. and Hartl, F.U. (1999) Principles of protein folding in the cellular environment. *Curr Opin Struct Biol*, **9**, 102-110.
- Ferbitz, L., Maier, T., Patzelt, H., Bukau, B., Deuerling, E. and Ban, N. (2004) Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. *Nature*, **431**, 590-596.

- Franke, J., Reimann, B., Hartmann, E., Kohlerl, M. and Wiedmann, B. (2001) Evidence for a nuclear passage of nascent polypeptide-associated complex subunits in yeast. *J Cell Sci*, **114**, 2641-2648.
- Frydman, J. (2001) Folding of newly translated proteins in vivo: the role of molecular chaperones. *Annu Rev Biochem*, **70**, 603-647.
- Frydman, J., Erdjument-Bromage, H., Tempst, P. and Hartl, F.U. (1999) Co-translational domain folding as the structural basis for the rapid de novo folding of firefly luciferase. *Nat Struct Biol*, **6**, 697-705.
- Gautschi, M., Just, S., Mun, A., Ross, S., Rucknagel, P., Dubaque, Y., Ehrenhofer-Murray, A. and Rospert, S. (2003) The yeast N(alpha)-acetyltransferase NatA is quantitatively anchored to the ribosome and interacts with nascent polypeptides. *Mol Cell Biol*, **23**, 7403-7414.
- Gautschi, M., Lilie, H., Funfschilling, U., Mun, A., Ross, S., Lithgow, T., Rucknagel, P. and Rospert, S. (2001) RAC, a stable ribosome-associated complex in yeast formed by the DnaK-DnaJ homologs Ssz1p and zuotin. *Proc Natl Acad Sci U S A*, **98**, 3762-3767.
- Gautschi, M., Mun, A., Ross, S. and Rospert, S. (2002) A functional chaperone triad on the yeast ribosome. *Proc Natl Acad Sci U S A*, **99**, 4209-4214.
- Gilbert, R.J., Fucini, P., Connell, S., Fuller, S.D., Nierhaus, K.H., Robinson, C.V., Dobson, C.M. and Stuart, D.I. (2004) Three-dimensional structures of translating ribosomes by Cryo-EM. *Mol Cell*, **14**, 57-66.
- Gorlich, D., Kurzchalia, T.V., Wiedmann, M. and Rapoport, T.A. (1991) Probing the molecular environment of translocating polypeptide chains by cross-linking. *Methods Cell Biol*, **34**, 241-262.
- Gorlich, D., Prehn, S., Hartmann, E., Kalies, K.U. and Rapoport, T.A. (1992) A mammalian homolog of SEC61p and SECYp is associated with ribosomes and nascent polypeptides during translocation. *Cell*, **71**, 489-503.
- Gouet, P., Courcelle, E., Stuart, D.I. and Metoz, F. (1999) ESPript: analysis of multiple sequence alignments in PostScript. *Bioinformatics*, **15**, 305-308.
- Grallath, S., Schwarz, J.P., Bottcher, U.M., Bracher, A., Hartl, F.U. and Siegers, K. (2005) L25 functions as a conserved ribosomal docking site shared by nascent chain-associated complex and signal-recognition particle. *EMBO Rep*.
- Harms, J., Schluenzen, F., Zarivach, R., Bashan, A., Gat, S., Agmon, I., Bartels, H., Franceschi, F. and Yonath, A. (2001) High resolution structure of the large ribosomal subunit from a mesophilic eubacterium. *Cell*, **107**, 679-688.
- Hartl, F.U. and Hayer-Hartl, M. (2002) Molecular chaperones in the cytosol: from nascent chain to folded protein. *Science*, **295**, 1852-1858.
- Hesterkamp, T., Hauser, S., Lutcke, H. and Bukau, B. (1996) Escherichia coli trigger factor is a prolyl isomerase that associates with nascent polypeptide chains. *Proc Natl Acad Sci U S A*, **93**, 4437-4441.
- Holm, L. and Sander, C. (1993) Protein structure comparison by alignment of distance matrices. *J Mol Biol*, **233**, 123-138.
- Hooft, R.W., Vriend, G., Sander, C. and Abola, E.E. (1996) Errors in protein structures. *Nature*, **381**, 272.
- Horwich, A. (2004) Cell biology: sight at the end of the tunnel. *Nature*, **431**, 520-522.
- Hu, G.Z. and Ronne, H. (1994) Yeast BTF3 protein is encoded by duplicated genes and inhibits the expression of some genes in vivo. *Nucleic Acids Res*, **22**, 2740-2743.
- Hundley, H., Eisenman, H., Walter, W., Evans, T., Hotokezaka, Y., Wiedmann, M. and Craig, E. (2002) The in vivo function of the ribosome-associated Hsp70, Ssz1,

- does not require its putative peptide-binding domain. *Proc Natl Acad Sci U S A*, **99**, 4203-4208.
- Hundley, H.A., Walter, W., Bairstow, S. and Craig, E.A. (2005) Human Mpp11 J protein: ribosome-tethered molecular chaperones are ubiquitous. *Science*, **308**, 1032-1034.
- Jones, T.A., Zou, J.Y., Cowan, S.W. and Kjeldgaard. (1991) Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr A*, **47 ( Pt 2)**, 110-119.
- Kabsch, W. (1993) Automatic processing of rotation diffraction data from crystals of initially unknown symmetry and cell constants. *J. Appl. Cryst.*, **26**, 795-800.
- Kalies, K.U., Gorlich, D. and Rapoport, T.A. (1994) Binding of ribosomes to the rough endoplasmic reticulum mediated by the Sec61p-complex. *J Cell Biol*, **126**, 925-934.
- Kanno, M., Chalut, C. and Egly, J.M. (1992) Genomic structure of the putative BTF3 transcription factor. *Gene*, **117**, 219-228.
- Kelley, L.A., MacCallum, R.M. and Sternberg, M.J. (2000) Enhanced genome annotation using structural profiles in the program 3D-PSSM. *J Mol Biol*, **299**, 499-520.
- Kim, S.H., Shim, K.S. and Lubec, G. (2002) Human brain nascent polypeptide-associated complex alpha subunit is decreased in patients with Alzheimer's disease and Down syndrome. *J Investig Med*, **50**, 293-301.
- Kolb, V.A., Makeyev, E.V. and Spirin, A.S. (2000) Co-translational folding of an eukaryotic multidomain protein in a prokaryotic translation system. *J Biol Chem*, **275**, 16597-16601.
- Kramer, G., Rauch, T., Rist, W., Vorderwulbecke, S., Patzelt, H., Schulze-Specking, A., Ban, N., Deuerling, E. and Bukau, B. (2002) L23 protein functions as a chaperone docking site on the ribosome. *Nature*, **419**, 171-174.
- Kramer, G., Rutkowska, A., Wegrzyn, R.D., Patzelt, H., Kurz, T.A., Merz, F., Rauch, T., Vorderwulbecke, S., Deuerling, E. and Bukau, B. (2004) Functional dissection of Escherichia coli trigger factor: unraveling the function of individual domains. *J Bacteriol*, **186**, 3777-3784.
- Kraulis, P.J. (1991) MOLSCRIPT: A Program to Produce Both Detailed and Schematic Plots of Protein Structures. *Journal of Applied Crystallography*, **24**, 946-950.
- Krissinel, E. and Henrick, K. (2004) Secondary-structure matching (SSM), a new tool for fast protein structure alignment in three dimensions. *Acta Crystallogr D Biol Crystallogr*, **60**, 2256-2268.
- Kroes, R.A., Jastrow, A., McLone, M.G., Yamamoto, H., Colley, P., Kersey, D.S., Yong, V.W., Mkrdichian, E., Cerullo, L., Leestma, J. and Moskal, J.R. (2000) The identification of novel therapeutic targets for the treatment of malignant brain tumors. *Cancer Lett*, **156**, 191-198.
- Lauring, B., Kreibich, G. and Wiedmann, M. (1995a) The intrinsic ability of ribosomes to bind to endoplasmic reticulum membranes is regulated by signal recognition particle and nascent-polypeptide-associated complex. *Proc Natl Acad Sci U S A*, **92**, 9435-9439.
- Lauring, B., Sakai, H., Kreibich, G. and Wiedmann, M. (1995b) Nascent polypeptide-associated complex protein prevents mistargeting of nascent chains to the endoplasmic reticulum. *Proc Natl Acad Sci U S A*, **92**, 5411-5415.
- Lauring, B., Wang, S., Sakai, H., Davis, T.A., Wiedmann, B., Kreibich, G. and Wiedmann, M. (1995c) Nascent-polypeptide-associated complex: a bridge between ribosome and cytosol. *Cold Spring Harb Symp Quant Biol*, **60**, 47-56.

- Lei, M., Podell, E.R., Baumann, P. and Cech, T.R. (2003) DNA self-recognition in the structure of Pot1 bound to telomeric single-stranded DNA. *Nature*, **426**, 198-203.
- Lopez, N., Halladay, J., Walter, W. and Craig, E.A. (1999) SSB, encoding a ribosome-associated chaperone, is coordinately regulated with ribosomal protein genes. *J Bacteriol*, **181**, 3136-3143.
- Macario, A.J. and Conway De Macario, E. (2001) The molecular chaperone system and other anti-stress mechanisms in archaea. *Front Biosci*, **6**, D262-283.
- Makarova, K.S., Aravind, L., Galperin, M.Y., Grishin, N.V., Tatusov, R.L., Wolf, Y.I. and Koonin, E.V. (1999) Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell. *Genome Res*, **9**, 608-628.
- Marchler-Bauer, A., Panchenko, A.R., Shoemaker, B.A., Thiessen, P.A., Geer, L.Y. and Bryant, S.H. (2002) CDD: a database of conserved domain alignments with links to domain three-dimensional structure. *Nucleic Acids Res*, **30**, 281-283.
- Markesich, D.C., Gajewski, K.M., Nazimiec, M.E. and Beckingham, K. (2000) bicaudal encodes the Drosophila beta NAC homolog, a component of the ribosomal translational machinery\*. *Development*, **127**, 559-572.
- Merritt, E.A. and Bacon, D.J. (1997) Raster3D Photorealistic Molecular Graphics. *Methods in Enzymology*, **277**, 505-524.
- Moller, I., Beatrix, B., Kreibich, G., Sakai, H., Lauring, B. and Wiedmann, M. (1998a) Unregulated exposure of the ribosomal M-site caused by NAC depletion results in delivery of non-secretory polypeptides to the Sec61 complex. *FEBS Lett*, **441**, 1-5.
- Moller, I., Jung, M., Beatrix, B., Levy, R., Kreibich, G., Zimmermann, R., Wiedmann, M. and Lauring, B. (1998b) A general mechanism for regulation of access to the translocon: competition for a membrane attachment site on ribosomes. *Proc Natl Acad Sci U S A*, **95**, 13425-13430.
- Moncollin, V., Fischer, L., Cavallini, B., Egly, J.M. and Chambon, P. (1992) Class II (B) general transcription factor (TFIIB) that binds to the template-committed preinitiation complex is different from general transcription factor BTF3. *Proc Natl Acad Sci U S A*, **89**, 397-401.
- Moncollin, V., Miyamoto, N.G., Zheng, X.M. and Egly, J.M. (1986) Purification of a factor specific for the upstream element of the adenovirus-2 major late promoter. *Embo J*, **5**, 2577-2584.
- Moreau, A., Yotov, W.V., Glorieux, F.H. and St-Arnaud, R. (1998) Bone-specific expression of the alpha chain of the nascent polypeptide-associated complex, a coactivator potentiating c-Jun-mediated transcription. *Mol Cell Biol*, **18**, 1312-1321.
- Mueller, T.D. and Feigon, J. (2002) Solution structures of UBA domains reveal a conserved hydrophobic surface for protein-protein interactions. *J Mol Biol*, **319**, 1243-1255.
- Mueller, T.D., Kamionka, M. and Feigon, J. (2004) Specificity of the interaction between ubiquitin-associated domains and ubiquitin. *J Biol Chem*, **279**, 11926-11936.
- Murshudov, G.N., Vagin, A.A. and Dodson, E.J. (1997) Refinement of Macromolecular Structure by the Maximum-Likelihood Method. *Acta Crystallogr D Biol Crystallogr*, **D53**, 240-255.
- Murzin, A.G., Lesk, A.M. and Chothia, C. (1994) Principles determining the structure of beta-sheet barrels in proteins. I. A theoretical analysis. *J Mol Biol*, **236**, 1369-1381.

- Netzer, W.J. and Hartl, F.U. (1997) Recombination of protein domains facilitated by co-translational folding in eukaryotes. *Nature*, **388**, 343-349.
- Netzer, W.J. and Hartl, F.U. (1998) Protein folding in the cytosol: chaperonin-dependent and -independent mechanisms. *Trends Biochem Sci*, **23**, 68-73.
- Neupert, W. and Lill, R. (1994) Protein synthesis. Cradle at the ribosome. *Nature*, **370**, 421-422.
- Nicholls, A. and Honig, B. (1991) A Rapid Finite Difference Algorithm, Utilizing Successive Over-Relaxation to Solve the Poisson-Boltzmann Equation. *J. Comp. Chem.*, **12**, 435-445.
- Nicola, A.V., Chen, W. and Helenius, A. (1999) Co-translational folding of an alphavirus capsid protein in the cytosol of living cells. *Nat Cell Biol*, **1**, 341-345.
- Notredame, C., Higgins, D.G. and Heringa, J. (2000) T-Coffee: A novel method for fast and accurate multiple sequence alignment. *J Mol Biol*, **302**, 205-217.
- Otto, H., Conz, C., Maier, P., Wolfle, T., Suzuki, C.K., Jeno, P., Rucknagel, P., Stahl, J. and Rospert, S. (2005) The chaperones MPP11 and Hsp70L1 form the mammalian ribosome-associated complex. *Proc Natl Acad Sci U S A*, **102**, 10064-10069.
- Otwinowski, Z. and Minor, W. (1997) Processing of X-ray Diffraction Data Collected in Oscillation Mode. *Methods in Enzymology*, **276**, 307-326.
- Parthun, M.R., Mangus, D.A. and Jaehning, J.A. (1992) The EGD1 product, a yeast homolog of human BTF3, may be involved in GAL4 DNA binding. *Mol Cell Biol*, **12**, 5683-5689.
- Pfund, C., Lopez-Hoyo, N., Ziegelhoffer, T., Schilke, B.A., Lopez-Buesa, P., Walter, W.A., Wiedmann, M. and Craig, E.A. (1998) The molecular chaperone Ssb from *Saccharomyces cerevisiae* is a component of the ribosome-nascent chain complex. *Embo J*, **17**, 3981-3989.
- Potter, H. (1988) Electroporation in biology: methods, applications, and instrumentation. *Anal Biochem*, **174**, 361-373.
- Raasi, S. and Pickart, C.M. (2003) Rad23 ubiquitin-associated domains (UBA) inhibit 26 S proteasome-catalyzed proteolysis by sequestering lysine 48-linked polyubiquitin chains. *J Biol Chem*, **278**, 8951-8959.
- Raasi, S., Varadan, R., Fushman, D. and Pickart, C.M. (2005) Diverse polyubiquitin interaction properties of ubiquitin-associated domains. *Nat Struct Mol Biol*, **12**, 708-714.
- Raden, D. and Gilmore, R. (1998) Signal recognition particle-dependent targeting of ribosomes to the rough endoplasmic reticulum in the absence and presence of the nascent polypeptide-associated complex. *Mol Biol Cell*, **9**, 117-130.
- Rees, B., Webster, G., Delarue, M., Boeglin, M. and Moras, D. (2000) Aspartyl tRNA-synthetase from *Escherichia coli*: flexibility and adaptability to the substrates. *J Mol Biol*, **299**, 1157-1164.
- Reimann, B., Bradsher, J., Franke, J., Hartmann, E., Wiedmann, M., Prehn, S. and Wiedmann, B. (1999) Initial characterization of the nascent polypeptide-associated complex in yeast. *Yeast*, **15**, 397-407.
- Rost, B. and Sander, C. (1993) Prediction of protein secondary structure at better than 70% accuracy. *J Mol Biol*, **232**, 584-599.
- Sambrook, J., Fritsch, E.F., Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual, 2nd Ed. *Cold Spring Harb Lab Press*, Cold Spring Harbor N.Y.
- Sanger, F., Nicklen, S. and Coulson, A.R. (1977) DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci U S A*, **74**, 5463-5467.

- Sanner, M.F., Olson, A.J. and Spehner, J.C. (1996) Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers*, **38**, 305-320.
- Scheuring, U.J., Corbeil, J., Mosier, D.E. and Theofilopoulos, A.N. (1998) Early modification of host cell gene expression induced by HIV-1. *Aids*, **12**, 563-570.
- Schlunzen, F., Tocilj, A., Zarivach, R., Harms, J., Gluehmann, M., Janell, D., Bashan, A., Bartels, H., Agmon, I., Franceschi, F. and Yonath, A. (2000) Structure of functionally activated small ribosomal subunit at 3.3 angstroms resolution. *Cell*, **102**, 615-623.
- Schlunzen, F., Wilson, D.N., Tian, P., Harms, J.M., McInnes, S.J., Hansen, H.A., Albrecht, R., Buerger, J., Wilbanks, S.M. and Fucini, P. (2005) The binding mode of the trigger factor on the ribosome: implications for protein folding and SRP interaction. *Structure (Camb)*, **13**, 1685-1694.
- Schubert, U., Anton, L.C., Gibbs, J., Norbury, C.C., Yewdell, J.W. and Bennink, J.R. (2000) Rapid degradation of a large fraction of newly synthesized proteins by proteasomes. *Nature*, **404**, 770-774.
- Schuwirth, B.S., Borovinskaya, M.A., Hau, C.W., Zhang, W., Vila-Sanjurjo, A., Holton, J.M. and Cate, J.H. (2005) Structures of the bacterial ribosome at 3.5 Å resolution. *Science*, **310**, 827-834.
- Schwede, T., Kopp, J., Guex, N. and Peitsch, M.C. (2003) SWISS-MODEL: An automated protein homology-modeling server. *Nucleic Acids Res*, **31**, 3381-3385.
- SHARP. Global Phasing (Cambridge, UK).
- Shi, X., Parthun, M.R. and Jaehning, J.A. (1995) The yeast EGD2 gene encodes a homologue of the alpha NAC subunit of the human nascent-polypeptide-associated complex. *Gene*, **165**, 199-202.
- Smith, P.K., Krohn, R.I., Hermanson, G.T., Mallia, A.K., Gartner, F.H., Provenzano, M.D., Fujimoto, E.K., Goeke, N.M., Olson, B.J. and Klenk, D.C. (1985) Measurement of protein using bicinchoninic acid. *Anal Biochem*, **150**, 76-85.
- Spahn, C.M., Beckmann, R., Eswar, N., Penczek, P.A., Sali, A., Blobel, G. and Frank, J. (2001) Structure of the 80S ribosome from *Saccharomyces cerevisiae*--tRNA-ribosome and subunit-subunit interactions. *Cell*, **107**, 373-386.
- Spreiter, T., Pech, M. and Beatrix, B. (2005) The crystal structure of archaeal nascent polypeptide-associated complex (NAC) reveals a unique fold and the presence of a ubiquitin-associated domain. *J Biol Chem*, **280**, 15849-15854.
- Stoller, G., Rucknagel, K.P., Nierhaus, K.H., Schmid, F.X., Fischer, G. and Rahfeld, J.U. (1995) A ribosome-associated peptidyl-prolyl cis/trans isomerase identified as the trigger factor. *Embo J*, **14**, 4939-4948.
- Storoni, L.C., McCoy, A.J. and Read, R.J. (2004) Likelihood-enhanced fast rotation functions. *Acta Crystallogr D Biol Crystallogr*, **60**, 432-438.
- Terwilliger, T.C. (2002) Automated structure solution, density modification and model building. *Acta Crystallogr D Biol Crystallogr*, **58**, 1937-1940.
- Terwilliger, T.C. and Berendzen, J. (1999) Automated MAD and MIR structure solution. *Acta Crystallogr D Biol Crystallogr*, **55 ( Pt 4)**, 849-861.
- Teter, S.A., Houry, W.A., Ang, D., Tradler, T., Rockabrand, D., Fischer, G., Blum, P., Georgopoulos, C. and Hartl, F.U. (1999) Polypeptide flux through bacterial Hsp70: DnaK cooperates with trigger factor in chaperoning nascent chains. *Cell*, **97**, 755-765.
- Theobald, D.L., Mitton-Fry, R.M. and Wuttke, D.S. (2003) Nucleic acid recognition by OB-fold proteins. *Annu Rev Biophys Biomol Struct*, **32**, 115-133.

- Thiede, B., Dimmler, C., Siejak, F. and Rudel, T. (2001) Predominant identification of RNA-binding proteins in Fas-induced apoptosis by proteome analysis. *J Biol Chem*, **276**, 26044-26050.
- Turner, G.C. and Varshavsky, A. (2000) Detecting and measuring cotranslational protein degradation in vivo. *Science*, **289**, 2117-2120.
- Uversky, V.N. (2002) Natively unfolded proteins: a point where biology waits for physics. *Protein Sci*, **11**, 739-756.
- Valent, Q.A., Kendall, D.A., High, S., Kusters, R., Oudega, B. and Luirink, J. (1995) Early events in preprotein recognition in *E. coli*: interaction of SRP and trigger factor with nascent polypeptides. *Embo J*, **14**, 5494-5505.
- Wang, S., Sakai, H. and Wiedmann, M. (1995) NAC covers ribosome-associated nascent chains thereby forming a protective environment for regions of nascent chains just emerging from the peptidyl transferase center. *J Cell Biol*, **130**, 519-528.
- Ward, J.J., Sodhi, J.S., McGuffin, L.J., Buxton, B.F. and Jones, D.T. (2004) Prediction and functional analysis of native disorder in proteins from the three kingdoms of life. *J Mol Biol*, **337**, 635-645.
- Wegrzyn, R.D. and Deuerling, E. (2005) Molecular guardians for newborn proteins: ribosome-associated chaperones and their role in protein folding. *Cell Mol Life Sci*, **62**, 2727-2738.
- Wegrzyn, R.D., Hofmann, D., Merz, F., Nikolay, R., Rauch, T., Graf, C. and Deuerling, E. (2005) A conserved motif is prerequisite for the interaction of NAC with ribosomal protein L23 and nascent chains. *J Biol Chem*.
- Weiss, M. (2000) Global indicators of X-ray data quality. *J. Appl. Cryst*, **34**, 130-135.
- White, B. (1993) *PCR Protocols: current methods and applications*.
- Widmann, M. and Christen, P. (2000) Comparison of folding rates of homologous prokaryotic and eukaryotic proteins. *J Biol Chem*, **275**, 18619-18622.
- Wiedmann, B. and Prehn, S. (1999) The nascent polypeptide-associated complex (NAC) of yeast functions in the targeting process of ribosomes to the ER membrane. *FEBS Lett*, **458**, 51-54.
- Wiedmann, B., Sakai, H., Davis, T.A. and Wiedmann, M. (1994) A protein complex required for signal-sequence-specific sorting and translocation. *Nature*, **370**, 434-440.
- Wild, K., Halic, M., Sinning, I. and Beckmann, R. (2004) SRP meets the ribosome. *Nat Struct Mol Biol*, **11**, 1049-1053.
- Wilson, D.N. and Nierhaus, K.H. (2003) The ribosome through the looking glass. *Angew Chem Int Ed Engl*, **42**, 3464-3486.
- Wimberly, B.T., Brodersen, D.E., Clemons, W.M., Jr., Morgan-Warren, R.J., Carter, A.P., Vonrhein, C., Hartsch, T. and Ramakrishnan, V. (2000) Structure of the 30S ribosomal subunit. *Nature*, **407**, 327-339.
- Winn, M.D., Isupov, M.N. and Murshudov, G.N. (2001) Use of TLS parameters to model anisotropic displacements in macromolecular refinement. *Acta Crystallogr D Biol Crystallogr*, **57**, 122-133.
- Woolhead, C.A., McCormick, P.J. and Johnson, A.E. (2004) Nascent membrane and secretory proteins differ in FRET-detected folding far inside the ribosome and in their exposure to ribosomal proteins. *Cell*, **116**, 725-736.
- Yan, W., Schilke, B., Pfund, C., Walter, W., Kim, S. and Craig, E.A. (1998) Zuotin, a ribosome-associated DnaJ molecular chaperone. *Embo J*, **17**, 4809-4817.
- Yewdell, J.W. (2001) Not such a dismal science: the economics of protein synthesis, folding, degradation and antigen processing. *Trends Cell Biol*, **11**, 294-297.

- Yotov, W.V., Moreau, A. and St-Arnaud, R. (1998) The alpha chain of the nascent polypeptide-associated complex functions as a transcriptional coactivator. *Mol Cell Biol*, **18**, 1303-1311.
- Yotov, W.V. and St-Arnaud, R. (1996a) Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle-specific transcription factor. *Genes Dev*, **10**, 1763-1772.
- Yotov, W.V. and St-Arnaud, R. (1996b) Mapping of the human gene for the alpha-NAC/1.9.2 (NACA/1.9.2) transcriptional coactivator to Chromosome 12q23-24.1. *Mamm Genome*, **7**, 163-164.
- Young, J.C., Agashe, V.R., Siegers, K. and Hartl, F.U. (2004) Pathways of chaperone-mediated protein folding in the cytosol. *Nat Rev Mol Cell Biol*, **5**, 781-791.
- Zheng, X.M., Black, D., Chambon, P. and Egly, J.M. (1990) Sequencing and expression of complementary DNA for the general transcription factor BTF3. *Nature*, **344**, 556-559.
- Zheng, X.M., Moncollin, V., Egly, J.M. and Chambon, P. (1987) A general transcription factor forms a stable complex with RNA polymerase B (II). *Cell*, **50**, 361-368.