

# Jay Ghurye

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7842040/publications.pdf>

Version: 2024-02-01

15  
papers

2,921  
citations

858243

12  
h-index

1113639

15  
g-index

21  
all docs

21  
docs citations

21  
times ranked

3720  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021, 39, 309-312.	9.4	109
2	A critical assessment of gene catalogs for metagenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2848-2857.	1.8	15
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
4	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	3.8	65
5	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	5.8	84
6	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
7	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	3.8	66
8	Modern technologies and algorithms for scaffolding assembled genomes. <i>PLoS Computational Biology</i> , 2019, 15, e1006994.	1.5	56
9	MetaCarvel: linking assembly graph motifs to biological variants. <i>Genome Biology</i> , 2019, 20, 174.	3.8	14
10	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	1.5	509
11	A chromosome-scale assembly of the major African malaria vector <i>Anopheles funestus</i> . <i>GigaScience</i> , 2019, 8, .	3.3	56
12	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , 2019, 20, 1000.	1.2	21
13	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. <i>Briefings in Bioinformatics</i> , 2019, 20, 1140-1150.	3.2	113
14	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	1.2	194
15	A Framework to Model Human Behavior at Large Scale during Natural Disasters. , 2016, , .		14