Karen H Miga

List of Publications by Year
in descending order

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	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
2	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	9.0	42
3	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	6.0	118
4	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	6.0	204
5	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science, 2022, 376, eabk3112.	6.0	146
6	DiMeLo-seq: a long-read, single-molecule method for mapping proteinâ€“DNA interactions genome wide. Nature Methods, 2022, 19, 711-723.	9.0	45
7	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
8	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
9	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	6.0	130
10	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
11	Satellite DNAs and human sex chromosome variation. Seminars in Cell and Developmental Biology, 2022, 128, 15-25.	2.3	3
12	Breaking through the unknowns of the human reference genome. Nature, 2021, 590, 217-218.	13.7	3
13	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	13.7	221
14	Expanding studies of chromosome structure and function in the era of T2T genomics. Human Molecular Genetics, 2021, 30, R198-R205.	1.4	4
15	The Need for a Human Pangenome Reference Sequence. Annual Review of Genomics and Human Genetics, 2021, 22, 81-102.	2.5	71
16	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	9.0	139
17	Variation and Evolution of Human Centromeres: A Field Guide and Perspective. Annual Review of Genetics, 2021, 55, 583-602.	3.2	36
18	PCR amplicons identify widespread copy number variation in human centromeric arrays and instability in cancer. Cell Genomics, 2021, 1, 100064.	3.0	14

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19	Human chromosomeâ€specific aneuploidy is influenced by <scp>DNA</scp> â€dependent centromeric features. EMBO Journal, 2020, 39, e102924.	3.5	79
20	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. Bioinformatics, 2020, 36, i75-i83.	1.8	40
21	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	13.7	549
22	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Research, 2020, 30, 1291-1305.	2.4	440
23	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	9.4	344
24	Centromere studies in the era of â€˜telomere-to-telomereâ€™ genomics. Experimental Cell Research, 2020, 394, 112127.	1.2	34
25	Human Artificial Chromosomes that Bypass Centromeric DNA. Cell, 2019, 178, 624-639.e19.	13.5	74
26	DNA replication acts as an error correction mechanism to maintain centromere identity by restricting CENP-A to centromeres. Nature Cell Biology, 2019, 21, 743-754.	4.6	65
27	Centromeric Satellite DNAs: Hidden Sequence Variation in the Human Population. Genes, 2019, 10, 352.	1.0	75
28	Haplotypes spanning centromeric regions reveal persistence of large blocks of archaic DNA. ELife, 2019, 8, .	2.8	54
29	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	9.4	1,443
30	Linear assembly of a human centromere on the Y chromosome. Nature Biotechnology, 2018, 36, 321-323.	9.4	216
31	Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer. Molecular Cell, 2018, 70, 842-853.e7.	4.5	96
32	Human centromeric CENP-A chromatin is a homotypic, octameric nucleosome at all cell cycle points. Journal of Cell Biology, 2017, 216, 607-621.	2.3	53
33	The Promises and Challenges of Genomic Studies of Human Centromeres. Progress in Molecular and Subcellular Biology, 2017, 56, 285-304.	0.9	15
34	Chromosome-Specific Centromere Sequences Provide an Estimate of the Ancestral Chromosome 2 Fusion Event in Hominin Genomes. Journal of Heredity, 2017, 108, 45-52.	1.0	18
35	Alpha-CENTAURI: assessing novel centromeric repeat sequence variation with long read sequencing. Bioinformatics, 2016, 32, 1921-1924.	1.8	43
36	Utilizing mapping targets of sequences underrepresented in the reference assembly to reduce false positive alignments. Nucleic Acids Research, 2015, 43, gkv671.	6.5	29

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37	Improved data analysis for the MinION nanopore sequencer. Nature Methods, 2015, 12, 351-356.	9.0	557
38	The UCSC Genome Browser database: 2015 update. Nucleic Acids Research, 2015, 43, D670-D681.	6.5	891
39	Completing the human genome: the progress and challenge of satellite DNA assembly. Chromosome Research, 2015, 23, 421-426.	1.0	74
40	Genomic Characterization of Large Heterochromatic Gaps in the Human Genome Assembly. PLoS Computational Biology, 2014, 10, e1003628.	1.5	99
41	Replication of alpha-satellite DNA arrays in endogenous human centromeric regions and in human artificial chromosome. Nucleic Acids Research, 2014, 42, 11502-11516.	6.5	42
42	Centromere reference models for human chromosomes X and Y satellite arrays. Genome Research, 2014, 24, 697-707.	2.4	210