# Xian F Mallory

List of Publications by Year
in descending order



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|---|---|---|---|
| 20 papers | 4,876 citations | 567281 15 h-index | 752698 20 g-index |
| 22 all docs | 22 docs citations | 22 times ranked | 11483 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81. | 27.8 | 1,994 |
| 2 | Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098. | 27.0 | 688 |
| 3 | Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784. | 12.8 | 636 |
| 4 | CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654. | 19.0 | 451 |
| 5 | A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355. | 17.5 | 233 |
| 6 | Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582. | 11.1 | 199 |
| 7 | BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11. | 25.8 | 135 |
| 8 | novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67. | 19.0 | 93 |
| 9 | Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455. | 8.2 | 91 |
| 10 | Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274. | 3.2 | 83 |
| 11 | TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317. | 5.5 | 81 |
| 12 | Methods for copy number aberration detection from single-cell DNA-sequencing data. Genome Biology, 2020, 21, 208. | 8.8 | 72 |
| 13 | Assessing the performance of methods for copy number aberration detection from single-cell DNA sequencing data. PLoS Computational Biology, 2020, 16, e1008012. | 3.2 | 33 |
| 14 | HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800. | 5.5 | 32 |
| 15 | BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87. | 9.6 | 25 |
| 16 | Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299. | 2.6 | 10 |
| 17 | SimSCSnTree: a simulator of single-cell DNA sequencing data. Bioinformatics, 2022, 38, 2912-2914. | 4.1 | 7 |
| 18 | BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122. | 4.1 | 5 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Theoretical Analysis Reveals the Cost and Benefit of Proofreading in Coronavirus Genome Replication. Journal of Physical Chemistry Letters, 2021, 12, 2691-2698. | 4.6 | 4 |
| 20 | Integrated genotyping of structural variation. , 2013, , . | | 0 |