

Serghei Mangul

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,785
citations

361413

20
h-index

345221

36
g-index

63
all docs

63
docs citations

63
times ranked

4133
citing authors

#	ARTICLE	IF	CITATIONS
1	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure". <i>MSystems</i> , 2022, , e0144721.	3.8	2
2	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
3	Virtual meetings promise to eliminate geographical and administrative barriers and increase accessibility, diversity and inclusivity. <i>Nature Biotechnology</i> , 2022, 40, 133-137.	17.5	30
4	A comprehensive benchmarking of WGS-based deletion structural variant callers. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	9
5	The Gene Expression Deconvolution Interactive Tool (GEDIT): accurate cell type quantification from gene expression data. <i>GigaScience</i> , 2021, 10, .	6.4	33
6	Improving the completeness of public metadata accompanying omics studies. <i>Genome Biology</i> , 2021, 22, 106.	8.8	22
7	Detection of viral gene expression in risk-stratified biopsies reveals no active HPV in cutaneous squamous cell carcinoma. <i>Experimental Dermatology</i> , 2021, 30, 1711-1716.	2.9	4
8	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021, 18, 588-591.	19.0	40
9	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. <i>Nucleic Acids Research</i> , 2021, 49, e102-e102.	14.5	36
10	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	56
11	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	8.8	51
12	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	10
13	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	3.8	26
14	Ancestral diversity is limited in published T cell receptor sequencing studies. <i>Immunity</i> , 2021, 54, 2177-2179.	14.3	3
15	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.	1.0	0
16	PUMAA: A Platform for Accessible Microbiome Analysis in the Undergraduate Classroom. <i>Frontiers in Microbiology</i> , 2020, 11, 584699.	3.5	10
17	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	210
18	Metalign: efficient alignment-based metagenomic profiling via containment min hash. <i>Genome Biology</i> , 2020, 21, 242.	8.8	29

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19	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020, 9, .	6.4	83
20	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. <i>Cell</i> , 2020, 181, 1612-1625.e13.	28.9	436
21	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020, 21, 71.	8.8	26
22	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. <i>Nature Communications</i> , 2020, 11, 3126.	12.8	44
23	Telescope: an interactive tool for managing large-scale analysis from mobile devices. <i>GigaScience</i> , 2020, 9, .	6.4	0
24	Challenges and recommendations to improve the installability and archival stability of omics computational tools. <i>PLoS Biology</i> , 2019, 17, e3000333.	5.6	54
25	Transcriptional profiling of single fiber cells in a transgenic paradigm of an inherited childhood cataract reveals absence of molecular heterogeneity. <i>Journal of Biological Chemistry</i> , 2019, 294, 13530-13544.	3.4	5
26	Interpreting and integrating big data in the life sciences. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 335-341.	2.6	2
27	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. <i>BMC Genomics</i> , 2019, 20, 423.	2.8	22
28	Improving the usability and archival stability of bioinformatics software. <i>Genome Biology</i> , 2019, 20, 47.	8.8	62
29	How bioinformatics and open data can boost basic science in countries and universities with limited resources. <i>Nature Biotechnology</i> , 2019, 37, 324-326.	17.5	25
30	Systematic benchmarking of omics computational tools. <i>Nature Communications</i> , 2019, 10, 1393.	12.8	111
31	Involving undergraduates in genomics research to narrow the educationâ€™research gap. <i>Nature Biotechnology</i> , 2018, 36, 369-371.	17.5	2
32	Spatial Analysis of Single Fiber Cells of the Developing Ocular Lens Reveals Regulated Heterogeneity of Gene Expression. <i>IScience</i> , 2018, 10, 66-79.	4.1	15
33	A Comprehensive Map of Genetic Variation in the Worldâ€™s Largest Ethnic Groupâ€™Han Chinese. <i>Molecular Biology and Evolution</i> , 2018, 35, 2736-2750.	8.9	86
34	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.	8.8	42
35	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.	1.6	14
36	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. <i>Trends in Biotechnology</i> , 2017, 35, 901-903.	9.3	22

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37	Reference-free comparison of microbial communities via de Bruijn graphs. , 2016, , .		3
38	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. Genetics, 2016, 204, 1057-1064.	2.9	17
39	Accurate viral population assembly from ultra-deep sequencing data. Bioinformatics, 2014, 30, i329-i337.	4.1	48
40	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. , 2013, , .		0
41	Monte-Carlo Regression algorithm for isoform frequency estimation from RNA-Seq data. , 2013, , .		1