Udo Heinemann, Dr. rer. nat., leads the *Macromolecular Structure and Interaction* Laboratory at the Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin. He has recently retired from his position as full professor at the Chemistry and Biochemistry Department of Freie Universität Berlin. He received his doctoral degree from Georg August University in Göttingen, Germany, worked as a postdoctoral researcher in the Molecular Biology Institute of the University of California at Los Angeles and was appointed to his current position at the Max Delbrück Center after independent research at Freie Universität Berlin, partly funded by a Heisenberg Fellowship from the German Research Foundation (DFG), and a year as non-tenured associate professor in the Organic Chemistry Department of the University of Stuttgart, Germany. Professor Heinemann's research combines biochemistry and molecular biology with protein crystallography. He was Chair of the German National Committee for Crystallography, President of the German Crystallographic Society and is currently the President of the European Crystallographic Association. Throughout his scientific career, he has been interested in the structural basis of gene expression regulation. Recently, his laboratory studied the regulation of let-7 microRNA biogenesis by the RNA-binding protein Lin28 and proposed a model for the sequential binding of the Lin28 cold-shock and zinc knuckle domains to let-7 precursor RNA. A second protein active in translational gene expression control, Roquin-1, was shown to bind mRNA 3'UTR sequences via its conserved ROQUIN domain, mediating their degradation and down-regulation of genes in the immune system. In transcriptional regulation, two classical transcription factor families were structurally characterized. Here, recognition of DNA target sequences by Krueppel-like factor 4 (Klf4) on one side and the Grainyhead-like proteins 1 and 2 (Grhl1,2) followed very different strategies. In both cases, the full landscape of transcription factor-binding sequences remained unexplored by biochemical and structural studies. To achieve a comprehensive description of DNA target recognition by some transcription factors is the Heinemann laboratory's aim within this Research Unit.

Publications (selection):

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3 Sachs, R.*, Max, K.E.A.*, Heinemann, U.# & Balbach, J.# (2012) RNA single strands bind to a conserved surface of the major cold shock protein in crystals and solution. *RNA* **18**, 65-76.

4 Schuetz, A., Murakawa, Y., Rosenbaum, E., Landthaler, M. & Heinemann, U. (2014) Roquin binding to target mRNAs involves a winged helix-turn-helix motif. *Nat. Commun.* **5**:5701.

5 Murakawa, Y., Hinz, M., Mothes, J., Schuetz, A., Uhl, M., Wyler, E., Yasuda, T., Mastrobuoni, G., Friedel, C.C., Dölken, L., Kempa, S., Schmidt-Supprian, M., Blüthgen, N., Backofen, R., Heinemann, U., Wolf, J., Scheidereit, C. & Landthaler, M. (2015) RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-κB pathway. *Nat. Commun*. **6**:8367.

6 Ming, Q., Roske, Y., Schuetz, A., Walentin, K., Ibraimi, I., Schmidt-Ott, K.M. & Heinemann, U. (2018) Structural basis of gene regulation by the Grainyhead/CP2 transcription factor family. *Nucleic Acids Res*. **46**, 2082-2095.