

# Karen H Miga

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

8,831  
citations

147726  
31  
h-index

265120  
42  
g-index

62  
all docs

62  
docs citations

62  
times ranked

9880  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	9.4	1,443
2	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
3	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
4	Improved data analysis for the MinION nanopore sequencer. <i>Nature Methods</i> , 2015, 12, 351-356.	9.0	557
5	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
6	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , 2020, 30, 1291-1305.	2.4	440
7	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
8	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	13.7	221
9	Linear assembly of a human centromere on the Y chromosome. <i>Nature Biotechnology</i> , 2018, 36, 321-323.	9.4	216
10	Centromere reference models for human chromosomes X and Y satellite arrays. <i>Genome Research</i> , 2014, 24, 697-707.	2.4	210
11	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	6.0	204
12	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	13.7	192
13	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.	6.0	146
14	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	6.0	144
15	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , 2021, 18, 1322-1332.	9.0	139
16	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	6.0	130
17	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	6.0	118
18	Genomic Characterization of Large Heterochromatic Gaps in the Human Genome Assembly. <i>PLoS Computational Biology</i> , 2014, 10, e1003628.	1.5	99

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19	Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer. <i>Molecular Cell</i> , 2018, 70, 842-853.e7.	4.5	96
20	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	9.4	90
21	Human chromosome-specific aneuploidy is influenced by <scp>DNA</scp> -dependent centromeric features. <i>EMBO Journal</i> , 2020, 39, e102924.	3.5	79
22	Centromeric Satellite DNAs: Hidden Sequence Variation in the Human Population. <i>Genes</i> , 2019, 10, 352.	1.0	75
23	Completing the human genome: the progress and challenge of satellite DNA assembly. <i>Chromosome Research</i> , 2015, 23, 421-426.	1.0	74
24	Human Artificial Chromosomes that Bypass Centromeric DNA. <i>Cell</i> , 2019, 178, 624-639.e19.	13.5	74
25	The Need for a Human Pangenome Reference Sequence. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 81-102.	2.5	71
26	DNA replication acts as an error correction mechanism to maintain centromere identity by restricting CENP-A to centromeres. <i>Nature Cell Biology</i> , 2019, 21, 743-754.	4.6	65
27	Haplotypes spanning centromeric regions reveal persistence of large blocks of archaic DNA. <i>ELife</i> , 2019, 8, .	2.8	54
28	Human centromeric CENP-A chromatin is a homotypic, octameric nucleosome at all cell cycle points. <i>Journal of Cell Biology</i> , 2017, 216, 607-621.	2.3	53
29	DiMeLo-seq: a long-read, single-molecule method for mapping protein-DNA interactions genome wide. <i>Nature Methods</i> , 2022, 19, 711-723.	9.0	45
30	Alpha-CENTAURI: assessing novel centromeric repeat sequence variation with long read sequencing. <i>Bioinformatics</i> , 2016, 32, 1921-1924.	1.8	43
31	Replication of alpha-satellite DNA arrays in endogenous human centromeric regions and in human artificial chromosome. <i>Nucleic Acids Research</i> , 2014, 42, 11502-11516.	6.5	42
32	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	9.0	42
33	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. <i>Bioinformatics</i> , 2020, 36, i75-i83.	1.8	40
34	Variation and Evolution of Human Centromeres: A Field Guide and Perspective. <i>Annual Review of Genetics</i> , 2021, 55, 583-602.	3.2	36
35	Centromere studies in the era of "telomere-to-telomere" genomics. <i>Experimental Cell Research</i> , 2020, 394, 112127.	1.2	34
36	Utilizing mapping targets of sequences underrepresented in the reference assembly to reduce false positive alignments. <i>Nucleic Acids Research</i> , 2015, 43, gkv671.	6.5	29

#	ARTICLE	IF	CITATIONS
37	Chromosome-Specific Centromere Sequences Provide an Estimate of the Ancestral Chromosome 2 Fusion Event in Hominin Genomes. <i>Journal of Heredity</i> , 2017, 108, 45-52.	1.0	18
38	The Promises and Challenges of Genomic Studies of Human Centromeres. <i>Progress in Molecular and Subcellular Biology</i> , 2017, 56, 285-304.	0.9	15
39	PCR amplicons identify widespread copy number variation in human centromeric arrays and instability in cancer. <i>Cell Genomics</i> , 2021, 1, 100064.	3.0	14
40	Expanding studies of chromosome structure and function in the era of T2T genomics. <i>Human Molecular Genetics</i> , 2021, 30, R198-R205.	1.4	4
41	Breaking through the unknowns of the human reference genome. <i>Nature</i> , 2021, 590, 217-218.	13.7	3
42	Satellite DNAs and human sex chromosome variation. <i>Seminars in Cell and Developmental Biology</i> , 2022, 128, 15-25.	2.3	3