

William H Majoros

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

19,174
citations

304743

22
h-index

434195

31
g-index

34
all docs

34
docs citations

34
times ranked

21570
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351. | 12.6 | 12,623 |
| 2 | The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149. | 12.6 | 1,859 |
| 3 | Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156. | 27.8 | 1,272 |
| 4 | Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286. | 5.6 | 657 |
| 5 | A viral microRNA functions as an orthologue of cellular miR-155. <i>Nature</i> , 2007, 450, 1096-1099. | 27.8 | 541 |
| 6 | Multiplex CRISPR/Cas9-based genome editing for correction of dystrophin mutations that cause Duchenne muscular dystrophy. <i>Nature Communications</i> , 2015, 6, 6244. | 12.8 | 383 |
| 7 | A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671. | 12.6 | 344 |
| 8 | Translocation of Sickle Cell Erythrocyte MicroRNAs into <i>Plasmodium falciparum</i> Inhibits Parasite Translation and Contributes to Malaria Resistance. <i>Cell Host and Microbe</i> , 2012, 12, 187-199. | 11.0 | 272 |
| 9 | Direct GR Binding Sites Potentiate Clusters of TF Binding across the Human Genome. <i>Cell</i> , 2016, 166, 1269-1281.e19. | 28.9 | 158 |
| 10 | Genomics and natural language processing. <i>Nature Reviews Genetics</i> , 2002, 3, 601-610. | 16.3 | 126 |
| 11 | Targeted long-read sequencing identifies missing disease-causing variation. <i>American Journal of Human Genetics</i> , 2021, 108, 1436-1449. | 6.2 | 105 |
| 12 | Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284. | 5.5 | 102 |
| 13 | Massively parallel quantification of the regulatory effects of noncoding genetic variation in a human cohort. <i>Genome Research</i> , 2015, 25, 1206-1214. | 5.5 | 100 |
| 14 | Correction of Dystrophin Expression in Cells From Duchenne Muscular Dystrophy Patients Through Genomic Excision of Exon 51 by Zinc Finger Nucleases. <i>Molecular Therapy</i> , 2015, 23, 523-532. | 8.2 | 100 |
| 15 | Pre-established Chromatin Interactions Mediate the Genomic Response to Glucocorticoids. <i>Cell Systems</i> , 2018, 7, 146-160.e7. | 6.2 | 82 |
| 16 | Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. <i>Genetics</i> , 2016, 203, 699-714. | 2.9 | 76 |
| 17 | Gene Discovery in the Genome. <i>Protist</i> , 2005, 156, 203-214. | 1.5 | 74 |
| 18 | GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. <i>Nucleic Acids Research</i> , 2003, 31, 3601-3604. | 14.5 | 60 |

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|----|---|------|-----------|
| 19 | MicroRNA target site identification by integrating sequence and binding information. <i>Nature Methods</i> , 2013, 10, 630-633. | 19.0 | 56 |
| 20 | Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128. | 5.5 | 40 |
| 21 | Human genome-wide measurement of drug-responsive regulatory activity. <i>Nature Communications</i> , 2018, 9, 5317. | 12.8 | 34 |
| 22 | Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. <i>PLoS ONE</i> , 2017, 12, e0181604. | 2.5 | 31 |
| 23 | Full-length dystrophin restoration via targeted exon integration by AAV-CRISPR in a humanized mouse model of Duchenne muscular dystrophy. <i>Molecular Therapy</i> , 2021, 29, 3243-3257. | 8.2 | 27 |
| 24 | Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. <i>Genome Biology and Evolution</i> , 2019, 11, 3035-3053. | 2.5 | 12 |
| 25 | Modeling the Evolution of Regulatory Elements by Simultaneous Detection and Alignment with Phylogenetic Pair HMMs. <i>PLoS Computational Biology</i> , 2010, 6, e1001037. | 3.2 | 11 |
| 26 | Correcting signal biases and detecting regulatory elements in STARR-seq data. <i>Genome Research</i> , 2021, 31, 877-889. | 5.5 | 11 |
| 27 | Improved transcript isoform discovery using ORF graphs. <i>Bioinformatics</i> , 2014, 30, 1958-1964. | 4.1 | 5 |
| 28 | Predicting gene structure changes resulting from genetic variants via exon definition features. <i>Bioinformatics</i> , 2018, 34, 3616-3623. | 4.1 | 3 |
| 29 | A preliminary comparison of the mouse and human genomes. <i>International Congress Series</i> , 2002, 1246, 169-181. | 0.2 | 2 |
| 30 | High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. <i>Bioinformatics</i> , 2017, 33, 1437-1446. | 4.1 | 2 |
| 31 | Bayesian estimation of genetic regulatory effects in high-throughput reporter assays. <i>Bioinformatics</i> , 2020, 36, 331-338. | 4.1 | 0 |