M Kendell Clement

List of Publications by Citations

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	CRISPResso2 provides accurate and rapid genome editing sequence analysis. *Nature Biotechnology*, **2019**, 37, 224-226	44.5	326
53	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. *Nature Genetics*, **2015**, 47, 469-78	36.3	288
52	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. *Nature Biotechnology*, **2019**, 37, 276-282	44.5	235
51	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. *Nature Biotechnology*, **2018**, 36, 977-982	44.5	224
50	Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. *Cancer Cell*, **2014**, 26, 813-825	24.3	216
49	In vivo CRISPR editing with no detectable genome-wide off-target mutations. *Nature*, **2018**, 561, 416-419	50.4	202
48	Highly efficient therapeutic gene editing of human hematopoietic stem cells. *Nature Medicine*, **2019**, 25, 776-783	50.5	197
47	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. *Nature Biotechnology*, **2015**, 33, 1173-81	44.5	192
46	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. *Genome Biology*, **2012**, 13, R92	18.3	183
45	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. *Nature*, **2017**, 548, 219-223	50.4	135
44	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. *Nature*, **2019**, 569, 576-580	50.4	104
43	Assessment of computational methods for the analysis of single-cell ATAC-seq data. *Genome Biology*, **2019**, 20, 241	18.3	97
42	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. *Nature*, **2017**, 549, 543-547	50.4	86
41	Genome-wide tracking of dCas9-methyltransferase footprints. *Nature Communications*, **2018**, 9, 597	17.4	85
40	Genetic determinants and epigenetic effects of pioneer-factor occupancy. *Nature Genetics*, **2018**, 50, 250-258	36.3	85
39	Therapeutic base editing of human hematopoietic stem cells. *Nature Medicine*, **2020**, 26, 535-541	50.5	84
38	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. *Cell*, **2018**, 173, 624-633.e8	56.2	71

37	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. *Nature Biotechnology*, **2014**, 32, 1223-30	44.5	71
36	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. *Nature Methods*, **2018**, 15, 732-740	21.6	44
35	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. *Cell Stem Cell*, **2017**, 20, 706-719.e7	18	43
34	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. *Cell Stem Cell*, **2019**, 25, 622-638.e13	18	35
33	Age- and pregnancy-associated DNA methylation changes in mammary epithelial cells. *Stem Cell Reports*, **2015**, 4, 297-311	8	35
32	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. *Cell Stem Cell*, **2018**, 23, 289-305.e5	18	34
31	Global delay in nascent strand DNA methylation. *Nature Structural and Molecular Biology*, **2018**, 25, 327-332	17.6	32
30	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	18	31
29	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. *Nature Biotechnology*, **2021**,	44.5	30
28	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nature Methods*, **2018**, 15, 238-239	21.6	25
27	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. *Cell Stem Cell*, **2018**, 22, 575-588.e7	18	24
26	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. *Nature Methods*, **2018**, 15, 992-993	21.6	17
25	Targets and genomic constraints of ectopic Dnmt3b expression. *ELife*, **2018**, 7,	8.9	16
24	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. *Bioinformatics*, **2018**, 34, i202-i210	7.2	15
23	A Code of Ethics for Gene Drive Research. *CRISPR Journal*, **2021**, 4, 19-24	2.5	14
22	Comparative genomic analysis of embryonic, lineage-converted and stem cell-derived motor neurons. *Development (Cambridge)*, **2018**, 145,	6.6	8
21	Technologies and Computational Analysis Strategies for CRISPR Applications. *Molecular Cell*, **2020**, 79, 11-29	17.6	7
20	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. *Science Translational Medicine*, **2020**, 12,	17.5	7

19	Unexpected mutations after CRISPR-Cas9 editing in vivo are most likely pre-existing sequence variants and not nuclease-induced mutations		6
18	High-precision CRISPR-Cas9 base editors with minimized bystander and off-target mutations		6
17	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. *Blood Cancer Discovery*, **2021**, 2, 54-69	7	6
16	PathGen: a transitive gene pathway generator. *Bioinformatics*, **2010**, 26, 423-5	7.2	5
15	In vivo CRISPR-Cas gene editing with no detectable genome-wide off-target mutations		5
14	Increased Local Disorder of DNA Methylation Forms the Basis of High Intra-Leukemic Epigenetic Heterogeneity and Enhances CLL Evolution. *Blood*, **2013**, 122, 596-596	2.2	4
13	Analysis and comparison of genome editing using CRISPResso2		4
12	Assessment of computational methods for the analysis of single-cell ATAC-seq data		4
11	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. *Blood*, **2019**, 134, 684-684	2.2	2
10	Epigenomics and chromatin dynamics **2012**, 13, 313		2
9	Global-scale CRISPR gene editor specificity profiling by ONE-seq identifies population-specific, variant off-target effects		2
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	2.2	1
7	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from Hemoglobinopathy Patients for Fetal Hemoglobin Induction. *Blood*, **2018**, 132, 3482-3482	2.2	1
6	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. *Blood*, **2016**, 128, 1047-1047	2.2	1
5	DNA methylation is a key mechanism for maintaining monoallelic expression on autosomes		1
4	Loss of TET2 Function in Myelodysplastic Syndrome Results in Intragenic Hypermethylation and Alterations in mRNA Splicing. *Blood*, **2014**, 124, 775-775	2.2	0
3	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. *Blood*, **2021**, 138, 504-504	2.2	
2	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). *Blood*, **2018**, 132, 820-820	2.2	

List of Publications

1	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). *Blood*, **2019**, 134, 516-516	2.2