Bo Li

List of Publications by Year
in descending order

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	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	9.4	127
2	A Capsidless Virus Is *trans*-Encapsidated by a Bisegmented Botybirnavirus. Journal of Virology, 2022, 96, e0029622.	1.5	11
3	IntroSpect: Motif-Guided Immunopeptidome Database Building Tool to Improve the Sensitivity of HLA I Binding Peptide Identification by Mass Spectrometry. Biomolecules, 2022, 12, 579.	1.8	3
4	Interannual dynamics, diversity and evolution of the virome in *Sclerotinia sclerotiorum* from a single crop field. Virus Evolution, 2021, 7, veab032.	2.2	56
5	Comparative Transcriptome Analysis Reveals Putative Genes Responsible for High Theacrine Content in Kucha (Camellia kucha (Chang et Wang) Chang). Tropical Plant Biology, 2021, 14, 82-92.	1.0	3
6	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	13.7	537
7	The Known Unknowns of the Immune Response to Coccidioides. Journal of Fungi (Basel, Switzerland), 2021, 7, 377.	1.5	6
8	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	13.7	73
9	Genome profiles of pathologist-defined cell clusters by multiregional LCM and G&T-seq in one triple-negative breast cancer patient. Cell Reports Medicine, 2021, 2, 100404.	3.3	5
10	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
11	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
12	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	15.2	381
13	First Draft Genome of the Sable, Martes zibellina. Genome Biology and Evolution, 2020, 12, 59-65.	1.1	5
14	Linking indirect effects of cytomegalovirus in transplantation to modulation of monocyte innate immune function. Science Advances, 2020, 6, eaax9856.	4.7	20
15	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
16	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. Methods in Molecular Biology, 2020, 2120, 249-262.	0.4	18
17	TIMER2.0 for analysis of tumor-infiltrating immune cells. Nucleic Acids Research, 2020, 48, W509-W514.	6.5	2,546
18	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. Nature Communications, 2019, 10, 2907.	5.8	117

#	Article	IF	Citations
19	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	13.7	392
20	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
21	Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, 2019, 20, 70.	3.8	82
22	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. Cell, 2018, 175, 998-1013.e20.	13.5	1,260
23	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. Scientific Reports, 2018, 8, 15338.	1.6	45
24	PROBer Provides a General Toolkit for Analyzing Sequencing-Based Toeprinting Assays. Cell Systems, 2017, 4, 568-574.e7.	2.9	15
25	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. Nature Communications, 2017, 8, 1136.	5.8	686
26	Metrics for rapid quality control in RNA structure probing experiments. Bioinformatics, 2016, 32, 3575-3583.	1.8	15
27	Divergence of dim-light vision among bats (order: Chiroptera) as estimated by molecular and electrophysiological methods. Scientific Reports, 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. PLoS Computational Biology, 2015, 11, e1004491.	1.5	11
29	Evaluation of de novo transcriptome assemblies from RNA-Seq data. Genome Biology, 2014, 15, 553.	3.8	256
30	RSEM. , 2014, , 41-74.		31
31	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
32	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics, 2011, 12, 323.	1.2	16,042
33	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
34	RNA-Seq gene expression estimation with read mapping uncertainty. Bioinformatics, 2010, 26, 493-500.	1.8	1,012
35	How Low Can You Go? Calling Robust ATAC-Seq Peaks Through Read Down-Sampling. SSRN Electronic Journal, 0, , .	0.4	0