Name Dr. Katrin Mercedes Schüle

Institution: Institute of Experimental and Clinical Pharmacology and Toxicology, Faculty of Medicine

Contact: Phone: +49 761 203 96822, Email: katrin.schuele@pharmakol.uni-freiburg.de

Position: Junior Group Leader

Academic education including academic degrees

PhD Biology Institute of Molecular Biology (IMB) Mainz, University Mainz
01/2016-10/2019

Master of Science Biochemistry Goethe-University Frankfurt
10/2013-10/2015

Bachelor of Science Biochemistry Goethe-University Frankfurt
10/2010-07/2013

Scientific graduation

October 16th, 2019 PhD in Biology

Employment

Scientist Institute of Experimental and Clinical Pharmacology and Toxicology Albert-Ludwigs-University Freiburg, Prof. Dr. Sebastian Arnold
Since 02/2020

Scientist Institute of Molecular Biology (IMB) Mainz, Prof. Dr. Christof Niehrs
11/2019-01/2020

Other activities, awards and honours

2023-2024	CIBSS Launchpad Research Funding
2022-2023	Hans A. Krebs Medical Scientist Fellow
2021	MEDEP Young Investigator Award
01/2016-10/2019	International PhD Programme Fellowship from IMB Mainz
2015	„Merz-Förderpreis“ for the best degree in the course of studies Biochemistry, Chemistry and Pharmacy
10/2014-01/2015	Travel-Scholarship of the German Academic Exchange Service (DAAD)
2014	Dr. Albrecht Magen-Scholarship (Steuben-Schurz-Society)
2013-2015	Scholarship „Deutschlandstipendium“

Key words

Epigenetic mechanisms, transcription factor specificity, early mouse development, lineage segregation, mouse embryonic stem cells

Research description

Our scientific goal is to gain a deeper molecular understanding of how signalling cues and epigenetic changes during early mouse development are integrated to regulate transcription factor specificity. Transcription factor (TF) binding is sequence specific with each TF possessing its distinct DNA binding motif. However, variations in binding site occupancy and thus TF functions in different cell types imply additional regulatory mechanisms for TF binding specificity. One key example for variation in TF functions occurs during early embryonic development, when two of the most fundamental lineage decisions, segregation between inner cell mass (ICM) and trophectoderm (TE), and specification of the three germ layers neuroectoderm (NE), mesoderm and endoderm (ME), are made. These two lineage decisions are regulated by overlapping sets of transcription factors, including CDX and TBX factors. However, the underlying mechanisms that account for differences of TF functions between these two lineage choices and the integration of signalling cascades and epigenetic regulation are largely unexplored.

Ten most important publications

Schüle KM*[,1], Weckerle J, Probst S, Wehmeyer AE, Zissel L, Schröder CM, Tekman M, Kim G-J. Schlägl I-M, Sagar, Arnold SJ[1] (2023) Eomes restricts Brachyury function at the onset of mammalian gastrulation. bioRxiv doi.org/10.1101/2023.01.27.525830, Developmental Cell: in revisions

Wang S, Klein SO, Urban S, Staudt M, Barthes NPF, Willmann D, Bacher J, Sum M, Bauer H, Peng L, Rennar GA, Gratzke C, **Schüle KM**, Zhang L, Einsle O, Greschik H, MacLeod C, Thomson CG, Jung M, Eric Metzger E, Schüle R (2023) Structure-guided design of a selective inhibitor of the methyltransferase KMT9 with cellular activity. Nature Communications 15 (43), doi: 0.1038/s41467-023-44243-6

Wehmeyer AE, **Schüle KM**, Conrad A, Schröder SM, Probst S, Arnold SJ (2022) Chimeric 3D gastruloids – a versatile tool for studies of mammalian peri-gastrulation development. Development 149, dev200812.

Schüle KM*, Leichsenring M*, Andreani T, Vastolo V, Mallick M, Musheev MU, Karaulanov E, Niehrs C (2019) GADD45 promotes locus-specific DNA demethylation and 2C cycling in embryonic stem cells. Genes and Development 33, 782-798

Han D*, Schomacher L*, **Schüle KM***, Mallick M, Musheev MU, Karaulanov E, Krebs L, von Seggern A, Niehrs C (2019) NEIL1 and NEIL2 DNA glycosylases protect neural crest development against mitochondrial oxidative stress. eLife 8, 49044

Metzger E, Willmann D, McMillan J, Forne I, Metzger P, Gerhardt S, Petroll K, von Maessenhausen A, Urban S, Schott AK, Espejo A, Eberlin A, Wohlwend D, **Schüle KM**, Schleicher M, Perner S, Bedford MT, Jung M, Dengjel J, Flaig R, Imhof A, Einsle O, Schüle R (2016) Assembly of methylated KDM1A and CHD1 drives androgen receptor-dependent transcription and translocation. Nature Structural & Molecular Biology 23, 132-139