

Erez Lieberman Aiden

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

23,949
citations

109311

35
h-index

88628

70
g-index

115
all docs

115
docs citations

115
times ranked

23101
citing authors

#	ARTICLE	IF	CITATIONS
1	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. <i>Cell</i> , 2014, 159, 1665-1680.	28.9	6,520
2	Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments. <i>Cell Systems</i> , 2016, 3, 95-98.	6.2	2,057
3	Quantitative Analysis of Culture Using Millions of Digitized Books. <i>Science</i> , 2011, 331, 176-182.	12.6	2,010
4	De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> , 2017, 356, 92-95.	12.6	1,513
5	Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6456-65.	7.1	1,464
6	Cohesin Loss Eliminates All Loop Domains. <i>Cell</i> , 2017, 171, 305-320.e24.	28.9	1,454
7	Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom. <i>Cell Systems</i> , 2016, 3, 99-101.	6.2	1,199
8	Evolutionary dynamics on graphs. <i>Nature</i> , 2005, 433, 312-316.	27.8	1,044
9	Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. <i>Nature Genetics</i> , 2019, 51, 1664-1669.	21.4	631
10	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
11	The Energetics and Physiological Impact of Cohesin Extrusion. <i>Cell</i> , 2018, 173, 1165-1178.e20.	28.9	399
12	Quantifying the evolutionary dynamics of language. <i>Nature</i> , 2007, 449, 713-716.	27.8	346
13	Genome Organization Drives Chromosome Fragility. <i>Cell</i> , 2017, 170, 507-521.e18.	28.9	311
14	Transferable model for chromosome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12168-12173.	7.1	291
15	Using deep learning and Google Street View to estimate the demographic makeup of neighborhoods across the United States. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13108-13113.	7.1	282
16	The expanding scope of DNA sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1084-1094.	17.5	280
17	Juicebox.js Provides a Cloud-Based Visualization System for Hi-C Data. <i>Cell Systems</i> , 2018, 6, 256-258.e1.	6.2	271
18	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. <i>Molecular Cell</i> , 2017, 67, 1037-1048.e6.	9.7	242

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19	Deletion of <i>DXZ4</i> on the human inactive X chromosome alters higher-order genome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4504-12.	7.1	239
20	Walking along chromosomes with super-resolution imaging, contact maps, and integrative modeling. <i>PLoS Genetics</i> , 2018, 14, e1007872.	3.5	209
21	De novo prediction of human chromosome structures: Epigenetic marking patterns encode genome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12126-12131.	7.1	193
22	A Pliable Mediator Acts as a Functional Rather Than an Architectural Bridge between Promoters and Enhancers. <i>Cell</i> , 2019, 178, 1145-1158.e20.	28.9	176
23	Myc Regulates Chromatin Decompaction and Nuclear Architecture during B Cell Activation. <i>Molecular Cell</i> , 2017, 67, 566-578.e10.	9.7	174
24	Polycomb-mediated chromatin loops revealed by a subkilobase-resolution chromatin interaction map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8764-8769.	7.1	150
25	H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. <i>Nature Communications</i> , 2021, 12, 719.	12.8	140
26	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	21.4	139
27	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	12.6	132
28	The fundamental role of chromatin loop extrusion in physiological V(D)J recombination. <i>Nature</i> , 2019, 573, 600-604.	27.8	126
29	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
30	Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. <i>ELife</i> , 2021, 10, .	6.0	87
31	Large DNA Methylation Nadirs Anchor Chromatin Loops Maintaining Hematopoietic Stem Cell Identity. <i>Molecular Cell</i> , 2020, 78, 506-521.e6.	9.7	72
32	Analysis of Hi-C data using SIP effectively identifies loops in organisms from <i>C. elegans</i> to mammals. <i>Genome Research</i> , 2020, 30, 447-458.	5.5	70
33	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic β^2 Cell Identity and Function. <i>Cell Reports</i> , 2019, 26, 788-801.e6.	6.4	68
34	CTCF loss has limited effects on global genome architecture in <i>Drosophila</i> despite critical regulatory functions. <i>Nature Communications</i> , 2021, 12, 1011.	12.8	60
35	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (<i>Microcebus murinus</i>). <i>BMC Biology</i> , 2017, 15, 110.	3.8	53
36	Chromatin architecture transitions from zebrafish sperm through early embryogenesis. <i>Genome Research</i> , 2021, 31, 981-994.	5.5	48

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37	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (<i>Canis lupus</i>) Tj ETQq1.1.0.784314 rgBT / Overlock 10	6.4	47
38	Exploring chromosomal structural heterogeneity across multiple cell lines. <i>ELife</i> , 2020, 9, .	6.0	43
39	CTCF looping is established during gastrulation in medaka embryos. <i>Genome Research</i> , 2021, 31, 968-980.	5.5	37
40	Robust CTCF-Based Chromatin Architecture Underpins Epigenetic Changes in the Heart Failure Stressâ€Gene Response. <i>Circulation</i> , 2019, 139, 1937-1956.	1.6	36
41	Cohesin depleted cells rebuild functional nuclear compartments after endomitosis. <i>Nature Communications</i> , 2020, 11, 6146.	12.8	35
42	Genome-wide diversity in the California condor tracks its prehistoric abundance and decline. <i>Current Biology</i> , 2021, 31, 2939-2946.e5.	3.9	35
43	Topologically Associated Domains Delineate Susceptibility to Somatic Hypermutation. <i>Cell Reports</i> , 2019, 29, 3902-3915.e8.	6.4	33
44	Essential role of Cp190 in physical and regulatory boundary formation. <i>Science Advances</i> , 2022, 8, eabl8834.	10.3	27
45	Chromatin Is Frequently Unknotted at the Megabase Scale. <i>Biophysical Journal</i> , 2020, 118, 2268-2279.	0.5	26
46	Chromosomalâ€level genome assembly of the scimitarâ€horned oryx: Insights into diversity and demography of a species extinct in the wild. <i>Molecular Ecology Resources</i> , 2020, 20, 1668-1681.	4.8	26
47	Gene architecture directs splicing outcome in separate nuclear spatial regions. <i>Molecular Cell</i> , 2022, 82, 1021-1034.e8.	9.7	26
48	Chromosome-length genome assembly and structural variations of the primal Basenji dog (<i>Canis lupus</i>) Tj ETQq0.0.0 rgBT / Overlock 10	2.8	22
49	MCPH1 inhibits Condensin II during interphase by regulating its SMC2-Kleisin interface. <i>ELife</i> , 2021, 10, .	6.0	21
50	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	9.5	20
51	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	2.9	19
52	Somatic Rearrangement in B Cells: Itâ€™s (Mostly) Nuclear Physics. <i>Cell</i> , 2015, 162, 708-711.	28.9	14
53	The Easter Egg Weevil (<i>Pachyrhynchus</i>) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. <i>PLoS Genetics</i> , 2021, 17, e1009745.	3.5	14
54	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	10.3	14

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55	Delineating the Tnt1 Insertion Landscape of the Model Legume <i>Medicago truncatula</i> cv. R108 at the Hi-C Resolution Using a Chromosome-Length Genome Assembly. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4326.	4.1	13
56	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation. <i>PLoS Pathogens</i> , 2022, 18, e1010288.	4.7	13
57	RedChIP identifies noncoding RNAs associated with genomic sites occupied by Polycomb and CTCF proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	13
58	GSDB: a database of 3D chromosome and genome structures reconstructed from Hi-C data. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 60.	2.0	12
59	Chromosome Modeling on Downsampled Hi-C Maps Enhances the Compartmentalization Signal. <i>Journal of Physical Chemistry B</i> , 2021, 125, 8757-8767.	2.6	12
60	Somatic structural variant formation is guided by and influences genome architecture. <i>Genome Research</i> , 2022, 32, 643-655.	5.5	12
61	A chromosome-level genome sequence assembly of the red raspberry (<i>Rubus idaeus</i> L.). <i>PLoS ONE</i> , 2022, 17, e0265096.	2.5	11
62	A pan-genome and chromosome-length reference genome of narrow-leaved lupin (<i>Lupinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Journal, 0, , .	5.7	9
63	Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. <i>GigaScience</i> , 2022, 11, .	6.4	8
64	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020, 9, .	6.4	6
65	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 33.	1.8	6
66	De novo chromosome-length assembly of the mule deer (<i>Odocoileus hemionus</i>) genome. <i>GigaByte</i> , 0, 2021, 1-13.	0.0	5
67	Culturomicsâ€™ Response. <i>Science</i> , 2011, 332, 36-37.	12.6	4
68	Nuclear Biology: Whatâ€™s Been Most Surprising?. <i>Cell</i> , 2013, 152, 1207-1208.	28.9	3
69	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	1.8	3
70	Zoom!. <i>Science</i> , 2011, 334, 1222-1223.	12.6	2
71	Chromatin Extrusion Explains Key Features of Loop and Domain Formation in Wild-type and Engineered Genomes. <i>FASEB Journal</i> , 2016, 30, 588.1.	0.5	2
72	Response to Bakker et al.. <i>Current Biology</i> , 2022, 32, R358-R359.	3.9	1

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73	A Chromosome-Length Assembly of the Hawaiian Monk Seal (<i>Neomonachus schauinslandi</i>): A History of Genetic Purgings and Genomic Stability. <i>Genes</i> , 2022, 13, 1270.	2.4	1
74	Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
75	High Order Chromatin Structure Regulates Gene Expression in Hematopoietic Stem Cell Self-Renewal and Erythroid Differentiation. <i>Blood</i> , 2016, 128, 1033-1033.	1.4	0
76	Large DNA Methylation Canyons Anchor Chromatin Loops Maintaining Hematopoietic Stem Cell Identity. <i>Blood</i> , 2018, 132, 534-534.	1.4	0
77	Topologically Associated Domains Delineate Susceptibility to Somatic Hypermutation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
78	Three-D Codes in the Human Genome. <i>Blood</i> , 2019, 134, SCI-50-SCI-50.	1.4	0
79	Le g�nome, un fouillis bien ordonn�. <i>Pourlascience Fr</i> , 2020, N� 517 - novembre, 34-43.	0.0	0