

Bo Li

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

18,051
citations

19
h-index

47
g-index

47
ext. papers

26,546
ext. citations

18.2
avg, IF

7.29
L-index

#	Paper	IF	Citations
43	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. <i>BMC Bioinformatics</i> , 2011 , 12, 323	3.6	9564
42	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013 , 8, 1494-512	18.8	4563
41	TIMER2.0 for analysis of tumor-infiltrating immune cells. <i>Nucleic Acids Research</i> , 2020 , 48, W509-W514	20.1	808
40	RNA-Seq gene expression estimation with read mapping uncertainty. <i>Bioinformatics</i> , 2010 , 26, 493-500	7.2	740
39	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. <i>Cell</i> , 2018 , 175, 998-1013.e20	56.2	631
38	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. <i>Nature Communications</i> , 2017 , 8, 1136	17.4	409
37	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019 , 574, 365-371	50.4	200
36	Evaluation of de novo transcriptome assemblies from RNA-Seq data. <i>Genome Biology</i> , 2014 , 15, 553	18.3	170
35	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , 2019 , 20, 213	18.3	163
34	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , 2020 , 26, 792-802	50.5	130
33	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021 , 595, 107-113	50.4	124
32	STAR-Fusion: Fast and Accurate Fusion Transcript Detection from RNA-Seq		80
31	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019 , 10, 2907	17.4	62
30	Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of CHIP-Seq data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002111	5	60
29	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019 , 20, 70	18.3	47
28	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. <i>Nature Methods</i> , 2020 , 17, 793-798	21.6	44
27	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020 , 586, 769-775	50.4	32

26	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020 , 52, 1088-1104.e6	32.3	31
25	Interannual dynamics, diversity and evolution of the virome in from a single crop field. <i>Virus Evolution</i> , 2021 , 7, veab032	3.7	20
24	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. <i>Scientific Reports</i> , 2018 , 8, 15338	4.9	19
23	RSEM 2014 , 41-74		18
22	Thousands of novel unannotated proteins expand the MHC I immunopeptidome in cancer		15
21	A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 2021 ,		15
20	Metrics for rapid quality control in RNA structure probing experiments. <i>Bioinformatics</i> , 2016 , 32, 3575-3583	5.8	14
19	PROBer Provides a General Toolkit for Analyzing Sequencing-Based Toeprinting Assays. <i>Cell Systems</i> , 2017 , 4, 568-574.e7	10.6	13
18	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2021 ,	44.5	13
17	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021 , 598, 327-331	50.4	10
16	Divergence of dim-light vision among bats (order: Chiroptera) as estimated by molecular and electrophysiological methods. <i>Scientific Reports</i> , 2015 , 5, 11531	4.9	9
15	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	5.1	7
14	Cumulus: a cloud-based data analysis framework for large-scale single-cell and single-nucleus RNA-seq		7
13	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020 , 2120, 249-262	1.4	6
12	Evaluation of de novo transcriptome assemblies from RNA-Seq data 2014 ,		5
11	Linking indirect effects of cytomegalovirus in transplantation to modulation of monocyte innate immune function. <i>Science Advances</i> , 2020 , 6, eaax9856	14.3	4
10	A single-cell and single-nucleus RNA-seq toolbox for fresh and frozen human tumors		3
9	A Capsidless Virus Is -Encapsidated by a Bisegmented Botybirnavirus.. <i>Journal of Virology</i> , 2022 , e00296226	2.6	2

8	First Draft Genome of the Sable, <i>Martes zibellina</i> . <i>Genome Biology and Evolution</i> , 2020 , 12, 59-65	3.9	1
7	Biology-inspired data-driven quality control for scientific discovery in single-cell transcriptomics		1
6	Prober: A general toolkit for analyzing sequencing-based Deepprinting assays		1
5	The Known Unknowns of the Immune Response to. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	1
4	Intrinsic and extrinsic regulation of human fetal bone marrow haematopoiesis and perturbations in Down syndrome		1
3	Comparative Transcriptome Analysis Reveals Putative Genes Responsible for High Theacrine Content in Kucha (<i>Camellia kucha</i> (Chang et Wang) Chang). <i>Tropical Plant Biology</i> , 2021 , 14, 82-92	1.6	1
2	IntroSpect: motif-guided immunopeptidome database building tool to improve the sensitivity of HLA binding peptide identification		1
1	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	18	0