

Johnie N Jenkins

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

114 papers	1,985 citations	26 h-index	38 g-index
118 ext. papers	2,452 ext. citations	3.1 avg, IF	4.65 L-index

#	Paper	IF	Citations
114	Genomic interrogation of a MAGIC population highlights genetic factors controlling fiber quality traits in cotton.. <i>Communications Biology</i> , 2022 , 5, 60	6.7	0
113	Assessing the Weed-Suppressing Potential of Cotton Chromosome Substitution Lines Using the Stair-Step Assay. <i>Plants</i> , 2021 , 10,	4.5	1
112	Pelleted biosolids and cover crop effects on major Southern row crops. <i>Journal of Plant Nutrition</i> , 2021 , 44, 2677-2690	2.3	
111	Alteration of root and shoot morphologies by interspecific replacement of individual Upland cotton chromosome or chromosome segment pairs. <i>Euphytica</i> , 2021 , 217, 1	2.1	1
110	Application of the Cottonscope for determining fiber maturity and fineness of an upland cotton MAGIC population. <i>Crop Science</i> , 2020 , 60, 2266-2279	2.4	3
109	Effect of physical damage to early- and late-maturing cotton cultivars. <i>Agronomy Journal</i> , 2020 , 112, 1140-1147	2.2	
108	Managing harvest of Russell and Mifton 44 Bermudagrass receiving broiler litter for nutritive value and phosphorus removal. <i>Crop, Forage and Turfgrass Management</i> , 2020 , 6, e20013	0.5	1
107	Effect of chromosome substitutions from <i>Gossypium barbadense</i> L., <i>G. tomentosum</i> Nutt. Ex Seem and <i>G. mustelinum</i> Watt into <i>G. hirsutum</i> L. on cottonseed protein and oil content. <i>Euphytica</i> , 2020 , 216, 1	2.1	1
106	Analysis of Cotton Chromosome 11 and 14 Root-Knot Nematode Resistance Quantitative Trait Loci Effects on Root-Knot Nematode Postinfection Development, Egg Mass Formation, and Fecundity. <i>Phytopathology</i> , 2020 , 110, 927-932	3.8	2
105	Effects of inter-species chromosome substitution on cottonseed mineral and protein nutrition profiles. <i>Agronomy Journal</i> , 2020 , 112, 3963-3974	2.2	7
104	Registration of four upland cotton germplasm lines with elevated levels of seed oil oleic acid. <i>Journal of Plant Registrations</i> , 2020 , 14, 64-71	0.7	2
103	Management Strategies on an Upland Soil for Improving Soil Properties. <i>Communications in Soil Science and Plant Analysis</i> , 2020 , 51, 413-429	1.5	6
102	Effects of Interspecific Chromosome Substitution in Upland Cotton on Cottonseed Micronutrients. <i>Plants</i> , 2020 , 9,	4.5	3
101	High-Temperature and Drought-Resilience Traits among Interspecific Chromosome Substitution Lines for Genetic Improvement of Upland Cotton. <i>Plants</i> , 2020 , 9,	4.5	4
100	Evaluation of genomic selection methods for predicting fiber quality traits in Upland cotton. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 67-79	3.1	16
99	Assessment of Surface Water Resources in the Big Sunflower River Watershed Using Coupled SWAT-MODFLOW Model. <i>Water (Switzerland)</i> , 2019 , 11, 528	3	17
98	Genetic and transcriptomic dissection of the fiber length trait from a cotton (<i>Gossypium hirsutum</i> L.) MAGIC population. <i>BMC Genomics</i> , 2019 , 20, 112	4.5	26

97	Consequences of pelletized poultry litter applications on soil physical and hydraulic properties in reduced tillage, continuous cotton system. <i>Soil and Tillage Research</i> , 2019 , 194, 104309	6.5	6
96	The effect of cotton growth stage on response to a sublethal concentration of 2,4-D. <i>Weed Technology</i> , 2019 , 33, 321-328	1.4	1
95	Simulating Potential Weekly Stream and Pond Water Available for Irrigation in the Big Sunflower River Watershed of Mississippi Delta. <i>Water (Switzerland)</i> , 2019 , 11, 1271	3	1
94	A novel variant of Gh_D02G0276 is required for root-knot nematode resistance on chromosome 14 (D02) in Upland cotton. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 1425-1434	6	8
93	Registration of RMBHMTUP-C4, a Random-Mated Cotton Population Containing Alleles from Four Gossypium Species. <i>Journal of Plant Registrations</i> , 2019 , 13, 411-415	0.7	1
92	Poultry Litter and Cover Crop Integration into No-till Cotton on Upland Soil. <i>Agronomy Journal</i> , 2019 , 111, 2097-2107	2.2	12
91	Whole genome sequencing of a MAGIC population identified genomic loci and candidate genes for major fiber quality traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019 , 132, 989-999	6	26
90	Introgression of <i>Gossypium barbadense</i> L. into Upland cotton germplasm RMBUP-C4S1. <i>Euphytica</i> , 2018 , 214, 1	2.1	3
89	Registration of Two CS-B17-derived Upland Cotton Recombinant Inbred Lines with Improved Fiber Micronaire. <i>Journal of Plant Registrations</i> , 2018 , 12, 97-100	0.7	1
88	Harvest Management Effects on Mifton 44 Bermudagrass Phosphorus Removal and Nutritive Value. <i>Agronomy Journal</i> , 2018 , 110, 879-889	2.2	6
87	Rainwater Deficit and Irrigation Demand for Row Crops in Mississippi Blackland Prairie. <i>Soil Science Society of America Journal</i> , 2018 , 82, 423-435	2.5	11
86	Morph-physiological responses of cotton interspecific chromosome substitution lines to low temperature and drought stresses. <i>Euphytica</i> , 2018 , 214, 1	2.1	6
85	Genetic diversity of day-neutral converted landrace <i>Gossypium hirsutum</i> L. accessions. <i>Euphytica</i> , 2018 , 214, 1	2.1	3
84	The P450 gene CYP749A16 is required for tolerance to the sulfonylurea herbicide trifloxysulfuron sodium in cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Plant Biology</i> , 2018 , 18, 186	5.3	11
83	Rain Water Deficit and Irrigation Demand of Major Row Crops in the Mississippi Delta. <i>Transactions of the ASABE</i> , 2018 , 61, 927-935	0.9	10
82	Effects on Selected Soil Properties of Subsurface Banding and Surface Broadcasting Pelletized Poultry Litter on Cotton. <i>Soil Science</i> , 2018 , 183, 112-120	0.9	2
81	Evaluation of Reference Evapotranspiration Methods in Arid, Semiarid, and Humid Regions. <i>Journal of the American Water Resources Association</i> , 2017 , 53, 791-808	2.1	18
80	A Model to Estimate Hydrological Processes and Water Budget in an Irrigation Farm Pond. <i>Water Resources Management</i> , 2017 , 31, 2225-2241	3.7	13

79	Individual and combined contributions of the Ren barb1, Ren barb2, and Ren barb3 quantitative trait loci to reniform nematode (<i>Rotylenchulus reniformis</i> Linford & Oliveira) resistance in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2017 , 213, 1	2.1	7
78	Genetic Effects of Chromosomes 1, 4, and 18 from Three Tetraploid <i>Gossypium</i> Species in Topcrosses with Five Elite Cultivars. <i>Crop Science</i> , 2017 , 57, 1338-1346	2.4	4
77	Genotypic comparisons of chromosomes 01, 04, and 18 from three tetraploid species of <i>Gossypium</i> in topcrosses with five elite cultivars of <i>G. hirsutum</i> L.. <i>Euphytica</i> , 2017 , 213, 1	2.1	5
76	Tri-Species Shuffling of Chromosomes to Study the Effects on Fiber Traits Using Chromosome Substitution Lines. <i>Crop Science</i> , 2017 , 57, 1211-1226	2.4	6
75	QTL mapping for flowering-time and photoperiod insensitivity of cotton <i>Gossypium darwinii</i> Watt. <i>PLoS ONE</i> , 2017 , 12, e0186240	3.7	5
74	Subsurface Band Placement of Pelletized Poultry Litter in Cotton. <i>Agronomy Journal</i> , 2016 , 108, 1356-1366	3.6	10
73	Coupling of MIC-3 overexpression with the chromosomes 11 and 14 root-knot nematode (RKN) (<i>Meloidogyne incognita</i>) resistance QTLs provides insights into the regulation of the RKN resistance response in Upland cotton (<i>Gossypium hirsutum</i>). <i>Theoretical and Applied Genetics</i> , 2016 , 129, 1759-67	6	2
72	Trend Analysis and Forecast of Precipitation, Reference Evapotranspiration, and Rainfall Deficit in the Blackland Prairie of Eastern Mississippi. <i>Journal of Applied Meteorology and Climatology</i> , 2016 , 55, 1425-1439	2.7	43
71	Estimating the ratio of pond size to irrigated soybean land in Mississippi: a case study. <i>Water Science and Technology: Water Supply</i> , 2016 , 16, 1639-1647	1.4	9
70	Optimum Poultry Litter Rates for Maximum Profit versus Yield in Cotton Production. <i>Crop Science</i> , 2016 , 56, 3307-3317	2.4	8
69	A MAGIC population-based genome-wide association study reveals functional association of GhRBB1_A07 gene with superior fiber quality in cotton. <i>BMC Genomics</i> , 2016 , 17, 903	4.5	71
68	Comparative assessment of genetic diversity in cytoplasmic and nuclear genome of upland cotton. <i>Genetica</i> , 2016 , 144, 289-306	1.5	3
67	Small RNA sequencing and degradome analysis of developing fibers of short fiber mutants Ligon-lintles-1 (Li 1) and -2 (Li 2) revealed a role for miRNAs and their targets in cotton fiber elongation. <i>BMC Genomics</i> , 2016 , 17, 360	4.5	18
66	Simulating soybean productivity under rainfed conditions for major soil types using APEX model in East Central Mississippi. <i>Agricultural Water Management</i> , 2016 , 177, 379-391	5.9	15
65	Field experimental design comparisons to detect field effects associated with agronomic traits in upland cotton. <i>Euphytica</i> , 2015 , 206, 747-757	2.1	2
64	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1187-209	3.2	117
63	Overexpression of MIC-3 indicates a direct role for the MIC gene family in mediating Upland cotton (<i>Gossypium hirsutum</i>) resistance to root-knot nematode (<i>Meloidogyne incognita</i>). <i>Theoretical and Applied Genetics</i> , 2015 , 128, 199-209	6	8
62	Detection, Validation, and Application of Genotyping-by-Sequencing Based Single Nucleotide Polymorphisms in Upland Cotton. <i>Plant Genome</i> , 2015 , 8, eplantgenome2014.07.0034	4.4	35

61	Simulating the Fate of Fall- and Spring-Applied Poultry Litter Nitrogen in Corn Production. <i>Soil Science Society of America Journal</i> , 2015 , 79, 1804-1814	2.5	12
60	Molecular confirmation of <i>Gossypium hirsutum</i> chromosome substitution lines. <i>Euphytica</i> , 2015 , 205, 459-473	2.1	11
59	Genetic mapping of non-target-site resistance to a sulfonylurea herbicide (Envoke®) in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Molecular Breeding</i> , 2014 , 33, 341-348	3.4	7
58	Molecular characterization of the reniform nematode C-type lectin gene family reveals a likely role in mitigating environmental stresses during plant parasitism. <i>Gene</i> , 2014 , 537, 269-78	3.8	9
57	Quantitative trait loci analysis of fiber quality traits using a random-mated recombinant inbred population in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2014 , 15, 397	4.5	69
56	Phytochrome RNAi enhances major fibre quality and agronomic traits of the cotton <i>Gossypium hirsutum</i> L. <i>Nature Communications</i> , 2014 , 5, 3062	17.4	40
55	Genetic analysis without replications: model evaluation and application in spring wheat. <i>Euphytica</i> , 2013 , 190, 447-458	2.1	8
54	SSR markers for marker assisted selection of root-knot nematode (<i>Meloidogyne incognita</i>) resistant plants in cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2012 , 183, 49-54	2.1	21
53	Genetic effects of nine <i>Gossypium barbadense</i> L. chromosome substitution lines in top crosses with five elite Upland cotton <i>G. hirsutum</i> L. cultivars. <i>Euphytica</i> , 2012 , 187, 161-173	2.1	16
52	Detecting epistatic effects associated with cotton traits by a modified MDR approach. <i>Euphytica</i> , 2012 , 187, 289-301	2.1	13
51	Broiler Litter Type and Placement Effects on Corn Growth, Nitrogen Utilization, and Residual Soil Nitrate-Nitrogen in a No-Till Field. <i>Agronomy Journal</i> , 2012 , 104, 43-48	2.2	10
50	A categorical, improper probability method for combining NDVI and LiDAR elevation information for potential cotton precision agricultural applications. <i>Computers and Electronics in Agriculture</i> , 2012 , 82, 15-22	6.5	6
49	A cotton-fiber-associated cyclin-dependent kinase a gene: characterization and chromosomal location. <i>International Journal of Plant Genomics</i> , 2012 , 2012, 613812		5
48	Identification of QTL regions and SSR markers associated with resistance to reniform nematode in <i>Gossypium barbadense</i> L. accession GB713. <i>Theoretical and Applied Genetics</i> , 2011 , 122, 271-80	6	39
47	Molecular evolution of the clustered MIC-3 multigene family of <i>Gossypium</i> species. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 1359-73	6	4
46	Clustering, haplotype diversity and locations of MIC-3: a unique root-specific defense-related gene family in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2010 , 120, 587-606	6	8
45	Genetic dissection of chromosome substitution lines of cotton to discover novel <i>Gossypium barbadense</i> L. alleles for improvement of agronomic traits. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 1193-205	6	27
44	Cotton chromosome substitution lines crossed with cultivars: genetic model evaluation and seed trait analyses. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 1473-83	6	20

43	SSR markers closely associated with genes for resistance to root-knot nematode on chromosomes 11 and 14 of Upland cotton. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 1323-37	6	49
42	Designing experiments to evaluate the effectiveness of precision agricultural practices on research fields: part 1 concepts for their formulation. <i>Operational Research</i> , 2010 , 10, 329-348	1.6	6
41	Characterization and promoter analysis of a cotton RING-type ubiquitin ligase (E3) gene. <i>Molecular Biotechnology</i> , 2010 , 46, 140-8	3	12
40	Use of fiber and fuzz mutants to detect QTL for yield components, seed, and fiber traits of upland cotton. <i>Euphytica</i> , 2010 , 172, 21-34	2.1	40
39	Genetic effects of individual chromosomes in cotton cultivars detected by using chromosome substitution lines as genetic probes. <i>Genetica</i> , 2010 , 138, 1171-9	1.5	4
38	Integrative placement and orientation of non-redundant SSR loci in cotton linkage groups by deficiency analysis. <i>Molecular Breeding</i> , 2009 , 23, 693-707	3.4	11
37	Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton. <i>Euphytica</i> , 2009 , 165, 231-245	2.1	72
36	Seed trait evaluation of <i>Gossypium barbadense</i> L. chromosomes/arms in a <i>G. hirsutum</i> L. background. <i>Euphytica</i> , 2009 , 167, 371-380	2.1	20
35	Genetic variance components and genetic effects among eleven diverse upland cotton lines and their F2 hybrids. <i>Euphytica</i> , 2009 , 167, 397-408	2.1	34
34	Defining the experimental unit for the design and analysis of site-specific experiments in commercial cotton fields. <i>Agricultural Systems</i> , 2008 , 96, 237-249	6.1	19
33	Genetic association of cotton yield with its component traits in derived primitive accessions crossed by elite upland cultivars using the conditional ADAA genetic model. <i>Euphytica</i> , 2008 , 161, 337-352 ¹	2.1	17
32	BAC-derived SSR markers chromosome locations in cotton. <i>Euphytica</i> , 2008 , 161, 361-370	2.1	19
31	QTLs for node of first fruiting branch in a cross of an upland cotton, <i>Gossypium hirsutum</i> L., cultivar with primitive accession Texas 701. <i>Euphytica</i> , 2008 , 163, 113-122	2.1	41
30	Genetic association of lint yield with its components in cotton chromosome substitution lines. <i>Euphytica</i> , 2008 , 164, 199-207	2.1	14
29	Cotton (<i>Gossypium</i> spp.) R2R3-MYB transcription factors SNP identification, phylogenomic characterization, chromosome localization, and linkage mapping. <i>Theoretical and Applied Genetics</i> , 2008 , 116, 1015-26	6	37
28	Molecular characterization and temporal expression analyses indicate that the MIC (Meloidogyne Induced Cotton) gene family represents a novel group of root-specific defense-related genes in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Planta</i> , 2008 , 228, 111-23	4.7	15
27	Use of Primitive Derived Cotton Accessions for Agronomic and Fiber Traits Improvement: Variance Components and Genetic Effects. <i>Crop Science</i> , 2007 , 47, 100-110	2.4	22
26	Genetic Effects of Thirteen <i>Gossypium barbadense</i> L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: II. Fiber Quality Traits. <i>Crop Science</i> , 2007 , 47, 561-570	2.4	49

25	Molecular and SNP characterization of two genome specific transcription factor genes GhMyb8 and GhMyb10 in cotton species. <i>Euphytica</i> , 2007 , 159, 259-273	2.1	12
24	Transcriptome profiling, sequence characterization, and SNP-based chromosomal assignment of the EXPANSIN genes in cotton. <i>Molecular Genetics and Genomics</i> , 2007 , 278, 539-53	3.1	45
23	An additive-dominance model to determine chromosomal effects in chromosome substitution lines and other gemplasms. <i>Theoretical and Applied Genetics</i> , 2006 , 112, 391-9	6	26
22	Effects of chromosome-specific introgression in upland cotton on fiber and agronomic traits. <i>Genetics</i> , 2006 , 172, 1927-38	4	70
21	Genetic Effects of Thirteen Gossypium barbadense L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: I. Yield and Yield Components. <i>Crop Science</i> , 2006 , 46, 1169-1178	2.4	48
20	Association of Root-Knot Nematode Resistance Genes with Simple Sequence Repeat Markers on Two Chromosomes in Cotton. <i>Crop Science</i> , 2006 , 46, 2670-2674	2.4	51
19	A recursive approach to detect multivariable conditional variance components and conditional random effects. <i>Computational Statistics and Data Analysis</i> , 2006 , 50, 285-300	1.6	7
18	Genetic diversity for agronomic and fiber traits in day-neutral accessions derived from primitive cotton germplasm. <i>Euphytica</i> , 2006 , 148, 283-293	2.1	15
17	Effects of chromosome 5sh from Gossypium barbadense L. on flower production in G. hirsutum L.. <i>Euphytica</i> , 2006 , 152, 99-107	2.1	12
16	Primitive Accession Derived Germplasm by Cultivar Crosses as Sources for Cotton Improvement. <i>Crop Science</i> , 2004 , 44, 1226-1230	2.4	45
15	Primitive Accession Derived Germplasm by Cultivar Crosses as Sources for Cotton Improvement. <i>Crop Science</i> , 2004 , 44, 1231-1235	2.4	30
14	Genetic association of yield with its component traits in a recombinant inbred line population of cotton. <i>Euphytica</i> , 2004 , 140, 171-179	2.1	24
13	Molecular and cytological characterization of a cytoplasmic-specific mutant in pima cotton (Gossypium barbadense L.). <i>Euphytica</i> , 2004 , 139, 187-197	2.1	23
12	Molecular cloning, differential expression, and functional characterization of a family of class I ubiquitin-conjugating enzyme (E2) genes in cotton (Gossypium). <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2003 , 1625, 269-79		21
11	A novel root-specific gene, MIC-3, with increased expression in nematode-resistant cotton (Gossypium hirsutum L.) after root-knot nematode infection. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002 , 1576, 214-8		11
10	Registration of 16 Day Length-Neutral Flowering Primitive Cotton Germplasm Lines. <i>Crop Science</i> , 2002 , 42, 1755-1756	2.4	9
9	Use of Cross-Species Simple Sequence Repeat (SSR) Primers for Developing Polymorphic DNA Markers. <i>Journal of New Seeds</i> , 1999 , 1, 25-37		1
8	Caloric Analyses of the Distribution of Energy in Ripened Cotton (Gossypium hirsutum L.). <i>Journal of Agricultural and Food Chemistry</i> , 1997 , 45, 3258-3261	5.7	1

7	Combining Ability Analysis of Root-Knot Nematode Resistance in Cotton. <i>Crop Science</i> , 1995 , 35, 373	2.4	21
6	Use of <i>Bacillus thuringiensis</i> Genes in Transgenic Cotton To Control Lepidopterous Insects. <i>ACS Symposium Series</i> , 1993 , 267-280	0.4	2
5	Registration of 79 Day-Neutral Primitive Cotton Germplasm Lines. <i>Crop Science</i> , 1993 , 33, 351	2.4	15
4	F2 Hybrids of Host Plant Germplasm and Cotton Cultivars: I. Heterosis and Combining Ability for Lint Yield and Yield Components. <i>Crop Science</i> , 1993 , 33, 700-705	2.4	38
3	F2 Hybrids of Host Plant Germplasm and Cotton Cultivars: II. Heterosis and Combining Ability for Fiber Properties. <i>Crop Science</i> , 1993 , 33, 706-710	2.4	31
2	A GENERALIZED APPROACH AND COMPUTER TOOL FOR QUANTITATIVE GENETICS STUDY. <i>Conference on Applied Statistics in Agriculture</i> ,		13
1	TESTING VARIANCE COMPONENTS BY TWO JACKKNIFE METHODS. <i>Conference on Applied Statistics in Agriculture</i> ,		10