

Jane Grimwood

List of Publications by Year in descending order

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131
papers

64,044
citations

8181

76
h-index

12946

131
g-index

139
all docs

139
docs citations

139
times ranked

61555
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
3	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	27.8	2,642
4	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. Science, 2007, 318, 245-250.	12.6	2,354
5	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
6	The genomic basis of adaptive evolution in threespine sticklebacks. Nature, 2012, 484, 55-61.	27.8	1,600
7	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. Nature, 2008, 456, 239-244.	27.8	1,458
8	Widespread Parallel Evolution in Sticklebacks by Repeated Fixation of Ectodysplasin Alleles. Science, 2005, 307, 1928-1933.	12.6	1,299
9	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
10	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	21.4	1,159
11	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	21.4	1,031
12	Insights into Land Plant Evolution Garnered from the Marchantia polymorpha Genome. Cell, 2017, 171, 287-304.e15.	28.9	973
13	Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a <i>Pitx1</i> Enhancer. Science, 2010, 327, 302-305.	12.6	901
14	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	17.5	864
15	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . Nature, 2016, 538, 336-343.	27.8	849
16	The Arabidopsis lyrata genome sequence and the basis of rapid genome size change. Nature Genetics, 2011, 43, 476-481.	21.4	814
17	The Trichoplax genome and the nature of placozoans. Nature, 2008, 454, 955-960.	27.8	801
18	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	27.8	725

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19	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . Science, 2010, 328, 633-636.	12.6	708
20	Comparative genomes of Chlamydia pneumoniae and C. trachomatis. Nature Genetics, 1999, 21, 385-389.	21.4	636
21	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . Science, 2009, 324, 268-272.	12.6	591
22	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nature Biotechnology, 2014, 32, 656-662.	17.5	572
23	Insights into bilaterian evolution from three spiralian genomes. Nature, 2013, 493, 526-531.	27.8	564
24	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7705-7710.	7.1	563
25	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . Science, 2010, 329, 223-226.	12.6	536
26	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispersome Structure, Chromosome Plasticity, and Stealth Pathogenesis. PLoS Genetics, 2011, 7, e1002070.	3.5	532
27	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
28	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	27.8	460
29	Coding potential of laboratory and clinical strains of human cytomegalovirus. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14976-14981.	7.1	450
30	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . Nature Biotechnology, 2007, 25, 319-326.	17.5	449
31	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . Nature Genetics, 2019, 51, 877-884.	21.4	439
32	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. Plant Journal, 2018, 93, 338-354.	5.7	431
33	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . Nature Biotechnology, 2011, 29, 922-927.	17.5	428
34	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
35	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. PLoS Genetics, 2009, 5, e1000618.	3.5	402
36	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	27.8	377

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37	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	21.4	374
38	Longitudinal serum concentrations of placental growth factor: Evidence for abnormal placental angiogenesis in pathologic pregnancies. <i>American Journal of Obstetrics and Gynecology</i> , 2003, 188, 177-182.	1.3	373
39	The Master Sex-Determination Locus in Threespine Sticklebacks Is on a Nascent Y Chromosome. <i>Current Biology</i> , 2004, 14, 1416-1424.	3.9	367
40	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
41	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. <i>Nature Biotechnology</i> , 2016, 34, 562-570.	17.5	340
42	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	5.5	329
43	A role for a neo-sex chromosome in stickleback speciation. <i>Nature</i> , 2009, 461, 1079-1083.	27.8	327
44	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
45	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
46	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	7.1	260
47	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
48	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
49	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
50	Comparative DNA Sequence Analysis of Mouse and Human Protocadherin Gene Clusters. <i>Genome Research</i> , 2001, 11, 389-404.	5.5	224
51	A Genome-wide SNP Genotyping Array Reveals Patterns of Global and Repeated Species-Pair Divergence in Sticklebacks. <i>Current Biology</i> , 2012, 22, 83-90.	3.9	212
52	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	7.3	210
53	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
54	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180

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55	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. PLoS Genetics, 2016, 12, e1006108.	3.5	177
56	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
57	Quality assessment of the human genome sequence. Nature, 2004, 429, 365-368.	27.8	172
58	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . Science, 2010, 328, 351-354.	12.6	159
59	The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994.	27.8	156
60	The Chlamydomonas genome project: a decade on. Trends in Plant Science, 2014, 19, 672-680.	8.8	145
61	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. Nature, 2021, 590, 438-444.	27.8	144
62	Evolving New Skeletal Traits by cis -Regulatory Changes in Bone Morphogenetic Proteins. Cell, 2016, 164, 45-56.	28.9	132
63	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
64	The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. ELife, 2018, 7, .	6.0	120
65	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. Plant Journal, 2018, 95, 168-182.	5.7	115
66	Construction and comparison of three reference-quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
67	Toxoplasma gondii: the role of parasite surface and secreted proteins in host cell invasion. International Journal for Parasitology, 1996, 26, 169-173.	3.1	104
68	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	17.5	103
69	The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274.	27.8	102
70	The genomic landscape of molecular responses to natural drought stress in Panicum hallii. Nature Communications, 2018, 9, 5213.	12.8	101
71	Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. Genome Research, 2004, 14, 354-366.	5.5	100
72	Toxoplasma gondii: The role of a 30-kDa surface protein in host cell invasion. Experimental Parasitology, 1992, 74, 106-111.	1.2	98

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73	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	6.6	98
74	Computational Analysis of the Polymorphic Membrane Protein Superfamily of <i>Chlamydia trachomatis</i> and <i>Chlamydia pneumoniae</i> . <i>Microbial & Comparative Genomics</i> , 1999, 4, 187-201.	0.4	95
75	A Hypervariable Invertebrate Allodeterminant. <i>Current Biology</i> , 2009, 19, 583-589.	3.9	95
76	A Comparative Epigenomic Analysis of Polyploidy-Derived Genes in Soybean and Common Bean. <i>Plant Physiology</i> , 2015, 168, 1433-1447.	4.8	88
77	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	3.9	79
78	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
79	PEATmoss (<i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	5.7	74
80	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	5.5	73
81	Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. <i>Genome Research</i> , 2004, 14, 2397-2405.	5.5	70
82	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	5.7	70
83	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass (<i>Panicum virgatum</i> L.). <i>Plant Journal</i> , 2013, 74, 160-173.	5.7	70
84	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
85	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	12.8	67
86	Expression of <i>Chlamydia pneumoniae</i> Polymorphic Membrane Protein Family Genes. <i>Infection and Immunity</i> , 2001, 69, 2383-2389.	2.2	66
87	Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3622-3627.	7.1	65
88	New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine Sticklebacks. <i>Behaviour</i> , 2004, 141, 1331-1344.	0.8	64
89	Hydractinia Allodeterminant alr1 Resides in an Immunoglobulin Superfamily-like Gene Complex. <i>Current Biology</i> , 2010, 20, 1122-1127.	3.9	61
90	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59

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91	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
92	The GC-Rich Mitochondrial and Plastid Genomes of the Green Alga <i>Coccomyxa</i> Give Insight into the Evolution of Organelle DNA Nucleotide Landscape. <i>PLoS ONE</i> , 2011, 6, e23624.	2.5	53
93	Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin 14 Cluster. <i>American Journal of Human Genetics</i> , 2003, 72, 621-635.	6.2	51
94	Comprehensive analysis of Hox gene expression in the amphipod crustacean <i>Parhyale hawaiiensis</i> . <i>Developmental Biology</i> , 2016, 409, 297-309.	2.0	51
95	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	2.5	50
96	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
97	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
98	Closing the Gaps on Human Chromosome 19 Revealed Genes With a High Density of Repetitive Tandemly Arrayed Elements. <i>Genome Research</i> , 2004, 14, 239-246.	5.5	47
99	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	2.0	43
100	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
101	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
102	Toward a Reference Sequence of the Soybean Genome: A Multiagency Effort. <i>Crop Science</i> , 2006, 46, S-55.	1.8	37
103	Sequencing of 15,622 genes bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
104	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020, 110, 1180-1188.	2.2	34
105	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351.	3.6	30
106	Widespread polycistronic gene expression in green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
107	Complete Plastome Sequences from <i>Glycine syndetika</i> and Six Additional Perennial Wild Relatives of Soybean. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2023-2033.	1.8	26
108	Phylogenomics of the genus <i>Glycine</i> sheds light on polyploid evolution and life-strategy transition. <i>Nature Plants</i> , 2022, 8, 233-244.	9.3	26

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109	Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. ISME Journal, 2022, 16, 1074-1085.	9.8	25
110	Fowl sequence. Nature, 2004, 432, 679-680.	27.8	24
111	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Ove 7, 15274.	3.3	23
112	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . Communications Biology, 2021, 4, 537.	4.4	21
113	Legacy genetics of <i>Arachis cardenasii</i> in the peanut crop shows the profound benefits of international seed exchange. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	18
114	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. Plant Physiology, 2022, 189, 516-526.	4.8	18
115	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. New Phytologist, 2022, 234, 2111-2125.	7.3	18
116	Genomic variation within the maize stiff-stalk heterotic germplasm pool. Plant Genome, 2021, 14, e20114.	2.8	14
117	Exploring the loblolly pine (<i>Pinus taeda</i> L.) genome by BAC sequencing and Cot analysis. Gene, 2018, 663, 165-177.	2.2	13
118	Targeted Switchgrass BAC Library Screening and Sequence Analysis Identifies Predicted Biomass and Stress Response-Related Genes. Bioenergy Research, 2016, 9, 109-122.	3.9	10
119	Comparative Transcriptomics of Non-Embryogenic and Embryogenic Callus in Semi-Recalcitrant and Non-Recalcitrant Upland Cotton Lines. Plants, 2021, 10, 1775.	3.5	10
120	Chloroplast genome sequences of <i>Carya illinoensis</i> from two distinct geographic populations. Tree Genetics and Genomes, 2020, 16, 1.	1.6	9
121	The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange. Science Advances, 2022, 8, eabj4633.	10.3	9
122	Kinetics of the growth and variation in infectivity of <i>Toxoplasma gondii</i> in mice. Annals of Tropical Medicine and Parasitology, 1991, 85, 659-661.	1.6	8
123	Six is seventh. Nature, 2003, 425, 775-776.	27.8	8
124	LCM and RNA-seq analyses revealed roles of cell cycle and translational regulation and homoeolog expression bias in cotton fiber cell initiation. BMC Genomics, 2021, 22, 309.	2.8	7
125	The Common Bean V Gene Encodes Flavonoid 3-Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. Frontiers in Plant Science, 2022, 13, 869582.	3.6	7
126	Gene disruption by structural mutations drives selection in US rice breeding over the last century. PLoS Genetics, 2021, 17, e1009389.	3.5	6

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127	A draft genome provides hypotheses on drought tolerance in a keystone plant species in Western North America threatened by climate change. Ecology and Evolution, 2021, 11, 15417-15429.	1.9	6
128	Attachment of Toxoplasma gondii to a Specific Membrane Fraction of CHO Cells. Infection and Immunity, 2000, 68, 7198-7201.	2.2	5
129	A generalistâ€“specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2118879119.	7.1	5
130	Genome organization of the vg1 and nodal3 gene clusters in the allotetraploid frog Xenopus laevis. Developmental Biology, 2017, 426, 236-244.	2.0	4
131	eP144: Long-read genome sequencing secondary processing pipelines provide variant call accuracy that exceeds current clinical standards for short-read genome sequencing. Genetics in Medicine, 2022, 24, S89.	2.4	0