

M Kendell Clement

List of Publications by Year in Descending Order

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Version: 2024-04-09

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54 papers	3,352 citations	26 h-index	57 g-index
60 ext. papers	4,720 ext. citations	22 avg, IF	5.06 L-index

#	Paper	IF	Citations
54	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. <i>Blood</i> , 2021 , 138, 504-504	2.2	
53	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. <i>Nature Biotechnology</i> , 2021 ,	44.5	30
52	Preneoplastic Alterations Define CLL DNA Methyome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021 , 2, 54-69	7	6
51	A Code of Ethics for Gene Drive Research. <i>CRISPR Journal</i> , 2021 , 4, 19-24	2.5	14
50	Therapeutic base editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2020 , 26, 535-541	50.5	84
49	Technologies and Computational Analysis Strategies for CRISPR Applications. <i>Molecular Cell</i> , 2020 , 79, 11-29	17.6	7
48	Multiplexed CRISPR In Vivo Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. <i>Blood</i> , 2020 , 136, 2-3	2.2	1
47	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	7
46	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019 , 25, 622-638.e13	18	35
45	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019 , 569, 576-580	50.4	104
44	Highly efficient therapeutic gene editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2019 , 25, 776-783	50.5	197
43	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	44.5	235
42	CRISPResso2 provides accurate and rapid genome editing sequence analysis. <i>Nature Biotechnology</i> , 2019 , 37, 224-226	44.5	326
41	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	2.2	2
40	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). <i>Blood</i> , 2019 , 134, 516-516	2.2	
39	Assessment of computational methods for the analysis of single-cell ATAC-seq data. <i>Genome Biology</i> , 2019 , 20, 241	18.3	97
38	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	18	24

37	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018 , 173, 624-633.e8	56.2	71
36	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018 , 9, 597	17.4	85
35	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018 , 50, 250-258	36.3	85
34	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018 , 15, 238-239	20.6	25
33	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 327-332	37.6	32
32	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. <i>Nature Biotechnology</i> , 2018 , 36, 977-982	44.5	224
31	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018 , 23, 289-305.e5	18	34
30	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018 , 15, 732-740	21.6	44
29	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from Hemoglobinopathy Patients for Fetal Hemoglobin Induction. <i>Blood</i> , 2018 , 132, 3482-3482	2.2	1
28	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018 , 7,	8.9	16
27	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018 , 132, 820-820	2.2	
26	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. <i>Nature Methods</i> , 2018 , 15, 992-993	21.6	17
25	Comparative genomic analysis of embryonic, lineage-converted and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	8
24	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018 , 561, 416-419	30.4	202
23	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	18	31
22	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. <i>Bioinformatics</i> , 2018 , 34, i202-i210	7.2	15
21	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017 , 20, 706-719.e7	18	43
20	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017 , 548, 219-223	50.4	135

19	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017 , 549, 543-547	50.4	86
18	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016 , 128, 1047-1047	2.2	1
17	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015 , 47, 469-78	36.3	288
16	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. <i>Nature Biotechnology</i> , 2015 , 33, 1173-81	44.5	192
15	Age- and pregnancy-associated DNA methylation changes in mammary epithelial cells. <i>Stem Cell Reports</i> , 2015 , 4, 297-311	8	35
14	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. <i>Nature Biotechnology</i> , 2014 , 32, 1223-30	44.5	71
13	Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. <i>Cancer Cell</i> , 2014 , 26, 813-825	24.3	216
12	Loss of TET2 Function in Myelodysplastic Syndrome Results in Intragenic Hypermethylation and Alterations in mRNA Splicing. <i>Blood</i> , 2014 , 124, 775-775	2.2	0
11	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	2.2	4
10	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012 , 13, R92	18.3	183
9	Epigenomics and chromatin dynamics 2012 , 13, 313		2
8	PathGen: a transitive gene pathway generator. <i>Bioinformatics</i> , 2010 , 26, 423-5	7.2	5
7	Unexpected mutations after CRISPR-Cas9 editing in vivo are most likely pre-existing sequence variants and not nuclease-induced mutations		6
6	DNA methylation is a key mechanism for maintaining monoallelic expression on autosomes		1
5	In vivo CRISPR-Cas gene editing with no detectable genome-wide off-target mutations		5
4	High-precision CRISPR-Cas9 base editors with minimized bystander and off-target mutations		6
3	Analysis and comparison of genome editing using CRISPResso2		4
2	Assessment of computational methods for the analysis of single-cell ATAC-seq data		4

1	Global-scale CRISPR gene editor specificity profiling by ONE-seq identifies population-specific, variant off-target effects	2
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