Lior S Pachter

List of Publications by Year
in descending order

166 papers	89,632 citations	18482 62 h-index	6836 155 g-index
224 all docs	224 docs citations	224 times ranked	108766 citing authors

#	Article	IF	Citations
1	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotechnology, 2010, 28, 511-515.	17.5	13,805
2	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nature Protocols, 2012, 7, 562-578.	12.0	11,433
3	TopHat: discovering splice junctions with RNA-Seq. Bioinformatics, 2009, 25, 1105-1111.	4.1	11,265
4	Near-optimal probabilistic RNA-seq quantification. Nature Biotechnology, 2016, 34, 525-527.	17.5	7,322
5	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
6	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
7	Differential analysis of gene regulation at transcript resolution with RNA-seq. Nature Biotechnology, 2013, 31, 46-53.	17.5	3,256
8	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
9	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
10	The ENCODE (ENCyclopedia Of DNA Elements) Project. Science, 2004, 306, 636-640.	12.6	2,121
11	VISTA: computational tools for comparative genomics. Nucleic Acids Research, 2004, 32, W273-W279.	14.5	2,033
12	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
13	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
14	Disordered Microbial Communities in Asthmatic Airways. PLoS ONE, 2010, 5, e8578.	2.5	1,436
15	Differential analysis of RNA-seq incorporating quantification uncertainty. Nature Methods, 2017, 14, 687-690.	19.0	1,296
16	Improving RNA-Seq expression estimates by correcting for fragment bias. Genome Biology, 2011, 12, R22.	9.6	1,164
17	Identification of novel transcripts in annotated genomes using RNA-Seq. Bioinformatics, 2011, 27, 2325-2329.	4.1	906
18	Streaming fragment assignment for real-time analysis of sequencing experiments. Nature Methods, 2013, 10, 71-73.	19.0	901

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19	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in Drosophila simulans. PLoS Biology, 2007, 5, e310.	5.6	583
20	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	27.8	573
21	Phylogenetic Shadowing of Primate Sequences to Find Functional Regions of the Human Genome. Science, 2003, 299, 1391-1394.	12.6	466
22	AVID: A Global Alignment Program. Genome Research, 2003, 13, 97-102.	5.5	405
23	<tt>rVista</tt>for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. Genome Research, 2002, 12, 832-839.	5.5	384
24	A Genome-Wide Map of Conserved MicroRNA Targets in C. elegans. Current Biology, 2006, 16, 460-471.	3.9	380
25	Museum of spatial transcriptomics. Nature Methods, 2022, 19, 534-546.	19.0	356
26	Multiplexed RNA structure characterization with selective 2â€²-hydroxyl acylation analyzed by primer extension sequencing (SHAPE-Seq). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11063-11068.	7.1	346
27	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
28	Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction. Genome Research, 2000, 10, 950-958.	5.5	303
29	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	3.2	302
30	Bioinformatics for Whole-Genome Shotgun Sequencing of Microbial Communities. PLoS Computational Biology, 2005, 1, e24.	3.2	292
31	Active Conservation of Noncoding Sequences Revealed by Three-Way Species Comparisons. Genome Research, 2000, 10, 1304-1306.	5.5	279
32	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. Nature Biotechnology, 2021, 39, 813-818.	17.5	252
33	MAVID: Constrained Ancestral Alignment of Multiple Sequences. Genome Research, 2004, 14, 693-699.	5.5	232
34	A Python library for probabilistic analysis of single-cell omics data. Nature Biotechnology, 2022, 40, 163-166.	17.5	216
35	Identification and correction of systematic error in high-throughput sequence data. BMC Bioinformatics, 2011, 12, 451.	2.6	201
36	Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis. Science, 2015, 350, 1251-1255.	12.6	201

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37	Viral Population Estimation Using Pyrosequencing. PLoS Computational Biology, 2008, 4, e1000074.	3.2	197
38	Strategies and Tools for Whole-Genome Alignments. Genome Research, 2003, 13, 73-80.	5.5	190
39	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. Cell, 2019, 179, 713-728.e17.	28.9	186
40	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
41	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. PLoS Biology, 2010, 8, e1000343.	5.6	184
42	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
43	A dynamic intron retention program enriched in RNA processing genes regulates gene expression during terminal erythropoiesis. Nucleic Acids Research, 2016, 44, 838-851.	14.5	162
44	A curated database reveals trends in single-cell transcriptomics. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	148
45	SLAM: Cross-Species Gene Finding and Alignment with a Generalized Pair Hidden Markov Model. Genome Research, 2003, 13, 496-502.	5.5	141
46	A discriminative learning approach to differential expression analysis for single-cell RNA-seq. Nature Methods, 2019, 16, 163-166.	19.0	123
47	Interpretable factor models of single-cell RNA-seq via variational autoencoders. Bioinformatics, 2020, 36, 3418-3421.	4.1	123
48	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. Molecular Cancer Research, 2010, 8, 961-974.	3.4	121
49	The barcode, UMI, set format and BUStools. Bioinformatics, 2019, 35, 4472-4473.	4.1	117
50	Genome methylation in D. melanogaster is found at specific short motifs and is independent of DNMT2 activity. Genome Research, 2014, 24, 821-830.	5.5	113
51	Modeling and automation of sequencing-based characterization of RNA structure. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11069-11074.	7.1	109
52	Fast and accurate single-cell RNA-seq analysis by clustering of transcript-compatibility counts. Genome Biology, 2016, 17, 112.	8.8	109
53	Gene-level differential analysis at transcript-level resolution. Genome Biology, 2018, 19, 53.	8.8	108
54	Mapping and identification of essential gene functions on the X chromosome ofDrosophila. EMBO Reports, 2002, 3, 34-38.	4.5	105

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55	Association mapping from sequencing reads using k-mers. ELife, 2018, 7, .	6.0	88
56	Why Neighbor-Joining Works. Algorithmica, 2009, 54, 1-24.	1.3	83
57	Human Intestinal Tissue with Adult Stem Cell Properties Derived from Pluripotent Stem Cells. Stem Cell Reports, 2014, 2, 838-852.	4.8	83
58	Highly multiplexed single-cell RNA-seq by DNA oligonucleotide tagging of cellular proteins. Nature Biotechnology, 2020, 38, 35-38.	17.5	83
59	CGAL: computing genome assembly likelihoods. Genome Biology, 2013, 14, R8.	9.6	77
60	Tropical geometry of statistical models. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16132-16137.	7.1	76
61	A dynamic alternative splicing program regulates gene expression during terminal erythropoiesis. Nucleic Acids Research, 2014, 42, 4031-4042.	14.5	76
62	Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems. Journal of Computational Biology, 2002, 9, 389-399.	1.6	73
63	Multiple alignment by sequence annealing. Bioinformatics, 2007, 23, e24-e29.	4.1	67
64	SHAPEâ€“Seq: Highâ€Throughput RNA Structure Analysis. Current Protocols in Chemical Biology, 2012, 4, 275-297.	1.7	67
65	Accurate design of translational output by a neural network model of ribosome distribution. Nature Structural and Molecular Biology, 2018, 25, 577-582.	8.2	67
66	Reference based annotation with GeneMapper. Genome Biology, 2006, 7, R29.	9.6	66
67	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	17.5	64
68	Development of a Low Bias Method for Characterizing Viral Populations Using Next Generation Sequencing Technology. PLoS ONE, 2010, 5, e13564.	2.5	58
69	HMM sampling and applications to gene finding and alternative splicing. Bioinformatics, 2003, 19, ii36-ii41.	4.1	56
70	RNA Velocity: Molecular Kinetics from Single-Cell RNA-Seq. Molecular Cell, 2018, 72, 7-9.	9.7	56
71	Analysis of epistatic interactions and fitness landscapes using a new geometric approach. BMC Evolutionary Biology, 2007, 7, 60.	3.2	54
72	MAVID multiple alignment server. Nucleic Acids Research, 2003, 31, 3525-3526.	14.5	52

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73	Shape-based peak identification for ChIP-Seq. BMC Bioinformatics, 2011, 12, 15.	2.6	52
74	Isoform cell-type specificity in the mouse primary motor cortex. Nature, 2021, 598, 195-199.	27.8	52
75	Parametric inference for biological sequence analysis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16138-16143.	7.1	51
76	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56.	2.9	51
77	Protein velocity and acceleration from single-cell multiomics experiments. Genome Biology, 2020, 21, 39.	8.8	49
78	Forcing matchings on square grids. Discrete Mathematics, 1998, 190, 287-294.	0.7	48
79	Constrained Optimization for UAV Task Assignment. , 2004, , .		48
80	A diverse epigenetic landscape at human exons with implication for expression. Nucleic Acids Research, 2015, 43, 3498-3508.	14.5	48
81	Whole-animal multiplexed single-cell RNA-seq reveals transcriptional shifts across Clytia medusa cell types. Science Advances, 2021, 7, eabh1683.	10.3	47
82	Optimization of air vehicles operations using mixed-integer linear programming. Journal of the Operational Research Society, 2007, 58, 516-527.	3.4	46
83	Convex Rank Tests and Semigraphoids. SIAM Journal on Discrete Mathematics, 2009, 23, 1117-1134.	0.8	46
84	Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples. Nature Biomedical Engineering, 2021, 5, 657-665.	22.5	46
85	Identification of transposable elements using multiple alignments of related genomes. Genome Research, 2005, 16, 260-270.	5.5	45
86	Intraspecies sequence comparisons for annotating genomes. Genome Research, 2004, 14, 2406-2411.	5.5	44
87	Multiple-sequence functional annotation and the generalized hidden Markov phylogeny. Bioinformatics, 2004, 20, 1850-1860.	4.1	44
88	Reconstructing trees from subtree weights. Applied Mathematics Letters, 2004, 17, 615-621.	2.7	44
89	UAV Task Assignment with Timing Constraints via Mixed-Integer Linear Programming. , 2004, , .		44
90	Principles of open source bioinstrumentation applied to the poseidon syringe pump system. Scientific Reports, 2019, 9, 12385.	3.3	44

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91	Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. Genome Research, 2011, 21, 2049-2057.	5.5	43
92	Parametric Alignment of Drosophila Genomes. PLoS Computational Biology, 2006, 2, e73.	3.2	38
93	Comparison of Pattern Detection Methods in Microarray Time Series of the Segmentation Clock. PLoS ONE, 2008, 3, e2856.	2.5	38
94	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	4.1	35
95	The Mathematics of Phylogenomics. SIAM Review, 2007, 49, 3-31.	9.5	34
96	RNA structure characterization from chemical mapping experiments. , 2011, , .		34
97	On the optimality of the neighbor-joining algorithm. Algorithms for Molecular Biology, 2008, 3, 5.	1.2	31
98	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	4.4	30
99	Estimating intrinsic and extrinsic noise from single-cell gene expression measurements. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 447-471.	0.6	30
100	Odd-paired is a pioneer-like factor that coordinates with Zelda to control gene expression in embryos. ELife, 2020, 9, .	6.0	30
101	Accurate Identification of Novel Human Genes Through Simultaneous Gene Prediction in Human, Mouse, and Rat. Genome Research, 2004, 14, 661-664.	5.5	28
102	Rational experiment design for sequencing-based RNA structure mapping. Rna, 2014, 20, 1864-1877.	3.5	28
103	Combining statistical alignment and phylogenetic footprinting to detect regulatory elements. Bioinformatics, 2008, 24, 1236-1242.	4.1	27
104	Expression reflects population structure. PLoS Genetics, 2018, 14, e1007841.	3.5	27
105	The neighbor-net algorithm. Advances in Applied Mathematics, 2011, 47, 240-258.	0.7	26
106	Beyond Pairwise Distances: Neighbor-Joining with Phylogenetic Diversity Estimates. Molecular Biology and Evolution, 2006, 23, 491-498.	8.9	25
107	Normalization of single-cell RNA-seq counts byâ€‚log(x + 1)â€‚orâ€‚log(1 + x). Bioinformatics, 2021, 37, 2223-2224.	4.1	25
108	A Dictionary-Based Approach for Gene Annotation. Journal of Computational Biology, 1999, 6, 419-430.	1.6	23

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109	Identification of Evolutionary Hotspots in the Rodent Genomes. Genome Research, 2004, 14, 574-579.	5.5	23
110	Updating RNA-Seq analyses after re-annotation. Bioinformatics, 2013, 29, 1631-1637.	4.1	23
111	rVista for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. Genome Research, 2002, 12, 832-839.	5.5	23
112	RNA-Seq and find: entering the RNA deep field. Genome Medicine, 2011, 3, 74.	8.2	22
113	Fragment assignment in the cloud with eXpress-D. BMC Bioinformatics, 2013, 14, 358.	2.6	22
114	Finding Convex Sets Among Points in the Plane. Discrete and Computational Geometry, 1998, 19, 405-410.	0.6	21
115	Modeling bursty transcription and splicing with the chemical master equation. Biophysical Journal, 2022, 121, 1056-1069.	0.5	21
116	Subtree power analysis and species selection for comparative genomics. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7900-7905.	7.1	19
117	Toward the Human Genotope. Bulletin of Mathematical Biology, 2007, 69, 2723-2735.	1.9	19
118	Pregnancy-Induced Changes in Systemic Gene Expression among Healthy Women and Women with Rheumatoid Arthritis. PLoS ONE, 2015, 10, e0145204.	2.5	19
119	Special function methods for bursty models of transcription. Physical Review E, 2020, 102, 022409.	2.1	18
120	Picking Alignments from (Steiner) Trees. Journal of Computational Biology, 2003, 10, 509-520.	1.6	17
121	Barcode identification for single cell genomics. BMC Bioinformatics, 2019, 20, 32.	2.6	17
122	Combinatorial Approaches and Conjectures for 2-Divisibility Problems Concerning Domino Tilings of Polyominoes. Electronic Journal of Combinatorics, 1997, 4, .	0.4	17
123	Forcing numbers of stop signs. Theoretical Computer Science, 2003, 303, 409-416.	0.9	15
124	Visualization of Multiple Genome Annotations and Alignments With the K-BROWSER. Genome Research, 2004, 14, 716-720.	5.5	15
125	Interpreting the unculturable majority. Nature Methods, 2007, 4, 479-480.	19.0	15
126	PROBer Provides a General Toolkit for Analyzing Sequencing-Based Toeprinting Assays. Cell Systems, 2017, 4, 568-574.e7.	6.2	15

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127	Combinatorics of least-squares trees. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13206-13211.	7.1	14
128	The Lair: a resource for exploratory analysis of published RNA-Seq data. BMC Bioinformatics, 2016, 17, 490.	2.6	13
129	Reliable and accurate diagnostics from highly multiplexed sequencing assays. Scientific Reports, 2020, 10, 21759.	3.3	13
130	RefShannon: A genome-guided transcriptome assembler using sparse flow decomposition. PLoS ONE, 2020, 15, e0232946.	2.5	13
131	MetMap Enables Genome-Scale Methyltyping for Determining Methylation States in Populations. PLoS Computational Biology, 2010, 6, e1000888.	3.2	11
132	Transcriptomic response of Drosophila melanogaster pupae developed in hypergravity. Genomics, 2016, 108, 158-167.	2.9	11
133	The computational challenges of applying comparative-based computational methods to whole genomes. Briefings in Bioinformatics, 2002, 3, 18-22.	6.5	10
134	SLAM web server for comparative gene finding and alignment. Nucleic Acids Research, 2003, 31, 3507-3509.	14.5	10
135	Coverage statistics for sequence census methods. BMC Bioinformatics, 2010, 11, 430.	2.6	10
136	Pregnancy-induced gene expression changes in vivo among women with rheumatoid arthritis: a pilot study. Arthritis Research and Therapy, 2017, 19, 104.	3.5	9
137	Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes. Lecture Notes in Computer Science, 2006, , 265-280.	1.3	9
138	Low-cost, scalable, and automated fluid sampling for fluidics applications. HardwareX, 2021, 10, e00201.	2.2	8
139	Large Multiple Organism Gene Finding by Collapsed Gibbs Sampling. Journal of Computational Biology, 2005, 12, 599-608.	1.6	7
140	The Cyclohedron Test for Finding Periodic Genes in Time Course Expression Studies. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article 21.	0.6	7
141	A closer look at RNA editing. Nature Biotechnology, 2012, 30, 246-247.	17.5	7
142	Zika infection of neural progenitor cells perturbs transcription in neurodevelopmental pathways. PLoS ONE, 2017, 12, e0175744.	2.5	7
143	Constructing status injective graphs. Discrete Applied Mathematics, 1997, 80, 107-113.	0.9	6
144	Human and mouse gene structure. , 2000, , .		6

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145	Applications of generalized pair hidden Markov models to alignment and gene finding problems. , 2001, , .		6
146	Quantifying uniformity of mapped reads. Bioinformatics, 2012, 28, 2680-2682.	4.1	6
147	Patterns of gene duplication and intron loss in the ENCODE regions suggest a confounding factor. Genomics, 2007, 90, 44-48.	2.9	5
148	Tracing the Most Parsimonious Indel History. Journal of Computational Biology, 2011, 18, 967-986.	1.6	5
149	Affine and Projective Tree Metric Theorems. Annals of Combinatorics, 2013, 17, 205-228.	0.6	5
150	Structural Variation among Wild and Industrial Strains of Penicillium chrysogenum. PLoS ONE, 2014, 9, e96784.	2.5	5
151	BUTTERFLY: addressing the pooled amplification paradox with unique molecular identifiers in single-cell RNA-seq. Genome Biology, 2021, 22, 174.	8.8	5
152	Multiple organism gene finding by collapsed gibbs sampling. , 2004, , .		4
153	Controlling for conservation in genome-wide DNA methylation studies. BMC Genomics, 2015, 16, 420.	2.8	4
154	SWALO: scaffolding with assembly likelihood optimization. Nucleic Acids Research, 2021, 49, e117-e117.	14.5	3
155	Picking alignments from (steiner) trees. , 2002, , .		2
156	Pair hidden Markov models. , 2005, , .		2
157	A faster implementation of association mapping from k-mers. Bio-protocol, 2020, 10, e3815.	0.4	2
158	Computation. , 2005, , 43-84.		1
159	Determining Coding CpG Islands by Identifying Regions Significant for Pattern Statistics on Markov Chains. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	1
160	Identification and correction of systematic error in high-throughput sequence data. Nature Precedings, 2011, , .	0.1	1
161	Factor analysis for survival time prediction with informative censoring and diverse covariates. Statistics in Medicine, 2019, 38, 3719-3732.	1.6	1
162	Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. PLoS ONE, 2010, 5, e11645.	2.5	0

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163	Deterministic column subset selection for single-cell RNA-Seq. PLoS ONE, 2019, 14, e0210571.	2.5	0
164	Transcript Abundance Estimation and the Laminar Packing Problem. Lecture Notes in Computer Science, 2019, , 203-211.	1.3	0
165	GENOME-WIDE ANALYSIS AND COMPARATIVE GENOMICS. , 2001, , .		0
166	Session Introduction. , 2002, , .		0