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	Multiplex structural variant detection by whole-genome mapping and nanopore sequencing. Scientific Reports, 2022, 12, 6512.	3.3	3
2	Customized optical mapping by CRISPRâ€“Cas9 mediated DNA labeling with multiple sgRNAs. Nucleic Acids Research, 2021, 49, e8-e8.	14.5	15
3	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
4	Multicolor Whole-Genome Mapping in Nanochannels for Genetic Analysis. Analytical Chemistry, 2021, 93, 9808-9816.	6.5	6
5	Characterization of full-length LINE-1 insertions in 154 genomes. Genomics, 2021, 113, 3804-3810.	2.9	2
6	The Driver of Extreme Human-Specific Olduvai Repeat Expansion Remains Highly Active in the Human Genome. Genetics, 2020, 214, 179-191.	2.9	14
7	Single-molecule analysis of subtelomeres and telomeres in Alternative Lengthening of Telomeres (ALT) cells. BMC Genomics, 2020, 21, 485.	2.8	8
8	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
9	Towards a reference genome that captures global genetic diversity. Nature Communications, 2020, 11, 5482.	12.8	34
10	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. PLoS Genetics, 2020, 16, e1008347.	3.5	31
11	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0
12	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0
13	Comprehensive Analysis of Human Subtelomeres by Whole Genome Mapping. , 2020, 16, e1008347.		0
14	A micropatterned substrate for on-surface enzymatic labelling of linearized long DNA molecules. Scientific Reports, 2019, 9, 15059.	3.3	6
15	The 22q11 low copy repeats are characterized by unprecedented size and structural variability. Genome Research, 2019, 29, 1389-1401.	5.5	39
16	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
17	Genome maps across 26 human populations reveal population-specific patterns of structural variation. Nature Communications, 2019, 10, 1025.	12.8	123
18	REXTAL: Regional Extension of Assemblies Using Linked-Reads. Lecture Notes in Computer Science, 2018, 10847, 63-78.	1.3	2

#	Article	IF	Citations
19	OMBlast: alignment tool for optical mapping using a seed-and-extend approach. Bioinformatics, 2017, 33, 311-319.	4.1	39
20	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
21	High-throughput single-molecule telomere characterization. Genome Research, 2017, 27, 1904-1915.	5.5	46
22	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
23	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. Genetics, 2016, 202, 351-362.	2.9	126
24	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
25	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
26	Genome mapping on nanochannel arrays for structural variation analysis and sequence assembly. Nature Biotechnology, 2012, 30, 771-776.	17.5	586
27	Direct determination of haplotypes from single DNA molecules. Nature Methods, 2009, 6, 199-201.	19.0	32
28	Rapid DNA mapping by fluorescent single molecule detection. Nucleic Acids Research, 2007, 35, e16-e16.	14.5	91
29	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
30	A simple DNA stretching method for fluorescence imaging of single DNA molecules. Nucleic Acids Research, 2006, 34, e113-e113.	14.5	40