

# William J Greenleaf

## List of Publications by Year in descending order

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Version: 2024-02-01

110  
papers

28,056  
citations

22099

59  
h-index

27345

106  
g-index

162  
all docs

162  
docs citations

162  
times ranked

34809  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Molecule Multikilobase-Scale Profiling of Chromatin Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq. <i>Methods in Molecular Biology</i> , 2022, 2458, 269-298.	0.4	1
2	Reduced chromatin accessibility to CD4 T cell super-enhancers encompassing susceptibility loci of rheumatoid arthritis. <i>EBioMedicine</i> , 2022, 76, 103825.	2.7	1
3	Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment. <i>Cell Reports Methods</i> , 2022, 2, 100188.	1.4	9
4	High-throughput biochemical profiling reveals functional adaptation of a bacterial Argonaute. <i>Molecular Cell</i> , 2022, 82, 1329-1342.e8.	4.5	8
5	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.	0.3	0
6	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.	3.3	19
7	NEAT-seq: simultaneous profiling of intra-nuclear proteins, chromatin accessibility and gene expression in single cells. <i>Nature Methods</i> , 2022, 19, 547-553.	9.0	56
8	Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. <i>Nature Genetics</i> , 2022, 54, 985-995.	9.4	77
9	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. <i>Nature Genetics</i> , 2022, 54, 1133-1144.	9.4	31
10	Quantification of Cas9 binding and cleavage across diverse guide sequences maps landscapes of target engagement. <i>Science Advances</i> , 2021, 7, .	4.7	28
11	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.	1.5	5
12	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.	7.1	110
13	ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. <i>Nature Genetics</i> , 2021, 53, 403-411.	9.4	610
14	p53 is a central regulator driving neurodegeneration caused by C9orf72 poly(PR). <i>Cell</i> , 2021, 184, 689-708.e20.	13.5	104
15	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate <i>Breviolum minutum</i> . <i>Nature Genetics</i> , 2021, 53, 613-617.	9.4	38
16	High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer. <i>Nature Communications</i> , 2021, 12, 2969.	5.8	73
17	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	139
18	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, .	3.3	36

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19	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. <i>Nature Cell Biology</i> , 2021, 23, 915-924.	4.6	26
20	High-throughput dissection of the thermodynamic and conformational properties of a ubiquitous class of RNA tertiary contact motifs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
21	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. <i>Cell</i> , 2021, 184, 5053-5069.e23.	13.5	209
22	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.	0.5	3
23	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
24	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021, 6, eabh3768.	5.6	19
25	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , 2021, 53, 1564-1576.	9.4	45
26	Increased ACTL6A occupancy within mSWI/SNF chromatin remodelers drives human squamous cell carcinoma. <i>Molecular Cell</i> , 2021, 81, 4964-4978.e8.	4.5	19
27	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. <i>Molecular Cell</i> , 2021, 81, 4861-4875.e7.	4.5	42
28	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.	9.4	217
29	Comprehensive sequence-to-function mapping of cofactor-dependent RNA catalysis in the glmS ribozyme. <i>Nature Communications</i> , 2020, 11, 1663.	5.8	21
30	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , 2020, 17, 319-327.	9.0	93
31	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	6.0	187
32	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.	3.3	38
33	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. <i>Nature Biotechnology</i> , 2019, 37, 925-936.	9.4	622
34	High-Throughput Analysis Reveals Rules for Target RNA Binding and Cleavage by AGO2. <i>Molecular Cell</i> , 2019, 75, 741-755.e11.	4.5	107
35	Automated Design of Diverse Stand-Alone Riboswitches. <i>ACS Synthetic Biology</i> , 2019, 8, 1838-1846.	1.9	34
36	Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. <i>Nature Communications</i> , 2019, 10, 3221.	5.8	33

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37	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019, 10, 4063.	5.8	104
38	Chromatin accessibility and the regulatory epigenome. <i>Nature Reviews Genetics</i> , 2019, 20, 207-220.	7.7	1,112
39	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019, 16, 489-492.	9.0	70
40	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.	3.3	157
41	Brief Report: Cell Cycle Dynamics of Human Pluripotent Stem Cells Primed for Differentiation. <i>Stem Cells</i> , 2019, 37, 1151-1157.	1.4	7
42	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. <i>Molecular Cell</i> , 2019, 74, 966-981.e18.	4.5	55
43	Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip. <i>Molecular Cell</i> , 2019, 73, 1075-1082.e4.	4.5	42
44	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.	3.3	21
45	Demonstration of protein cooperativity mediated by RNA structure using the human protein PUM2. <i>Rna</i> , 2019, 25, 702-712.	1.6	14
46	Omega-3 Fatty Acids Activate Ciliary FFAR4 to Control Adipogenesis. <i>Cell</i> , 2019, 179, 1289-1305.e21.	13.5	159
47	Landscape of stimulation-responsive chromatin across diverse human immune cells. <i>Nature Genetics</i> , 2019, 51, 1494-1505.	9.4	196
48	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. <i>Nature Biotechnology</i> , 2019, 37, 1458-1465.	9.4	321
49	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. <i>Cell</i> , 2019, 176, 361-376.e17.	13.5	215
50	Linking RNA Sequence, Structure, and Function on Massively Parallel High-Throughput Sequencers. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032300.	2.3	17
51	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.	5.2	44
52	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	15.2	124
53	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. <i>Nucleic Acids Research</i> , 2018, 46, e42-e42.	6.5	7
54	Rapid chromatin repression by Aire provides precise control of immune tolerance. <i>Nature Immunology</i> , 2018, 19, 162-172.	7.0	69

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55	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	13.5	545
56	INO80 Chromatin Remodeling Coordinates Metabolic Homeostasis with Cell Division. <i>Cell Reports</i> , 2018, 22, 611-623.	2.9	28
57	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. <i>Nature Genetics</i> , 2018, 50, 1716-1727.	9.4	135
58	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	3.2	61
59	Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. <i>Nature Communications</i> , 2018, 9, 4590.	5.8	76
60	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
61	A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. <i>Cell Systems</i> , 2018, 7, 310-322.e4.	2.9	38
62	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. <i>Cancer Discovery</i> , 2018, 8, 1316-1331.	7.7	123
63	High-throughput chromatin accessibility profiling at single-cell resolution. <i>Nature Communications</i> , 2018, 9, 3647.	5.8	124
64	Unsupervised clustering and epigenetic classification of single cells. <i>Nature Communications</i> , 2018, 9, 2410.	5.8	100
65	Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. <i>Cell Stem Cell</i> , 2018, 23, 412-425.e10.	5.2	59
66	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. <i>Nature Genetics</i> , 2017, 49, 377-386.	9.4	76
67	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , 2017, 18, 15.	3.8	92
68	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.	3.6	66
69	Epigenomics of human CD8 T cell differentiation and aging. <i>Science Immunology</i> , 2017, 2, .	5.6	181
70	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.	3.3	165
71	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. <i>Nature Communications</i> , 2017, 8, 15178.	5.8	284
72	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. <i>Cancer Cell</i> , 2017, 32, 27-41.e4.	7.7	136

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73	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.	3.3	54
74	Variable chromatin structure revealed by in situ spatially correlated DNA cleavage mapping. <i>Nature</i> , 2017, 541, 237-241.	13.7	132
75	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.	7.2	71
76	Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers. <i>Angewandte Chemie</i> , 2017, 129, 762-765.	1.6	6
77	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	9.4	419
78	chromVAR: inferring transcription-factor-associated accessibility from single-cell epigenomic data. <i>Nature Methods</i> , 2017, 14, 975-978.	9.0	1,021
79	Discovery of stimulation-responsive immune enhancers with CRISPR activation. <i>Nature</i> , 2017, 549, 111-115.	13.7	247
80	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.	5.2	106
81	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	9.4	255
82	Origin and differentiation of human memory CD8 T cells after vaccination. <i>Nature</i> , 2017, 552, 362-367.	13.7	412
83	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017, 35, 1128-1132.	9.4	19
84	Chromatin accessibility dynamics reveal novel functional enhancers in <i>C. elegans</i> . <i>Genome Research</i> , 2017, 27, 2096-2107.	2.4	142
85	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. <i>Nature Methods</i> , 2017, 14, 959-962.	9.0	1,653
86	Nfib Promotes Metastasis through a Widespread Increase in Chromatin Accessibility. <i>Cell</i> , 2016, 166, 328-342.	13.5	304
87	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203.	9.4	952
88	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016, 13, 919-922.	9.0	853
89	ATAC-seq reveals the accessible genome by transposase-mediated imaging and sequencing. <i>Nature Methods</i> , 2016, 13, 1013-1020.	9.0	199
90	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. <i>Nature Genetics</i> , 2016, 48, 117-125.	9.4	80

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91	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	2,391
92	Single-cell chromatin accessibility reveals principles of regulatory variation. <i>Nature</i> , 2015, 523, 486-490.	13.7	1,798
93	Unraveling the 3D genome: genomics tools for multiscale exploration. <i>Trends in Genetics</i> , 2015, 31, 357-372.	2.9	62
94	Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions. <i>Genome Research</i> , 2015, 25, 1757-1770.	2.4	334
95	Beyond the Linear Genome: Paired-End Sequencing as a Biophysical Tool. <i>Trends in Cell Biology</i> , 2015, 25, 716-719.	3.6	1
96	Individuality and Variation of Personal Regulomes in Primary Human T Cells. <i>Cell Systems</i> , 2015, 1, 51-61.	2.9	128
97	Assaying the epigenome in limited numbers of cells. <i>Methods</i> , 2015, 72, 51-56.	1.9	16
98	Exome sequencing identifies a DNAJB6 mutation in a family with dominantly-inherited limb-girdle muscular dystrophy. <i>Neuromuscular Disorders</i> , 2014, 24, 431-435.	0.3	35
99	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014, 344, 1042-1047.	6.0	280
100	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. <i>Nature Biotechnology</i> , 2014, 32, 562-568.	9.4	202
101	A Conditional System to Specifically Link Disruption of Protein-Coding Function with Reporter Expression in Mice. <i>Cell Reports</i> , 2014, 7, 2078-2086.	2.9	9
102	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, 1213-1218.	9.0	5,209
103	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, 852-864.	2.6	284
104	Direct Observation of Hierarchical Folding in Single Riboswitch Aptamers. <i>Science</i> , 2008, 319, 630-633.	6.0	361
105	High-Resolution, Single-Molecule Measurements of Biomolecular Motion. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007, 36, 171-190.	18.3	425
106	Single-Molecule, Motion-Based DNA Sequencing Using RNA Polymerase. <i>Science</i> , 2006, 313, 801-801.	6.0	102
107	Passive All-Optical Force Clamp for High-Resolution Laser Trapping. <i>Physical Review Letters</i> , 2005, 95, 208102.	2.9	201
108	Increased ACTL6A Occupancy within mSWI/SNF Chromatin Remodelers Drives Human Squamous Cell Carcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

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109	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21
110	HiChIRP: RNA-centric chromatin conformation. Protocol Exchange, 0, , .	0.3	1