

Christian Schmidl

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

8,105
citations

186209

28
h-index

345118

36
g-index

39
all docs

39
docs citations

39
times ranked

17781
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting clinical epigenetic reprogramming for chemoprevention of metabolic and viral hepatocellular carcinoma. <i>Gut</i> , 2021, 70, 157-169.	6.1	57
2	Cancer-associated cells release citrate to support tumour metastatic progression. <i>Life Science Alliance</i> , 2021, 4, e202000903.	1.3	21
3	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory T cells. <i>Immunity</i> , 2021, 54, 702-720.e17.	6.6	78
4	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. <i>Immunity</i> , 2020, 52, 295-312.e11.	6.6	140
5	Targeting Nuclear NOTCH2 by Gliotoxin Recovers a Tumor-Suppressor NOTCH3 Activity in CLL. <i>Cells</i> , 2020, 9, 1484.	1.8	7
6	Structural cells are key regulators of organ-specific immune responses. <i>Nature</i> , 2020, 583, 296-302.	13.7	292
7	Mechanisms governing the pioneering and redistribution capabilities of the non-classical pioneer PU.1. <i>Nature Communications</i> , 2020, 11, 402.	5.8	76
8	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. <i>Nature Communications</i> , 2020, 11, 577.	5.8	69
9	Genome-wide cooperation of EMT transcription factor ZEB1 with YAP and AP1 in breast cancer. <i>EMBO Journal</i> , 2020, 39, e103209.	3.5	104
10	Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethality in human cancers. <i>Nature Genetics</i> , 2019, 51, 1399-1410.	9.4	92
11	Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL. <i>Nature Chemical Biology</i> , 2019, 15, 232-240.	3.9	34
12	High-throughput ChIPmentation: freely scalable, single day ChIPseq data generation from very low cell-numbers. <i>BMC Genomics</i> , 2019, 20, 59.	1.2	30
13	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. <i>Nature Genetics</i> , 2019, 51, 990-998.	9.4	61
14	HCV-Induced Epigenetic Changes Associated With Liver Cancer Risk Persist After Sustained Virologic Response. <i>Gastroenterology</i> , 2019, 156, 2313-2329.e7.	0.6	184
15	Rbpj expression in regulatory T cells is critical for restraining TH2 responses. <i>Nature Communications</i> , 2019, 10, 1621.	5.8	41
16	Epigenetic mechanisms regulating T-cell responses. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 728-743.	1.5	100
17	The Peripheral and Intratumoral Immune Cell Landscape in Cancer Patients: A Proxy for Tumor Biology and a Tool for Outcome Prediction. <i>Biomedicines</i> , 2018, 6, 25.	1.4	19
18	Pooled CRISPR screening with single-cell transcriptome readout. <i>Nature Methods</i> , 2017, 14, 297-301.	9.0	749

#	ARTICLE	IF	CITATIONS
19	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
20	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>Biotechnology and Bioengineering</i> , 2016, 113, 2241-2253.	1.7	112
21	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. <i>Nature Communications</i> , 2016, 7, 11938.	5.8	131
22	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	1.5	23
23	Epigenome Mapping Reveals Distinct Modes of Gene Regulation and Widespread Enhancer Reprogramming by the Oncogenic Fusion Protein EWS-FLI1. <i>Cell Reports</i> , 2015, 10, 1082-1095.	2.9	183
24	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. <i>Nature Methods</i> , 2015, 12, 963-965.	9.0	417
25	Genome-wide identification of hypoxia-inducible factor-1 and -2 binding sites in hypoxic human macrophages alternatively activated by IL-10. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 10-22.	0.9	54
26	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
27	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
28	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	0.6	77
29	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	0.6	157
30	Mechanisms of in vivo binding site selection of the hematopoietic master transcription factor PU.1. <i>Nucleic Acids Research</i> , 2013, 41, 6391-6402.	6.5	76
31	Dominant Th2 Differentiation of Human Regulatory T Cells upon Loss of FOXP3 Expression. <i>Journal of Immunology</i> , 2012, 188, 1275-1282.	0.4	60
32	Epigenetic reprogramming of the <i>RORC</i> locus during in vitro expansion is a distinctive feature of human memory but not naïve Treg. <i>European Journal of Immunology</i> , 2011, 41, 1491-1498.	1.6	57
33	Isolation of intact genomic DNA from FOXP3-sorted human regulatory T cells for epigenetic analyses. <i>European Journal of Immunology</i> , 2010, 40, 1510-1512.	1.6	11
34	Lineage-specific DNA methylation in T cells correlates with histone methylation and enhancer activity. <i>Genome Research</i> , 2009, 19, 1165-1174.	2.4	206
35	Aldehyde oxidase 1 is highly abundant in hepatic steatosis and is downregulated by adiponectin and fenofibric acid in hepatocytes in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 731-735.	1.0	74