

Andrey V Bzikadze

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6189775/publications.pdf>

Version: 2024-02-01

13
papers

2,630
citations

1051969

10
h-index

1336881

12
g-index

21
all docs

21
docs citations

21
times ranked

2407
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads. <i>Nature Biotechnology</i> , 2022, 40, 1075-1081.	9.4	41
2	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	9.0	42
3	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	6.0	204
4	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
5	Automated annotation of human centromeres with HORmon. <i>Genome Research</i> , 2022, , gr.276362.121.	2.4	11
6	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	13.7	221
7	CentromereArchitect: inference and analysis of the architecture of centromeres. <i>Bioinformatics</i> , 2021, 37, i196-i204.	1.8	15
8	Automated assembly of centromeres from ultra-long error-prone reads. <i>Nature Biotechnology</i> , 2020, 38, 1309-1316.	9.4	45
9	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. <i>Bioinformatics</i> , 2020, 36, i75-i83.	1.8	40
10	The string decomposition problem and its applications to centromere analysis and assembly. <i>Bioinformatics</i> , 2020, 36, i93-i101.	1.8	28
11	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
12	Reconstructing Antibody Repertoires from Error-Prone Immunosequencing Reads. <i>Journal of Immunology</i> , 2017, 199, 3369-3380.	0.4	37
13	On some statistical properties of the "Book Stack" transformation. <i>Vestnik St Petersburg University: Mathematics</i> , 2016, 49, 305-312.	0.1	0