Lior S Pachter

List of Publications by Year
in descending order

166 papers	89,632 citations	21215 62 h-index	7836 155 g-index
224 all docs	224 docs citations	224 times ranked	120183 citing authors

#	Article	IF	Citations
1	Modeling bursty transcription and splicing with the chemical master equation. Biophysical Journal, 2022, 121, 1056-1069.	0.2	21
2	A Python library for probabilistic analysis of single-cell omics data. Nature Biotechnology, 2022, 40, 163-166.	9.4	216
3	Museum of spatial transcriptomics. Nature Methods, 2022, 19, 534-546.	9.0	356
4	Normalization of single-cell RNA-seq counts by␣log(x + 1)␣or␣log(1 + x). Bioinformatics, 2021, 37, 2223-2224.	1.8	25
5	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. Nature Biotechnology, 2021, 39, 813-818.	9.4	252
6	BUTTERFLY: addressing the pooled amplification paradox with unique molecular identifiers in single-cell RNA-seq. Genome Biology, 2021, 22, 174.	3.8	5
7	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.	11.6	46
8	SWALO: scaffolding with assembly likelihood optimization. Nucleic Acids Research, 2021, 49, e117-e117.	6.5	3
9	Low-cost, scalable, and automated fluid sampling for fluidics applications. HardwareX, 2021, 10, e00201.	1.1	8
10	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	13.7	166
11	Isoform cell-type specificity in the mouse primary motor cortex. Nature, 2021, 598, 195-199.	13.7	52
12	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	13.7	316
13	Whole-animal multiplexed single-cell RNA-seq reveals transcriptional shifts across *Clytia* medusa cell types. Science Advances, 2021, 7, eabh1683.	4.7	47
14	Highly multiplexed single-cell RNA-seq by DNA oligonucleotide tagging of cellular proteins. Nature Biotechnology, 2020, 38, 35-38.	9.4	83
15	A curated database reveals trends in single-cell transcriptomics. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	148
16	Special function methods for bursty models of transcription. Physical Review E, 2020, 102, 022409.	0.8	18
17	Reliable and accurate diagnostics from highly multiplexed sequencing assays. Scientific Reports, 2020, 10, 21759.	1.6	13
18	RefShannon: A genome-guided transcriptome assembler using sparse flow decomposition. PLoS ONE, 2020, 15, e0232946.	1.1	13

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19	Interpretable factor models of single-cell RNA-seq via variational autoencoders. Bioinformatics, 2020, 36, 3418-3421.	1.8	123
20	Protein velocity and acceleration from single-cell multiomics experiments. Genome Biology, 2020, 21, 39.	3.8	49
21	Odd-paired is a pioneer-like factor that coordinates with Zelda to control gene expression in embryos. ELife, 2020, 9, .	2.8	30
22	A faster implementation of association mapping from k-mers. Bio-protocol, 2020, 10, e3815.	0.2	2
23	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. Cell, 2019, 179, 713-728.e17.	13.5	186
24	Principles of open source bioinstrumentation applied to the poseidon syringe pump system. Scientific Reports, 2019, 9, 12385.	1.6	44
25	A discriminative learning approach to differential expression analysis for single-cell RNA-seq. Nature Methods, 2019, 16, 163-166.	9.0	123
26	Deterministic column subset selection for single-cell RNA-Seq. PLoS ONE, 2019, 14, e0210571.	1.1	0
27	Barcode identification for single cell genomics. BMC Bioinformatics, 2019, 20, 32.	1.2	17
28	Transcript Abundance Estimation and the Laminar Packing Problem. Lecture Notes in Computer Science, 2019, , 203-211.	1.0	0
29	Factor analysis for survival time prediction with informative censoring and diverse covariates. Statistics in Medicine, 2019, 38, 3719-3732.	0.8	1
30	The barcode, UMI, set format and BUStools. Bioinformatics, 2019, 35, 4472-4473.	1.8	117
31	Gene-level differential analysis at transcript-level resolution. Genome Biology, 2018, 19, 53.	3.8	108
32	Expression reflects population structure. PLoS Genetics, 2018, 14, e1007841.	1.5	27
33	RNA Velocity: Molecular Kinetics from Single-Cell RNA-Seq. Molecular Cell, 2018, 72, 7-9.	4.5	56
34	Accurate design of translational output by a neural network model of ribosome distribution. Nature Structural and Molecular Biology, 2018, 25, 577-582.	3.6	67
35	Association mapping from sequencing reads using k-mers. ELife, 2018, 7, .	2.8	88
36	PROBer Provides a General Toolkit for Analyzing Sequencing-Based Toeprinting Assays. Cell Systems, 2017, 4, 568-574.e7.	2.9	15

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37	Differential analysis of RNA-seq incorporating quantification uncertainty. Nature Methods, 2017, 14, 687-690.	9.0	1,296
38	Pregnancy-induced gene expression changes in vivo among women with rheumatoid arthritis: a pilot study. Arthritis Research and Therapy, 2017, 19, 104.	1.6	9
39	Zika infection of neural progenitor cells perturbs transcription in neurodevelopmental pathways. PLoS ONE, 2017, 12, e0175744.	1.1	7
40	Near-optimal probabilistic RNA-seq quantification. Nature Biotechnology, 2016, 34, 525-527.	9.4	7,322
41	Transcriptomic response of Drosophila melanogaster pupae developed in hypergravity. Genomics, 2016, 108, 158-167.	1.3	11
42	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	9.4	64
43	The Lair: a resource for exploratory analysis of published RNA-Seq data. BMC Bioinformatics, 2016, 17, 490.	1.2	13
44	Estimating intrinsic and extrinsic noise from single-cell gene expression measurements. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 447-471.	0.2	30
45	Fast and accurate single-cell RNA-seq analysis by clustering of transcript-compatibility counts. Genome Biology, 2016, 17, 112.	3.8	109
46	A dynamic intron retention program enriched in RNA processing genes regulates gene expression during terminal erythropoiesis. Nucleic Acids Research, 2016, 44, 838-851.	6.5	162
47	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	2.2	30
48	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
49	Controlling for conservation in genome-wide DNA methylation studies. BMC Genomics, 2015, 16, 420.	1.2	4
50	Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis. Science, 2015, 350, 1251-1255.	6.0	201
51	A diverse epigenetic landscape at human exons with implication for expression. Nucleic Acids Research, 2015, 43, 3498-3508.	6.5	48
52	Pregnancy-Induced Changes in Systemic Gene Expression among Healthy Women and Women with Rheumatoid Arthritis. PLoS ONE, 2015, 10, e0145204.	1.1	19
53	Structural Variation among Wild and Industrial Strains of Penicillium chrysogenum. PLoS ONE, 2014, 9, e96784.	1.1	5
54	A dynamic alternative splicing program regulates gene expression during terminal erythropoiesis. Nucleic Acids Research, 2014, 42, 4031-4042.	6.5	76

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55	Genome methylation in <i>D. melanogaster</i> is found at specific short motifs and is independent of DNMT2 activity. Genome Research, 2014, 24, 821-830.	2.4	113
56	Rational experiment design for sequencing-based RNA structure mapping. Rna, 2014, 20, 1864-1877.	1.6	28
57	Human Intestinal Tissue with Adult Stem Cell Properties Derived from Pluripotent Stem Cells. Stem Cell Reports, 2014, 2, 838-852.	2.3	83
58	CGAL: computing genome assembly likelihoods. Genome Biology, 2013, 14, R8.	13.9	77
59	Affine and Projective Tree Metric Theorems. Annals of Combinatorics, 2013, 17, 205-228.	0.3	5
60	Fragment assignment in the cloud with eXpress-D. BMC Bioinformatics, 2013, 14, 358.	1.2	22
61	Differential analysis of gene regulation at transcript resolution with RNA-seq. Nature Biotechnology, 2013, 31, 46-53.	9.4	3,256
62	Streaming fragment assignment for real-time analysis of sequencing experiments. Nature Methods, 2013, 10, 71-73.	9.0	901
63	Updating RNA-Seq analyses after re-annotation. Bioinformatics, 2013, 29, 1631-1637.	1.8	23
64	SHAPE–Seq: High–Throughput RNA Structure Analysis. Current Protocols in Chemical Biology, 2012, 4, 275-297.	1.7	67
65	A closer look at RNA editing. Nature Biotechnology, 2012, 30, 246-247.	9.4	7
66	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nature Protocols, 2012, 7, 562-578.	5.5	11,433
67	Quantifying uniformity of mapped reads. Bioinformatics, 2012, 28, 2680-2682.	1.8	6
68	RNA-Seq and find: entering the RNA deep field. Genome Medicine, 2011, 3, 74.	3.6	22
69	Tracing the Most Parsimonious Indel History. Journal of Computational Biology, 2011, 18, 967-986.	0.8	5
70	Multiplexed RNA structure characterization with selective 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.	3.3	346
71	Determining Coding CpG Islands by Identifying Regions Significant for Pattern Statistics on Markov Chains. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	1
72	Identification of novel transcripts in annotated genomes using RNA-Seq. Bioinformatics, 2011, 27, 2325-2329.	1.8	906

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73	Improving RNA-Seq expression estimates by correcting for fragment bias. Genome Biology, 2011, 12, R22.	13.9	1,164
74	Identification and correction of systematic error in high-throughput sequence data. Nature Precedings, 2011, , .	0.1	1
75	Identification and correction of systematic error in high-throughput sequence data. BMC Bioinformatics, 2011, 12, 451.	1.2	201
76	Shape-based peak identification for ChIP-Seq. BMC Bioinformatics, 2011, 12, 15.	1.2	52
77	The neighbor-net algorithm. Advances in Applied Mathematics, 2011, 47, 240-258.	0.4	26
78	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.	3.3	109
79	Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. Genome Research, 2011, 21, 2049-2057.	2.4	43
80	RNA structure characterization from chemical mapping experiments. , 2011, , .		34
81	Coverage statistics for sequence census methods. BMC Bioinformatics, 2010, 11, 430.	1.2	10
82	Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. PLoS ONE, 2010, 5, e11645.	1.1	0
83	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. Molecular Cancer Research, 2010, 8, 961-974.	1.5	121
84	Development of a Low Bias Method for Characterizing Viral Populations Using Next Generation Sequencing Technology. PLoS ONE, 2010, 5, e13564.	1.1	58
85	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. PLoS Biology, 2010, 8, e1000343.	2.6	184
86	MetMap Enables Genome-Scale Methyltyping for Determining Methylation States in Populations. PLoS Computational Biology, 2010, 6, e1000888.	1.5	11
87	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotechnology, 2010, 28, 511-515.	9.4	13,805
88	Disordered Microbial Communities in Asthmatic Airways. PLoS ONE, 2010, 5, e8578.	1.1	1,436
89	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	1.5	302
90	Why Neighbor-Joining Works. Algorithmica, 2009, 54, 1-24.	1.0	83

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91	TopHat: discovering splice junctions with RNA-Seq. Bioinformatics, 2009, 25, 1105-1111.	1.8	11,265
92	Convex Rank Tests and Semigraphoids. SIAM Journal on Discrete Mathematics, 2009, 23, 1117-1134.	0.4	46
93	On the optimality of the neighbor-joining algorithm. Algorithms for Molecular Biology, 2008, 3, 5.	0.3	31
94	Combining statistical alignment and phylogenetic footprinting to detect regulatory elements. Bioinformatics, 2008, 24, 1236-1242.	1.8	27
95	Combinatorics of least-squares trees. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13206-13211.	3.3	14
96	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	1.8	35
97	Viral Population Estimation Using Pyrosequencing. PLoS Computational Biology, 2008, 4, e1000074.	1.5	197
98	Comparison of Pattern Detection Methods in Microarray Time Series of the Segmentation Clock. PLoS ONE, 2008, 3, e2856.	1.1	38
99	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in Drosophila simulans. PLoS Biology, 2007, 5, e310.	2.6	583
100	The Mathematics of Phylogenomics. SIAM Review, 2007, 49, 3-31.	4.2	34
101	The Cyclohedron Test for Finding Periodic Genes in Time Course Expression Studies. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article 21.	0.2	7
102	Multiple alignment by sequence annealing. Bioinformatics, 2007, 23, e24-e29.	1.8	67
103	Optimization of air vehicles operations using mixed-integer linear programming. Journal of the Operational Research Society, 2007, 58, 516-527.	2.1	46
104	Patterns of gene duplication and intron loss in the ENCODE regions suggest a confounding factor. Genomics, 2007, 90, 44-48.	1.3	5
105	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
106	Interpreting the unculturable majority. Nature Methods, 2007, 4, 479-480.	9.0	15
107	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
108	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573

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109	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
110	Analysis of epistatic interactions and fitness landscapes using a new geometric approach. BMC Evolutionary Biology, 2007, 7, 60.	3.2	54
111	Toward the Human Genotope. Bulletin of Mathematical Biology, 2007, 69, 2723-2735.	0.9	19
112	Reference based annotation with GeneMapper. Genome Biology, 2006, 7, R29.	13.9	66
113	A Genome-Wide Map of Conserved MicroRNA Targets in C. elegans. Current Biology, 2006, 16, 460-471.	1.8	380
114	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56.	1.4	51
115	Parametric Alignment of Drosophila Genomes. PLoS Computational Biology, 2006, 2, e73.	1.5	38
116	Beyond Pairwise Distances: Neighbor-Joining with Phylogenetic Diversity Estimates. Molecular Biology and Evolution, 2006, 23, 491-498.	3.5	25
117	Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes. Lecture Notes in Computer Science, 2006, , 265-280.	1.0	9
118	Computation. , 2005, , 43-84.		1
119	Bioinformatics for Whole-Genome Shotgun Sequencing of Microbial Communities. PLoS Computational Biology, 2005, 1, e24.	1.5	292
120	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.	3.3	19
121	Large Multiple Organism Gene Finding by Collapsed Gibbs Sampling. Journal of Computational Biology, 2005, 12, 599-608.	0.8	7
122	Identification of transposable elements using multiple alignments of related genomes. Genome Research, 2005, 16, 260-270.	2.4	45
123	Pair hidden Markov models. , 2005, , .		2
124	Multiple organism gene finding by collapsed gibbs sampling. , 2004, , .		4
125	Intraspecies sequence comparisons for annotating genomes. Genome Research, 2004, 14, 2406-2411.	2.4	44
126	MAVID: Constrained Ancestral Alignment of Multiple Sequences. Genome Research, 2004, 14, 693-699.	2.4	232

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127	Parametric inference for biological sequence analysis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16138-16143.	3.3	51
128	Visualization of Multiple Genome Annotations and Alignments With the K-BROWSER. Genome Research, 2004, 14, 716-720.	2.4	15
129	Tropical geometry of statistical models. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16132-16137.	3.3	76
130	Identification of Evolutionary Hotspots in the Rodent Genomes. Genome Research, 2004, 14, 574-579.	2.4	23
131	Multiple-sequence functional annotation and the generalized hidden Markov phylogeny. Bioinformatics, 2004, 20, 1850-1860.	1.8	44
132	Accurate Identification of Novel Human Genes Through Simultaneous Gene Prediction in Human, Mouse, and Rat. Genome Research, 2004, 14, 661-664.	2.4	28
133	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
134	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	13.7	2,421
135	Reconstructing trees from subtree weights. Applied Mathematics Letters, 2004, 17, 615-621.	1.5	44
136	Constrained Optimization for UAV Task Assignment. , 2004, , .		48
137	UAV Task Assignment with Timing Constraints via Mixed-Integer Linear Programming. , 2004, , .		44
138	VISTA: computational tools for comparative genomics. Nucleic Acids Research, 2004, 32, W273-W279.	6.5	2,033
139	The ENCODE (ENCyclopedia Of DNA Elements) Project. Science, 2004, 306, 636-640.	6.0	2,121
140	Forcing numbers of stop signs. Theoretical Computer Science, 2003, 303, 409-416.	0.5	15
141	Phylogenetic Shadowing of Primate Sequences to Find Functional Regions of the Human Genome. Science, 2003, 299, 1391-1394.	6.0	466
142	Picking Alignments from (Steiner) Trees. Journal of Computational Biology, 2003, 10, 509-520.	0.8	17
143	Strategies and Tools for Whole-Genome Alignments. Genome Research, 2003, 13, 73-80.	2.4	190
144	MAVID multiple alignment server. Nucleic Acids Research, 2003, 31, 3525-3526.	6.5	52

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145	SLAM web server for comparative gene finding and alignment. Nucleic Acids Research, 2003, 31, 3507-3509.	6.5	10
146	SLAM: Cross-Species Gene Finding and Alignment with a Generalized Pair Hidden Markov Model. Genome Research, 2003, 13, 496-502.	2.4	141
147	AVID: A Global Alignment Program. Genome Research, 2003, 13, 97-102.	2.4	405
148	HMM sampling and applications to gene finding and alternative splicing. Bioinformatics, 2003, 19, ii36-ii41.	1.8	56
149	<tt>rVista</tt>for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. Genome Research, 2002, 12, 832-839.	2.4	384
150	The computational challenges of applying comparative-based computational methods to whole genomes. Briefings in Bioinformatics, 2002, 3, 18-22.	3.2	10
151	Picking alignments from (steiner) trees. , 2002, , .		2
152	Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems. Journal of Computational Biology, 2002, 9, 389-399.	0.8	73
153	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
154	Mapping and identification of essential gene functions on the X chromosome ofDrosophila. EMBO Reports, 2002, 3, 34-38.	2.0	105
155	rVista for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. Genome Research, 2002, 12, 832-839.	2.4	23
156	Session Introduction. , 2002, , .		0
157	Applications of generalized pair hidden Markov models to alignment and gene finding problems. , 2001, , .		6
158	GENOME-WIDE ANALYSIS AND COMPARATIVE GENOMICS. , 2001, , .		0
159	Human and mouse gene structure. , 2000, , .		6
160	Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction. Genome Research, 2000, 10, 950-958.	2.4	303
161	Active Conservation of Noncoding Sequences Revealed by Three-Way Species Comparisons. Genome Research, 2000, 10, 1304-1306.	2.4	279
162	A Dictionary-Based Approach for Gene Annotation. Journal of Computational Biology, 1999, 6, 419-430.	0.8	23

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163	Forcing matchings on square grids. Discrete Mathematics, 1998, 190, 287-294.	0.4	48
164	Finding Convex Sets Among Points in the Plane. Discrete and Computational Geometry, 1998, 19, 405-410.	0.4	21
165	Constructing status injective graphs. Discrete Applied Mathematics, 1997, 80, 107-113.	0.5	6
166	Combinatorial Approaches and Conjectures for 2-Divisibility Problems Concerning Domino Tilings of Polyominoes. Electronic Journal of Combinatorics, 1997, 4, .	0.2	17