

Prof. Dirk Heinz: List of Publications (as of July 2023)

1. M. K. Groenewold *et al.*, Virulence of *Agrobacterium tumefaciens* requires lipid homeostasis mediated by the lysyl-phosphatidylglycerol hydrolase AcvB. *Molecular microbiology* 111, 269-286 (2019).
2. M. K. Groenewold *et al.*, A phosphatidic acid-binding protein is important for lipid homeostasis and adaptation to anaerobic biofilm conditions in *Pseudomonas aeruginosa*. *The Biochemical journal* 475, 1885-1907 (2018).
3. J. Krausze *et al.*, Dimerization of the plant molybdenum insertase Cnx1E is required for synthesis of the molybdenum cofactor. *The Biochemical journal* 474, 163-178 (2017).
4. J. Debarry, D. Heinz, M. P. Manns, [Individualized infection medicine: Challenges and opportunities]. *Der Internist* 58, 647-649 (2017).
5. A. Kling *et al.*, Targeting DnaN for tuberculosis therapy using novel griselimycins. *Science* 348, 1106-1112 (2015).
6. S. Hebecker *et al.*, Structures of two bacterial resistance factors mediating tRNA-dependent aminoacylation of phosphatidylglycerol with lysine or alanine. *Proceedings of the National Academy of Sciences of the United States of America* 112, 10691-10696 (2015).
7. F. Kolditz, J. Krausze, D. W. Heinz, H. H. Niemann, C. C. Müller-Goymann, Wound healing potential of a dimeric InlB variant analyzed by in vitro experiments on re-epithelialization of human skin models. *European journal of pharmaceuticals and biopharmaceutics : official journal of Arbeitsgemeinschaft für Pharmazeutische Verfahrenstechnik e.V* 86, 277-283 (2014).
8. K. Haufschildt *et al.*, The crystal structure of siroheme decarboxylase in complex with iron-uroporphyrin III reveals two essential histidine residues. *Journal of molecular biology* 426, 3272-3286 (2014).
9. J. Moser *et al.*, Structure of ADP-aluminium fluoride-stabilized protochlorophyllide oxidoreductase complex. *Proceedings of the National Academy of Sciences of the United States of America* 110, 2094-2098 (2013).
10. M. Kudryashev *et al.*, In situ structural analysis of the *Yersinia enterocolitica* injectisome. *eLife* 2, e00792 (2013).
11. T. Hofmeyer *et al.*, Arranged sevenfold: structural insights into the C-terminal oligomerization domain of human C4b-binding protein. *Journal of molecular biology* 425, 1302-1317 (2013).
12. D. W. Heinz, Secrets of a secretin. *Structure (London, England : 1993)* 21, 2098-2099 (2013).
13. B. Glotzbach *et al.*, Structural characterization of *Spinacia oleracea* trypsin inhibitor III (SOTI-III). *Acta crystallographica. Section D, Biological crystallography* 69, 114-120 (2013).
14. C. Fradrich *et al.*, Purification, crystallization and preliminary X-ray analysis of the effector domain of AlsR, an LysR-type transcriptional regulator from *Bacillus subtilis*. *Acta crystallographica. Section F, Structural biology and crystallization communications* 69, 581-584 (2013).
15. M. Tischler *et al.*, Braces for the peptide backbone: insights into structure-activity relationships of protease inhibitor mimics with locked amide conformations. *Angewandte Chemie (International ed. in English)* 51, 3708-3712 (2012).
16. N. Quade *et al.*, Structural basis for intrinsic thermosensing by the master virulence regulator RovA of *Yersinia*. *The Journal of biological chemistry* 287, 35796-35803 (2012).
17. N. Quade, D. W. Heinz, R. Müller, Biosynthesis of secondary and natural materials: Where do unusual side chains in polyketides come from? *BioSpektrum* 18, 789-792 (2012).
18. H. H. Niemann, E. Gherardi, W. M. Bley Müller, D. W. Heinz, Engineered variants of InlB with an additional leucine-rich repeat discriminate between physiologically relevant and packing contacts in crystal structures of the InlB:MET complex. *Protein science : a publication of the Protein Society* 21, 1528-1539 (2012).
19. J. Kugler *et al.*, High affinity peptide inhibitors of the hepatitis C virus NS3-4A protease refractory to common resistant mutants. *The Journal of biological chemistry* 287, 39224-39232 (2012).
20. S. Wilke *et al.*, Streamlining homogeneous glycoprotein production for biophysical and structural applications by targeted cell line development. *PloS one* 6, e27829 (2011).
21. C. P. Strube *et al.*, Polysaccharide synthesis of the levansucrase SacB from *Bacillus megaterium* is controlled by distinct surface motifs. *The Journal of biological chemistry* 286, 17593-17600 (2011).

22. S. Storbeck *et al.*, Crystal structure of the heme d1 biosynthesis enzyme NirE in complex with its substrate reveals new insights into the catalytic mechanism of S-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferases. *The Journal of biological chemistry* 286, 26754-26767 (2011).
23. N. Quade, L. Huo, S. Rachid, D. W. Heinz, R. Muller, Unusual carbon fixation gives rise to diverse polyketide extender units. *Nature chemical biology* 8, 117-124 (2011).
24. N. Quade *et al.*, Structure of the effector-binding domain of the LysR-type transcription factor RovM from *Yersinia pseudotuberculosis*. *Acta crystallographica. Section D, Biological crystallography* 67, 81-90 (2011).
25. J. C. de Groot *et al.*, Structural basis for complex formation between human IRSp53 and the translocated intimin receptor Tir of enterohemorrhagic *E. coli*. *Structure (London, England : 1993)* 19, 1294-1306 (2011).
26. K. Rand *et al.*, The oxygen-independent coproporphyrinogen III oxidase HemN utilizes harderoporphyrinogen as a reaction intermediate during conversion of coproporphyrinogen III to protoporphyrinogen IX. *Biological chemistry* 391, 55-63 (2010).
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28. B. U. Klink *et al.*, Structure of *Shigella* IpgB2 in complex with human RhoA: implications for the mechanism of bacterial guanine nucleotide exchange factor mimicry. *The Journal of biological chemistry* 285, 17197-17208 (2010).
29. D. W. Heinz, C. Betzel, M. Wilmanns, Highlight: of systems and structures. *Biological chemistry* 391, 717-718 (2010).
30. I. U. Heinemann *et al.*, Structure of the heme biosynthetic *Pseudomonas aeruginosa* porphobilinogen synthase in complex with the antibiotic alaremycin. *Antimicrobial agents and chemotherapy* 54, 267-272 (2010).
31. M. Haffke, A. Menzel, Y. Carius, D. Jahn, D. W. Heinz, Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. *Acta crystallographica. Section D, Biological crystallography* 66, 979-987 (2010).
32. D. M. Ferraris, E. Gherardi, Y. Di, D. W. Heinz, H. H. Niemann, Ligand-mediated dimerization of the Met receptor tyrosine kinase by the bacterial invasion protein InlB. *Journal of molecular biology* 395, 522-532 (2010).
33. M. J. Brocker *et al.*, Crystal structure of the nitrogenase-like dark operative protochlorophyllide oxidoreductase catalytic complex (ChlN/ChlB)₂. *The Journal of biological chemistry* 285, 27336-27345 (2010).
34. U. Wiesand *et al.*, Structure of the type III secretion recognition protein YscU from *Yersinia enterocolitica*. *Journal of molecular biology* 385, 854-866 (2009).
35. M. Marin, D. W. Heinz, D. H. Pieper, B. U. Klink, Crystal structure and catalytic mechanism of 4-methylmuconolactone methylisomerase. *The Journal of biological chemistry* 284, 32709-32716 (2009).
36. G. Hagelueken *et al.*, The absolute configuration of rhizopodin and its inhibition of actin polymerization by dimerization. *Angewandte Chemie (International ed. in English)* 48, 595-598 (2009).
37. M. Bublitz *et al.*, Structural basis for autoinhibition and activation of Auto, a virulence-associated peptidoglycan hydrolase of *Listeria monocytogenes*. *Molecular microbiology* 71, 1509-1522 (2009).
38. K. U. Wendt, M. S. Weiss, P. Cramer, D. W. Heinz, Structures and diseases. *Nature structural & molecular biology* 15, 117-120 (2008).
39. H. H. Niemann *et al.*, X-ray and neutron small-angle scattering analysis of the complex formed by the Met receptor and the *Listeria monocytogenes* invasion protein InlB. *Journal of molecular biology* 377, 489-500 (2008).
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41. M. Bublitz *et al.*, Crystal structure and standardized geometric analysis of InlJ, a listerial virulence factor and leucine-rich repeat protein with a novel cysteine ladder. *Journal of molecular biology* 378, 87-96 (2008).

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43. T. Wollert *et al.*, Extending the host range of *Listeria monocytogenes* by rational protein design. *Cell* 129, 891-902 (2007).
44. T. Wollert, D. W. Heinz, W. D. Schubert, Thermodynamically reengineering the listerial invasion complex InlA/E-cadherin. *Proceedings of the National Academy of Sciences of the United States of America* 104, 13960-13965 (2007).
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46. C. Luer *et al.*, Glutamate recognition and hydride transfer by *Escherichia coli* glutamyl-tRNA reductase. *The FEBS journal* 274, 4609-4614 (2007).
47. G. Hagelueken *et al.*, Crystal structure of the electron transfer complex rubredoxin rubredoxin reductase of *Pseudomonas aeruginosa*. *Proceedings of the National Academy of Sciences of the United States of America* 104, 12276-12281 (2007).
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51. G. Layer *et al.*, The substrate radical of *Escherichia coli* oxygen-independent coproporphyrinogen III oxidase HemN. *The Journal of biological chemistry* 281, 15727-15734 (2006).
52. D. W. Heinz, M. S. Weiss, K. U. Wendt, Biomacromolecular interactions, assemblies and machines: a structural view. *Chembiochem : a European journal of chemical biology* 7, 203-208 (2006).
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