

# Maika Malig

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3609767/publications.pdf>

Version: 2024-02-01

18  
papers

5,920  
citations

516710

16  
h-index

839539

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

11642  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	27.8	1,994
2	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
3	Resolving the complexity of the human genome using single-molecule sequencing. <i>Nature</i> , 2015, 517, 608-611.	27.8	714
4	Diversity of Human Copy Number Variation and Multicopy Genes. <i>Science</i> , 2010, 330, 641-646.	12.6	609
5	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	12.6	368
6	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. <i>Cell</i> , 2012, 149, 912-922.	28.9	341
7	Reconstructing complex regions of genomes using long-read sequencing technology. <i>Genome Research</i> , 2014, 24, 688-696.	5.5	222
8	Evolution and diversity of copy number variation in the great ape lineage. <i>Genome Research</i> , 2013, 23, 1373-1382.	5.5	161
9	Structural diversity and African origin of the 17q21.31 inversion polymorphism. <i>Nature Genetics</i> , 2012, 44, 872-880.	21.4	129
10	The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017, 1, 69.	7.8	123
11	Emergence of a <i>Homo sapiens</i> -specific gene family and chromosome 16p11.2 CNV susceptibility. <i>Nature</i> , 2016, 536, 205-209.	27.8	102
12	Palindromic GOLGA8 core duplicons promote chromosome 15q13.3 microdeletion and evolutionary instability. <i>Nature Genetics</i> , 2014, 46, 1293-1302.	21.4	96
13	Interplay between DNA sequence and negative superhelicity drives R-loop structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6260-6269.	7.1	93
14	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. <i>Nature Genetics</i> , 2010, 42, 745-750.	21.4	89
15	Ultra-deep Coverage Single-molecule R-loop Footprinting Reveals Principles of R-loop Formation. <i>Journal of Molecular Biology</i> , 2020, 432, 2271-2288.	4.2	52
16	Epigenetic origin of evolutionary novel centromeres. <i>Scientific Reports</i> , 2017, 7, 41980.	3.3	30
17	An evolutionary driver of interspersed segmental duplications in primates. <i>Genome Biology</i> , 2020, 21, 202.	8.8	19
18	Characterization of R-Loop Structures Using Single-Molecule R-Loop Footprinting and Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2161, 209-228.	0.9	6