

## Dahl, Andreas, PhD (Z02)

### Personal Data

Title	Dr.
First name	Andreas
Name	Dahl
Current position	Head of DRESDEN-concept Genome Center; permanent position
Current institution(s)/site(s), country	Technische Universität Dresden (TUD), Center for Molecular and Cellular Bioengineering, DRESDEN-concept Genome Center, Fetscherstr. 74, 01307 Dresden, Germany
Identifiers/ORCID	ORCID-ID: 0000-0002-2668-8371

### Qualifications and Career

Stages	Periods and Details
Degree programme: Nutritional sciences	1995 – 2000, Diploma, University of Potsdam, Germany
Doctorate	05.07.2007: Supervisor: Hans Lehrach, <i>Development of a miniaturised platform for PCR based assays with application in gene expression analysis and SNP genotyping</i> , MPI for Molecular Genetics Berlin / Freie Universität (FU) Berlin, Germany
Stages of academic/ professional career	
Since 2013	Head of DRESDEN-concept Genome Center Dresden, Germany
Since 2010	Head of Deep Sequencing Group, BIOTEC TU Dresden, Germany
2007 – 2010	Junior Group Leader, Max Planck Institute for Molecular Genetics, Miniaturization in Functional Genomics, Technology Development Group, MOLGEN Berlin, Germany

### Scientific Results

#### Category A, \* contributed equally, # open access

- Willenborg S, Roscito JG, Gerbaulet A, Roers A, **Dahl A**, Eming SA & Reinhardt S. Isolation of macrophages from mouse skin wounds for single-cell RNA sequencing. **STAR Protoc** 2022; 3(2):101337. doi: 10.1016/j.xpro.2022.101337. # ([methods development for single cell transcriptomics](#))
- Morcos MNF, Li C, Munz CM, Greco A, Dressel N, Reinhardt S, Sameith K, **Dahl A**, Becker NB, Roers A, Höfer T & Gerbaulet A. Fate mapping of hematopoietic stem cells reveals two pathways of native thrombopoiesis. **Nat Commun** 2022; 13(1). doi: 10.1038/s41467-022-31914-z. # ([methods development for single cell transcriptomics](#))
- Kraus G, Weigelt M, Reinhardt S, Petzold A, **Dahl A**, Bonifacio E. Reproducibility of 10x Genomics single cell RNA sequencing method in the immune cell environment. **J**

- Immunol Methods** 2022; 502:113227. doi: 10.1016/j.jim.2022.113227 ([single cell transcriptomics benchmarking](#))
4. Wigger L, Barovic M, Brunner AD, Marzetta F, Schöniger E, Mehl F, Kipke N, Friedland D, Burdet F, Kessler C, Lesche M, Thorens B, Bonifacio E, Legido-Quigley C, Barbier Saint Hilaire P, Delerive P, **Dahl A**, Klose C, Gerl MJ, Simons K, Aust D, Weitz J, Distler M, Schulte AM, Mann M, Ibberson M, Solimena M. Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. **Nat Metab** 2021; 3(7):1017–1031. doi: 10.1038/s42255-021-00420-9 ([methods development low input transcriptomics](#))
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  6. Kalafati L, Kourtzelis I, Schulte-Schrepping J, Li X, Hatzioannou A, Grinenko T, Hagag E, Sinha A, Ha, C, Diet, S, de Jesus Domingues AM, Nati M, Sormendi S, Neuwirth A, Chatzigeorgiou A, Ziogas A, Lesche M, **Dahl A**, Henry I, Subramanian P, Wielockx B, Murray P, Mirtschink P, Chung KJ, Schultze JL, Netea MG, Hajishengallis G, Verginis P, Mitroulis I, Chavakis T. Innate Immune Training of Granulopoiesis Promotes Anti-tumor Activity. **Cell** 2020; 183(3):771-785.e12. doi: 10.1016/j.cell.2020.09.058. # ([methods for low input transcriptome analysis](#))
  7. Cosacak MI, Bhattarai P, Reinhardt S, Petzold A, **Dahl A**, Zhang Y, Kizil C. Single-Cell Transcriptomics Analyses of Neural Stem Cell Heterogeneity and Contextual Plasticity in a Zebrafish Brain Model of Amyloid Toxicity. **Cell Rep** 2019; 27(4):1307-1318.e3. doi: 10.1016/j.celrep.2019.03.090. # ([methods development low input transcriptomics](#))
  8. Brosch M, Kattler K, Herrmann A, von Schönfels W, Nordström K, Seehofer D, Damm G, Becker T, Zeissig S, Nehring S, Reichel F, Moser V, Thangapandi RV, Stickel F, Baretton G, Röcken C, Muders M, Matz-Soja M, Krawczak M, Gasparoni G, Hartmann H, **Dahl A**, Schafmayer C, Walter J, Hampe J. Epigenomic map of human liver reveals principles of zoned morphogenic and metabolic control. **Nat Commun** 2018; 9(1):4150. doi: 10.1038/s41467-018-06611-5. # ([liver biology](#))
  9. Nowoshilow S, Schloissnig S, Fei JF, **Dahl A**, Pang AWC, Pippel M, Winkler S, Hastie AR, Young G, Roscito JG, Falcon F, Knapp D, Powell S, Cruz A, Cao H, Habermann B, Hiller M, Tanaka EM, Myers EW. The axolotl genome and the evolution of key tissue formation regulators. **Nature** 2018; 554(7690):50-55. doi: 10.1038/nature25458. Epub 2018 Jan 24. Erratum in: *Nature* 2018 Jul;559(7712):E2. PMID: 29364872. ([long read sequencing technologies](#))
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