

Prof. Dr. Michael J. Ziller

Personal Data

Date of birth: 17/07/1983

Place of birth: Hamm (Germany)

Nationality: German

h-index: 28

Cumulated IF: 702

Total citations: 9,961

Research Experience

- | | |
|------------|---|
| Since 2020 | Full Professor for Functional Genomics in Psychiatry, Clinic for Mental Health, WWU Muenster |
| Since 2016 | Principal Investigator and Independent Group Leader, Max-Planck Institute of Psychiatry, Germany |
| 2014-2015 | Postdoctoral Fellow in the Department of Stem Cell and Regenerative Biology, Harvard University, USA |
| 2009-2015 | Graduate Research Assistant, The Broad Institute of Harvard and MIT, USA |
| 2010-2014 | PhD student in the Department of Stem Cell and Regenerative Biology, Harvard University and the Broad Institute of Harvard and MIT, USA |
| 2009-2010 | Visiting student in the Department of Stem Cell and Regenerative Biology, Harvard University and the Broad Institute, USA |

Education

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| 2010-2014 | Dr. rer. nat. in Bioinformatics, summa cum laude University of Tübingen, Germany (2014), Advisors:
Prof. Alex Meissner (Harvard University, USA)
Prof. Oliver Kohlbacher (University of Tübingen, Germany) |
| 2004-2010 | Diplom in Physics University of Tübingen, Germany - with honors
Major: Mathematical/ Computational Physics
Theses: Simulation of Protein Charge Distributions Under the Influence of Salt |
| 2003-2009 | Diplom in Bioinformatics, University of Tübingen, Germany - with honors
Major: Molecular Biology/ Genetics
Automated Mathematical Modeling of Biochemical Reaction Networks |

Key publications

Ziller MJ, Ortega JA, Quinlan KA, Santos DP, Gu H, Galonska C, Pop R, Martin EJ, Maidl S, Di Pardo A, Huang M, Meltzer HY, Heckman CJ, Gnirke A, Meissner A, Kiskinis E. Dissecting

the role of de Novo DNA methylation dynamics in the development and function of human motor neurons, *Cell Stem Cell*, 2018

Galonska C*, **Ziller MJ***, Karnik R, Meissner A, Ground state conditions induce rapid reorganization of core pluripotency factor binding that precede global epigenetic reprogramming, *Cell Stem Cell*, 2015

Cacchiarelli D*, Trapnell C*, **Ziller MJ***, Soumillon M, Cesana M, Smith ZD, Karnik R, Ratanasirintrao S, Zhang X, Wu Z, Akopian V, Gifford CA, Rinn JL, Daley GQ, Meissner A, Lander ES, Mikkelsen TS, A scalable cellular reprogramming system and integrative genomic approaches reveal ordered transitions towards pluripotency in human cells, *Cell*, 2015

Roadmap Epigenomics Consortium - **Co-leader integrative analysis**, Integrative analysis of 111 reference human epigenomes, *Nature*, 2015 – Featured as cover story

Ziller MJ, Reuven E, Yaffe Y, Donaghey J, Pop R, Mallard W, Issner R, Gifford CA, Goren A, Xing J, Gu H, Cacchiarelli D, Tsankov A, Epstein C, Rinn JL, Mikkelsen TS, Kohlbacher O, Gnirke A, Bernstein BE, Elkabetz Y, Meissner A, Dissecting neural differentiation regulatory networks through epigenetic footprinting, *Nature*, 2014 – Featured in News & Views, *Nature* 518, p.314-316 and the *Economist*, Feb 18th 2015

Ziller MJ, Hansen KD, Meissner A, Aryee MJ, Coverage and replicate requirements for whole genome bisulfite sequencing, *Nature Methods*, 2014

Ziller MJ, Gu H, Müller F, Donaghey J, Tsai LT, Kohlbacher O, De Jager PL, Rosen ED, Bennett DA, Bernstein BE, Gnirke A, Meissner A, Charting a dynamic DNA methylation landscape of the human genome, *Nature*, 2013 – Featured as cover story

Gifford CA*, **Ziller MJ***, Gu H, Trapnell C, Donaghey J, Tsankov A, Shalek AK, Kelley DR, Shishkin AA, Issner R, Zhang X, Coyne M, Fostel JL, Holmes L, Meldrim J, Guttman M, Epstein C, Park H, Kohlbacher O, Rinn J, Gnirke A, Lander ES, Bernstein BE, Meissner A, Transcriptional and epigenetic dynamics during specification of human embryonic stem cells, *Cell*, 2013

Ziller MJ*, Müller F*, Liao J, Zhang Y, Gu H, Bock C, Boyle P, Epstein CB, Bernstein BE, Lengauer T, Gnirke A, Meissner A, Genomic Distribution and Inter-Sample Variation of non-CpG Methylation Across Human Cell Types, *PloS Genetics*, 2011 – Featured as research highlight by *Nature Reviews in Genetics*, 13,75 2012

* Equal contribution

Co-Authored Publications

Genga RMJ, Kernfeld EM, Parsi KM, Parsons TJ, **Ziller MJ**, Maehr R Single-Cell RNA-Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Early Human Endoderm Development, *Cell Rep.*, 2019

Giulitti S, Pellegrini M, Zorzan I, Martini P, Gagliano O, Mutarelli M, **Ziller MJ**, Cacchiarelli D, Romualdi C, Elvassore N, Martello G Direct generation of human naive induced pluripotent stem cells from somatic cells in microfluidics, *Nat Cell Biol.*, 2019

Hoffmann A, **Ziller MJ**, Spengler D, Childhood-Onset Schizophrenia: Insights from Induced Pluripotent Stem Cells, *Int J Mol Sci.*, 2018 Review

Sheng C, Jungverdorben J, Wiethoff H, Lin Q, Flitsch LJ, Eckert D, Heibisch M, Fischer J, Kesavan J, Weykopf B, Schneider L, Holtkamp D, Beck H, Till A, Wüllner U, **Ziller MJ**, Wagner W, Peitz M, Brüstle O A stably self-renewing adult blood-derived induced neural stem cell exhibiting patternability and epigenetic rejuvenation, *Nat Commun.*, 2018

Ahmad R, Sportelli V, **Ziller MJ**, Spengler D, Hoffmann A Tracing Early Neurodevelopment in Schizophrenia with Induced Pluripotent Stem Cells, *Cells*. 2018 Review

Cacchiarelli D, Qiu X, Srivatsan S, Manfredi A, **Ziller MJ**, Overbey E, Grimaldi A, Grimsby J, Pokharel P, Livak KJ, Li S, Meissner A, Mikkelsen TS, Rinn JL, Trapnell C Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome, *Cell Syst.*, 2018

Charlton J, Downing TJ, Smith ZD, Gu H, Clement K, Pop R, Akopian V, Klages S, Santos D, Tsankov A, Timmermann B, **Ziller MJ**, Kiskinis E, Gnirke A, Meissner A, Global delay in nascent strand DNA methylation, *Nature Structural and Molecular Biology*, 2018

Galonska C, Charlton J, Mattei AL, Donaghey J, Clement K, Gu H, Mohammad A, Stamenova E, Cacchiarelli D, Klages S, Timmermann B, Cantz T, Schöler HR, Gnirke A, **Ziller MJ**, Meissner AM, Genome-wide tracking of dCas9-methyltransferase footprints, *Nature Communications*. 2018

Donaghey J, Thakurela S, Charlton J, Chen JS, Smith ZD, Gu H, Pop R, Clement K, Stamenova EK, Karnik R, Kelley DR, Gifford CA, Cacchiarelli D, Rinn JL, Gnirke A, **Ziller MJ**, Meissner A, Genetic determinants and epigenetic effects of pioneer-factor occupancy, *Nature Genetics*, 2018

Ziller MJ, Stamenova EK, Gu H, Gnirke A, Meissner A, Targeted bisulfite sequencing of the dynamic DNA methylome, *Epigenetics Chromatin*, 2016

Hoffmann A, **Ziller MJ**, Spengler D, The Future is The Past: Methylation QTLs in Schizophrenia, *Genes*, 2016

Yu VW, Yusuf RZ, Oki T, Wu J, Saez B, Wang X, Cook C, Baryawno N, **Ziller MJ**, Lee E, Gu H, Meissner A, Lin CP, Kharchenko PV, Scadden DT, Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells, *Cell*, 2016

Libertini E, Heath SC, Hamoudi RA, Gut M, **Ziller MJ**, Herrero J, Czyz A, Ruotti V, Stunnenberg HG, Frontini M, Ouwehand WH, Meissner A, Gut IG, Beck S, Saturation analysis for whole-genome bisulfite sequencing data, *Nat Biotechnol.*, 2016

Libertini E, Heath SC, Hamoudi RA, Gut M, **Ziller MJ**, Czyz A, Ruotti V, Stunnenberg HG, Frontini M, Ouwehand WH, Meissner A, Gut IG, Beck S, Information recovery from low coverage whole-genome bisulfite sequencing, *Nat Commun.*, 2016

Shea JM, Serra RW, Carone BR, Shulha HP, Kucukural A, **Ziller MJ**, Vallaster MP, Gu H, Tapper AR, Gardner PD, Meissner A, Garber M, Rando OJ, Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome, *Developmental Cell*, 2016

Jing L*, Karnik R*, Gu H, **Ziller MJ**, Clement K, Tsankov A, Akopian V, Gifford CA, Donaghey J, Galonska C, Gnirke A, Meissner A, Targeted disruption of DNMT1, 3A and 3B in human embryonic stem cells, *Nature Genetics*, 2015

Edri R*, Yaffe Y*, **Ziller MJ**, Ziv O, Mashenko D, Zaritski A, David E, Jacob-Hirsch J, Rechavi G, Gat-Vics I, Wolf L, Meissner A, Elkabetz Y, Prospective isolation of distinct human ES cell derived neural progenitor cells provides a cell culture model for CNS establishment and cerebral development, *Nature Communications*, 2015

Tsankov A, Gu H, Akopian A, **Ziller MJ**, Amit I, Meissner A, Modular and context dependent rewiring of transcription factor networks during human ESC differentiation, in *Nature*, 2015

Landau DA*, Clement K*, **Ziller MJ**, Boyle P, Gu H, Stevenson K, Sougnez C, Zhang W, Ghandi M, Garraway L, Kiezun A, Fernandes SM, Tesar B, Gabriel S, Gnirke A, Lander ES, Brown JR, Neuberg D, Hacohen D, Getz G, Meissner A, Wu CJ, Locally disordered DNA methylation contributes to intraleukemic epigenetic heterogeneity and clonal evolution, *Cancer Cell*, 2014

Ichida JK*, TCW J*, Williams LA*, Carter AC, Shi Y, Moura MT, **Ziller MJ**, Singh S, Amabile G, Bock C, Umezawa A, Rubin LL, Bradner JE, Akutsu H, Meissner AM, Eggan K, Notch inhibition allows oncogene-independent generation of iPS cells, *Nature Chemical Biology*, 2014

25. Kiskinis E*, Sandoe J*, Williams LA, Boulting GL, Moccia R, Wainger BJ, Han S, Peng T, Thams S, Mikkilineni S, Mellin C, Merkle FT, Davis-Dusenbery BN, **Ziller MJ**, Oakley D, Ichida J, Di Costanzo S, Atwater N, Maeder ML, Goodwin MJ, Nemesh J, Handsaker RE, Paull D, Noggle S, McCarroll SA, Joung JK, Woolf CJ, Brown RH, Eggan K, Pathways disrupted in human ALS motor neurons identified through genetic correction of mutant SOD1, *Cell Stem Cell*, 2014

Kearns NA, Genga RM*, **Ziller MJ***, Kapinas K, Peters H, Brehm MA, Meissner A, Maehr R, Generation of organized anterior foregut epithelia from pluripotent stem cells using small molecules, *Stem Cell Res*, 2013

Keller R, Dörr A, Tabira A, Funahashi A, **Ziller MJ**, Adams R, Rodriguez N, Novère NL, Hiroi N, Planatscher H, Zell A, Dräger A, The systems biology simulation core algorithm, *BMC Syst Biol* 2013

Akopian V, Chan MM, Clement K, Galonska C, Gifford CA, Lehtola E, Liao J, Samavarchi-Tehrani P, Sindhu C, Smith ZD, Tsankov AM, Webster J, Zhang Y, **Ziller MJ**, Meissner A, Epigenomics and chromatin dynamics, *Genome Biology*, 2012

Boyle P*, Clement K*, Gu H, Smith ZD, **Ziller MJ**, Fostel JL, Holmes L, Meldrim J, Kelly F, Gnirke A, Meissner A, Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling, *Genome Biology*, 2011

Bock C*, Kiskinis E*, Verstappen G*, Gu H, Boulting G, Smith ZD, **Ziller MJ**, Croft GF, Amoroso MW, Oakley DH, Gnirke A, Eggan K, Meissner A., Reference Maps of human ES and iPS cell variation enable high-throughput characterization of pluripotent cell lines, *Cell*, 2011

Zhang F, Weggler S, **Ziller MJ**, Ianeselli L, Heck BS, Hildebrandt A, Kohlbacher O, Skoda MW, Jacobs RM, Schreiber F., Universality of protein reentrant condensation in solution induced by multivalent metal ions, *Proteins*, 2010

Dräger A, Kronfeld M, **Ziller MJ**, Supper J, Planatscher H, Magnus JB, Oldiges M, Kohlbacher O, Zell A, Modeling Metabolic Networks in *C. glutamicum*: A Comparison of Rate Laws in Combination with Various Parameter Optimization Strategies, *BMC Sys Biol*, 2009

Awards and Fellowships

2010-2013 PhD fellowship by Studienstiftung des Deutschen Volkes

2009 DAAD Master Thesis Fellowship for Conducting Research Abroad

Third party funding

2019-2023	BMBF Computational Life Science Grant: MERGE- Model Exchange for regulatory genomics, 275K€ (810K€) Co-PI
2018-2021	„Schlüsselprojekt“ Else-Kröner-Fresenius Stiftung: Decoding the molecular basis of bipolar disorder, 625K€, PI
2017-2019	BMBF eMed Grant: Aberrant transcriptome influencing risk of common diseases, 150K€ (450K€) Co-PI
2016-2021	BMBF eMed Grant (01ZX1504): Research Group in Systems Medicine: Project DINGS, 1.9M€, PI
2016-2021	DFG Emmy Noether Grant, 1.4M€, PI, declined
2016-2021	NIH DP3 (1DP3DK111898-01) - Deciphering the molecular basis of T1D in human cells using functional genomics 450K€, Subcontractor