

Alvis Brazma

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.

17
papers

1,571
citations

10
h-index

18
g-index

18
ext. papers

1,877
ext. citations

18.6
avg. IF

4.25
L-index

#	Paper	IF	Citations
17	ArrayExpress--a public repository for microarray gene expression data at the EBI. <i>Nucleic Acids Research</i> , 2003 , 31, 68-71	20.1	637
16	ArrayExpress update--from an archive of functional genomics experiments to the atlas of gene expression. <i>Nucleic Acids Research</i> , 2009 , 37, D868-72	20.1	346
15	Minimum Information About a Microarray Experiment (MIAME)--successes, failures, challenges. <i>Scientific World Journal, The</i> , 2009 , 9, 420-3	2.2	160
14	Standards for systems biology. <i>Nature Reviews Genetics</i> , 2006 , 7, 593-605	30.1	114
13	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020 , 586, E14-E16	50.4	85
12	ArrayExpress: a public database of gene expression data at EBI. <i>Comptes Rendus - Biologies</i> , 2003 , 326, 1075-8	1.4	58
11	The BioSample Database (BioSD) at the European Bioinformatics Institute. <i>Nucleic Acids Research</i> , 2012 , 40, D64-70	20.1	47
10	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. <i>Nature Communications</i> , 2020 , 11, 736	17.4	32
9	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020 , 17, 621-628	21.6	30
8	REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021 , 18, 1418-1422	21.6	16
7	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , 2021 , 8, 115	8.2	10
6	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020 , 38, 1384-1386	44.5	9
5	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021 , 18, 327-328	21.6	9
4	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021 , 12, 5854	17.4	7
3	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021 , 12, 1137	17.4	5
2	Using Deep Learning to Extrapolate Protein Expression Measurements. <i>Proteomics</i> , 2020 , 20, e2000009	4.8	3
1	Blood transcriptome profile induced by an efficacious vaccine formulated with salivary antigens from cattle ticks. <i>Npj Vaccines</i> , 2019 , 4, 53	9.5	3

