Alexander Dobin

List of Publications by Year in Descending Order

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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.

15 papers	19,233 citations	10 h-index	19 g-index
19 ext. papers	30,645 ext. citations	12.4 avg, IF	6.62 L-index

#	Paper	IF	Citations
15	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. *Cell Systems*, **2021**, 12, 827-838.e5	10.6	3
14	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. *Frontiers in Plant Science*, **2020**, 11, 289	6.2	3
13	A limited set of transcriptional programs define major cell types. *Genome Research*, **2020**, 30, 1047-1059	9.7	15
12	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. *Genome Biology*, **2019**, 20, 213	18.3	163
11	Is it time to change the reference genome?. *Genome Biology*, **2019**, 20, 159	18.3	72
10	The fractured landscape of RNA-seq alignment: the default in our STARs. *Nucleic Acids Research*, **2018**, 46, 5125-5138	20.1	10
9	A benchmark for RNA-seq quantification pipelines. *Genome Biology*, **2016**, 17, 74	18.3	117
8	Optimizing RNA-Seq Mapping with STAR. *Methods in Molecular Biology*, **2016**, 1415, 245-62	1.4	90
7	Mapping RNA-seq Reads with STAR. *Current Protocols in Bioinformatics*, **2015**, 51, 11.14.1-11.14.19	24.2	446
6	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. *Genome Research*, **2013**, 23, 169-80	9.7	133
5	STAR: ultrafast universal RNA-seq aligner. *Bioinformatics*, **2013**, 29, 15-21	7.2	18121
4	The fractured landscape of RNA-seq alignment: The default in our STARs		1
3	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
2	A limited set of transcriptional programs define major cell types		3
1	STARsolo: accurate, fast and versatile mapping/quantification of single-cell and single-nucleus RNA-seq data		23