

# Erez Lieberman Aiden

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

23,949  
citations

109321  
35  
h-index

88630  
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

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

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