

6 Literaturverzeichnis

- Alonso**, J.C., Ayora, S., Canosa, I., Weise, F. und Rojo, F. (1996). Site-specific recombination in gram-positive theta-replicating plasmids. *FEMS Microbiol. Lett.*, **142**, 1-10.
- Amor**, J.C., Harrison, D.H., Kahn, R.A. und Ringe, D. (1994). Structure of the human ADP-ribosylation factor 1 complexed with GDP. *Nature* **372** pp.704-708.
- Arndt**, U.W. und Wonacott, A.J. (1977). The rotation method in crystallography. *Amsterdam:North Holland*.
- Barilla**, D., Rosenberg, M.F., Nobbmann, U. und Hayes, F., (2005). Bacterial DNA segregation dynamics mediated by the polymerizing protein ParF. *EMBO J.* **24** (7),1453-64.
- Barilla**, D., Carmelo E. und Hayes, F. (2007). The tail of the ParG DNA segregation protein remodels ParF polymers and enhances ATP hydrolysis via an arginine finger-like motif. *Proc. Natl. Acad. Sci. USA* **104(6)**, 1811-1816.
- Barilla**, D. und Hayes, F. (2003). Architecture of the ParF*ParG protein complex involved in prokaryotic DNA segregation. *Mol. Microbiol.*, **49**, 487-499.
- Bignell**, C. und Thomas, C.M. (2001). The bacterial ParA-ParB partitioning proteins. *J. Biotechnol.*, **91**, 1-34.
- Bork**, P., Sander, C., und Valencia, A. (1992). An ATPase domain common to prokaryotic cell cycle proteins, sugar kinases, actin, and hsp70 heat shock proteins. *Proc. Natl. Acad. Sci. USA* **89**, 7290- 7294.
- Bouet**, J.Y. und Funnell, B.E. (1999). P1 ParA interacts with the P1 partition complex at *parS* and an ATP-ADP switch controls ParA activities. *EMBO J.*, **18**, 1415-1424.
- 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.
- Branden**, C. und Tooze, J. (1991). Introduction to Protein Structure. *Garland Publishing, Inc., New York und London*, pp. 99-110.
- Brantl**, S., Behnke, D. und Alonso, J.C. (1990). Molecular analysis of the replication region of the conjugative *Streptococcus agalactiae* plasmid pIP501 in *Bacillus subtilis*. Comparison with plasmids pAM beta 1 and pSM19035. *Nucleic Acids Res.*, **18**, 4783 4790.
- Brantl**, S. (1994). The *copR* gene product of plasmid pIP501 acts as a transcriptional repressor at the essential *repR* promoter. *Mol. Microbiol.*, **14**, 473-483.
- Brantl**, S. und Wagner, E.G. (1997). Dual function of the *copR* gene product of plasmid pIP501. *J. Bacteriol.*, **179**, 7016-7024.

- Brennan, R.G.** und **Matthews, B.W.** (1989a). The helix-turn-helix DNA binding motif. *J. Biol. Chem.*, **264**, 1903-1906.
- Brennan, R.G.** und **Matthews, B.W.** (1989b). Structural basis of DNA-protein recognition. *Trends Biochem. Sci.*, **14**, 286-290.
- Brunger, A.T.** (1992). The free R value: a novel statistical quantity for assessing the accuracy of crystal structures. *Nature*, **355**, 472-474.
- Camacho, A. G.**, **Misselwitz, R.**, **Behlke, J.**, **Ayora, S.**, **Welfle, K.**, **Meinhart, A.**, **Lara, B.**, **Saenger, W.**, **Welfle, H.**, und **Alonso, J. C.** (2002). *In vitro* and *in vivo* stability of the epsilon2zeta2 protein complex of the broad host-range *Streptococcus pyogenes* pSM19035 addiction system. *Biol. Chem.* **383**, 1701-1713.
- CCP4** (1994). The CCP4 Suite: Programs for Protein Crystallography. *Acta Cryst.*, **D50**, 760-763.
- Ceglowski, P.** und **Alonso, J.C.** (1994). Gene organization of the *Streptococcus pyogenes* plasmid pDB101: sequence analysis of the orf zeta-copS region. *Gene*, **145**, 33-39.
- Ceglowski, P.**, **Boitsov, A.**, **Chai, S.** und **Alonso, J.C.** (1993a). Analysis of the stabilization system of pSM19035-derived plasmid pBT233 in *Bacillus subtilis*. *Gene*, **136**, 1-12.
- Ceglowski, P.**, **Boitsov, A.**, **Karamyan, N.**, **Chai, S.** und **Alonso, J.C.** (1993b). Characterization of the effectors required for stable inheritance of *Streptococcus pyogenes* pSM19035-derived plasmids in *Bacillus subtilis*. *Mol. Gen. Genet.*, **241**, 579-585.
- Ceglowski, P.**, **Lurz, R.** und **Alonso, J.C.** (1993c). Functional analysis of pSM19035 derived replicons in *Bacillus subtilis*. *FEMS Microbiol. Lett.*, **109**, 145-150.
- Cheung, D. T.** und **M.E. Nimni**, (1982). Mechanism of crosslinking of proteins by glutardialdehyde I: reaction with model compounds. *Connect. Tissue Res.* **10**, 187-199.
- Chothia, C.**, **Lesk, A.M.**, **Tramontano, A.**, **Levitt, M.**, **Smith-Gill, S.J.**, **Air, G.**, **Sheriff, S.**, **Padlan, E.A.**, **Davies, D.**, **Tulip, W.R.** *et al.* (1989). Conformations of immunoglobulin hypervariable regions. *Nature*, **342**, 877-883.
- Colloms, S.D.**, **McCulloch, R.**, **Grant, K.**, **Neilson, L.**, und **Sherratt, D.J.**, (1996). Xer -mediated site-specific recombination *in vitro*. *EMBO J* **15**, 1172- 1181
- Cordell, S.C.** und **Lowe, J.** (2001). Crystal structure of the bacterial cell division regulator MinD. *FEBS Lett*, **492**, 160-165.
- D'Arcy, A.** (1994). Crystallizing proteins - a rational approach? *Acta Cryst.*, **50**, 469-471.
- Davis, M. A.**, und **Austin, S. J.** (1988). Recognition of the P1 plasmid centromere analog involves binding of the ParB protein and is modified by a specific host factor. *EMBO J.*, **7**, 1881-1888.

- Davis**, M.A., Radnedge, L., Martin, K.A., Hayes, F., Youngren, B. und Austin, S.J. (1996). The P1 ParA protein and its ATPase activity play a direct role in the segregation of plasmid copies to daughter cells. *Mol. Microbiol.*, **21**, 1029-1036.
- de Boer**, P.A., Crossley, R.E., Hand, A.R., und Rothfield, L.I. (1991). The MinD protein is a membrane ATPase required for the correct placement of the *Escherichia coli* division site. *EMBO J* **10**, 4371–4380.
- de Boer**, P.A.J., Crossley, R.E., und Rothfield, L.I. (1992). Roles of MinC and MinD in the site-specific septation block mediated by the MinCDE system of *Escherichia coli*. *J. Bacteriol.* **174**, 63–70.
- de la Hoz**, A.B., Ayora, S., Sitkiewicz, I., Fernandez, S., Pankiewicz, R., Alonso, J.C. und Ceglowski, P. (2000). Plasmid copy-number control and better-than-random segregation genes of pSM19035 share a common regulator. *Proc. Natl. Acad. Sci. USA*, **97**, 728-733.
- de la Hoz**, A.B., Pratto, F., Misselwitz, R., Speck, C., Weihofen, W., Welfle, K., Saenger, W., Welfle, H. und Alonso, J.C. (2004). Recognition of DNA by ω protein from the broad-host range *Streptococcus pyogenes* plasmid pSM19035: analysis of binding to operator DNA with one to four heptad repeats. *Nucleic Acids Res.*, **32**, 3136-3147.
- del Solar**, G., Alonso, J. C., Espinosa, M., und Diaz-Orejas, R. (1996). Broad-host-range plasmid replication: an open question. *Mol. Microbiol.*, **21**, 661-666.
- del Solar**, G., Hernandez-Arriaga, A.M., Gomis-Ruth, F.X., Coll, M. und Espinosa, M. (2002). A genetically economical family of plasmid-encoded transcriptional repressors involved in control of plasmid copy number. *J. Bacteriol.*, **184**, 4943-4951.
- Dmowski**, M., Sitkiewicz, I., und Ceglowski, P. (2006). Characterization of a novel partition system encoded by the delta and omega genes from the streptococcal plasmid pSM19035. *J. Bacteriol.*, **188**, 4362-4372.
- Dobrovinski**, K. und M. Howard (2005). Stochastic model for Soj relocation dynamics in *Bacillus subtilis*. *Proc Natl Acad Sci U S A*. **102** :9808-13
- Dostál**, L., Pratto, F., Alonso, J. C., und Welfle, H. (2006). Binding of Regulatory Protein Omega From *Streptococcus pyogenes* Plasmid pSM19035 to Direct and Inverted 7-Base Pair Repeats of Operator DNA. *J. Raman Spectrosc.*
- Dreusicke**, D. und Schulz, G.E. (1986). The glycin-rich loop of adenylate kinase forms a giant anion hole. *FEBS letters*. **208**, 301-304.
- Ducruix**, A. und Giegé, R. (1992). Crystallization of nucleic acids and proteins, A practical approach. The practical approach series, IRL Press, Oxford University Press, Oxford-New Yourk-Tokyo.
- Ducruix**, A. und Giegé, R. (1999). Crystallization of nucleic acids and proteins: a practical approach. *Oxford University Press, Oxford; New York*.

- Easter J. Jr.** und **Gober J.W.** (2002). ParB-stimulated nucleotide exchange regulates a switch in functionally distinct ParA activities. *Mol. Cell* **10**, 427–434.
- Ebersbach, G.**, and **Gerdes, K.** (2001). The double par locus of virulence factor pB171: DNA segregation is correlated with oscillation of ParA. *Proc. Natl. Acad. Sci. USA* **98**, 15078–15083.
- Ebersbach, G.** und **Gerdes, K.** (2004). Bacterial mitosis: partitioning protein ParA oscillates in spiral-shaped structures and positions plasmids at mid-cell. *Mol. Microbiol.*, **52**, 385-398.
- Ebersbach, G.** und **Gerdes, K.** (2005). Plasmid Segregation Mechanisms. *Annu. Rev. Genet.* **39**,453-479.
- Edwards, D.H.** und **Errington, J.** (1997). The *Bacillus subtilis* DivIVA protein targets to the division septum and controls the site specificity of cell division. *Mol. Microbiol.* **24**, 905-915.
- Engh, R.** und **Huber, R.** (1991). Accurate Bond and Angle Parameters for X-ray Protein-Structure Refinement. *Acta Cryst.*, **A47**, 392-400.
- Erickson H.P.**, **Taylor D.W.**, **Taylor K.A.** und **Bramhill D.** (1996). Bacterial cell division protein FtsZ assembles into proto filament sheets and mini rings, structural homologs of tubulin polymers. *Proc. Natl. Acad. Sci.USA* **93**, 519–23.
- Errington J.**, **Daniel R.A.**, **Scheffers D. J.** (2003). Cytokinesis in bacteria. *Microbiol. Mol. Biol. Rev.* **67**, 52–65.
- Ferre-d'Amare, A.R.** und **Doudna, J.A.** (1997). Establishing suitability of RNA preparations for crystallization. Determination of polydispersity. *Methods Mol. Biol.*, **74**, 371-377.
- Figge, R.M.**, **Easter, J.** und **Gober, J.W.** (2003). Productive interaction between the chromosome partitioning proteins, ParA and ParB, is required for the progression of the cell cycle in *Caulobacter crescentus*. *Mol. Microbiol.*, **47**, 1225-1237.
- Freymann, D.M.**, **Keenan, R.J.**, **Stroud, R.M.** und **Walter, P.** (1999). Functional changes in the structure of the SRP GTPase on binding GDP and Mg²⁺+GDP. *Nat.Struct.Biol.* **6** 793-801.
- Funnell, B. E.** (1988). Participation of *Escherichia coli* integration host factor in the P1 plasmid partition system. *Proc. Natl. Acad. Sci. U S A* **85**, 6657-6661.
- Funnell, B. E.** (2005). Partition-mediated plasmid pairing. *Plasmid* **53**, 119-125.
- Fung, E.**, **Bouet, J.Y.** und **Funnell, B.E.** (2001). Probing the ATP-binding site of P1 ParA: partition and repression have different requirements for ATP binding and hydrolysis. *EMBO J.*, **20**, 4901-4911.
- Gaspar, R.**, **Scrima, A.** und **Wittinghofer, A.** (2006). Structural insights into HypB, a GTP-binding protein that regulates metal binding. *J.Biol.Chem.* **281**, 27492-27502.

- Georgiadis, M.M.**, Komiya, H., Chakrabarti, P., Woo, D., Kornuc, J.J., und Rees, D.C. (1992). Crystallographic structure of the nitrogenase iron protein from *Azotobacter vinelandii*. *Science* **257**, 1653–1659.
- Gerdes, K.**, Gulyaev, A.P., Franch, T., Pedersen, K. und Mikkelsen, N.D. (1997). Antisense RNA regulated programmed cell death. *Annu. Rev. Genet.*, **31**, 1-31.
- Gerdes, K.**, Moller-Jensen J. und Bugge Jensen R. (2000). Plasmid and chromosome partitioning: surprises from phylogeny. *Mol Microbiol.*, **37**(3), 455-66. Review.
- Gerdes, K.**, (2000). Toxin-antitoxin modules may regulate synthesis of macromolecules during nutritional stress. *J. Bacteriol.*, **182**, 561-572.
- Gerdes, K.**, Moller-Jensen, J., Ebersbach, G., Kruse, T. und Nordstrom, K. (2004). Bacterial mitotic machineries. *Cell*, **116**, 359-366.
- Gordon, G.S.**, Sitnikov, D., Webb, C.D., Teleman, A., Straight, A., Losick, R., Murray, A.W. und Wright, A. (1997). Chromosome and low copy plasmid segregation in *E. coli*: visual evidence for distinct mechanisms. *Cell*, **90**, 1113-1121.
- Gordon, G.S.** und Wright, A., (2000). DNA segregation in bacteria. *Annu. Rev. Microbiol.* **54**, 681–708.
- Guex, N.** und Peitsch, M.C. (1997). SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling. *Electrophoresis* **18**, 2714-2723.
- Hayashi, I.**, Oyama, T., und Morikawa, K. (2001). Structural and functional studies of MinD ATPase: implications for the molecular recognition of the bacterial cell division apparatus. *EMBO J.*, **20**, 1819–1828.
- Hayes, F.**, Radnedge, L., Davis, M.A., und Austin, S.J. (1994). The homologous operons for P1 and P7 plasmid partition are autoregulated from dissimilar operator sites. *Mol. Microbiol.* **11**, 249-260.
- Hayes, F.** (2000). The partition system of multidrug resistance plasmid TP228 includes a novel protein that epitomizes an evolutionarily distinct subgroup of the ParA superfamily. *Mol. Microbiol.* **37**, 528–541.
- Hayes, F.**, und Barilla, D. (2006). The bacterial segrosome: a dynamic nucleoprotein machine for DNA trafficking and segregation. *Nat. Rev. Microbiol.* **4**, 133-143.
- Hengge-Aronis, R.** (2002) Recent Insights into the General Stress Response Regulatory Network in *Escherichia coli*. *J. Mol. Microbiol. Biotechnol.* **4** (3), 341–346.
- Hengge-Aronis, R.** (2000) The general stress response in *Escherichia coli*. In Storz, G. and Hengge-Aronis, R. (eds.), *Bacterial Stress Responses*. ASM Press, Washington, D.C., pp. 161-178.
- Hester, C. M.** und J. Lutkenhaus (2007) Soj (ParA) DNA binding is mediated by conserved

- arginines and is essential for plasmid segregation. *Proc. Natl. Acad. Sci. USA*, **104**, 20326–20331
- Hiraga**, S. (1992). Chromosome and plasmid partition in *Escherichia coli*. *Annu. Rev. Biochem.*, **61**, 283-306.
- Hiraga**, S., (2000). Dynamic localization of bacterial and plasmid chromosomes. *Annu. Rev. Genet.* **34**, 21–59.
- Holm**, L., Sander, C. (1993) Dali ver. 2.0.: *J.Mol.Biol.* **233**,123-138
- Hoof**t, R.W., Vriend, G., Sander, C. und Abola, E.E. (1996). Errors in protein structures. *Nature*, **381**, 272.
- Holm** L. und Park, J.(2000). DaliLite workbench for protein structure comparison. *Bioinformatics* **16**, 566-567.
- Hu**, Z., und Lutkenhaus, J. (2001). Topological regulation of cell division in *E. coli*. spatiotemporal oscillation of MinD requires stimulation of its ATPase by MinE and phospholipid. *Mol. Cell*, **7**, 1337–1343.
- Hu**, Z., Gogol, E.P. and Lutkenhaus, J. (2002) Dynamic assembly of MinD on phospholipid vesicles regulated by ATP and MinE. *Proc. Natl. Acad. Sci. U S A*, **99**, 6761-6766.
- Huang**, J., Cao, C. und Lutkenhaus, J. (1996). Interaction between FtsZ and inhibitors of cell division. *J. Bacteriol.*,**178**, 5080- 5085.
- Ireton** K, Gunther N. W. und Grossman A.D. (1994). spo0J is required for normal chromosome segregation as well as the initiation of sporulation in *Bacillus subtilis*. *J. Bacteriol.*, **176**, 5320–5329.
- Jang**, S.B., Seefeldt, L.C., und Peters, J.W. (2000). Insights into nucleotide signal transduction in nitrogenase: structure of an iron protein with Mg-ADP bound. *Biochemistry* **39**:14745–14752.
- Jancarik**, J. und Kim, H.S. (1991). Sparse matrix sampling: a screening method for crystallization of proteins. *J. Appl. Cryst.*, **24**, 409-411.
- Jensen**, R.B. und Gerdes, K. (1995). Programmed cell death in bacteria: proteic plasmid stabilization systems. *Mol. Microbiol.*, **17**, 205-210.
- Jensen**, R.B. und Gerdes,K. (1997). Partitioning of plasmid R1. The ParM protein exhibits ATPase activity and interacts with the centromere-likeParR-parC complex. *J. Mol. Biol.*, **269**, 505-513.
- Jensen**, R.B., Lurz,R. und Gerdes,K. (1998). Mechanism of DNA segregation in prokaryotes: replicon pairing by parC of plasmid R1. *Proc. Natl Acad. Sci. USA*, **95**, 8550-8555.
- Jiang** Y., Pogliano J., Helinski D.R. und Konieczny I. (2002). ParE toxin encoded by the broad-host-range plasmid RK2 is an inhibitor of *Escherichia coli* gyrase. *Mol. Microbiol.* **44**, 971-979.

- Jones**, L. J., Carballido- Lopez, R., und Errington, J. (2001). Control of cell shape in bacteria: helical, actin-like filaments in *Bacillus subtilis*. *Cell* **104**, 913–922.
- Jones**, T.A. (1978). A graphics model building und refinement system for macromolecules. *J. Appl. Cryst.*, **11**, 268-272.
- Jones** T.A., Zou J.Y., Cowan S.W. und Kjeldgaard M. (1991). Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr. A.*, **47**,110-9.
- Kabsch**, W. (1988). Evaluation of single-crystal X-ray diffraction from a position-sensitive detector. *J. Appl. Cryst.*, **21**, 916.
- Kalnin**, K., Stegalkina, S., und Yarmolinsky, M. (2000). pTAR encoded proteins in plasmid partitioning. *J. Bacteriol.*, **182**, 1889-1894.
- Koonin**, E.V. (1993). A superfamily of ATPases with diverse functions containing either classical or deviant ATP-binding motif. *J. Mol. Biol.*, **229**, 1165-1174.
- Koppes**, L. J., Woldringh, C.L. und Nanninga, N. (1999). *Escherichia coli* contains a DNA replication compartment in the cell center. *Biochimie*, **81**, 803–810.
- Kraulis**, P. J. (1991). MOLSCRIPT: A Program to Produce Both Detailed and Schematic Plots of Protein Structures. *J. Appl. Cryst.*, **24**, 946-950.
- Laemmli**, U. K. (1970). Cleavage of structural proteins during the assembly of the head bacteriophage T4. *Nature*, **227**, 680-685.
- Laskowski**, R.A., Mac Arthur, M.W., Moss, D.S. und Thornton, J.M. (1993). PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Cryst.*, **26**, 283-291.
- Leipe**, D.D., Wolf, Y.I., Koonin, E.V., und Aravind, L. (2002). Classification and evolution of P-loop GTPases and related ATPases. *J. Mol Biol.*, **317**, 41–72.
- Lemon**, K.P. und Grossman, A.D., (2000). Movement of replicating DNA through a stationary factory. *Mol. Cell* **6**, 1321–1330.
- Lemon**, K.P. und Grossman, A.D., (2001). The extrusion-capture model for chromosome partitioning in bacteria. *Genes Dev.***15**, 2031–2041.
- Leonard**, T.A., Butler, P.J. und Lowe, J. (2004). Structural analysis of the chromosome segregation protein Spo0J from *Thermus thermophilus*. *Mol. Microbiol.*, **53**, 419-432.
- Leonard**, T.A., Butler, P.J. und Lowe, J. (2005a). Bacterial chromosome segregation: structure and DNA binding of the Soj dimer - a conserved biological switch. *EMBO J*, **24**, 270-282.
- Leonard**, T.A., Moller-Jensen, J. und Lowe, J. (2005b). Towards understanding the molecular basis of bacterial DNA segregation. *Philos. Trans. R. Soc. Lond. B. Biol. Sci.*, **360**, 523-535.

- Libante V.**, Thion L. und Lane D., (2001). Role of the ATP-binding site of SopA protein in partition of F plasmid. *J. Mol. Biol.*, **314**, 387-399.
- Lin**, D.C. und Grossman, A.D. (1998) Identification and characterization of a bacterial chromosome partitioning site. *Cell*, **92**, 675-685.
- Lioy**, V. S., Martin, M. T., Camacho, A. G., Lurz, R., Antelmann, H., Hecker, M., Hitchin, E., Ridge, Y., Wells, J. M., und Alonso, J. C. (2006). pSM19035-encoded {zeta} toxin induces stasis followed by death in a subpopulation of cells. *Microbiology*, **152**, 2365-2379.
- Löwe** J. und Amos L. A. (1998). Crystal structure of the bacterial cell-division protein FtsZ. *Nature*, **391**, 203–6.
- Löwe** J. und Amos L.A. (1999). Tubulin like proto filaments in Ca²⁺-induced FtsZ sheets. *EMBO J.*, **18**, 2364–71.
- Löwe** J., Li H., Downing K. H. und Nogales E. (2001). Refined structure of alpha beta- tubulin at 3.5 resolution. *J. Mol. Biol.*, **313**:1045–57
- Lutkenhaus** J. und Addinall S. G. (1997). Bacterial cell division and the Z ring. *Annu. Rev. Biochem.* **66**, 93–116
- Lutkenhaus** J. und Sundaramoorthy M. (2003). MinD and role of the deviant Walker A motif, dimerization and membrane binding in oscillation. *Mol. Microbiol.*, **48**, 295–303.
- Ma**, L.Y., King G., und Rothfield L. (2003). Mapping the MinE site involved in interaction with the MinD division site selection protein of *Escherichia coli*. *J. Bacteriol.*, **185**, 4948-4955
- Marston**, A. L., und Errington, J. (1999). Dynamic movement of the ParA-like Soj protein of *B. subtilis* and its dual role in nucleoid organization and developmental regulation. *Mol. Cell* **4**, 673–682.
- Meinhart**, A., Alonso, J. C., Strater, N. und Saenger, W. (2003). Crystal structure of the plasmid maintenance system epsilon/zeta: functional mechanism of toxin zeta and inactivation by epsilon2zeta2 complex formation. *Proc. Natl. Acad. Sci. U S A*, **100**, 1661-1666.
- McPherson**, A. (1990). Current approaches to macromolecular crystallization. *Eur. J. Biochem.*, **189**, 1-23.
- Merritt**, E. A. und Bacon, D. J. (1997). Raster3D: Photorealistic Molecular Graphics. *Methods Enzymol.*, **277**, 505-524.
- Misselwitz**, R., de la Hoz, A. B., Ayora, S., Welfle, K., Behlke, J., Murayama, K., Saenger, W., Alonso, J.C. und Welfle, H. (2001). Stability and DNA-binding properties of the regulator protein from the broad-host range *Streptococcus pyogenes* plasmid pSM19035. *FEBS Lett.*, **505**, 436-440.
- Mohl**, D. A., und Gober, J. W. (1997). Cell cycle-dependent polar localization of chromosome partitioning proteins in *Caulobacter crescentus*. *Cell* **88**, 675-684.

-
- Moller-Jensen, J.**, Borch, J., Dam, M., Jensen, R.B., Roepstorff, P. und Gerdes, K. (2003). Bacterial mitosis: ParM of plasmid R1 moves plasmid DNA by an actin-like insertional polymerization mechanism. *Mol. Cell.*, **12**, 1477-1487.
- Moller-Jensen, J.**, Jensen, R. B. und Gerdes, K. (2000). Plasmid and chromosome segregation in prokaryotes. *Trends Microbiol.*, **8**, 313-320.
- Moller-Jensen, J.**, Jensen, R.B., Lowe, J. und Gerdes, K. (2002). Prokaryotic DNA segregation by an actin-like filament. *EMBO J.*, **21**, 3119-3127.
- Motallebi-Veshareh, M.**, Rouch, D.A. und Thomas, C.M. (1990). A family of ATPases involved in active partitioning of diverse bacterial plasmids. *Mol. Microbiol.*, **4**, 1455-1463.
- Mukherjee A.** und Lutkenhaus J. (1994). Guaninenucleotide-dependent assembly of FtsZ into filaments. *J. Bacteriol.* **176**, 2754–58.
- Murayama, K.**, Orth, P., de la Hoz, A. B., Alonso, J. C. und Saenger, W. (2001). Crystal structure of ω -transcriptional repressor encoded by *Streptococcus pyogenes* plasmid pSM19035 at 1.5 Å resolution. *J. Mol. Biol.*, **314**, 789-796.
- Murzin A. G.**, Brenner S. E., Hubbard T. und Chothia C. (1995). SCOP: a structural classification of proteins database for the investigation of sequences and structures. *J. Mol. Biol.* **247**, 536-540.
- Murshudov, G.N.**, Vagin, A.A. und Dodson, E.J. (1997). Refinement of macromolecular structures by the maximum-likelihood method. *Acta Cryst.*, **D53**, 240-255.
- Naar, A.M.**, Boutin, J.M., Lipkin, S.M., Yu, V.C., Holloway, J.M., Glass, C.K. und Rosenfeld, M.G. (1991). The orientation and spacing of core DNA-binding motifs dictate selective transcriptional responses to three nuclear receptors. *Cell*, **65**, 1267-1279.
- Niki, H.** und Hiraga, S. (1997). Subcellular distribution of actively partitioning F plasmid during the cell division cycle in *E. coli*. *Cell*, **90**, 951-957.
- Niki, H.**, Yamamaka und K., Hiraga, S., (2000a). Dynamic organization of chromosomal DNA in *Escherichia coli*. *Genes Dev.* **14**, 212–223.
- Niki, H.** und Hiraga, S., (2000b). Polar localisation of the replication origin and terminus in *Escherichia coli* nucleoids during chromosome partitioning. *Genes Dev.* **12**, 1036–1045.
- Nordström, K.** und Austin, S.J. (1989). Mechanisms that contribute to the stable segregation of plasmids. *Annu. Rev. Genet.*, **23**, 37-69.
- Nordström, K.** und Gerdes K., (2003). Clustering versus random segregation of plasmids lacking a partitioning function: a plasmid paradox? *Plasmid* **50**, 95–101.
- Otwinowski, Z.** und Minor, W. (1997). Processing of X-Ray Diffraction Data Collected in Oscillation Mode. In Carter C.W.Jr, S.R.M. (ed.), *Macromolecular Crystallography Part A*. Academic Press, Vol. **276**, pp. 307-326.

- Parkinson**, G., Vojtechovsky, J., Clowney, L., Brunger, A.T. und Berman, H.M. (1996). Newparameters for the refinement of nucleic acid-containing structures. *Acta Cryst.*, **D52**,57-64.
- Phillips**, S.E. (1994). The β -ribbon DNA recognition motif. *Annu. Rev. Biophys. Biomol. Struct.*, **23**, 671-701.
- Pike**, A.C.W., Yang, X., Colebrook, S., Gileadi, O., Sobott, F., Bray, J., Wen Hwa, L., Marsden, B., Zhao, Y., Schoch, G., Elkins, J., Debreczeni, J.E., Turnbull, A.P., Von Delft, F., Arrowsmith, C., Edwards, A., Weigelt, J., Sundstrom, M., Doyle, D. The Crystal Structure of the Human Rnd1 Gtpase in the Active GTP Bound State *To be Published* .
- Pujol**, C., Chedin, F., Ehrlich, S.D. und Janniere, L. (1998). Inhibition of a naturally occurring rolling-circle replicon in derivatives of the τ -replicating plasmid pIP501. *Mol. Microbiol.*, **29**, 709-718.
- Potter**, H. (1988). Electroporation in biology: methods, applications, and instrumentation. *Analyt. Biochem.*, **174**, 361-373.
- Quisel** J.D., Lin D.C. und Grossman A.D. (1999). Control of development by altered localization of a transcription factor in *B. subtilis*. *Mol Cell* **4**: 665–672.
- Quisel** J.D. und Grossman A.D. (2000). Control of sporulation gene expression in *B. subtilis* by the chromosome partitioning proteins Soj (ParA) and Spo0J (ParB). *J. Bacteriol.* **182**, 3446–3451.
- Radnedge** L., Youngren B., Davis M. und Austin S. (1998). Probing the structure of complex macromolecular interactions by homolog specificity scanning: the P1 and P7 plasmid partition systems. *EMBO J.* **17**, 6076–6085.
- Raumann**, B. E., Rould, M.A., Pabo, C.O. und Sauer, R.T. (1994). DNA recognition by β - sheets in the Arc repressor-operator crystal structure. *Nature*, **367**, 754-757.
- Raskin**, D. M., und de Boer, P.A. (1999). MinDE-dependent pole-to-pole oscillation of division inhibitor MinC in *Escherichia coli*. *J. Bacteriol.* **181**, 6419–6424.
- Ravin** N. V., Rech J. und Lane D. (2003). Mapping of functional domains in F plasmid partition proteins reveals a bipartite SopB-recognition domain in SopA. *J. Mol. Biol.*, **329**, 875–889.
- Read** T. D. und weitere 20 Mitarbeiter. (2003). The genome sequence of *Bacillus anthracis* Ames and comparison to closely related bacteria. *Nature*, **423** (6935), 81-6.
- Roberts**, R. C., Spangler, C. und Helinski, D.R. (1993). Characteristics and significance of DNA binding activity of plasmid stabilization protein ParD from the broad host- range plasmid RK2. *J. Biol. Chem.*, **268**, 27109-27117.

- Rost**, B. und Sander, C. (1993). Prediction of protein secondary structure at better than 70% accuracy. *J. Mol. Biol.*, **232**, 584-599.
- Rost**, B., Yachdav, G. und Liu, J. (2004). The Predict Protein server. *Nucleic Acids Res.*, **32**, W321-326.
- Rothfield** L, Justice S. und Garcia-Lara J. (1999). Bacterial cell division. *Annu. Rev.Genet.* **33**,423–48
- Rossmann**, M. G. und Blow, D. M. (1962). The detection of sub-units within the crystallographic asymmetric unit. *Acta. Cryst.*, **15**: 24-31.
- Sakai**, N., Yao, M., Itou, H., Watanabe, N., Yumoto, F., Tanokura, M. und Tanaka, I. (2001). The three-dimensional structure of septum site-determining protein MinD from *Pyrococcus horikoshii* OT3 in complex with Mg-ADP. *Structure* **9**,817-826.
- Salje**, Jeanne, Benoît Zuber und Jan Löwe (2009). Segregation Filament Bundles Involved in Plasmid DNA Electron Cryomicroscopy of *E. coli* Reveals. *Science* **323**, 509. DOI: 10.1126/science.1164346
- Sandalova**, T., Schneider, G., Kaeck, H., Lindqvist, Y. und Lorimer, G. (1999). The crystal structure of an ATP-dependent carboxylase, dethiobiotin synthase, at 1.65 Å Resolution. *RCBS- Daten Bank Eintrag*:1byi.
- Sanger**, F., Nicklen, S. und 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. und Spehner, J. C. (1996a). Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers*, **38**, 305-320.
- Sanner**, M. F., Spehner, J.-C. und Olson, A. J. (1996b). Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers. Biopolymers*, **38**, 305-320.
- Sawitzke**, J. und Austin, S. A., (2001). An analysis of the factory model for chromosome replication and segregation in bacteria. *Mol. Microbiol.* **40**, 786–794.
- Schildbach**, J. F., Karzai, A. W., Raumann, B. E. und Sauer, R. T.(1999). Origins of DNA binding specificity: role of protein contacts with the DNA backbone. *Proc. Natl. Acad. Sci. U S A*, **96**, 811-817.
- Schindelin**, H., Kisker, C., Schlessman, J. L., Howard, J. B., und Rees, D. C. (1997). Structure of ADP x AIF4 (-)-stabilized nitrogenase complex and its implications for signal transduction. *Nature* **387**, 370–376.
- Sen**, S., Krishnakumar, A., Mcclead, J., Johnson, M.K., Seefeldt, L.C., Szilagyi, R.K. und Peters, J.W. (2006). Insights into the role of nucleotide-dependent conformational change in nitrogenase catalysis: Structural characterisation of the nitrogenase Fe protein Leu127 deletion variant with bound Mg ATP. *RCSB- Daten Bank Eintrag*: **2c8v**.

- Sitkiewicz**, U., Zielenkiewicz, R., Pankiewicz, I., Kern, I., Alonso, J.C. und Ceglowski, P. (1999). Characterization of the region involved in a better-than-random segregation of streptococcal plasmid pSM19035. *Plasmid* **41**, 161-162.
- Song**, H., Parsons, M. R., Rowsell, S., Leonard, G. und Phillips, S. E. (1999). Crystal structure of intact elongation factor EF-Tu from *Escherichia coli* in GDP conformation at 2.05 Å resolution. *J.Mol.Biol.* **285**, 1245-1256 ,.
- Stirling**, C. J., Szatmari, G., Stewart, G., Smith, M. C. M., und Sherratt, D. J., (1988). The arginine repressor is essential for plasmid stabilizing site-specific recombination at the ColE1 *cer* locus. *EMBO J.*, **7**, 4389-4395.
- Stirling**, C.J., Colloms, S.D., Collins, J.F., Szatmari, G., und Sherratt, D.J., (1989). *xerB*, an *Escherichia coli* gene required for plasmid ColE1 site-specific recombination is identical to *pepA*, encoding aminopeptidase A, a protein with substantial similarity to bovine lens leucine aminopeptidase. *EMBO J.*, **8**, 1623-1627.
- Storoni**, L. C., McCoy, A. J. und Read, R. J. (2004). Likelihood-enhanced fast rotation functions. *Acta Cryst.*, **D60**, 432-438.
- Suefuji**, K., Valluzzi, R. and RayChaudhuri, D. (2002) Dynamic assembly of MinD into filament bundles modulated by ATP, phospholipids, and MinE. *Pro.c Natl. Acad. Sci. U S A*, **99**, 16776-16781.
- Summers**, D. (1998). Timing, self-control and a sense of direction are the secrets of multicopy plasmid stability. *Mol. Microbiol.*, **29**, 1137-1145.
- Surtees**, J. A., und Funnell, B. E. (1999). P1 ParB domain structure includes two independent multimerization domains. *J. Bacteriol.*, **181**, 5898-5908.
- Surtees**, J. A., und Funnell, B. E. (2003). Plasmid and chromosome traffic control: How ParA and parB drive partition. *Current Topic in Developmental Biology* **56**, 145-180.
- Suzuki**, M. (1995). DNA recognition by a β -sheet. *Protein Eng.*, **8**, 1-4.
- Suzuki**, M. und Yagi, N. (1995). Stereochemical basis of DNA bending by transcription factors. *Nucleic Acids Res.*, **23**, 2083-2091.
- Terwilliger**, T. C. (2000). Maximum-likelihood density modification. *Acta Cryst.*, **D56**, 965-972.
- Thomas**, C. M., (2000). Paradigms of plasmid organization. *Mol Microbiol. Rev.*(**3**), 485-91.
- Thomas**, C. M., (2006). Transcription regulatory circuits in bacterial plasmids. *Biochem. Soc. Trans.* (Pt **6**), 1072-4.
- Thompson**, J. D., Higgins, D. G. und Gibson, T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positionsspecific gap penalties and weight matrix choice. *Nucleic Acids Research* **22**, 4673-4680.

- Thorsted** P.B., Macartney D.P., Akhtar P., Haines A.S., Ali N., Davidson P., Stafford T., Pocklington M.J., Pansegrau W., Wilkins B.M., Lanka E., Thomas C. M. Complete sequence of the IncPbeta plasmid R751: implications for evolution and organisation of the IncP backbone. *J Mol Biol.* **282**, 969-90.
- Vagin**, A. und Teplyakov, A. (1997). MOLREP: an automated program for molecular replacement. *J. Appl. Cryst.*, **30**, 1022-1025.
- van den Ent**, F., Amos, L. und Löwe, J. (2001). Bacterial ancestry of actin and tubulin. *Curr. Opin. Microbiol.*, **4**, 634-638.
- van den Ent**, F., Moller-Jensen, J., Amos, L. A., Gerdes, K. und Lowe, J. (2002). F-actin-like filaments formed by plasmid segregation protein ParM. *EMBO J.*, **21**, 6935-6943.
- van Melderen** L., (2002). Molecular interactions of the CcdB poison with its bacterial target, the DNA gyrase. Review. *Int. J. Med. Microbiol.* **291**, 537
- Vonrhein**, C., Bonisch, H., Schafer, G., Schulz, G. E. (1998). The structure of a trimeric archaeal adenylate kinase. *J.Mol. Biol.* **282**.167-179.
- Walker**, J. E., Saraste, M., Runswick, M. J., und Gay, N. J. (1982). Distantly related sequences in the alpha- and beta-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold. *EMBO J.* **1**, 945-951.
- Wang**, J. D., Rokop, M. E., Barker, M. M., Hanson, N.R. und Grossman, A. D. (2004). Multicopy plasmids affect replisome positioning in *Bacillus subtilis*. *J. Bacteriol*, **186**, 7084-7090.
- Webb**, C. D., Teleman, A., Gordon, S., Straight, A., Belmont, A., Lin, D. C., et al. (1997). Bipolar localization of the replication origin regions of chromosomes in vegetative and sporulating cells of *B. subtilis*. *Cell* **88**, 667-674.
- Webb**, C. D., Graumann, P.L., Kahana, J. A., Teleman, A. A., Silver, P. A., und Losick, R. (1998). Use of time-lapse microscopy to visualize rapid movement of the replication origin region of the chromosome during the cell cycle in *Bacillus subtilis*. *Mol. Microbiol.*, **28**, 883-892.
- Weihofen**, W.A., Cicek, A., Pratto, F., Alonso, J.C. und Saenger, W. (2006) Structures of omega repressors bound to direct and inverted DNA repeats explain modulation of transcription. *Nucleic Acids Res*, **34**, 1450-1458.
- Welfle**, K., Pratto, F., Misselwitz, R., Behlke, J., Alonso, J. C., und Welfle, H. (2005). Role of the N-terminal region and of beta-sheet residue Thr29 on the activity of the omega2 global regulator from the broad-host range *Streptococcus pyogenes* plasmid pSM19035. *Biol. Chem.* **386**, 881-894.
- Wheeler**, R. T. und Shapiro, L. (1997). Bacterial chromosome segregation: is there a mitotic apparatus? *Cell*, **88**, 577-579.
- White**, B. A. (1993). *PCR protocols : current methods and applications*. Humana Press.

-
- Totowa, N. J.** Williams, D. R. und Thomas, C. M. (1992). Active partitioning of bacterial plasmids. *J. Gen. Microbiol.*, **138**, 1-16.
- Winter, R.** und Noll, F. (1998). Methoden der Biophysikalischen Chemie. *Teubner Studienbücher Chemie*, Stuttgart.
- Xu, X.**, Sun, Y. L. und Hoey, T. (1996). Cooperative DNA binding and sequence-selective recognition conferred by the STAT amino-terminal domain. *Science*, **273**, 794-797.
- Yap, K.L.**, Ames, J.B., Swindells, M.B. und Ikura, M. (1999). Diversity of conformational states and changes withing the EF-hand protein superfamily. *Proteins*, **37** 499-507.
- Zhou, T.**, Radaev, S., Rosen, B. P., und Gatti, D. L. (2000). Structure of the ArsA ATPase: the catalytic subunit of a heavy metal resistance pump. *EMBO J.* **19**, 4838–4845.
- Zhou, T.**, Radaev, S., Rosen, B. P., und Gatti, D. L. (2001). Conformational changes in four regions of the *Escherichiacoli* ArsA ATPase link ATP hydrolysis to ion translocation. *J. Biol. Chem.*, **276**, 30414–30422.