William H Majoros

List of Publications by Year
in descending order

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	Correcting signal biases and detecting regulatory elements in STARR-seq data. Genome Research, 2021, 31, 877-889.	5.5	11
2	Targeted long-read sequencing identifies missing disease-causing variation. American Journal of Human Genetics, 2021, 108, 1436-1449.	6.2	105
3	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.	8.2	27
4	Bayesian estimation of genetic regulatory effects in high-throughput reporter assays. Bioinformatics, 2020, 36, 331-338.	4.1	0
5	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. Genome Biology and Evolution, 2019, 11, 3035-3053.	2.5	12
6	Predicting gene structure changes resulting from genetic variants via exon definition features. Bioinformatics, 2018, 34, 3616-3623.	4.1	3
7	Human genome-wide measurement of drug-responsive regulatory activity. Nature Communications, 2018, 9, 5317.	12.8	34
8	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. Genome Research, 2018, 28, 1272-1284.	5.5	102
9	Pre-established Chromatin Interactions Mediate the Genomic Response to Glucocorticoids. Cell Systems, 2018, 7, 146-160.e7.	6.2	82
10	High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. Bioinformatics, 2017, 33, 1437-1446.	4.1	2
11	Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. PLoS ONE, 2017, 12, e0181604.	2.5	31
12	Direct GR Binding Sites Potentiate Clusters of TF Binding across the Human Genome. Cell, 2016, 166, 1269-1281.e19.	28.9	158
13	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. Genetics, 2016, 203, 699-714.	2.9	76
14	Multiplex CRISPR/Cas9-based genome editing for correction of dystrophin mutations that cause Duchenne muscular dystrophy. Nature Communications, 2015, 6, 6244.	12.8	383
15	Massively parallel quantification of the regulatory effects of noncoding genetic variation in a human cohort. Genome Research, 2015, 25, 1206-1214.	5.5	100
16	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.	8.2	100
17	Improved transcript isoform discovery using ORF graphs. Bioinformatics, 2014, 30, 1958-1964.	4.1	5
18	MicroRNA target site identification by integrating sequence and binding information. Nature Methods, 2013, 10, 630-633.	19.0	56

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19	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.	11.0	272
20	Modeling the Evolution of Regulatory Elements by Simultaneous Detection and Alignment with Phylogenetic Pair HMMs. PLoS Computational Biology, 2010, 6, e1001037.	3.2	11
21	A viral microRNA functions as an orthologue of cellular miR-155. Nature, 2007, 450, 1096-1099.	27.8	541
22	Macronuclear Genome Sequence of the Ciliate Tetrahymena thermophila, a Model Eukaryote. PLoS Biology, 2006, 4, e286.	5.6	657
23	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
24	Gene Discovery in the Genome. Protist, 2005, 156, 203-214.	1.5	74
25	Assessment of Genome-Wide Protein Function Classification for Drosophila melanogaster. Genome Research, 2003, 13, 2118-2128.	5.5	40
26	GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. Nucleic Acids Research, 2003, 31, 3601-3604.	14.5	60
27	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	12.6	344
28	The Genome Sequence of the Malaria Mosquito Anopheles gambiae. Science, 2002, 298, 129-149.	12.6	1,859
29	A preliminary comparison of the mouse and human genomes. International Congress Series, 2002, 1246, 169-181.	0.2	2
30	Genomics and natural language processing. Nature Reviews Genetics, 2002, 3, 601-610.	16.3	126
31	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623