

William J Greenleaf

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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.

129
papers

15,419
citations

49
h-index

124
g-index

162
ext. papers

23,051
ext. citations

22.6
avg, IF

6.97
L-index

#	Paper	IF	Citations
129	Single-Molecule Multikilobase-Scale Profiling of Chromatin Accessibility Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq.. <i>Methods in Molecular Biology</i> , 2022 , 2458, 269-298	1.4	
128	Reduced chromatin accessibility to CD4 T cell super-enhancers encompassing susceptibility loci of rheumatoid arthritis.. <i>EBioMedicine</i> , 2022 , 76, 103825	8.8	
127	Generation of a dual edited human induced pluripotent stem cell Myl7-GFP reporter line with inducible CRISPRi/dCas9.. <i>Stem Cell Research</i> , 2022 , 61, 102754	1.6	
126	Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular switches.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2112979119	11.5	0
125	NEAT-seq: simultaneous profiling of intra-nuclear proteins, chromatin accessibility and gene expression in single cells.. <i>Nature Methods</i> , 2022 , 19, 547-553	21.6	3
124	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. <i>Molecular Cell</i> , 2021 , 81, 4861-4875.e7	17.6	6
123	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021 , 6, eabh3768	28	1
122	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , 2021 , 53, 1564-1576	36.3	3
121	Increased ACTL6A occupancy within mSWI/SNF chromatin remodelers drives human squamous cell carcinoma. <i>Molecular Cell</i> , 2021 ,	17.6	2
120	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate <i>Breviolum minutum</i> . <i>Nature Genetics</i> , 2021 , 53, 613-617	36.3	10
119	High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer. <i>Nature Communications</i> , 2021 , 12, 2969	17.4	16
118	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	34
117	Dynamic chromatin regulatory landscape of human CAR T cell exhaustion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	9
116	Quantification of Cas9 binding and cleavage across diverse guide sequences maps landscapes of target engagement. <i>Science Advances</i> , 2021 , 7,	14.3	4
115	Finding needles in a haystack: dissecting tumor heterogeneity with single-cell transcriptomic and chromatin accessibility profiling. <i>Current Opinion in Genetics and Development</i> , 2021 , 66, 36-40	4.9	3
114	Single-cell transcriptomic analysis of the adult mouse spinal cord reveals molecular diversity of autonomic and skeletal motor neurons. <i>Nature Neuroscience</i> , 2021 , 24, 572-583	25.5	22
113	ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. <i>Nature Genetics</i> , 2021 , 53, 403-411	36.3	97

112	p53 is a central regulator driving neurodegeneration caused by C9orf72 poly(PR). <i>Cell</i> , 2021 , 184, 689-706.e20	26	26
111	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. <i>Nature Cell Biology</i> , 2021 , 23, 915-924	23.4	7
110	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. <i>Cell</i> , 2021 , 184, 5053-5069.e23	56.2	26
109	An optimized ATAC-seq protocol for genome-wide mapping of active regulatory elements in primary mouse cortical neurons. <i>STAR Protocols</i> , 2021 , 2, 100854	1.4	0
108	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
107	Comprehensive sequence-to-function mapping of cofactor-dependent RNA catalysis in the glmS ribozyme. <i>Nature Communications</i> , 2020 , 11, 1663	17.4	7
106	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , 2020 , 17, 319-327	21.6	36
105	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020 , 367,	33.3	76
104	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. <i>Nature Genetics</i> , 2020 , 52, 1158-1168	36.3	58
103	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019 , 10, 4063	17.4	49
102	Chromatin accessibility and the regulatory epigenome. <i>Nature Reviews Genetics</i> , 2019 , 20, 207-220	30.1	504
101	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019 , 16, 489-492	21.6	40
100	Epigenetic signature of PD-1+ TCF1+ CD8 T cells that act as resource cells during chronic viral infection and respond to PD-1 blockade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14113-14118	11.5	90
99	Brief Report: Cell Cycle Dynamics of Human Pluripotent Stem Cells Primed for Differentiation. <i>Stem Cells</i> , 2019 , 37, 1151-1157	5.8	7
98	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. <i>Molecular Cell</i> , 2019 , 74, 966-981.e18	17.6	23
97	Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip. <i>Molecular Cell</i> , 2019 , 73, 1075-1082.e4	17.6	18
96	Blind tests of RNA-protein binding affinity prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 8336-8341	11.5	6
95	Demonstration of protein cooperativity mediated by RNA structure using the human protein PUM2. <i>Rna</i> , 2019 , 25, 702-712	5.8	7

94	Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16847-16855	11.5	18
93	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. <i>Nature Biotechnology</i> , 2019 , 37, 925-936	44.5	244
92	High-Throughput Analysis Reveals Rules for Target RNA Binding and Cleavage by AGO2. <i>Molecular Cell</i> , 2019 , 75, 741-755.e11	17.6	41
91	Automated Design of Diverse Stand-Alone Riboswitches. <i>ACS Synthetic Biology</i> , 2019 , 8, 1838-1846	5.7	21
90	Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. <i>Nature Communications</i> , 2019 , 10, 3221	17.4	18
89	Omega-3 Fatty Acids Activate Ciliary FFAR4 to Control Adipogenesis. <i>Cell</i> , 2019 , 179, 1289-1305.e21	56.2	72
88	Landscape of stimulation-responsive chromatin across diverse human immune cells. <i>Nature Genetics</i> , 2019 , 51, 1494-1505	36.3	86
87	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. <i>Nature Biotechnology</i> , 2019 , 37, 1458-1465	44.5	128
86	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. <i>Cell</i> , 2019 , 176, 361-376.e17	56.2	119
85	Linking RNA Sequence, Structure, and Function on Massively Parallel High-Throughput Sequencers. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11,	10.2	9
84	Deterministic Somatic Cell Reprogramming Involves Continuous Transcriptional Changes Governed by Myc and Epigenetic-Driven Modules. <i>Cell Stem Cell</i> , 2019 , 24, 328-341.e9	18	25
83	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018 , 24, 580-590	50.5	93
82	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. <i>Nucleic Acids Research</i> , 2018 , 46, e42	20.1	2
81	Rapid chromatin repression by Aire provides precise control of immune tolerance. <i>Nature Immunology</i> , 2018 , 19, 162-172	19.1	25
80	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018 , 173, 1535-1548.e16	56.2	292
79	INO80 Chromatin Remodeling Coordinates Metabolic Homeostasis with Cell Division. <i>Cell Reports</i> , 2018 , 22, 611-623	10.6	18
78	Unsupervised clustering and epigenetic classification of single cells. <i>Nature Communications</i> , 2018 , 9, 2410	17.4	61
77	Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. <i>Cell Stem Cell</i> , 2018 , 23, 412-425.e10	18	27

76	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. <i>Nature Genetics</i> , 2018 , 50, 1716-1727	36.3	67
75	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018 , 14, e8594	12.2	32
74	Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. <i>Nature Communications</i> , 2018 , 9, 4590	17.4	41
73	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
72	A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. <i>Cell Systems</i> , 2018 , 7, 310-322.e4	22.64	24
71	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. <i>Cancer Discovery</i> , 2018 , 8, 1316-1331	24.4	65
70	High-throughput chromatin accessibility profiling at single-cell resolution. <i>Nature Communications</i> , 2018 , 9, 3647	17.4	73
69	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. <i>Nature Genetics</i> , 2017 , 49, 377-386	36.3	52
68	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , 2017 , 18, 15	18.3	61
67	TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 344-352	17.6	48
66	Epigenomics of human CD8 T cell differentiation and aging. <i>Science Immunology</i> , 2017 , 2,	28	110
65	High-throughput biochemical profiling reveals sequence determinants of dCas9 off-target binding and unbinding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 5461-5466	11.5	115
64	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. <i>Nature Communications</i> , 2017 , 8, 15178	17.4	148
63	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. <i>Cancer Cell</i> , 2017 , 32, 27-41.e4	24.3	96
62	Comprehensive and quantitative mapping of RNA-protein interactions across a transcribed eukaryotic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 3619-3624	11.5	31
61	Variable chromatin structure revealed by in situ spatially correlated DNA cleavage mapping. <i>Nature</i> , 2017 , 541, 237-241	50.4	102
60	Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 744-747	16.4	49
59	Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers. <i>Angewandte Chemie</i> , 2017 , 129, 762-765	3.6	4

58	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017 , 49, 1602-1612	36.3	253
57	chromVAR: inferring transcription-factor-associated accessibility from single-cell epigenomic data. <i>Nature Methods</i> , 2017 , 14, 975-978	21.6	388
56	Discovery of stimulation-responsive immune enhancers with CRISPR activation. <i>Nature</i> , 2017 , 549, 111-115.	50.4	158
55	Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci. <i>Cell Stem Cell</i> , 2017 , 21, 305-318.e8	18	79
54	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017 , 49, 1522-1528	36.3	158
53	Origin and differentiation of human memory CD8 T cells after vaccination. <i>Nature</i> , 2017 , 552, 362-367	50.4	257
52	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017 , 35, 1128-1132	44.5	16
51	Chromatin accessibility dynamics reveal novel functional enhancers in. <i>Genome Research</i> , 2017 , 27, 2096-2107	37.1	79
50	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. <i>Nature Methods</i> , 2017 , 14, 959-962	21.6	727
49	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016 , 48, 1193-203	36.3	555
48	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016 , 13, 919-922	21.6	505
47	ATAC-seq reveals the accessible genome by transposase-mediated imaging and sequencing. <i>Nature Methods</i> , 2016 , 13, 1013-1020	21.6	122
46	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. <i>Nature Genetics</i> , 2016 , 48, 117-25	36.3	60
45	Nfib Promotes Metastasis through a Widespread Increase in Chromatin Accessibility. <i>Cell</i> , 2016 , 166, 328-342	56.2	209
44	Single-cell chromatin accessibility reveals principles of regulatory variation. <i>Nature</i> , 2015 , 523, 486-90	50.4	1110
43	Unraveling the 3D genome: genomics tools for multiscale exploration. <i>Trends in Genetics</i> , 2015 , 31, 357-365	32.5	47
42	Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions. <i>Genome Research</i> , 2015 , 25, 1757-70	9.7	191
41	Beyond the Linear Genome: Paired-End Sequencing as a Biophysical Tool. <i>Trends in Cell Biology</i> , 2015 , 25, 716-719	18.3	1

40	Individuality and variation of personal regulomes in primary human T cells. <i>Cell Systems</i> , 2015 , 1, 51-61	10.6	98
39	Assaying the epigenome in limited numbers of cells. <i>Methods</i> , 2015 , 72, 51-6	4.6	15
38	ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide. <i>Current Protocols in Molecular Biology</i> , 2015 , 109, 21.29.1-21.29.9	2.9	1370
37	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014 , 344, 1042-7	33.3	209
36	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. <i>Nature Biotechnology</i> , 2014 , 32, 562-8	44.5	146
35	A conditional system to specifically link disruption of protein-coding function with reporter expression in mice. <i>Cell Reports</i> , 2014 , 7, 2078-86	10.6	6
34	Exome sequencing identifies a DNAJB6 mutation in a family with dominantly-inherited limb-girdle muscular dystrophy. <i>Neuromuscular Disorders</i> , 2014 , 24, 431-5	2.9	29
33	Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. <i>Nature Methods</i> , 2013 , 10, 1213-8	21.6	3263
32	Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. <i>American Journal of Human Genetics</i> , 2013 , 93, 852-64	11	221
31	Direct observation of hierarchical folding in single riboswitch aptamers. <i>Science</i> , 2008 , 319, 630-3	33.3	328
30	High-resolution, single-molecule measurements of biomolecular motion. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007 , 36, 171-90		384
29	Single-molecule, motion-based DNA sequencing using RNA polymerase. <i>Science</i> , 2006 , 313, 801	33.3	93
28	Passive all-optical force clamp for high-resolution laser trapping. <i>Physical Review Letters</i> , 2005 , 95, 2081024	10.6	179
27	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation		3
26	Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH		1
25	Prospects for recurrent neural network models to learn RNA biophysics from high-throughput data		1
24	High-throughput chromatin accessibility profiling at single-cell resolution		1
23	High-resolution mapping of cancer cell networks using co-functional interactions		1

22	Coupled single-cell CRISPR screening and epigenomic profiling reveals causal gene regulatory networks	1
21	Identification and mitigation of pervasive off-target activity in CRISPR-Cas9 screens for essential non-coding elements	1
20	A single cell framework for multi-omic analysis of disease identifies malignant regulatory signatures in mixed phenotype acute leukemia	1
19	Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular sensors	2
18	Omni-ATAC-seq: Improved ATAC-seq protocol. <i>Protocol Exchange</i> ,	10
17	Single-cell epigenomics maps the continuous regulatory landscape of human hematopoietic differentiation	7
16	Unsupervised clustering and epigenetic classification of single cells	3
15	Neutralizing Gatad2a-Chd4-Mbd3 Axis within the NuRD Complex Facilitates Deterministic Induction of Naïve Pluripotency	1
14	Single-cell epigenomic identification of inherited risk loci in Alzheimer's and Parkinson's disease	9
13	ArchR: An integrative and scalable software package for single-cell chromatin accessibility analysis	36
12	Size-independent mRNA synthesis and chromatin-based partitioning mechanisms generate and maintain constant amounts of protein per cell	3
11	High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer	4
10	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19	11
9	Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity	3
8	Nonparametric analysis of contributions to variance in genomics and epigenomics data	1
7	Large-scale, quantitative protein assays on a high-throughput DNA sequencing chip	1
6	A quantitative and predictive model for RNA binding by human Pumilio proteins	4
5	Landscape of stimulation-responsive chromatin across diverse human immune cells	7

4	Long-range single-molecule mapping of chromatin accessibility in eukaryotes	4
3	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion	7
2	Single-cell analyses reveal a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer	1
1	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks	4