

# Jonas Korlach

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8639835/publications.pdf>

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	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013, 10, 563-569.	19.0	4,029
2	Real-Time DNA Sequencing from Single Polymerase Molecules. <i>Science</i> , 2009, 323, 133-138.	12.6	3,160
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
4	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
5	Resolving the complexity of the human genome using single-molecule sequencing. <i>Nature</i> , 2015, 517, 608-611.	27.8	714
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
7	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
8	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017, 27, 677-685.	5.5	323
9	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
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	Population genomics of the critically endangered <i>herring gull</i> . <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
12	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	27.8	85
13	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
14	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	12.8	38
15	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
16	Africa: sequence 100,000 species to safeguard biodiversity. <i>Nature</i> , 2022, 603, 388-392.	27.8	19
17	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
18	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