Prof. Dr. Dirk Heinz: List of Publications (as of September 2026)

1. S. Lata & D. W. Heinz, ECLIPSE: exploring the dark proteome of ESKAPE pathogens through the sequence similarity network of the Protein Universe Atlas. *Bioinformatics* 42, btag613 (2026).

2. B. Yuan *et al.*, Molecular insights into the capsular polysaccharide transporter Wza-Wzc complex. *Nature Communications* 17, 1436 (2026).

3. O. Dmytrenko *et al.*, RNA-triggered Cas12a3 cleaves tRNA tails to execute bacterial immunity. *Nature* 649, 1312-1321 (2026).

4. S. Eisa *et al.*, Targeting isoprenoid-precursor biosynthesis in Klebsiella pneumoniae: Design, synthesis and evaluation of 1-deoxy-D-xylulose 5-phosphate synthase (DXPS) inhibitors. *Bioorg. Chem.* 164, 108877 (2025).

5. 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).

6. 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).

7. 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).

8. J. Debarry, D. Heinz, M. P. Manns, [Individualized infection medicine: Challenges and opportunities]. *Der Internist* 58, 647-649 (2017).

9. A. Kling *et al.*, Targeting DnaN for tuberculosis therapy using novel griselimycins. *Science* 348, 1106-1112 (2015).

10. 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).

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12. 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).

13. 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).

14. M. Kudryashev *et al.*, In situ structural analysis of the Yersinia enterocolitica injectisome. *eLife* 2, e00792 (2013).

15. 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).

16. D. W. Heinz, Secrets of a secretin. *Structure (London, England : 1993)* 21, 2098-2099 (2013).

17. B. Glotzbach *et al.*, Structural characterization of Spinacia oleracea trypsin inhibitor III (SOTI-III). *Acta crystallographica. Section D, Biological crystallography* 69, 114-120 (2013).

18. 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).

19. 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).

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