

# Sebastian Preissl

## List of Publications by Year in descending order

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Version: 2024-02-01

38  
papers

6,344  
citations

117453

34  
h-index

264894

42  
g-index

63  
all docs

63  
docs citations

63  
times ranked

9663  
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. <i>Cell Stem Cell</i> , 2019, 25, 558-569.e7.	5.2	520
2	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. <i>Nature</i> , 2016, 537, 548-552.	13.7	484
3	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
4	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
5	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018, 21, 432-439.	7.1	290
6	Single-cell multimodal omics: the power of many. <i>Nature Methods</i> , 2020, 17, 11-14.	9.0	277
7	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. <i>Nature Communications</i> , 2014, 5, 5288.	5.8	272
8	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
9	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	5.8	253
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
11	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. <i>Nature Genetics</i> , 2019, 51, 1380-1388.	9.4	236
12	A single-cell atlas of chromatin accessibility in the human genome. <i>Cell</i> , 2021, 184, 5985-6001.e19.	13.5	194
13	Distinct epigenetic programs regulate cardiac myocyte development and disease in the human heart in vivo. <i>Nature Communications</i> , 2018, 9, 391.	5.8	181
14	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. <i>Nature</i> , 2021, 594, 398-402.	13.7	170
15	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
16	Pdgfra marks a cellular lineage with distinct contributions to myofibroblasts in lung maturation and injury response. <i>ELife</i> , 2018, 7, .	2.8	137
17	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021, 598, 120-128.	13.7	135
18	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. <i>Cell Research</i> , 2018, 28, 204-220.	5.7	131

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19	MOF Acetyl Transferase Regulates Transcription and Respiration in Mitochondria. <i>Cell</i> , 2016, 167, 722-738.e23.	13.5	130
20	Single-cell multiomic profiling of human lungs reveals cell-type-specific and age-dynamic control of SARS-CoV2 host genes. <i>ELife</i> , 2020, 9, .	2.8	129
21	Single-cell chromatin accessibility identifies pancreatic islet cell type-specific and state-specific regulatory programs of diabetes risk. <i>Nature Genetics</i> , 2021, 53, 455-466.	9.4	100
22	Preclinical Development of a MicroRNA-Based Therapy for Elderly Patients With Myocardial Infarction. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1557-1571.	1.2	99
23	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	6.0	96
24	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	13.7	95
25	DNA methylation signatures follow preformed chromatin compartments in cardiac myocytes. <i>Nature Communications</i> , 2017, 8, 1667.	5.8	76
26	Characterizing cis-regulatory elements using single-cell epigenomics. <i>Nature Reviews Genetics</i> , 2023, 24, 21-43.	7.7	72
27	Deciphering the Epigenetic Code of Cardiac Myocyte Transcription. <i>Circulation Research</i> , 2015, 117, 413-423.	2.0	71
28	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. <i>Cell Reports</i> , 2019, 29, 495-510.e6.	2.9	66
29	Cardiac cell type-specific gene regulatory programs and disease risk association. <i>Science Advances</i> , 2021, 7, .	4.7	63
30	Single-cell chromatin accessibility maps reveal regulatory programs driving early mouse organogenesis. <i>Nature Cell Biology</i> , 2020, 22, 487-497.	4.6	62
31	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
32	Adrenergic Repression of the Epigenetic Reader MeCP2 Facilitates Cardiac Adaptation in Chronic Heart Failure. <i>Circulation Research</i> , 2015, 117, 622-633.	2.0	57
33	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021, 39, 1000-1007.	9.4	53
34	Ablation of biglycan attenuates cardiac hypertrophy and fibrosis after left ventricular pressure overload. <i>Journal of Molecular and Cellular Cardiology</i> , 2016, 101, 145-155.	0.9	42
35	Epigenetics in cardiac development, function, and disease. <i>Cell and Tissue Research</i> , 2014, 356, 585-600.	1.5	37
36	The MUC5B-associated variant rs35705950 resides within an enhancer subject to lineage- and disease-dependent epigenetic remodeling. <i>JCI Insight</i> , 2021, 6, .	2.3	21

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37	Enhanced nucleoplasmic Ca <sup>2+</sup> signaling in ventricular myocytes from young hypertensive rats. <i>Journal of Molecular and Cellular Cardiology</i> , 2016, 101, 58-68.	0.9	17
38	Development of an Assay for Complex I/Complex III of the Respiratory Chain Using Solid Supported Membranes and Its Application in Mitochondrial Toxicity Screening in Drug Discovery. <i>Assay and Drug Development Technologies</i> , 2011, 9, 147-156.	0.6	2