

Andreas Kloetgen

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,203
citations

361413
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docs citations

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times ranked

4611
citing authors

#	ARTICLE	IF	CITATIONS
1	Replication of SARS-CoV-2 in adipose tissue determines organ and systemic lipid metabolism in hamsters and humans. <i>Cell Metabolism</i> , 2022, 34, 1-2.	16.2	37
2	Valine tRNA levels and availability regulate complex I assembly in leukaemia. <i>Nature</i> , 2022, 601, 428-433.	27.8	34
3	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	27.8	155
4	H3K27ac bookmarking promotes rapid post-mitotic activation of the pluripotent stem cell program without impacting 3D chromatin reorganization. <i>Molecular Cell</i> , 2021, 81, 1732-1748.e8.	9.7	60
5	Regulatory T-cell Transcriptomic Reprogramming Characterizes Adverse Events by Checkpoint Inhibitors in Solid Tumors. <i>Cancer Immunology Research</i> , 2021, 9, 726-734.	3.4	19
6	Surface antigen-guided CRISPR screens identify regulators of myeloid leukemia differentiation. <i>Cell Stem Cell</i> , 2021, 28, 718-731.e6.	11.1	38
7	Offspring born to influenza A virus infected pregnant mice have increased susceptibility to viral and bacterial infections in early life. <i>Nature Communications</i> , 2021, 12, 4957.	12.8	25
8	Cohesin Core Complex Gene Dosage Contributes to Germinal Center Derived Lymphoma Phenotypes and Outcomes. <i>Frontiers in Immunology</i> , 2021, 12, 688493.	4.8	5
9	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. <i>Nature Immunology</i> , 2021, 22, 240-253.	14.5	24
10	A bipartite element with allele-specific functions safeguards DNA methylation imprints at the Dlk1-Dio3 locus. <i>Developmental Cell</i> , 2021, 56, 3052-3065.e5.	7.0	14
11	Therapeutic targeting of the E3 ubiquitin ligase SKP2 in T-ALL. <i>Leukemia</i> , 2020, 34, 1241-1252.	7.2	27
12	Defining the relative and combined contribution of CTCF and CTCFL to genomic regulation. <i>Genome Biology</i> , 2020, 21, 108.	8.8	37
13	Three-dimensional chromatin landscapes in T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2020, 52, 388-400.	21.4	118
14	YBX1 Indirectly Targets Heterochromatin-Repressed Inflammatory Response-Related Apoptosis Genes through Regulating CBX5 mRNA. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4453.	4.1	11
15	Functional omics analyses reveal only minor effects of microRNAs on human somatic stem cell differentiation. <i>Scientific Reports</i> , 2020, 10, 3284.	3.3	9
16	Epigenetic Silencing of CDR1as Drives IGF2BP3-Mediated Melanoma Invasion and Metastasis. <i>Cancer Cell</i> , 2020, 37, 55-70.e15.	16.8	200
17	The homeobox transcription factor HB9 induces senescence and blocks differentiation in hematopoietic stem and progenitor cells. <i>Haematologica</i> , 2019, 104, 35-46.	3.5	24
18	3D Chromosomal Landscapes in Hematopoiesis and Immunity. <i>Trends in Immunology</i> , 2019, 40, 809-824.	6.8	21

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19	KLF4 is involved in the organization and regulation of pluripotency-associated three-dimensional enhancer networks. <i>Nature Cell Biology</i> , 2019, 21, 1179-1190.	10.3	122
20	Targeting Mitochondrial Structure Sensitizes Acute Myeloid Leukemia to Venetoclax Treatment. <i>Cancer Discovery</i> , 2019, 9, 890-909.	9.4	186
21	Targeting an RNA-Binding Protein Network in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2019, 35, 369-384.e7.	16.8	238
22	Pediatric ALL relapses after allo-SCT show high individuality, clonal dynamics, selective pressure, and druggable targets. <i>Blood Advances</i> , 2019, 3, 3143-3156.	5.2	4
23	Functional and topographic effects on DNA methylation in IDH1/2 mutant cancers. <i>Scientific Reports</i> , 2019, 9, 16830.	3.3	29
24	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. <i>Nature Communications</i> , 2019, 10, 4843.	12.8	57
25	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. <i>Science Immunology</i> , 2019, 4, .	11.9	85
26	Histone 1 Mutations Drive Lymphomagenesis By Inducing Primitive Stem Cell Functions and Epigenetic Instructions through Profound 3D Re-Organization of the B-Cell Genome. <i>Blood</i> , 2019, 134, 23-23.	1.4	6
27	Tumor Necrosis Factor-Mediated Survival of CD169 ⁺ Cells Promotes Immune Activation during Vesicular Stomatitis Virus Infection. <i>Journal of Virology</i> , 2018, 92, .	3.4	16
28	Apoptotic cell-induced AhR activity is required for immunological tolerance and suppression of systemic lupus erythematosus in mice and humans. <i>Nature Immunology</i> , 2018, 19, 571-582.	14.5	137
29	Transcriptome-wide analysis uncovers the targets of the RNA-binding protein MSI2 and effects of MSI2's RNA-binding activity on IL-6 signaling. <i>Journal of Biological Chemistry</i> , 2018, 293, 15359-15369.	3.4	31
30	Therapeutic Targeting of an RNA Splicing Factor Network for the Treatment of Myeloid Neoplasms. <i>Blood</i> , 2018, 132, 427-427.	1.4	0
31	Osteonecrosis develops independently from radiological leukemic infiltration of bone in adolescents with acute lymphoblastic leukemia – first findings of the OPAL trial. <i>Leukemia and Lymphoma</i> , 2017, 58, 2363-2369.	1.3	8
32	Finding Genes in Genome Sequence. <i>Methods in Molecular Biology</i> , 2017, 1525, 271-291.	0.9	4
33	T-cell acute lymphoblastic leukemia in infants has distinct genetic and epigenetic features compared to childhood cases. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 159-167.	2.8	15
34	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , 2016, 101, 1380-1389.	3.5	43
35	The PARA-suite: PAR-CLIP specific sequence read simulation and processing. <i>PeerJ</i> , 2016, 4, e2619.	2.0	8
36	Biochemical and bioinformatic methods for elucidating the role of RNA-protein interactions in posttranscriptional regulation. <i>Briefings in Functional Genomics</i> , 2015, 14, 102-114.	2.7	10

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37	GABI-Kat SimpleSearch: new features of the Arabidopsis thaliana T-DNA mutant database. Nucleic Acids Research, 2012, 40, D1211-D1215.	14.5	336