Ming Xiao

List of Publications by Year
in descending order

30 papers	6,280 citations	471509 17 h-index	526287 27 g-index
31 all docs	31 docs citations	31 times ranked	12400 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
3	Genome mapping on nanochannel arrays for structural variation analysis and sequence assembly. Nature Biotechnology, 2012, 30, 771-776.	17.5	586
4	Rapid Genome Mapping in Nanochannel Arrays for Highly Complete and Accurate De Novo Sequence Assembly of the Complex Aegilops tauschii Genome. PLoS ONE, 2013, 8, e55864.	2.5	146
5	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. Genetics, 2016, 202, 351-362.	2.9	126
6	Genome maps across 26 human populations reveal population-specific patterns of structural variation. Nature Communications, 2019, 10, 1025.	12.8	123
7	Rapid DNA mapping by fluorescent single molecule detection. Nucleic Acids Research, 2007, 35, e16-e16.	14.5	91
8	High-throughput single-molecule telomere characterization. Genome Research, 2017, 27, 1904-1915.	5.5	46
9	CRISPR-CAS9 D10A nickase target-specific fluorescent labeling of double strand DNA for whole genome mapping and structural variation analysis. Nucleic Acids Research, 2016, 44, e11-e11.	14.5	44
10	A simple DNA stretching method for fluorescence imaging of single DNA molecules. Nucleic Acids Research, 2006, 34, e113-e113.	14.5	40
11	OMBlast: alignment tool for optical mapping using a seed-and-extend approach. Bioinformatics, 2017, 33, 311-319.	4.1	39
12	The 22q11 low copy repeats are characterized by unprecedented size and structural variability. Genome Research, 2019, 29, 1389-1401.	5.5	39
13	Towards a reference genome that captures global genetic diversity. Nature Communications, 2020, 11, 5482.	12.8	34
14	Direct determination of haplotypes from single DNA molecules. Nature Methods, 2009, 6, 199-201.	19.0	32
15	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. PLoS Genetics, 2020, 16, e1008347.	3.5	31
16	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. Genome Biology, 2017, 18, 230.	8.8	28
17	High-throughput single-molecule mapping links subtelomeric variants and long-range haplotypes with specific telomeres. Nucleic Acids Research, 2017, 45, e73-e73.	14.5	22
18	Optical mapping of the 22q11.2DS region reveals complex repeat structures and preferred locations for non-allelic homologous recombination (NAHR). Scientific Reports, 2020, 10, 12235.	3.3	20

#	Article	IF	Citations
19	Customized optical mapping by CRISPRâ€“Cas9 mediated DNA labeling with multiple sgRNAs. Nucleic Acids Research, 2021, 49, e8-e8.	14.5	15
20	The Driver of Extreme Human-Specific Olduvai Repeat Expansion Remains Highly Active in the Human Genome. Genetics, 2020, 214, 179-191.	2.9	14
21	Single-molecule analysis of subtelomeres and telomeres in Alternative Lengthening of Telomeres (ALT) cells. BMC Genomics, 2020, 21, 485.	2.8	8
22	A micropatterned substrate for on-surface enzymatic labelling of linearized long DNA molecules. Scientific Reports, 2019, 9, 15059.	3.3	6
23	Multicolor Whole-Genome Mapping in Nanochannels for Genetic Analysis. Analytical Chemistry, 2021, 93, 9808-9816.	6.5	6
24	Single-molecule telomere length characterization by optical mapping in nano-channel array: Perspective and review on telomere length measurement. Environmental Toxicology and Pharmacology, 2021, 82, 103562.	4.0	4
25	Multiplex structural variant detection by whole-genome mapping and nanopore sequencing. Scientific Reports, 2022, 12, 6512.	3.3	3
26	REXTAL: Regional Extension of Assemblies Using Linked-Reads. Lecture Notes in Computer Science, 2018, 10847, 63-78.	1.3	2
27	Characterization of full-length LINE-1 insertions in 154 genomes. Genomics, 2021, 113, 3804-3810.	2.9	2
28	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0
29	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0
30	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0