

Jonas Korlach

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

12,347
citations

567281

15
h-index

839539

18
g-index

24
all docs

24
docs citations

24
times ranked

16836
citing authors

#	ARTICLE	IF	CITATIONS
1	Africa: sequence 100,000 species to safeguard biodiversity. <i>Nature</i> , 2022, 603, 388-392.	27.8	19
2	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
3	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
4	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
5	Population genomics of the critically endangered <i>h</i> . <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
6	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	27.8	85
7	Extreme enrichment of VNTR-associated polymorphicity in human subtelomeres: genes with most VNTRs are predominantly expressed in the brain. <i>Translational Psychiatry</i> , 2020, 10, 369.	4.8	15
8	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	12.8	38
9	A high-quality genome assembly from a single, field-collected spotted lanternfly (<i>Lycorma delicatula</i>) using the PacBio Sequel II system. <i>GigaScience</i> , 2019, 8, .	6.4	35
10	A High-Quality De novo Genome Assembly from a Single Mosquito Using PacBio Sequencing. <i>Genes</i> , 2019, 10, 62.	2.4	121
11	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
12	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
13	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of <i>Hyposidra talaca</i> nuclear polyhedrosis virus. <i>Scientific Reports</i> , 2018, 8, 8924.	3.3	8
14	De novo PacBio long-read and phased avian genome assemblies correct and add to reference genes generated with intermediate and short reads. <i>GigaScience</i> , 2017, 6, 1-16.	6.4	165
15	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017, 27, 677-685.	5.5	323
16	Resolving the complexity of the human genome using single-molecule sequencing. <i>Nature</i> , 2015, 517, 608-611.	27.8	714
17	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013, 10, 563-569.	19.0	4,029
18	Real-Time DNA Sequencing from Single Polymerase Molecules. <i>Science</i> , 2009, 323, 133-138.	12.6	3,160