Eric S Lander

List of Publications by Year
in descending order

137 papers	234,624 citations	1371 108 h-index	11308 136 g-index
150 all docs	150 docs citations	150 times ranked	214566 citing authors

#	Article	IF	Citations
1	Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15545-15550.	7.1	38,922
2	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
3	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
4	Integrative genomics viewer. Nature Biotechnology, 2011, 29, 24-26.	17.5	11,708
5	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	12.6	7,170
6	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. Cell, 2014, 159, 1665-1680.	28.9	6,520
7	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
8	The Structure of Haplotype Blocks in the Human Genome. Science, 2002, 296, 2225-2229.	12.6	5,300
9	Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. Nature Genetics, 1995, 11, 241-247.	21.4	5,020
10	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. Cell, 2006, 125, 315-326.	28.9	4,773
11	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	27.8	4,761
12	Development and Applications of CRISPR-Cas9 for Genome Engineering. Cell, 2014, 157, 1262-1278.	28.9	4,607
13	The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 2006, 313, 1929-1935.	12.6	4,472
14	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	27.8	3,801
15	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. Nature, 2007, 448, 553-560.	27.8	3,733
16	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
17	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
18	Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. Nature, 2009, 462, 108-112.	27.8	2,707

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19	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	27.8	2,586
20	Genetic Screens in Human Cells Using the CRISPR-Cas9 System. Science, 2014, 343, 80-84.	12.6	2,414
21	Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature, 2008, 454, 766-770.	27.8	2,267
22	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215
23	Identification of Selective Inhibitors of Cancer Stem Cells by High-Throughput Screening. Cell, 2009, 138, 645-659.	28.9	2,200
24	An immunogenic personal neoantigen vaccine for patients with melanoma. Nature, 2017, 547, 217-221.	27.8	2,112
25	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. Nature Genetics, 2018, 50, 1219-1224.	21.4	2,111
26	Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments. Cell Systems, 2016, 3, 95-98.	6.2	2,057
27	Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome. Science, 1998, 280, 1077-1082.	12.6	1,993
28	Detecting recent positive selection in the human genome from haplotype structure. Nature, 2002, 419, 832-837.	27.8	1,881
29	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
30	lincRNAs act in the circuitry controlling pluripotency and differentiation. Nature, 2011, 477, 295-300.	27.8	1,749
31	The common PPARÎ³ Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. Nature Genetics, 2000, 26, 76-80.	21.4	1,672
32	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science, 2016, 353, aaf5573.	12.6	1,647
33	High-resolution haplotype structure in the human genome. Nature Genetics, 2001, 29, 229-232.	21.4	1,596
34	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
35	Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. Nature, 1988, 335, 721-726.	27.8	1,532
36	De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science, 2017, 356, 92-95.	12.6	1,513

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37	High-quality draft assemblies of mammalian genomes from massively parallel sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1513-1518.	7.1	1,476
38	Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6456-65.	7.1	1,464
39	Identification and characterization of essential genes in the human genome. Science, 2015, 350, 1096-1101.	12.6	1,461
40	Cohesin Loss Eliminates All Loop Domains. Cell, 2017, 171, 305-320.e24.	28.9	1,454
41	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. Cell, 2005, 120, 169-181.	28.9	1,348
42	Dissecting direct reprogramming through integrative genomic analysis. Nature, 2008, 454, 49-55.	27.8	1,344
43	The mystery of missing heritability: Genetic interactions create phantom heritability. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1193-1198.	7.1	1,322
44	Genetic Mapping in Human Disease. Science, 2008, 322, 881-888.	12.6	1,289
45	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	27.8	1,288
46	Ab initio reconstruction of cell typeâ€“specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology, 2010, 28, 503-510.	17.5	1,251
47	Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom. Cell Systems, 2016, 3, 99-101.	6.2	1,199
48	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. Cell, 2016, 167, 1853-1866.e17.	28.9	1,144
49	Lessons from the Cancer Genome. Cell, 2013, 153, 17-37.	28.9	1,133
50	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science, 2014, 345, 1369-1372.	12.6	1,083
51	On the allelic spectrum of human disease. Trends in Genetics, 2001, 17, 502-510.	6.7	1,057
52	Local regulation of gene expression by lncRNA promoters, transcription and splicing. Nature, 2016, 539, 452-455.	27.8	1,056
53	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5â€² Sites. Cell Reports, 2014, 8, 284-296.	6.4	972
54	The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3. Nature, 2015, 521, 232-236.	27.8	946

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55	Initial impact of the sequencing of the human genome. Nature, 2011, 470, 187-197.	27.8	919
56	The Xist lncRNA Exploits Three-Dimensional Genome Architecture to Spread Across the X Chromosome. Science, 2013, 341, 1237973.	12.6	846
57	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	9.4	821
58	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. Cell, 2014, 159, 148-162.	28.9	770
59	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. Science Translational Medicine, 2016, 8, 343ra81.	12.4	763
60	The diastrophic dysplasia gene encodes a novel sulfate transporter: Positional cloning by fine-structure linkage disequilibrium mapping. Cell, 1994, 78, 1073-1087.	28.9	731
61	The Plasticity of Dendritic Cell Responses to Pathogens and Their Components. Science, 2001, 294, 870-875.	12.6	730
62	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865.	6.4	671
63	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
64	An SNP map of the human genome generated by reduced representation shotgun sequencing. Nature, 2000, 407, 513-516.	27.8	658
65	Activity-by-contact model of enhancerâ€“promoter regulation from thousands of CRISPR perturbations. Nature Genetics, 2019, 51, 1664-1669.	21.4	631
66	Ploidy Regulation of Gene Expression. Science, 1999, 285, 251-254.	12.6	608
67	Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. Nature Biotechnology, 2012, 30, 271-277.	17.5	602
68	Searching for missing heritability: Designing rare variant association studies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E455-64.	7.1	570
69	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. Cell, 2013, 155, 1409-1421.	28.9	554
70	Linkage disequilibrium mapping in isolated founder populations: diastrophic dysplasia in Finland. Nature Genetics, 1992, 2, 204-211.	21.4	544
71	Integrative Genomic Approaches Identify IKBKE as a Breast Cancer Oncogene. Cell, 2007, 129, 1065-1079.	28.9	538
72	Gene Essentiality Profiling Reveals Gene Networks and Synthetic Lethal Interactions with Oncogenic Ras. Cell, 2017, 168, 890-903.e15.	28.9	535

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73	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. Cell, 2019, 177, 587-596.e9.	28.9	516
74	Systematic mapping of functional enhancerâ€“promoter connections with CRISPR interference. Science, 2016, 354, 769-773.	12.6	512
75	Distinguishing protein-coding and noncoding genes in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19428-19433.	7.1	503
76	Array of hope. Nature Genetics, 1999, 21, 3-4.	21.4	500
77	Highly parallel identification of essential genes in cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20380-20385.	7.1	499
78	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. Cell, 2010, 143, 156-169.	28.9	460
79	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. Science, 2010, 327, 883-886.	12.6	457
80	RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites. Cell, 2014, 159, 188-199.	28.9	425
81	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. Cell, 2019, 176, 928-943.e22.	28.9	411
82	Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. Nucleic Acids Research, 2013, 41, e67-e67.	14.5	407
83	The Heroes of CRISPR. Cell, 2016, 164, 18-28.	28.9	391
84	RNF43 is frequently mutated in colorectal and endometrial cancers. Nature Genetics, 2014, 46, 1264-1266.	21.4	388
85	Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12372-12377.	7.1	383
86	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. Cell, 2016, 165, 1519-1529.	28.9	378
87	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
88	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
89	Detection of regulatory variation in mouse genes. Nature Genetics, 2002, 32, 432-437.	21.4	348
90	Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood. Nature, 2017, 548, 343-346.	27.8	336

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91	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	27.8	332
92	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. Cell Host and Microbe, 2018, 24, 146-154.e4.	11.0	311
93	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. Nature, 2018, 561, 132-136.	27.8	303
94	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	28.9	296
95	Exome sequencing identifies GATA1 mutations resulting in Diamond-Blackfan anemia. Journal of Clinical Investigation, 2012, 122, 2439-2443.	8.2	292
96	Measuring missing heritability: Inferring the contribution of common variants. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5272-81.	7.1	279
97	Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7145-7150.	7.1	272
98	Whole-Genome Sequence Assembly for Mammalian Genomes: Arachne 2. Genome Research, 2003, 13, 91-96.	5.5	263
99	The SARS-CoV-2 RNAâ€“protein interactome in infected human cells. Nature Microbiology, 2021, 6, 339-353.	13.3	245
100	Altered translation of GATA1 in Diamond-Blackfan anemia. Nature Medicine, 2014, 20, 748-753.	30.7	243
101	Deletion of DXZ4 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
102	Comprehensive variation discovery in single human genomes. Nature Genetics, 2014, 46, 1350-1355.	21.4	214
103	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. Cell, 2015, 162, 412-424.	28.9	206
104	Assembly of polymorphic genomes: Algorithms and application to Ciona savignyi. Genome Research, 2005, 15, 1127-1135.	5.5	170
105	Identification of cancer driver genes based on nucleotide context. Nature Genetics, 2020, 52, 208-218.	21.4	170
106	Mapping transcriptomic vector fields of single cells. Cell, 2022, 185, 690-711.e45.	28.9	167
107	Systematic dissection of genomic features determining transcription factor binding and enhancer function. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1291-E1300.	7.1	150
108	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140

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109	A small-molecule inhibitor of TRPC5 ion channels suppresses progressive kidney disease in animal models. Science, 2017, 358, 1332-1336.	12.6	135
110	Small Molecule Targets TMED9 and Promotes Lysosomal Degradation to Reverse Proteinopathy. Cell, 2019, 178, 521-535.e23.	28.9	124
111	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
112	Direct isolation of polymorphic markers linked to a trait by genetically directed representational difference analysis. Nature Genetics, 1994, 6, 57-63.	21.4	118
113	Cyclin D3 coordinates the cell cycle during differentiation to regulate erythrocyte size and number. Genes and Development, 2012, 26, 2075-2087.	5.9	100
114	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. Cell, 2017, 171, 1424-1436.e18.	28.9	95
115	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. Nature Genetics, 2020, 52, 138-145.	21.4	73
116	Positional specificity of different transcription factor classes within enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7222-E7230.	7.1	72
117	Compatibility rules of human enhancer and promoter sequences. Nature, 2022, 607, 176-184.	27.8	67
118	Towards a treatment for genetic prion disease: trials and biomarkers. Lancet Neurology, The, 2020, 19, 361-368.	10.2	60
119	Recognition of related proteins by iterative template refinement (ITR). Protein Science, 1994, 3, 1315-1328.	7.6	48
120	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E327-E336.	7.1	39
121	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	12.8	38
122	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	19.0	33
123	Compressed sensing for highly efficient imaging transcriptomics. Nature Biotechnology, 2021, 39, 936-942.	17.5	33
124	Single Guide RNA Library Design and Construction. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot090803.	0.3	30
125	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. Cell Metabolism, 2021, 33, 615-628.e13.	16.2	28
126	Finding similarities and differences among genomes. Nature Genetics, 1993, 4, 5-6.	21.4	27

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127	Viral Packaging and Cell Culture for CRISPR-Based Screens. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot090811.	0.3	27
128	Rare Genetic Variants Associated With Sudden Cardiac Death in Adults. Journal of the American College of Cardiology, 2019, 74, 2623-2634.	2.8	27
129	Founding father. Nature, 1998, 396, 13-14.	27.8	25
130	HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequencing of DNA probes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 33404-33413.	7.1	21
131	Large-Scale Single Guide RNA Library Construction and Use for CRISPRâ€“Cas9-Based Genetic Screens. Cold Spring Harbor Protocols, 2016, 2016, pdb.top086892.	0.3	20
132	Genome-Wide CRISPR/Cas9 Screening for Identification of Cancer Genes in Cell Lines. Methods in Molecular Biology, 2019, 1907, 125-136.	0.9	16
133	Response to the ANZFSS council statement on the Presidentâ€™s Council Of Advisors On Science And Technology Report. Australian Journal of Forensic Sciences, 2017, 49, 366-368.	1.2	13
134	Prepare and Inspire. Science, 2010, 330, 151-151.	12.6	12
135	Gain-of-Function Claims for Type-2-Diabetes-Associated Coding Variants in SLC16A11 Are Not Supported by the Experimental Data. Cell Reports, 2019, 29, 778-780.	6.4	6
136	Reply to Lee: Downward bias in heritability estimation is not due to simplified linkage equilibrium SNP simulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5452-E5453.	7.1	1
137	2018 William Allan Award: Discovering the Genes for Common Disease: From Families to Populations. American Journal of Human Genetics, 2019, 104, 375-383.	6.2	0