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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9004104/publications.pdf>

Version: 2024-02-01

47
papers

5,792
citations

201575

27
h-index

223716

46
g-index

60
all docs

60
docs citations

60
times ranked

10280
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPResso2 provides accurate and rapid genome editing sequence analysis. <i>Nature Biotechnology</i> , 2019, 37, 224-226.	9.4	891
2	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. <i>Nature Biotechnology</i> , 2019, 37, 276-282.	9.4	439
3	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	9.4	409
4	Highly efficient therapeutic gene editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2019, 25, 776-783.	15.2	344
5	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. <i>Nature Biotechnology</i> , 2018, 36, 977-982.	9.4	328
6	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825.	7.7	323
7	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018, 561, 416-419.	13.7	274
8	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012, 13, R92.	13.9	244
9	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. <i>Nature Biotechnology</i> , 2015, 33, 1173-1181.	9.4	235
10	Assessment of computational methods for the analysis of single-cell ATAC-seq data. <i>Genome Biology</i> , 2019, 20, 241.	3.8	225
11	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017, 548, 219-223.	13.7	211
12	Therapeutic base editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2020, 26, 535-541.	15.2	196
13	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	13.7	195
14	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017, 549, 543-547.	13.7	146
15	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018, 50, 250-258.	9.4	139
16	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. <i>Nature Biotechnology</i> , 2022, 40, 189-193.	9.4	118
17	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018, 9, 597.	5.8	114
18	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018, 173, 624-633.e8.	13.5	113

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19	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. <i>Nature Biotechnology</i> , 2014, 32, 1223-1230.	9.4	89
20	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	5.2	82
21	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018, 15, 732-740.	9.0	74
22	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 706-719.e7.	5.2	63
23	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 289-305.e5.	5.2	60
24	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 327-332.	3.6	56
25	An Intermediate Pluripotent State Controlled by MicroRNAs Is Required for the Naive-to-Primed Stem Cell Transition. <i>Cell Stem Cell</i> , 2018, 22, 851-864.e5.	5.2	47
26	Age- and Pregnancy-Associated DNA Methylation Changes in Mammary Epithelial Cells. <i>Stem Cell Reports</i> , 2015, 4, 297-311.	2.3	45
27	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018, 22, 575-588.e7.	5.2	40
28	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. <i>Nature Methods</i> , 2018, 15, 992-993.	9.0	33
29	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. <i>Bioinformatics</i> , 2018, 34, i202-i210.	1.8	28
30	Technologies and Computational Analysis Strategies for CRISPR Applications. <i>Molecular Cell</i> , 2020, 79, 11-29.	4.5	28
31	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018, 7, .	2.8	26
32	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018, 15, 238-239.	9.0	25
33	A Code of Ethics for Gene Drive Research. <i>CRISPR Journal</i> , 2021, 4, 19-24.	1.4	24
34	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	17
35	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021, 2, 54-69.	2.6	16
36	Comparative genomic analysis of embryonic, lineage-converted, and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	10

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37	PathGen: a transitive gene pathway generator. <i>Bioinformatics</i> , 2010, 26, 423-425.	1.8	6
38	Increased Local Disorder of DNA Methylation Forms the Basis of High Intra-Leukemic Epigenetic Heterogeneity and Enhances CLL Evolution. <i>Blood</i> , 2013, 122, 596-596.	0.6	4
39	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from $\bar{A}\bar{Y}$ -Hemoglobinopathy Patients for Fetal Hemoglobin Induction. <i>Blood</i> , 2018, 132, 3482-3482.	0.6	2
40	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. <i>Blood</i> , 2019, 134, 684-684.	0.6	2
41	Loss of TET2 Function in Myelodysplastic Syndrome Results in Intragenic Hypermethylation and Alterations in mRNA Splicing. <i>Blood</i> , 2014, 124, 775-775.	0.6	2
42	Epigenomics and chromatin dynamics. <i>Genome Biology</i> , 2012, 13, 313.	13.9	2
43	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 1047-1047.	0.6	1
44	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. <i>Blood</i> , 2021, 138, 504-504.	0.6	1
45	Multiplexed CRISPR <i>In Vivo</i> Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. <i>Blood</i> , 2020, 136, 2-3.	0.6	1
46	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018, 132, 820-820.	0.6	0
47	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). <i>Blood</i> , 2019, 134, 516-516.	0.6	0