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List of Publications by Year
in descending order

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37 papers	1,470 citations	394421 19 h-index	434195 31 g-index
49 all docs	49 docs citations	49 times ranked	2794 citing authors

#	Article	IF	Citations
1	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	19.0	35
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
3	Virtual meetings promise to eliminate geographical and administrative barriers and increase accessibility, diversity and inclusivity. Nature Biotechnology, 2022, 40, 133-137.	17.5	30
4	The Gene Expression Deconvolution Interactive Tool (GEDIT): accurate cell type quantification from gene expression data. GigaScience, 2021, 10, .	6.4	33
5	Improving the completeness of public metadata accompanying omics studies. Genome Biology, 2021, 22, 106.	8.8	22
6	Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591.	19.0	40
7	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. Nucleic Acids Research, 2021, 49, e102-e102.	14.5	36
8	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	8.8	51
9	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. Briefings in Bioinformatics, 2021, 22, .	6.5	10
10	Ancestral diversity is limited in published T cell receptor sequencing studies. Immunity, 2021, 54, 2177-2179.	14.3	3
11	Integrating big data computational skills in education to facilitate reproducibility and transparency in pharmaceutical sciences. JACCP Journal of the American College of Clinical Pharmacy, 2021, 4, 1263-1266.	1.0	0
12	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
13	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
14	Metalign: efficient alignment-based metagenomic profiling via containment min hash. Genome Biology, 2020, 21, 242.	8.8	29
15	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	6.4	83
16	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	8.8	26
17	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. Nature Communications, 2020, 11, 3126.	12.8	44
18	Improving the usability and comprehensiveness of microbial databases. BMC Biology, 2020, 18, 37.	3.8	15

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19	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0
20	Telescope: an interactive tool for managing large-scale analysis from mobile devices. GigaScience, 2020, 9, .	6.4	0
21	Challenges and recommendations to improve the installability and archival stability of omics computational tools. PLoS Biology, 2019, 17, e3000333.	5.6	54
22	Interpreting and integrating big data in the life sciences. Emerging Topics in Life Sciences, 2019, 3, 335-341.	2.6	2
23	Improving the usability and archival stability of bioinformatics software. Genome Biology, 2019, 20, 47.	8.8	62
24	How bioinformatics and open data can boost basic science in countries and universities with limited resources. Nature Biotechnology, 2019, 37, 324-326.	17.5	25
25	Systematic benchmarking of omics computational tools. Nature Communications, 2019, 10, 1393.	12.8	111
26	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.	8.8	42
27	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. Journal of Computational Biology, 2017, 24, 558-570.	1.6	14
28	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. Trends in Biotechnology, 2017, 35, 901-903.	9.3	22
29	Accurate viral population assembly from ultra-deep sequencing data. Bioinformatics, 2014, 30, i329-i337.	4.1	48
30	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. BMC Genomics, 2014, 15, S7.	2.8	15
31	Workshop: Novel transcript reconstruction from paired-end RNA-Seq reads using fragment length distribution. , 2012, , .		0
32	Poster: Haplotype discovery from high-throughput sequencing data. , 2011, , .		0
33	Poster: ViSpA: Viral spectrum assembling method. , 2011, , .		0
34	Estimation of alternative splicing isoform frequencies from RNA-Seq data. Algorithms for Molecular Biology, 2011, 6, 9.	1.2	155
35	RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. , 2011, , .		3
36	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. In Silico Biology, 2011, 11, 251-61.	0.9	6

#	Article	IF	Citations
37	Data Availability of Open T-Cell Receptor Repertoire Data, a Systematic Assessment. Frontiers in Systems Biology, 0, 2, .	0.7	5