## Jan Philipp Junker

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Spatial transcriptomics unveils ZBTB11 as a regulator of cardiomyocyte degeneration in arrhythmogenic cardiomyopathy. Cardiovascular Research, 2023, 119, 477-491.	3.8	17
2	Single-cell-resolved dynamics of chromatin architecture delineate cell and regulatory states in zebrafish embryos. Cell Genomics, 2022, 2, 100083.	6.5	8
3	A single-cell atlas of <i>de novo</i> β-cell regeneration reveals the contribution of hybrid β/δ-cells to diabetes recovery in zebrafish. Development (Cambridge), 2022, 149, .	2.5	12
4	Variability of an Early Developmental Cell Population Underlies Stochastic Laterality Defects. Cell Reports, 2021, 34, 108606.	6.4	12
5	Single-cell genomics to study developmental cell fate decisions in zebrafish. Briefings in Functional Genomics, 2021, , .	2.7	1
6	Systematic identification of A-to-I RNA editing in zebrafish development and adult organs. Nucleic Acids Research, 2021, 49, 4325-4337.	14.5	21
7	Spatio-temporal mRNA tracking in the early zebrafish embryo. Nature Communications, 2021, 12, 3358.	12.8	25
8	Single cell biology—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
9	Multispecies RNA tomography reveals regulators of hematopoietic stem cell birth in the embryonic aorta. Blood, 2020, 136, 831-844.	1.4	28
10	Inclusion of temporal information in single cell transcriptomics. International Journal of Biochemistry and Cell Biology, 2020, 122, 105745.	2.8	4
11	The transcriptome dynamics of single cells during the cell cycle. Molecular Systems Biology, 2020, 16, e9946.	7.2	35
12	Detouring the roadblocks in gene expression. Nature Reviews Molecular Cell Biology, 2019, 20, 197-197.	37.0	2
13	RNA Tomography for Spatially Resolved Transcriptomics (Tomo-Seq). Methods in Molecular Biology, 2019, 1920, 129-141.	0.9	13
14	Transcription Factor Induction of Ectopic Vascular Blood Stem Cell Niches In Vivo. Blood, 2019, 134, 525-525.	1.4	5
15	Simultaneous lineage tracing and cell-type identification using CRISPR–Cas9-induced genetic scars. Nature Biotechnology, 2018, 36, 469-473.	17.5	396
16	Spatial Transcriptomics of C.Âelegans Males and Hermaphrodites Identifies Sex-Specific Differences in Gene Expression Patterns. Developmental Cell, 2018, 47, 801-813.e6.	7.0	55
17	Tomo-Seq Identifies SOX9 as a Key Regulator of Cardiac Fibrosis During Ischemic Injury. Circulation, 2017, 136, 1396-1409.	1.6	81
18	Methods for lineage tracing on the organism-wide level. Current Opinion in Cell Biology, 2017, 49, 16-21.	5.4	31

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19	Patched Receptors Sense, Interpret, and Establish an Epidermal Hedgehog SignalingÂGradient. Journal of Investigative Dermatology, 2017, 137, 179-186.	0.7	11
20	Tomo-seq. Methods in Cell Biology, 2016, 135, 299-307.	1.1	46
21	Spatially Resolved Genome-wide Transcriptional Profiling Identifies BMP Signaling as Essential Regulator of Zebrafish Cardiomyocyte Regeneration. Developmental Cell, 2016, 36, 36-49.	7.0	176
22	Genome-Wide RNA Tomography of the Hematopoietic Stem Cell Niche in Zebrafish Reveals Unexpected Functional Macrophage-Stem Cell Interactions. Blood, 2016, 128, 3882-3882.	1.4	0
23	DAZL regulates Tet1 translation in murine embryonic stem cells. EMBO Reports, 2015, 16, 791-802.	4.5	24
24	Single-Cell Transcriptomics Enters the Age of Mass Production. Molecular Cell, 2015, 58, 563-564.	9.7	17
25	Ascl2 Acts as an R-spondin/Wnt-Responsive Switch to Control Stemness in Intestinal Crypts. Cell Stem Cell, 2015, 16, 158-170.	11.1	217
26	Licensing of Primordial Germ Cells for Gametogenesis Depends on Genital Ridge Signaling. PLoS Genetics, 2015, 11, e1005019.	3.5	48
27	Genome-wide RNA tomography analysis of the microenvironment promoting hematopoietic stem cell emergence in the embryo aorta. Experimental Hematology, 2015, 43, S104.	0.4	0
28	A Gene Regulatory Program for Meiotic Prophase in the Fetal Ovary. PLoS Genetics, 2015, 11, e1005531.	3.5	93
29	A Predictive Model of Bifunctional Transcription Factor Signaling during Embryonic Tissue Patterning. Developmental Cell, 2014, 31, 448-460.	7.0	31
30	Every Cell Is Special: Genome-wide Studies Add a New Dimension to Single-Cell Biology. Cell, 2014, 157, 8-11.	28.9	177
31	Genome-wide RNA Tomography in the Zebrafish Embryo. Cell, 2014, 159, 662-675.	28.9	248
32	Single-molecule mRNA detection and counting in mammalian tissue. Nature Protocols, 2013, 8, 1743-1758.	12.0	187
33	Identification of molecular compartments and genetic circuitry in the developing mammalian kidney. Development (Cambridge), 2012, 139, 1863-1873.	2.5	51
34	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes and Development, 2012, 26, 2802-2816.	5.9	158
35	When Noisy Neighbors Are a Blessing: Analysis of Gene Expression Noise Identifies Coregulated Genes. Molecular Cell, 2012, 45, 437-438.	9.7	4
36	Evidence for a Broad Transitionâ€State Ensemble in Calmodulin Folding from Singleâ€Molecule Force Spectroscopy. Angewandte Chemie - International Edition, 2010, 49, 3306-3309.	13.8	23

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37	Single-molecule force spectroscopy distinguishes target binding modes of calmodulin. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14361-14366.	7.1	49
38	Ligand-Dependent Equilibrium Fluctuations of Single Calmodulin Molecules. Science, 2009, 323, 633-637.	12.6	203
39	Response to the Comment by Ainavarapu et al Biophysical Journal, 2006, 91, 2011-2012.	0.5	7
40	Cysteine engineering of polyproteins for single-molecule force spectroscopy. Nature Protocols, 2006, 1, 80-84.	12.0	71
41	Influence of Substrate Binding on the Mechanical Stability of Mouse Dihydrofolate Reductase. Biophysical Journal, 2005, 89, L46-L48.	0.5	59