

Sergey Aganezov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8358229/publications.pdf>

Version: 2024-02-01

15
papers

2,834
citations

933447

10
h-index

1058476

14
g-index

27
all docs

27
docs citations

27
times ranked

2542
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
2	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
4	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	6.5	77
5	Orienting Ordered Scaffolds: Complexity and Algorithms. <i>SN Computer Science</i> , 2022, 3, .	3.6	0
6	The human origin recognition complex is essential for pre-RC assembly, mitosis, and maintenance of nuclear structure. <i>ELife</i> , 2021, 10, .	6.0	14
7	Optimized sample selection for cost-efficient long-read population sequencing. <i>Genome Research</i> , 2021, 31, 910-918.	5.5	4
8	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	3.8	177
9	Reconstruction of clone- and haplotype-specific cancer genome karyotypes from bulk tumor samples. <i>Genome Research</i> , 2020, 30, 1274-1290.	5.5	12
10	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020, 30, 1258-1273.	5.5	72
11	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	12.8	56
12	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. <i>Cell</i> , 2020, 182, 145-161.e23.	28.9	464
13	Recovering rearranged cancer chromosomes from karyotype graphs. <i>BMC Bioinformatics</i> , 2019, 20, 641.	2.6	4
14	Reconstruction of Ancestral Genomes in Presence of Gene Gain and Loss. <i>Journal of Computational Biology</i> , 2016, 23, 150-164.	1.6	58
15	Scaffold assembly based on genome rearrangement analysis. <i>Computational Biology and Chemistry</i> , 2015, 57, 46-53.	2.3	12