

# Bo Li

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

31,863  
citations

331259

21  
h-index

377514

34  
g-index

47  
all docs

47  
docs citations

47  
times ranked

54032  
citing authors

#	ARTICLE	IF	CITATIONS
1	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics, 2011, 12, 323.	1.2	16,042
2	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. Nature Protocols, 2013, 8, 1494-1512.	5.5	7,054
3	TIMER2.0 for analysis of tumor-infiltrating immune cells. Nucleic Acids Research, 2020, 48, W509-W514.	6.5	2,546
4	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. Cell, 2018, 175, 998-1013.e20.	13.5	1,260
5	RNA-Seq gene expression estimation with read mapping uncertainty. Bioinformatics, 2010, 26, 493-500.	1.8	1,012
6	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. Nature Communications, 2017, 8, 1136.	5.8	686
7	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	13.7	537
8	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	13.7	392
9	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	15.2	381
10	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. Genome Biology, 2019, 20, 213.	3.8	379
11	Evaluation of de novo transcriptome assemblies from RNA-Seq data. Genome Biology, 2014, 15, 553.	3.8	256
12	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nature Methods, 2020, 17, 793-798.	9.0	134
13	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	9.4	127
14	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. Nature Communications, 2019, 10, 2907.	5.8	117
15	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
16	Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, 2019, 20, 70.	3.8	82
17	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. Immunity, 2020, 52, 1088-1104.e6.	6.6	79
18	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. PLoS Computational Biology, 2011, 7, e1002111.	1.5	73

#	ARTICLE	IF	CITATIONS
19	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	13.7	73
20	Interannual dynamics, diversity and evolution of the virome in <i>Sclerotinia sclerotiorum</i> from a single crop field. <i>Virus Evolution</i> , 2021, 7, veab032.	2.2	56
21	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. <i>Scientific Reports</i> , 2018, 8, 15338.	1.6	45
22	RSEM. , 2014, , 41-74.		31
23	Linking indirect effects of cytomegalovirus in transplantation to modulation of monocyte innate immune function. <i>Science Advances</i> , 2020, 6, eaax9856.	4.7	20
24	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020, 2120, 249-262.	0.4	18
25	Metrics for rapid quality control in RNA structure probing experiments. <i>Bioinformatics</i> , 2016, 32, 3575-3583.	1.8	15
26	PROBer Provides a General Toolkit for Analyzing Sequencing-Based Toeprinting Assays. <i>Cell Systems</i> , 2017, 4, 568-574.e7.	2.9	15
27	Divergence of dim-light vision among bats (order: Chiroptera) as estimated by molecular and electrophysiological methods. <i>Scientific Reports</i> , 2015, 5, 11531.	1.6	12
28	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015, 11, e1004491.	1.5	11
29	A Capsidless Virus Is <i>trans</i> -Encapsidated by a Bisegmented Botybirnavirus. <i>Journal of Virology</i> , 2022, 96, e0029622.	1.5	11
30	The Known Unknowns of the Immune Response to Coccidioides. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 377.	1.5	6
31	First Draft Genome of the Sable, <i>Martes zibellina</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 59-65.	1.1	5
32	Genome profiles of pathologist-defined cell clusters by multiregional LCM and G&T-seq in one triple-negative breast cancer patient. <i>Cell Reports Medicine</i> , 2021, 2, 100404.	3.3	5
33	Comparative Transcriptome Analysis Reveals Putative Genes Responsible for High Theacrine Content in <i>Kucha</i> ( <i>Camellia kucha</i> (Chang et Wang) Chang). <i>Tropical Plant Biology</i> , 2021, 14, 82-92.	1.0	3
34	IntroSpect: Motif-Guided Immuno-peptidome Database Building Tool to Improve the Sensitivity of HLA I Binding Peptide Identification by Mass Spectrometry. <i>Biomolecules</i> , 2022, 12, 579.	1.8	3
35	How Low Can You Go? Calling Robust ATAC-Seq Peaks Through Read Down-Sampling. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0