

# Matthew W Vaughn

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

10,735  
citations

159585

30  
h-index

161849

54  
g-index

69  
all docs

69  
docs citations

69  
times ranked

13371  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of whole-cell transcriptional response with machine learning. <i>Bioinformatics</i> , 2022, 38, 404-409.	4.1	8
2	Large-scale design and refinement of stable proteins using sequence-only models. <i>PLoS ONE</i> , 2022, 17, e0265020.	2.5	17
3	Large Scale Science on NSF's Frontera System. <i>Computing in Science and Engineering</i> , 2021, 23, 10-13.	1.2	0
4	Jetstream2: Accelerating cloud computing via Jetstream. , 2021, , .		15
5	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , 2021, 1, .	4.2	13
6	Arabidopsis DNA Replication Initiates in Intergenic, AT-Rich Open Chromatin. <i>Plant Physiology</i> , 2020, 183, 206-220.	4.8	9
7	Comparing DNA replication programs reveals large timing shifts at centromeres of endocycling cells in maize roots. <i>PLoS Genetics</i> , 2020, 16, e1008623.	3.5	4
8	Integrating Jupyter into Research Computing Ecosystems. , 2020, , .		4
9	Jetstreamâ€™ Early operations performance, adoption, and impacts. <i>Concurrency Computation Practice and Experience</i> , 2019, 31, e4683.	2.2	10
10	An â€œeFPâ€œ Browserâ€™ for visualizing and exploring <sc>RNA</sc> sequencing data. <i>Plant Journal</i> , 2019, 100, 641-654.	5.7	41
11	Subtle Perturbations of the Maize Methylome Reveal Genes and Transposons Silenced by Chromomethylase or RNA-Directed DNA Methylation Pathways. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1921-1932.	1.8	19
12	Genome-Wide Analysis of the Arabidopsis Replication Timing Program. <i>Plant Physiology</i> , 2018, 176, 2166-2185.	4.8	36
13	Platform for Automated Real-Time High Performance Analytics on Medical Image Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2018, 22, 318-324.	6.3	1
14	ThaleMine: A Warehouse for Arabidopsis Data Integration and Discovery. <i>Plant and Cell Physiology</i> , 2017, 58, pcw200.	3.1	39
15	Genomic Analysis of the DNA Replication Timing Program during Mitotic S Phase in Maize (<i>Zea mays</i>). <i>Plant Physiology</i> , 2017, 175, 1499-1509.	6.6	28
16	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	4.8	11
17	Repliscan: a tool for classifying replication timing regions. <i>BMC Bioinformatics</i> , 2017, 18, 362.	2.6	15
18	The iPlant Collaborative: Cyberinfrastructure for Enabling Data to Discovery for the Life Sciences. <i>PLoS Biology</i> , 2016, 14, e1002342.	5.6	306

#	ARTICLE	IF	CITATIONS
19	Jetstream. , 2016, , .		11
20	Bisulfite Sequence Analyses Using CyVerse Discovery Environment: From Mapping to DMRs. Current Protocols in Plant Biology, 2016, 1, 510-529.	2.8	4
21	Feature frequency profiles for automatic sample identification using PySpark. , 2015, , .		0
22	Araport: an application platform for data discovery. Concurrency Computation Practice and Experience, 2015, 27, 4412-4422.	2.2	9
23	Araport: the Arabidopsis Information Portal. Nucleic Acids Research, 2015, 43, D1003-D1009.	14.5	193
24	Jetstream. , 2015, , .		121
25	Examining the Causes and Consequences of Context-Specific Differential DNA Methylation in Maize. Plant Physiology, 2015, 168, 1262-1274.	4.8	62
26	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14728-14733.	7.1	179
27	Genomic Distribution of H3K9me2 and DNA Methylation in a Maize Genome. PLoS ONE, 2014, 9, e105267.	2.5	137
28	The Arabidopsis Information Portal: An Application Platform for Data Discovery. , 2014, , .		0
29	In Vivo Mapping of <i>Arabidopsis</i> Scaffold/Matrix Attachment Regions Reveals Link to Nucleosome-Disfavoring Poly(dA:dT) Tracts. Plant Cell, 2014, 26, 102-120.	6.6	19
30	Genetic Perturbation of the Maize Methylome. Plant Cell, 2014, 26, 4602-4616.	6.6	158
31	Discovery of biological networks using an optimized partial correlation coefficient with information theory algorithm on Stampede's Xeon and Xeon Phi processors. Concurrency Computation Practice and Experience, 2014, 26, 2178-2190.	2.2	8
32	Leveraging the national cyberinfrastructure for biomedical research. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 195-199.	4.4	12
33	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. Plant Cell, 2013, 25, 780-793.	6.6	91
34	Epigenetic and Genetic Influences on DNA Methylation Variation in Maize Populations. Plant Cell, 2013, 25, 2783-2797.	6.6	227
35	Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19639-19644.	7.1	131
36	Variation in DNA Methylation Patterns is More Common among Maize Inbreds than among Tissues. Plant Genome, 2013, 6, plantgenome2012.06.0009.	2.8	28

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37	National Center for Genome Analysis support leverages XSEDE to support life science research. , 2013, , .		3
38	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. PLoS Genetics, 2012, 8, e1003127.	3.5	166
39	Comparative Functional Genomics of the Fission Yeasts. Science, 2011, 332, 930-936.	12.6	458
40	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
41	CENP-B preserves genome integrity at replication forks paused by retrotransposon LTR. Nature, 2011, 469, 112-115.	27.8	79
42	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. Plant Cell, 2011, 23, 4221-4233.	6.6	189
43	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	3.5	150
44	Efficient parallel and out of core algorithms for constructing large bi-directed de Bruijn graphs. BMC Bioinformatics, 2010, 11, 560.	2.6	28
45	Arabidopsis thaliana Chromosome 4 Replicates in Two Phases That Correlate with Chromatin State. PLoS Genetics, 2010, 6, e1000982.	3.5	65
46	Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. Genome Research, 2009, 19, 1077-1083.	5.5	44
47	Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. Cell, 2009, 136, 461-472.	28.9	908
48	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
49	Genome-wide transposon tagging reveals location-dependent effects on transcription and chromatin organization in Arabidopsis. Plant Journal, 2008, 55, 514-525.	5.7	80
50	Lid2 Is Required for Coordinating H3K4 and H3K9 Methylation of Heterochromatin and Euchromatin. Cell, 2008, 135, 272-283.	28.9	127
51	Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. PLoS Biology, 2008, 6, e302.	5.6	179
52	The Fission Yeast Jmj2 Reverses Histone H3 Lysine 4 Trimethylation. Journal of Biological Chemistry, 2007, 282, 21662-21670.	3.4	28
53	S. pombe LSD1 Homologs Regulate Heterochromatin Propagation and Euchromatic Gene Transcription. Molecular Cell, 2007, 26, 89-101.	9.7	102
54	Epigenetic Natural Variation in Arabidopsis thaliana. PLoS Biology, 2007, 5, e174.	5.6	400

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55	MicroRNA-Targeted and Small Interfering RNA-Mediated mRNA Degradation Is Regulated by Argonaute, Dicer, and RNA-Dependent RNA Polymerase in Arabidopsis. <i>Plant Cell</i> , 2006, 18, 1559-1574.	6.6	141
56	Argonaute Slicing Is Required for Heterochromatic Silencing and Spreading. <i>Science</i> , 2006, 313, 1134-1137.	12.6	182
57	It's a Small RNA World, After All. <i>Science</i> , 2005, 309, 1525-1526.	12.6	29
58	Finding the Right Template: RNA Pol IV, a Plant-Specific RNA Polymerase. <i>Molecular Cell</i> , 2005, 17, 754-756.	9.7	21
59	Replication, Repair, and Reactivation. <i>Developmental Cell</i> , 2005, 9, 724-725.	7.0	3
60	Role of transposable elements in heterochromatin and epigenetic control. <i>Nature</i> , 2004, 430, 471-476.	27.8	1,103
61	Protein phosphorylation plays a key role in sucrose-mediated transcriptional regulation of a phloem-specific proton/sucrose symporter. <i>Planta</i> , 2003, 217, 483-489.	3.2	67
62	Sucrose-mediated transcriptional regulation of sucrose symporter activity in the phloem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10876-10880.	7.1	191