AG Schwarzer (UMG)

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Members:
Adrian Schwarzer, MD PhD (PI)
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Abstract: *(max. 100 words)*
We are developing and utilizing advanced functional genetic tools to model and investigate hematological malignancies. To achieve this, we are combining a wide range of methods including bioinformatics, conditional gene expression, inducible RNAi, CRISPR-Cas9 screens, transgenic mouse strains, and homologous recombination using CRISPR-Cas9 and adeno-associated viruses (AAV). Using these tools, we are creating leukemia mouse models that more accurately replicate the complexity, diversity, and plasticity of these diseases. We then systematically study these models *in vitro* and *in vivo* using high-throughput techniques such as CRISPR screens, single-cell RNA sequencing, and targeted protein degradation to identify novel genetic dependencies that can be exploited as therapeutic targets.

Key techniques:
- Viral gene/shRNAmiR/sgRNA transfer, CRISPR- and shRNA screens
- Conditional gene-expression and knockdown using Tet/ERT/AID systems
- HDR-genome editing using CRISPR-Cas9 RNP and AAV6
- Leukemia mouse models based on genetically engineered hematopoietic stem cells
- Development of Full-spectrum Flow Cytometry assays for MRD in AML

Special lab equipment: BD FACS Symphony A1, Keyence BZ-X800 Fluorescence Microscope, Vilber Fusion FX7 Edge, Spectramax ID3 Plate Reader

We seek cooperation in the field of: Bioinformatics, Proteomics, PROTACS

Key publications: (max. 3 references)

Schnoeder, TM, **Schwarzer, A**,..., Heidel, F. PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. ***Blood*** (2021). doi:10.1182/blood.2021012778

Schwarzer A, Talbot SR, …, Rothe M. Predicting genotoxicity of viral vectors for stem cell gene therapy using gene expression-based machine learning. ***Molecular Therapy*** *(*2021). doi: 10.1016/j.ymthe.2021.06.017

Schwarzer A, Emmrich S,..., Klusmann JH. The non-coding RNA landscape of human hematopoiesis and leukemia. ***Nature Communications*** (2017). doi: 10.1038/s41467-017-00212-4