

John M Burke

List of Publications by Year in descending order

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107
papers

9,453
citations

38742

50
h-index

40979

93
g-index

112
all docs

112
docs citations

112
times ranked

10324
citing authors

#	ARTICLE	IF	CITATIONS
1	GC content of plant genes is linked to past gene duplications. PLoS ONE, 2022, 17, e0261748.	2.5	6
2	Expression complementation of gene presence/absence polymorphisms in hybrids contributes importantly to heterosis in sunflower. Journal of Advanced Research, 2022, 42, 83-98.	9.5	12
3	Genomic regions associate with major axes of variation driven by gas exchange and leaf construction traits in cultivated sunflower (<i>Helianthus annuus</i> L.). Plant Journal, 2022, 111, 1425-1438.	5.7	4
4	Genetic control of arbuscular mycorrhizal colonization by Rhizophagus intraradices in <i>Helianthus annuus</i> (L.). Mycorrhiza, 2021, 31, 723-734.	2.8	9
5	Key Traits and Genes Associate with Salinity Tolerance Independent from Vigor in Cultivated Sunflower. Plant Physiology, 2020, 184, 865-880.	4.8	16
6	Phylogeography and the Evolutionary History of Sunflower (<i>Helianthus annuus</i> L.): Wild Diversity and the Dynamics of Domestication. Genes, 2020, 11, 266.	2.4	10
7	Impact of Deficit Irrigation on Shallow Saline Groundwater Contribution and Sunflower Productivity in the Imperial Valley, California. Water (Switzerland), 2020, 12, 571.	2.7	9
8	Massive haplotypes underlie ecotypic differentiation in sunflowers. Nature, 2020, 584, 602-607.	27.8	263
9	Genome-Wide Association Mapping of Floral Traits in Cultivated Sunflower (<i>Helianthus annuus</i>). Journal of Heredity, 2019, 110, 275-286.	2.4	16
10	Effect of Deficit Irrigation on Nitrogen Uptake of Sunflower in the Low Desert Region of California. Water (Switzerland), 2019, 11, 2340.	2.7	11
11	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. Nature Plants, 2019, 5, 54-62.	9.3	172
12	Genome-wide analysis of allele frequency change in sunflower crop-wild hybrid populations evolving under natural conditions. Molecular Ecology, 2018, 27, 233-247.	3.9	18
13	Multiple genomic regions influence root morphology and seedling growth in cultivated sunflower (<i>Helianthus annuus</i> L.) under well-watered and water-limited conditions. PLoS ONE, 2018, 13, e0204279.	2.5	24
14	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	27.8	579
15	Connectivity in gene coexpression networks negatively correlates with rates of molecular evolution in flowering plants. PLoS ONE, 2017, 12, e0182289.	2.5	36
16	Population Genetics of the Rubber-Producing Russian Dandelion (<i>Taraxacum kok-saghyz</i>). PLoS ONE, 2016, 11, e0146417.	2.5	22
17	Widespread natural variation of DNA methylation within angiosperms. Genome Biology, 2016, 17, 194.	8.8	436
18	Range-wide phenotypic and genetic differentiation in wild sunflower. BMC Plant Biology, 2016, 16, 249.	3.6	17

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19	Genetic Mapping of Millions of SNPs in Safflower (<i>Carthamus tinctorius</i> L.) via Whole-Genome Resequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2203-2211.	1.8	39
20	Environmental requirements trump genetic factors in explaining narrow endemism in two imperiled Florida sunflowers. <i>Conservation Genetics</i> , 2015, 16, 1277-1293.	1.5	4
21	A Unified Single Nucleotide Polymorphism Map of Sunflower (<i>Helianthus annuus</i> L.) Derived from Current Genomic Resources. <i>Crop Science</i> , 2015, 55, 1696-1702.	1.8	16
22	Association mapping in sunflower (<i>Helianthus annuus</i> L.) reveals independent control of apical vs. basal branching. <i>BMC Plant Biology</i> , 2015, 15, 84.	3.6	43
23	Transposome: a toolkit for annotation of transposable element families from unassembled sequence reads. <i>Bioinformatics</i> , 2015, 31, 1827-1829.	4.1	22
24	Evolutionary transitions in the Asteraceae coincide with marked shifts in transposable element abundance. <i>BMC Genomics</i> , 2015, 16, 623.	2.8	40
25	Selection on Crop-Derived Traits and QTL in Sunflower (<i>Helianthus annuus</i>) Crop-Wild Hybrids under Water Stress. <i>PLoS ONE</i> , 2014, 9, e102717.	2.5	9
26	A target enrichment method for gathering phylogenetic information from hundreds of loci: An example from the Compositae. <i>Applications in Plant Sciences</i> , 2014, 2, 1300085.	2.1	178
27	Chromosomal Evolution and Patterns of Introgression in <i>Helianthus</i> . <i>Genetics</i> , 2014, 197, 969-979.	2.9	52
28	Genetic analysis of safflower domestication. <i>BMC Plant Biology</i> , 2014, 14, 43.	3.6	40
29	Genomics of Compositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	4.8	45
30	Genetic diversity in <i>Carthamus tinctorius</i> (Asteraceae; safflower), an underutilized oilseed crop. <i>American Journal of Botany</i> , 2014, 101, 1640-1650.	1.7	25
31	Molecular Evolution of Candidate Genes for Crop-Related Traits in Sunflower (<i>Helianthus annuus</i> L.). <i>PLoS ONE</i> , 2014, 9, e99620.	2.5	11
32	Genetic diversity and population structure in the rare Algodones sunflower (<i>Helianthus niveus</i> ssp.). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.5	12
33	Sunflower as a biofuels crop: An analysis of Alignocellulosic chemical properties. <i>Biomass and Bioenergy</i> , 2013, 59, 208-217.	5.7	34
34	Sunflower genetic, genomic and ecological resources. <i>Molecular Ecology Resources</i> , 2013, 13, 10-20.	4.8	59
35	Genomic islands of divergence are not affected by geography of speciation in sunflowers. <i>Nature Communications</i> , 2013, 4, 1827.	12.8	263
36	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	27.8	464

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37	High Genetic Diversity and Low Population Structure in Porter's Sunflower (<i>Helianthus porteri</i>). <i>Journal of Heredity</i> , 2013, 104, 407-415.	2.4	24
38	Association Mapping and the Genomic Consequences of Selection in Sunflower. <i>PLoS Genetics</i> , 2013, 9, e1003378.	3.5	116
39	Sequence Validation of Candidates for Selectively Important Genes in Sunflower. <i>PLoS ONE</i> , 2013, 8, e71941.	2.5	4
40	Genetic Analysis of Floral Symmetry in Van Gogh's Sunflowers Reveals Independent Recruitment of CYCLOIDEA Genes in the Asteraceae. <i>PLoS Genetics</i> , 2012, 8, e1002628.	3.5	136
41	The sunflower (<i>Helianthus annuus</i> L.) genome reflects a recent history of biased accumulation of transposable elements. <i>Plant Journal</i> , 2012, 72, 142-153.	5.7	88
42	Evidence of selection on fatty acid biosynthetic genes during the evolution of cultivated sunflower. <i>Theoretical and Applied Genetics</i> , 2012, 125, 897-907.	3.6	51
43	Development of a 10,000 Locus Genetic Map of the Sunflower Genome Based on Multiple Crosses. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 721-729.	1.8	96
44	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	1.7	80
45	Development of an Ultra-Dense Genetic Map of the Sunflower Genome Based on Single-Feature Polymorphisms. <i>PLoS ONE</i> , 2012, 7, e51360.	2.5	12
46	SNP Discovery and Development of a High-Density Genotyping Array for Sunflower. <i>PLoS ONE</i> , 2012, 7, e29814.	2.5	100
47	Contributions of Flowering Time Genes to Sunflower Domestication and Improvement. <i>Genetics</i> , 2011, 187, 271-287.	2.9	82
48	Genetic diversity and population structure in cultivated sunflower and a comparison to its wild progenitor, <i>Helianthus annuus</i> L. <i>Theoretical and Applied Genetics</i> , 2011, 123, 693-704.	3.6	147
49	Progress towards a reference genome for sunflower. <i>Botany</i> , 2011, 89, 429-437.	1.0	67
50	Ecological patterns and genetic analysis of post-dispersal seed predation in sunflower (<i>Helianthus</i>) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	3.9	15
51	Population genetic analysis of safflower (<i>Carthamus tinctorius</i> ; Asteraceae) reveals a Near Eastern origin and five centers of diversity. <i>American Journal of Botany</i> , 2010, 97, 831-840.	1.7	53
52	Genetic Architecture of Novel Traits in the Hopi Sunflower. <i>Journal of Heredity</i> , 2010, 101, 727-736.	2.4	12
53	Widespread Gene Conversion in Centromere Cores. <i>PLoS Biology</i> , 2010, 8, e1000327.	5.6	109
54	Population Genetics of <i>Astragalus bibullatus</i> (Fabaceae) Using AFLPs. <i>Journal of Heredity</i> , 2009, 100, 424-431.	2.4	19

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55	Development, polymorphism, and cross-taxon utility of EST-SSR markers from safflower (<i>Carthamus</i>) Tj ETQq1 1,0,784314 rgBT /Oe 3.6 85P	1.0	78
56	Population genetic analysis reveals a homoploid hybrid origin of <i>Stephanomeria diegensis</i> (Asteraceae). <i>Molecular Ecology</i> , 2009, 18, 4049-4060.	3.9	16
57	Fitness effects and genetic architecture of plant-herbivore interactions in sunflower crop-wild hybrids. <i>New Phytologist</i> , 2009, 184, 828-841.	7.3	37
58	Karyotypic Evolution of the Common and Silverleaf Sunflower Genomes. <i>Plant Genome</i> , 2009, 2, .	2.8	19
59	Selection on domestication traits and quantitative trait loci in crop-wild sunflower hybrids. <i>Molecular Ecology</i> , 2008, 17, 666-677.	3.9	79
60	Molecular insights into the evolution of crop plants. <i>American Journal of Botany</i> , 2008, 95, 113-122.	1.7	130
61	Molecular evidence and the origin of the domesticated sunflower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, E46; author reply E49-50.	7.1	11
62	Positive Selection and Expression Divergence Following Gene Duplication in the Sunflower CYCLOIDEA Gene Family. <i>Molecular Biology and Evolution</i> , 2008, 25, 1260-1273.	8.9	132
63	A Genomic Scan for Selection Reveals Candidates for Genes Involved in the Evolution of Cultivated Sunflower (<i>Helianthus annuus</i>). <i>Plant Cell</i> , 2008, 20, 2931-2945.	6.6	269
64	Quantitative Trait Locus Analysis of the Early Domestication of Sunflower. <i>Genetics</i> , 2007, 176, 2589-2599.	2.9	78
65	Single Nucleotide Polymorphisms and Linkage Disequilibrium in Sunflower. <i>Genetics</i> , 2007, 177, 457-468.	2.9	77
66	Crop evolution: from genetics to genomics. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 525-532.	3.3	74
67	EST-SSRs as a resource for population genetic analyses. <i>Heredity</i> , 2007, 99, 125-132.	2.6	499
68	GENETIC DIVERGENCE AND HYBRID SPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1773-1780.	2.3	142
69	DNA sequence diversity and the origin of cultivated safflower (<i>Carthamus tinctorius</i> L.; Asteraceae). <i>BMC Plant Biology</i> , 2007, 7, 60.	3.6	69
70	Universal markers for comparative mapping and phylogenetic analysis in the Asteraceae (Compositae). <i>Theoretical and Applied Genetics</i> , 2007, 115, 747-755.	3.6	79
71	Patterns of Nucleotide Diversity in Wild and Cultivated Sunflower. <i>Genetics</i> , 2006, 173, 321-330.	2.9	177
72	Letting the gene out of the bottle: the population genetics of genetically modified crops. <i>New Phytologist</i> , 2006, 170, 429-443.	7.3	156

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73	High genetic diversity in a rare and endangered sunflower as compared to a common congener. <i>Molecular Ecology</i> , 2006, 15, 2345-2355.	3.9	91
74	Polluting gene flow from crops: Radishes gone wild. <i>Heredity</i> , 2006, 97, 379-380.	2.6	3
75	Chloroplast DNA Variation Confirms a Single Origin of Domesticated Sunflower (<i>Helianthus annuus</i>) <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	2.4	55
76	EST Databases as a Source for Molecular Markers: Lessons from <i>Helianthus</i> . <i>Journal of Heredity</i> , 2006, 97, 381-388.	2.4	174
77	Chloroplast SSR polymorphisms in the Compositae and the mode of organellar inheritance in <i>Helianthus annuus</i> . <i>Theoretical and Applied Genetics</i> , 2005, 110, 941-947.	3.6	51
78	Parallel genotypic adaptation: when evolution repeats itself. <i>Genetica</i> , 2005, 123, 157-170.	1.1	199
79	Genetic Consequences of Selection During the Evolution of Cultivated Sunflower. <i>Genetics</i> , 2005, 171, 1933-1940.	2.9	80
80	Extensive Chromosomal Repatterning and the Evolution of Sterility Barriers in Hybrid Sunflower Species. <i>Genetics</i> , 2005, 171, 291-303.	2.9	175
81	Parallel genotypic adaptation: when evolution repeats itself. , 2005, , 157-170.		7
82	Comparative Mapping and Rapid Karyotypic Evolution in the Genus <i>Helianthus</i> . <i>Genetics</i> , 2004, 167, 449-457.	2.9	100
83	CONTRASTING GENETIC STRUCTURE OF ADULTS AND PROGENY IN A LOUISIANA IRIS HYBRID POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2669.	2.3	0
84	WHEN GOOD PLANTS GO BAD?. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 1637.	2.3	0
85	CONTRASTING GENETIC STRUCTURE OF ADULTS AND PROGENY IN A LOUISIANA IRIS HYBRID POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2669-2681.	2.3	17
86	WHEN GOOD PLANTS GO BAD?. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 1637-1638.	2.3	3
87	The genetic architecture necessary for transgressive segregation is common in both natural and domesticated populations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2003, 358, 1141-1147.	4.0	240
88	Fitness Effects of Transgenic Disease Resistance in Sunflowers. <i>Science</i> , 2003, 300, 1250-1250.	12.6	134
89	Genetic Variation and Evidence of Hybridization in the Genus <i>Rhus</i> (Anacardiaceae). , 2002, 93, 37-41.		9
90	Directional selection is the primary cause of phenotypic diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12242-12245.	7.1	183

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91	The potential for gene flow between cultivated and wild sunflower (<i>Helianthus annuus</i>) in the United States. <i>American Journal of Botany</i> , 2002, 89, 1550-1552.	1.7	84
92	Genetic Analysis of Sunflower Domestication. <i>Genetics</i> , 2002, 161, 1257-1267.	2.9	252
93	Genetics and the Fitness of Hybrids. <i>Annual Review of Genetics</i> , 2001, 35, 31-52.	7.6	480
94	The biological reality of species: gene flow, selection, and collective evolution. <i>Taxon</i> , 2001, 50, 47-67.	0.7	155
95	A genic view of species integration. <i>Journal of Evolutionary Biology</i> , 2001, 14, 883-886.	1.7	45
96	Nectar Characteristics of Interspecific Hybrids and Their Parents in <i>Aesculus</i> (Hippocastanaceae) and <i>Iris</i> (Iridaceae). <i>Journal of the Torrey Botanical Society</i> , 2000, 127, 200.	0.3	9
97	FREQUENCY AND SPATIAL PATTERNING OF CLONAL REPRODUCTION IN LOUISIANA IRIS HYBRID POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 137-144.	2.3	48
98	FREQUENCY AND SPATIAL PATTERNING OF CLONAL REPRODUCTION IN LOUISIANA IRIS HYBRID POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 137.	2.3	6
99	Isolation and characterization of microsatellites in iris. <i>Molecular Ecology</i> , 1999, 8, 1091-1092.	3.9	9
100	How reliable is science information on the web?. <i>Nature</i> , 1999, 402, 722-722.	27.8	20
101	NATURAL HYBRIDIZATION: HOW LOW CAN YOU GO AND STILL BE IMPORTANT?. <i>Ecology</i> , 1999, 80, 371-381.	3.2	142
102	Genetic Interactions and Natural Selection in Louisiana Iris Hybrids. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 1304.	2.3	30
103	Hybrid Fitness in the Louisiana Irises: Analysis of Parental and F 1 Performance. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 37.	2.3	38
104	GENETIC INTERACTIONS AND NATURAL SELECTION IN LOUISIANA IRIS HYBRIDS. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 1304-1310.	2.3	80
105	HYBRID FITNESS IN THE LOUISIANA IRISES: ANALYSIS OF PARENTAL AND F 1 PERFORMANCE. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 37-43.	2.3	84
106	NATURAL FORMATION OF IRIS HYBRIDS: EXPERIMENTAL EVIDENCE ON THE ESTABLISHMENT OF HYBRID ZONES. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 2504-2509.	2.3	50
107	Natural Formation of Iris Hybrids: Experimental Evidence on the Establishment of Hybrid Zones. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 2504.	2.3	23