

William H Majoros

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1093565/publications.pdf>

Version: 2024-02-01

31
papers

19,174
citations

304602

22
h-index

434063

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. <i>Genome Research</i> , 2021, 31, 877-889.	2.4	11
2	Targeted long-read sequencing identifies missing disease-causing variation. <i>American Journal of Human Genetics</i> , 2021, 108, 1436-1449.	2.6	105
3	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.	3.7	27
4	Bayesian estimation of genetic regulatory effects in high-throughput reporter assays. <i>Bioinformatics</i> , 2020, 36, 331-338.	1.8	0
5	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. <i>Genome Biology and Evolution</i> , 2019, 11, 3035-3053.	1.1	12
6	Predicting gene structure changes resulting from genetic variants via exon definition features. <i>Bioinformatics</i> , 2018, 34, 3616-3623.	1.8	3
7	Human genome-wide measurement of drug-responsive regulatory activity. <i>Nature Communications</i> , 2018, 9, 5317.	5.8	34
8	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284.	2.4	102
9	Pre-established Chromatin Interactions Mediate the Genomic Response to Glucocorticoids. <i>Cell Systems</i> , 2018, 7, 146-160.e7.	2.9	82
10	High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. <i>Bioinformatics</i> , 2017, 33, 1437-1446.	1.8	2
11	Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. <i>PLoS ONE</i> , 2017, 12, e0181604.	1.1	31
12	Direct GR Binding Sites Potentiate Clusters of TF Binding across the Human Genome. <i>Cell</i> , 2016, 166, 1269-1281.e19.	13.5	158
13	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. <i>Genetics</i> , 2016, 203, 699-714.	1.2	76
14	Multiplex CRISPR/Cas9-based genome editing for correction of dystrophin mutations that cause Duchenne muscular dystrophy. <i>Nature Communications</i> , 2015, 6, 6244.	5.8	383
15	Massively parallel quantification of the regulatory effects of noncoding genetic variation in a human cohort. <i>Genome Research</i> , 2015, 25, 1206-1214.	2.4	100
16	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.	3.7	100
17	Improved transcript isoform discovery using ORF graphs. <i>Bioinformatics</i> , 2014, 30, 1958-1964.	1.8	5
18	MicroRNA target site identification by integrating sequence and binding information. <i>Nature Methods</i> , 2013, 10, 630-633.	9.0	56

#	ARTICLE	IF	CITATIONS
19	Translocation of Sickle Cell Erythrocyte MicroRNAs into Plasmodium falciparum Inhibits Parasite Translation and Contributes to Malaria Resistance. <i>Cell Host and Microbe</i> , 2012, 12, 187-199.	5.1	272
20	Modeling the Evolution of Regulatory Elements by Simultaneous Detection and Alignment with Phylogenetic Pair HMMs. <i>PLoS Computational Biology</i> , 2010, 6, e1001037.	1.5	11
21	A viral microRNA functions as an orthologue of cellular miR-155. <i>Nature</i> , 2007, 450, 1096-1099.	13.7	541
22	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
23	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
24	Gene Discovery in the Genome. <i>Protist</i> , 2005, 156, 203-214.	0.6	74
25	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
26	GlimmerM, Economy and Unveil: three ab initio eukaryotic genefinders. <i>Nucleic Acids Research</i> , 2003, 31, 3601-3604.	6.5	60
27	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	6.0	344
28	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
29	A preliminary comparison of the mouse and human genomes. <i>International Congress Series</i> , 2002, 1246, 169-181.	0.2	2
30	Genomics and natural language processing. <i>Nature Reviews Genetics</i> , 2002, 3, 601-610.	7.7	126
31	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623