M Kendell Clement

List of Publications by Year
in descending order

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

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47	5,792	201674	223800
papers	citations	27 h-index	46 g-index

60	60	60	10280
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. Nature Biotechnology, 2022, 40, 189-193.	17.5	118
2	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. Blood Cancer Discovery, 2021, 2, 54-69.	5.0	16
3	A Code of Ethics for Gene Drive Research. CRISPR Journal, 2021, 4, 19-24.	2.9	24
4	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. Blood, 2021, 138, 504-504.	1.4	1
5	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. Science Translational Medicine, 2020, 12, .	12.4	17
6	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	30.7	196
7	Technologies and Computational Analysis Strategies for CRISPR Applications. Molecular Cell, 2020, 79, 11-29.	9.7	28
8	Multiplexed CRISPR In Vivo Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. Blood, 2020, 136, 2-3.	1.4	1
9	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. Cell Stem Cell, 2019, 25, 622-638.e13.	11.1	82
10	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. Nature, 2019, 569, 576-580.	27.8	195
11	Highly efficient therapeutic gene editing of human hematopoietic stem cells. Nature Medicine, 2019, 25, 776-783.	30.7	344
12	Engineered CRISPRâ€“Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	17.5	439
13	CRISPResso2 provides accurate and rapid genome editing sequence analysis. Nature Biotechnology, 2019, 37, 224-226.	17.5	891
14	Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241.	8.8	225
15	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. Blood, 2019, 134, 684-684.	1.4	2
16	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). Blood, 2019, 134, 516-516.	1.4	0
17	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. Cell Stem Cell, 2018, 22, 575-588.e7.	11.1	40
18	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. Cell, 2018, 173, 624-633.e8.	28.9	113

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19	Genome-wide tracking of dCas9-methyltransferase footprints. Nature Communications, 2018, 9, 597.	12.8	114
20	Genetic determinants and epigenetic effects of pioneer-factor occupancy. Nature Genetics, 2018, 50, 250-258.	21.4	139
21	Response to â€œUnexpected mutations after CRISPRâ€“Cas9 editing in vivoâ€• Nature Methods, 2018, 15, 238-239.	19.0	25
22	Global delay in nascent strand DNA methylation. Nature Structural and Molecular Biology, 2018, 25, 327-332.	8.2	56
23	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	19.0	33
24	Comparative genomic analysis of embryonic, lineage-converted, and stem cell-derived motor neurons. Development (Cambridge), 2018, 145, .	2.5	10
25	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	27.8	274
26	An Intermediate Pluripotent State Controlled by MicroRNAs Is Required for the Naive-to-Primed Stem Cell Transition. Cell Stem Cell, 2018, 22, 851-864.e5.	11.1	47
27	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. Bioinformatics, 2018, 34, i202-i210.	4.1	28
28	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. Nature Biotechnology, 2018, 36, 977-982.	17.5	328
29	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. Cell Stem Cell, 2018, 23, 289-305.e5.	11.1	60
30	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. Nature Methods, 2018, 15, 732-740.	19.0	74
31	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from ÃŸ-Hemoglobinopathy Patients for Fetal Hemoglobin Induction. Blood, 2018, 132, 3482-3482.	1.4	2
32	Targets and genomic constraints of ectopic Dnmt3b expression. ELife, 2018, 7, .	6.0	26
33	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). Blood, 2018, 132, 820-820.	1.4	0
34	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 706-719.e7.	11.1	63
35	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. Nature, 2017, 549, 543-547.	27.8	146
36	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. Nature, 2017, 548, 219-223.	27.8	211

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37	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. Blood, 2016, 128, 1047-1047.	1.4	1
38	Age- and Pregnancy-Associated DNA Methylation Changes in Mammary Epithelial Cells. Stem Cell Reports, 2015, 4, 297-311.	4.8	45
39	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. Nature Genetics, 2015, 47, 469-478.	21.4	409
40	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. Nature Biotechnology, 2015, 33, 1173-1181.	17.5	235
41	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	16.8	323
42	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. Nature Biotechnology, 2014, 32, 1223-1230.	17.5	89
43	Loss of TET2 Function in Myelodysplastic Syndrome Results in Intragenic Hypermethylation and Alterations in mRNA Splicing. Blood, 2014, 124, 775-775.	1.4	2
44	Increased Local Disorder of DNA Methylation Forms the Basis of High Intra-Leukemic Epigenetic Heterogeneity and Enhances CLL Evolution. Blood, 2013, 122, 596-596.	1.4	4
45	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. Genome Biology, 2012, 13, R92.	9.6	244
46	Epigenomics and chromatin dynamics. Genome Biology, 2012, 13, 313.	9.6	2
47	PathGen: a transitive gene pathway generator. Bioinformatics, 2010, 26, 423-425.	4.1	6