William H Majoros

List of Publications by Year
in descending order

31	19,174	304602	434063
papers	citations	22 h-index	31 g-index

34	34	34	21570
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
2	The Genome Sequence of the Malaria MosquitoAnopheles gambiae. Science, 2002, 298, 129-149.	6.0	1,859
3	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	13.7	1,272
4	Macronuclear Genome Sequence of the Ciliate Tetrahymena thermophila, a Model Eukaryote. PLoS Biology, 2006, 4, e286.	2.6	657
5	A viral microRNA functions as an orthologue of cellular miR-155. Nature, 2007, 450, 1096-1099.	13.7	541
6	Multiplex CRISPR/Cas9-based genome editing for correction of dystrophin mutations that cause Duchenne muscular dystrophy. Nature Communications, 2015, 6, 6244.	5.8	383
7	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	6.0	344
8	Translocation of Sickle Cell Erythrocyte MicroRNAs into Plasmodium falciparum Inhibits Parasite Translation and Contributes to Malaria Resistance. Cell Host and Microbe, 2012, 12, 187-199.	5.1	272
9	Direct GR Binding Sites Potentiate Clusters of TF Binding across the Human Genome. Cell, 2016, 166, 1269-1281.e19.	13.5	158
10	Genomics and natural language processing. Nature Reviews Genetics, 2002, 3, 601-610.	7.7	126
11	Targeted long-read sequencing identifies missing disease-causing variation. American Journal of Human Genetics, 2021, 108, 1436-1449.	2.6	105
12	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. Genome Research, 2018, 28, 1272-1284.	2.4	102
13	Massively parallel quantification of the regulatory effects of noncoding genetic variation in a human cohort. Genome Research, 2015, 25, 1206-1214.	2.4	100
14	Correction of Dystrophin Expression in Cells From Duchenne Muscular Dystrophy Patients Through Genomic Excision of Exon 51 by Zinc Finger Nucleases. Molecular Therapy, 2015, 23, 523-532.	3.7	100
15	Pre-established Chromatin Interactions Mediate the Genomic Response to Glucocorticoids. Cell Systems, 2018, 7, 146-160.e7.	2.9	82
16	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. Genetics, 2016, 203, 699-714.	1.2	76
17	Gene Discovery in the Genome. Protist, 2005, 156, 203-214.	0.6	74
18	GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. Nucleic Acids Research, 2003, 31, 3601-3604.	6.5	60

#	Article	IF	Citations
19	MicroRNA target site identification by integrating sequence and binding information. Nature Methods, 2013, 10, 630-633.	9.0	56
20	Assessment of Genome-Wide Protein Function Classification for Drosophila melanogaster. Genome Research, 2003, 13, 2118-2128.	2.4	40
21	Human genome-wide measurement of drug-responsive regulatory activity. Nature Communications, 2018, 9, 5317.	5.8	34
22	Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. PLoS ONE, 2017, 12, e0181604.	1.1	31
23	Full-length dystrophin restoration via targeted exon integration by AAV-CRISPR in a humanized mouse model of Duchenne muscular dystrophy. Molecular Therapy, 2021, 29, 3243-3257.	3.7	27
24	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. Genome Biology and Evolution, 2019, 11, 3035-3053.	1.1	12
25	Modeling the Evolution of Regulatory Elements by Simultaneous Detection and Alignment with Phylogenetic Pair HMMs. PLoS Computational Biology, 2010, 6, e1001037.	1.5	11
26	Correcting signal biases and detecting regulatory elements in STARR-seq data. Genome Research, 2021, 31, 877-889.	2.4	11
27	Improved transcript isoform discovery using ORF graphs. Bioinformatics, 2014, 30, 1958-1964.	1.8	5
28	Predicting gene structure changes resulting from genetic variants via exon definition features. Bioinformatics, 2018, 34, 3616-3623.	1.8	3
29	A preliminary comparison of the mouse and human genomes. International Congress Series, 2002, 1246, 169-181.	0.2	2
30	High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. Bioinformatics, 2017, 33, 1437-1446.	1.8	2
31	Bayesian estimation of genetic regulatory effects in high-throughput reporter assays. Bioinformatics, 2020, 36, 331-338.	1.8	0