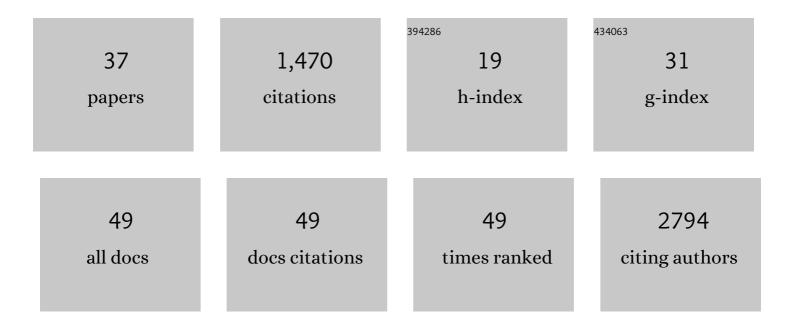
Serghei Mangul

List of Publications by Year in descending order

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SEDCHEL MANCHI

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

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#	Article	IF	CITATIONS
19	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	3.8	26
20	How bioinformatics and open data can boost basic science in countries and universities with limited resources. Nature Biotechnology, 2019, 37, 324-326.	9.4	25
21	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. Trends in Biotechnology, 2017, 35, 901-903.	4.9	22
22	Improving the completeness of public metadata accompanying omics studies. Genome Biology, 2021, 22, 106.	3.8	22
23	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. BMC Genomics, 2014, 15, S7.	1.2	15
24	Improving the usability and comprehensiveness of microbial databases. BMC Biology, 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. Journal of Computational Biology, 2017, 24, 558-570.	0.8	14
26	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. Briefings in Bioinformatics, 2021, 22, .	3.2	10
27	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. In Silico Biology, 2011, 11, 251-61.	0.4	6
28	Data Availability of Open T-Cell Receptor Repertoire Data, a Systematic Assessment. Frontiers in Systems Biology, 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. Immunity, 2021, 54, 2177-2179.	6.6	3
31	Interpreting and integrating big data in the life sciences. Emerging Topics in Life Sciences, 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. JACCP Journal of the American College of Clinical Pharmacy, 2021, 4, 1263-1266.	0.5	0
36	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0

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