

Serghei Mangul

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,470
citations

394286

19
h-index

434063

31
g-index

49
all docs

49
docs citations

49
times ranked

2794
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	210
2	Estimation of alternative splicing isoform frequencies from RNA-Seq data. <i>Algorithms for Molecular Biology</i> , 2011, 6, 9.	0.3	155
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
4	Systematic benchmarking of omics computational tools. <i>Nature Communications</i> , 2019, 10, 1393.	5.8	111
5	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020, 9, .	3.3	83
6	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	3.8	68
7	Improving the usability and archival stability of bioinformatics software. <i>Genome Biology</i> , 2019, 20, 47.	3.8	62
8	Challenges and recommendations to improve the installability and archival stability of omics computational tools. <i>PLoS Biology</i> , 2019, 17, e3000333.	2.6	54
9	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	3.8	51
10	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , 2014, 30, i329-i337.	1.8	48
11	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. <i>Nature Communications</i> , 2020, 11, 3126.	5.8	44
12	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. <i>Genome Biology</i> , 2018, 19, 36.	3.8	42
13	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021, 18, 588-591.	9.0	40
14	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. <i>Nucleic Acids Research</i> , 2021, 49, e102-e102.	6.5	36
15	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
16	The Gene Expression Deconvolution Interactive Tool (GEDIT): accurate cell type quantification from gene expression data. <i>GigaScience</i> , 2021, 10, .	3.3	33
17	Virtual meetings promise to eliminate geographical and administrative barriers and increase accessibility, diversity and inclusivity. <i>Nature Biotechnology</i> , 2022, 40, 133-137.	9.4	30
18	Metalign: efficient alignment-based metagenomic profiling via containment min hash. <i>Genome Biology</i> , 2020, 21, 242.	3.8	29

#	ARTICLE	IF	CITATIONS
19	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020, 21, 71.	3.8	26
20	How bioinformatics and open data can boost basic science in countries and universities with limited resources. <i>Nature Biotechnology</i> , 2019, 37, 324-326.	9.4	25
21	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. <i>Trends in Biotechnology</i> , 2017, 35, 901-903.	4.9	22
22	Improving the completeness of public metadata accompanying omics studies. <i>Genome Biology</i> , 2021, 22, 106.	3.8	22
23	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, S7.	1.2	15
24	Improving the usability and comprehensiveness of microbial databases. <i>BMC Biology</i> , 2020, 18, 37.	1.7	15
25	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Journal of Computational Biology</i> , 2017, 24, 558-570.	0.8	14
26	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
27	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. <i>In Silico Biology</i> , 2011, 11, 251-61.	0.4	6
28	Data Availability of Open T-Cell Receptor Repertoire Data, a Systematic Assessment. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	5
29	RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. , 2011, , .		3
30	Ancestral diversity is limited in published T cell receptor sequencing studies. <i>Immunity</i> , 2021, 54, 2177-2179.	6.6	3
31	Interpreting and integrating big data in the life sciences. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 335-341.	1.1	2
32	Poster: Haplotype discovery from high-throughput sequencing data. , 2011, , .		0
33	Poster: ViSpA: Viral spectrum assembling method. , 2011, , .		0
34	Workshop: Novel transcript reconstruction from paired-end RNA-Seq reads using fragment length distribution. , 2012, , .		0
35	Integrating big data computational skills in education to facilitate reproducibility and transparency in pharmaceutical sciences. <i>JACCP Journal of the American College of Clinical Pharmacy</i> , 2021, 4, 1263-1266.	0.5	0
36	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0

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37	Telescope: an interactive tool for managing large-scale analysis from mobile devices. GigaScience, 2020, 9, .	3.3	0