

# Erez Lieberman Aiden

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

23,949  
citations

125106

35  
h-index

100535

70  
g-index

115  
all docs

115  
docs citations

115  
times ranked

25723  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	4.4	20
2	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, .	3.3	124
3	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation. <i>PLoS Pathogens</i> , 2022, 18, e1010288.	2.1	13
4	Somatic structural variant formation is guided by and influences genome architecture. <i>Genome Research</i> , 2022, 32, 643-655.	2.4	12
5	Gene architecture directs splicing outcome in separate nuclear spatial regions. <i>Molecular Cell</i> , 2022, 82, 1021-1034.e8.	4.5	26
6	A chromosome-level genome sequence assembly of the red raspberry ( <i>Rubus idaeus</i> L.). <i>PLoS ONE</i> , 2022, 17, e0265096.	1.1	11
7	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, .	3.3	13
8	Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. <i>GigaScience</i> , 2022, 11, .	3.3	8
9	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	4.7	14
10	Response to Bakker et al.. <i>Current Biology</i> , 2022, 32, R358-R359.	1.8	1
11	Essential role of Cp190 in physical and regulatory boundary formation. <i>Science Advances</i> , 2022, 8, eabl8834.	4.7	27
12	A Chromosome-Length Assembly of the Hawaiian Monk Seal ( <i>Neomonachus schauinslandi</i> ): A History of Genetic Purging and Genomic Stability. <i>Genes</i> , 2022, 13, 1270.	1.0	1
13	H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. <i>Nature Communications</i> , 2021, 12, 719.	5.8	140
14	CTCF loss has limited effects on global genome architecture in <i>Drosophila</i> despite critical regulatory functions. <i>Nature Communications</i> , 2021, 12, 1011.	5.8	60
15	Chromosome-length genome assembly and structural variations of the primal Basenji dog ( <i>Canis lupus</i> ) Tj ETQq1 1,0,784314,rgBT /Omel 1,2	1.2	22
16	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.	1.8	13
17	Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. <i>ELife</i> , 2021, 10, .	2.8	87
18	Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. <i>FASEB Journal</i> , 2021, 35, .	0.2	0

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19	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	1.3	19
20	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	6.0	132
21	CTCF looping is established during gastrulation in medaka embryos. <i>Genome Research</i> , 2021, 31, 968-980.	2.4	37
22	Chromatin architecture transitions from zebrafish sperm through early embryogenesis. <i>Genome Research</i> , 2021, 31, 981-994.	2.4	48
23	Chromosome Modeling on Downsampled Hi-C Maps Enhances the Compartmentalization Signal. <i>Journal of Physical Chemistry B</i> , 2021, 125, 8757-8767.	1.2	12
24	Genome-wide diversity in the California condor tracks its prehistoric abundance and decline. <i>Current Biology</i> , 2021, 31, 2939-2946.e5.	1.8	35
25	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.	1.5	14
26	MCPH1 inhibits Condensin II during interphase by regulating its SMC2-Kleisin interface. <i>ELife</i> , 2021, 10, .	2.8	21
27	Chromatin Is Frequently Unknotted at the Megabase Scale. <i>Biophysical Journal</i> , 2020, 118, 2268-2279.	0.2	26
28	Cohesin depleted cells rebuild functional nuclear compartments after endomitosis. <i>Nature Communications</i> , 2020, 11, 6146.	5.8	35
29	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020, 9, .	3.3	6
30	GSDB: a database of 3D chromosome and genome structures reconstructed from Hi-C data. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 60.	1.0	12
31	Chromosomal-level genome assembly of the scimitar-horned oryx: Insights into diversity and demography of a species extinct in the wild. <i>Molecular Ecology Resources</i> , 2020, 20, 1668-1681.	2.2	26
32	Large DNA Methylation Nadirs Anchor Chromatin Loops Maintaining Hematopoietic Stem Cell Identity. <i>Molecular Cell</i> , 2020, 78, 506-521.e6.	4.5	72
33	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.	2.4	70
34	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog ( <i>Canis lupus</i> ) Tj ETQq0,0,0 rgt / Overlock 1	3.3	47
35	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	0.9	3
36	Exploring chromosomal structural heterogeneity across multiple cell lines. <i>ELife</i> , 2020, 9, .	2.8	43

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37	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. Wellcome Open Research, 2020, 5, 33.	0.9	6
38	Le génome, un fouillis bien ordonné. Pour la science Fr, 2020, N° 517 - novembre, 34-43.	0.0	0
39	A Pliable Mediator Acts as a Functional Rather Than an Architectural Bridge between Promoters and Enhancers. Cell, 2019, 178, 1145-1158.e20.	13.5	176
40	The fundamental role of chromatin loop extrusion in physiological V(D)J recombination. Nature, 2019, 573, 600-604.	13.7	126
41	Robust CTCF-Based Chromatin Architecture Underpins Epigenetic Changes in the Heart Failure Stress-Induced Gene Response. Circulation, 2019, 139, 1937-1956.	1.6	36
42	Topologically Associated Domains Delineate Susceptibility to Somatic Hypermutation. Cell Reports, 2019, 29, 3902-3915.e8.	2.9	33
43	Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. Nature Genetics, 2019, 51, 1664-1669.	9.4	631
44	Multomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic $\beta^2$ Cell Identity and Function. Cell Reports, 2019, 26, 788-801.e6.	2.9	68
45	Three-D Codes in the Human Genome. Blood, 2019, 134, SCI-50-SCI-50.	0.6	0
46	The Energetics and Physiological Impact of Cohesin Extrusion. Cell, 2018, 173, 1165-1178.e20.	13.5	399
47	Juicebox.js Provides a Cloud-Based Visualization System for Hi-C Data. Cell Systems, 2018, 6, 256-258.e1.	2.9	271
48	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. Nature, 2018, 563, 501-507.	13.7	426
49	Walking along chromosomes with super-resolution imaging, contact maps, and integrative modeling. PLoS Genetics, 2018, 14, e1007872.	1.5	209
50	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	9.4	139
51	Large DNA Methylation Canyons Anchor Chromatin Loops Maintaining Hematopoietic Stem Cell Identity. Blood, 2018, 132, 534-534.	0.6	0
52	De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. Science, 2017, 356, 92-95.	6.0	1,513
53	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.	3.3	193
54	Cohesin Loss Eliminates All Loop Domains. Cell, 2017, 171, 305-320.e24.	13.5	1,454

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55	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. <i>Molecular Cell</i> , 2017, 67, 1037-1048.e6.	4.5	242
56	Genome Organization Drives Chromosome Fragility. <i>Cell</i> , 2017, 170, 507-521.e18.	13.5	311
57	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.	3.3	150
58	Myc Regulates Chromatin Decompaction and Nuclear Architecture during B Cell Activation. <i>Molecular Cell</i> , 2017, 67, 566-578.e10.	4.5	174
59	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.	3.3	282
60	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur ( <i>Microcebus murinus</i> ). <i>BMC Biology</i> , 2017, 15, 110.	1.7	53
61	Transferable model for chromosome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12168-12173.	3.3	291
62	Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom. <i>Cell Systems</i> , 2016, 3, 99-101.	2.9	1,199
63	Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments. <i>Cell Systems</i> , 2016, 3, 95-98.	2.9	2,057
64	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.	3.3	239
65	Chromatin Extrusion Explains Key Features of Loop and Domain Formation in Wild-Type and Engineered Genomes. <i>FASEB Journal</i> , 2016, 30, 588.1.	0.2	2
66	High Order Chromatin Structure Regulates Gene Expression in Hematopoietic Stem Cell Self-Renewal and Erythroid Differentiation. <i>Blood</i> , 2016, 128, 1033-1033.	0.6	0
67	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.	3.3	1,464
68	Somatic Rearrangement in B Cells: It's (Mostly) Nuclear Physics. <i>Cell</i> , 2015, 162, 708-711.	13.5	14
69	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. <i>Cell</i> , 2014, 159, 1665-1680.	13.5	6,520
70	Nuclear Biology: What's Been Most Surprising?. <i>Cell</i> , 2013, 152, 1207-1208.	13.5	3
71	The expanding scope of DNA sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1084-1094.	9.4	280
72	Quantitative Analysis of Culture Using Millions of Digitized Books. <i>Science</i> , 2011, 331, 176-182.	6.0	2,010

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73	Culturomicsâ€™Response. Science, 2011, 332, 36-37.	6.0	4
74	Zoom!. Science, 2011, 334, 1222-1223.	6.0	2
75	Quantifying the evolutionary dynamics of language. Nature, 2007, 449, 713-716.	13.7	346
76	Evolutionary dynamics on graphs. Nature, 2005, 433, 312-316.	13.7	1,044
77	Topologically Associated Domains Delineate Susceptibility to Somatic Hypermutation. SSRN Electronic Journal, 0, , .	0.4	0
78	De novo chromosome-length assembly of the mule deer ( <i>Odocoileus hemionus</i> ) genome. GigaByte, 0, 2021, 1-13.	0.0	5
79	A panâ€™genome and chromosomeâ€™length reference genome of narrowâ€™leafed lupin ( <i>Lupinus</i> ) Tj ETQq1 1 0.784314 rgBT /Over Journal, 0, , .	2.8	9