

Nolan C Kane

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

5,878
citations

66315

42
h-index

85498

71
g-index

118
all docs

118
docs citations

118
times ranked

7704
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitochondrial genomes do not appear to regulate flowering pattern / reproductive strategy in <i>Cannabis sativa</i> . <i>AoB PLANTS</i> , 2022, 14, plab068.	1.2	1
2	Effective strategies for isolating DNA from members of Asteraceae with high concentrations of secondary metabolites. <i>BioTechniques</i> , 2022, , .	0.8	7
3	Editorial 2022. <i>Molecular Ecology</i> , 2022, 31, 1-30.	2.0	5
4	Rapid evolutionary changes in gene expression in response to climate fluctuations. <i>Molecular Ecology</i> , 2021, 30, 193-206.	2.0	27
5	Sharing and reporting benefits from biodiversity research. <i>Molecular Ecology</i> , 2021, 30, 1103-1107.	2.0	19
6	Genetic loci underlying quantitative resistance to necrotrophic pathogens <i>Sclerotinia</i> and <i>Diaporthe</i> (<i>Phomopsis</i>), and correlated resistance to both pathogens. <i>Theoretical and Applied Genetics</i> , 2021, 134, 249-259.	1.8	6
7	Patterns of genetic variation in a prairie wildflower, <i>Silphium integrifolium</i> , suggest a non-prairie origin and locally adaptive variation. <i>American Journal of Botany</i> , 2021, 108, 145-158.	0.8	9
8	Breeding for sustainable oilseed crop yield and quality in a changing climate. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1817-1827.	1.8	19
9	Evolution of pathogen response genes associated with increased disease susceptibility during adaptation to an extreme drought in a <i>Brassica rapa</i> plant population. <i>Bmc Ecology and Evolution</i> , 2021, 21, 61.	0.7	4
10	Widely assumed phenotypic associations in <i>Cannabis sativa</i> lack a shared genetic basis. <i>PeerJ</i> , 2021, 9, e10672.	0.9	18
11	Author response to Tagirdzhanova et al. (2021): "Lichen fungi do not depend on alga for ATP production: A comment on Pogoda et al. (2018)". <i>Molecular Ecology</i> , 2021, 30, 4160-4161.	2.0	1
12	Genomic Evidence That Governmentally Produced <i>Cannabis sativa</i> Poorly Represents Genetic Variation Available in State Markets. <i>Frontiers in Plant Science</i> , 2021, 12, 668315.	1.7	9
13	Aberrant RNA splicing due to genetic incompatibilities in sunflower hybrids. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 2747-2758.	1.1	7
14	Editorial 2021. <i>Molecular Ecology</i> , 2021, 30, 1-25.	2.0	4
15	Mating compatibility and fertility studies in an herbaceous perennial <i>Aster</i> undergoing de novo domestication to enhance agroecosystems. <i>Agronomy for Sustainable Development</i> , 2020, 40, 1.	2.2	8
16	Complete mitochondrial genomes provide current refined phylogenomic hypotheses for relationships among ten <i>Hirundo</i> species. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2881-2885.	0.2	1
17	A taxonomically broad metagenomic survey of 339 species spanning 57 families suggests cystobasidiomycete yeasts are not ubiquitous across all lichens. <i>American Journal of Botany</i> , 2019, 106, 1090-1095.	0.8	29
18	Extensive chloroplast genome rearrangement amongst three closely related <i>Halamphora</i> spp. (<i>Bacillariophyceae</i>), and evidence for rapid evolution as compared to land plants. <i>PLoS ONE</i> , 2019, 14, e0217824.	1.1	16

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19	Assessment of the biogeographical variation of seed size and seed oil traits in wild <i>Silphium integrifolium</i> Michx. genotypes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2019, 17, 427-436.	0.4	17
20	Editorial 2019. <i>Molecular Ecology</i> , 2019, 28, 1-28.	2.0	9
21	Genome streamlining via complete loss of introns has occurred multiple times in lichenized fungal mitochondria. <i>Ecology and Evolution</i> , 2019, 9, 4245-4263.	0.8	46
22	The complete mitochondrial genome of Gunnison's prairie dog subspecies (<i>Cynomys gunnisoni</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Part B: Resources, 2019, 4, 397-398.	0.2	2
23	Stochastic processes drive rapid genomic divergence during experimental range expansions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190231.	1.2	8
24	Gene copy number is associated with phytochemistry in <i>Cannabis sativa</i> . <i>AoB PLANTS</i> , 2019, 11, plz074.	1.2	38
25	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. <i>Nature Plants</i> , 2019, 5, 54-62.	4.7	172
26	Comparative analysis of the mitochondrial genomes of six newly sequenced diatoms reveals group II introns in the barcoding region of <i>cox1</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 43-51.	0.7	24
27	Evidence of substrate endemism of lichens on Fox Hills Sandstone: Discovery and description of <i>Lecanora lendemeri</i> as new to science. <i>Bryologist</i> , 2019, 122, 246.	0.1	5
28	The complete mitochondrial genomes of five lichenized fungi in the genus <i>Usnea</i> (Ascomycota:) Tj ETQq0 0 0 rgBT /Overlock 10 16	0.2	16
29	Reductions in complexity of mitochondrial genomes in lichen-forming fungi shed light on genome architecture of obligate symbioses. <i>Molecular Ecology</i> , 2018, 27, 1155-1169.	2.0	39
30	Demographic inference in barn swallows using whole-genome data shows signal for bottleneck and subspecies differentiation during the Holocene. <i>Molecular Ecology</i> , 2018, 27, 4200-4212.	2.0	29
31	Genomic insights into the mitochondria of 11 eastern North American species of <i>Cladonia</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 508-512.	0.2	10
32	Diversity and evolution of the repetitive genomic content in <i>Cannabis sativa</i> . <i>BMC Genomics</i> , 2018, 19, 156.	1.2	31
33	Two contrasting laboratory methods improve <i>Silphium integrifolium</i> Michx. germination rate to agronomically acceptable levels. <i>Euphytica</i> , 2018, 214, 1.	0.6	6
34	Genetics of alternative splicing evolution during sunflower domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6768-6773.	3.3	40
35	<i>Lecanora markjohnstonii</i> (Lecanoraceae, lichenized Ascomycetes), a new sorediate crustose lichen from the southeastern United States. <i>Bryologist</i> , 2018, 121, 498-512.	0.1	10
36	Following the Fate of Facilitated Migration In A Small Desert Spring. <i>Southwestern Naturalist</i> , 2018, 63, 8.	0.1	0

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37	Compromised External Validity: Federally Produced Cannabis Does Not Reflect Legal Markets. <i>Scientific Reports</i> , 2017, 7, 46528.	1.6	73
38	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152.	13.7	579
39	Effects of assortative mate choice on the genomic and morphological structure of a hybrid zone between two bird subspecies. <i>Molecular Ecology</i> , 2017, 26, 6430-6444.	2.0	34
40	Genomic variation across two barn swallow hybrid zones reveals traits associated with divergence in sympatry and allopatry. <i>Molecular Ecology</i> , 2017, 26, 5676-5691.	2.0	48
41	Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, <i>Helianthus annuus</i> . <i>New Phytologist</i> , 2017, 214, 412-423.	3.5	185
42	Accelerating <i>Silphium</i> Domestication: An Opportunity to Develop New Crop Ideotypes and Breeding Strategies Informed by Multiple Disciplines. <i>Crop Science</i> , 2017, 57, 1274-1284.	0.8	61
43	Genetic Architecture of Capitulate Glandular Trichome Density in Florets of Domesticated Sunflower (<i>Helianthus annuus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 2227.	1.7	7
44	The complete mitochondrial genome for <i>Cannabis sativa</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 715-716.	0.2	16
45	Genetic and Genomic Tools for <i>Cannabis sativa</i> . <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 364-377.	2.7	70
46	Current and Future Needs and Applications for Cannabis. <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 425-426.	2.7	8
47	Genomic and Chemical Diversity in <i>Cannabis</i> . <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 349-363.	2.7	115
48	Complete Mitochondrial Genome Sequence of Sunflower (<i>Helianthus annuus</i> L.). <i>Genome Announcements</i> , 2016, 4, .	0.8	13
49	Rapid genome-wide evolution in <i>Brassica rapa</i> populations following drought revealed by sequencing of ancestral and descendant gene pools. <i>Molecular Ecology</i> , 2016, 25, 3622-3631.	2.0	79
50	The complete chloroplast genomes of <i>Cannabis sativa</i> and <i>Humulus lupulus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3793-3794.	0.7	35
51	The complete mitochondrial genome of the Warm Springs pupfish, <i>Cyprinodon nevadensis pectoralis</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2349-2350.	0.7	5
52	Genomic analysis of a migratory divide reveals candidate genes for migration and implicates selective sweeps in generating islands of differentiation. <i>Molecular Ecology</i> , 2015, 24, 1873-1888.	2.0	106
53	Ecogeography and utility to plant breeding of the crop wild relatives of sunflower (<i>Helianthus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 101	1.7	57
54	Genome scans reveal candidate domestication and improvement genes in cultivated sunflower, as well as post-domestication introgression with wild relatives. <i>New Phytologist</i> , 2015, 206, 830-838.	3.5	79

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55	Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. <i>Molecular Ecology</i> , 2015, 24, 2194-2211.	2.0	59
56	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 698.	1.5	62
57	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (<i>Helianthus annuus</i> L.) Genome. <i>Biology</i> , 2014, 3, 295-319.	1.3	16
58	Bridging physiological and evolutionary time scales in a gene regulatory network. <i>New Phytologist</i> , 2014, 203, 685-696.	3.5	15
59	Genomics of <i>C</i> ompositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	2.2	45
60	Genome skimming reveals the origin of the Jerusalem Artichoke tuber crop species: neither from Jerusalem nor an artichoke. <i>New Phytologist</i> , 2014, 201, 1021-1030.	3.5	151
61	Editorial 2014. <i>Molecular Ecology</i> , 2014, 23, 1-15.	2.0	1
62	The genomics of adaptation, divergence and speciation: a congealing theory. <i>Molecular Ecology</i> , 2014, 23, 3938-3940.	2.0	7
63	Transposon fingerprinting using low coverage whole genome shotgun sequencing in Cacao (<i>Theobroma cacao</i> L.) and related species. <i>BMC Genomics</i> , 2013, 14, 502.	1.2	15
64	Complex origin of Trinitario-type <i>Theobroma cacao</i> (Malvaceae) from Trinidad and Tobago revealed using plastid genomics. <i>Tree Genetics and Genomes</i> , 2013, 9, 829-840.	0.6	18
65	The repetitive component of the sunflower genome as shown by different procedures for assembling next generation sequencing reads. <i>BMC Genomics</i> , 2013, 14, 686.	1.2	52
66	Sunflower genetic, genomic and ecological resources. <i>Molecular Ecology Resources</i> , 2013, 13, 10-20.	2.2	59
67	Recent nonhybrid origin of sunflower ecotypes in a novel habitat. <i>Molecular Ecology</i> , 2013, 22, 799-813.	2.0	47
68	Editorial 2013. <i>Molecular Ecology</i> , 2013, 22, 1-14.	2.0	1
69	A road map for molecular ecology. <i>Molecular Ecology</i> , 2013, 22, 2605-2626.	2.0	100
70	RNA-Seq Analysis of Allele-Specific Expression, Hybrid Effects, and Regulatory Divergence in Hybrids Compared with Their Parents from Natural Populations. <i>Genome Biology and Evolution</i> , 2013, 5, 1309-1323.	1.1	131
71	Mandated data archiving greatly improves access to research data. <i>FASEB Journal</i> , 2013, 27, 1304-1308.	0.2	139
72	Ultra-barcoding in cacao (<i>Theobroma</i> spp.; Malvaceae) using whole chloroplast genomes and nuclear ribosomal DNA. <i>American Journal of Botany</i> , 2012, 99, 320-329.	0.8	228

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73	Recommendations for utilizing and reporting population genetic analyses: the reproducibility of genetic clustering using the program <sc>structure</sc>. <i>Molecular Ecology</i> , 2012, 21, 4925-4930.	2.0	236
74	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.	2.8	88
75	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	0.8	80
76	Preparation of Normalized cDNA Libraries for 454 Titanium Transcriptome Sequencing. <i>Methods in Molecular Biology</i> , 2012, 888, 119-133.	0.4	12
77	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. <i>Biology</i> , 2012, 1, 575-596.	1.3	34
78	Editorial 2012. <i>Molecular Ecology</i> , 2012, 21, 1-22.	2.0	14
79	REDUCED DROUGHT TOLERANCE DURING DOMESTICATION AND THE EVOLUTION OF WEEDINESS RESULTS FROM TOLERANCE-GROWTH TRADE-OFFS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3803-3814.	1.1	80
80	Editorial - 20 years of <i>Molecular Ecology</i> . <i>Molecular Ecology</i> , 2011, 20, 1-21.	2.0	8
81	Increased growth in sunflower correlates with reduced defences and altered gene expression in response to biotic and abiotic stress. <i>Molecular Ecology</i> , 2011, 20, 4683-4694.	2.0	68
82	Effective Population Size Is Positively Correlated with Levels of Adaptive Divergence among Annual Sunflowers. <i>Molecular Biology and Evolution</i> , 2011, 28, 1569-1580.	3.5	88
83	Sunflower domestication alleles support single domestication center in eastern North America. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14360-14365.	3.3	97
84	Molecular Evolution across the Asteraceae: Micro- and Macroevolutionary Processes. <i>Molecular Biology and Evolution</i> , 2011, 28, 3225-3235.	3.5	19
85	Editorial and retrospective 2010. <i>Molecular Ecology</i> , 2010, 19, 1-22.	2.0	11
86	The genetics of adaptation to novel environments: selection on germination timing in <i>Arabidopsis thaliana</i> . <i>Molecular Ecology</i> , 2010, 19, 1270-1272.	2.0	6
87	Pushing north one bottleneck at a time: site frequency spectra tell the history of Sitka spruce. <i>Molecular Ecology</i> , 2010, 19, 3837-3839.	2.0	0
88	EvoPipes.net: Bioinformatic Tools for Ecological and Evolutionary Genomics. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5861.	0.6	83
89	Establishing genomic tools and resources for <i>Guizotia abyssinica</i> (L.f.) Cass. the development of a library of expressed sequence tags, microsatellite loci, and the sequencing of its chloroplast genome. <i>Molecular Ecology Resources</i> , 2010, 10, 1048-1058.	2.2	52
90	Editorial and retrospective 2008. <i>Molecular Ecology</i> , 2009, 18, 1-13.	2.0	16

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91	Using parentage analysis to examine gene flow and spatial genetic structure. <i>Molecular Ecology</i> , 2009, 18, 1551-1552.	2.0	6
92	Plant genomes do a balancing act. <i>Molecular Ecology</i> , 2009, 18, 2743-2745.	2.0	3
93	COMPARATIVE GENOMIC AND POPULATION GENETIC ANALYSES INDICATE HIGHLY POROUS GENOMES AND HIGH LEVELS OF GENE FLOW BETWEEN DIVERGENT <i>HELIANTHUS</i> SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2061-2075.	1.1	107
94	Genetics and evolution of weedy <i>Helianthus annuus</i> populations: adaptation of an agricultural weed. <i>Molecular Ecology</i> , 2008, 17, 384-394.	2.0	74
95	Botany without borders: barcoding in focus. <i>Molecular Ecology</i> , 2008, 17, 5175-5176.	2.0	54
96	Natural Variation in Gene Expression Between Wild and Weedy Populations of <i>Helianthus annuus</i> . <i>Genetics</i> , 2008, 179, 1881-1890.	1.2	64
97	Multiple Paleopolyploidizations during the Evolution of the Compositae Reveal Parallel Patterns of Duplicate Gene Retention after Millions of Years. <i>Molecular Biology and Evolution</i> , 2008, 25, 2445-2455.	3.5	322
98	Selective Sweeps Reveal Candidate Genes for Adaptation to Drought and Salt Tolerance in Common Sunflower, <i>Helianthus annuus</i> . <i>Genetics</i> , 2007, 175, 1823-1834.	1.2	112
99	Rampant Gene Exchange Across a Strong Reproductive Barrier Between the Annual Sunflowers, <i>Helianthus annuus</i> and <i>H. petiolaris</i> . <i>Genetics</i> , 2007, 175, 1883-1893.	1.2	154
100	The origins of weedy rice. <i>Molecular Ecology</i> , 2007, 16, 4423-4425.	2.0	17
101	Maize Genetics: The Treasure of the Sierra Madre. <i>Current Biology</i> , 2005, 15, R137-R139.	1.8	1
102	Frequency and Microenvironmental Pattern of Selection on Plastic Shade Avoidance Traits in a Natural Population of <i>Impatiens capensis</i> . <i>American Naturalist</i> , 2004, 163, 548-563.	1.0	92
103	SELECTION ON LEAF ECOPHYSIOLOGICAL TRAITS IN A DESERT HYBRID <i>HELIANTHUS</i> SPECIES AND EARLY-GENERATION HYBRIDS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2682.	1.1	9
104	TESTING ADAPTIVE PLASTICITY TO UV: COSTS AND BENEFITS OF STEM ELONGATION AND LIGHT-INDUCED PHENOLICS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2645.	1.1	2
105	Reconstructing the Origin of <i>Helianthus deserticola</i> : Survival and Selection on the Desert Floor. <i>American Naturalist</i> , 2004, 164, 145-156.	1.0	64
106	TESTING ADAPTIVE PLASTICITY TO UV: COSTS AND BENEFITS OF STEM ELONGATION AND LIGHT-INDUCED PHENOLICS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2645-2656.	1.1	40
107	SELECTION ON LEAF ECOPHYSIOLOGICAL TRAITS IN A DESERT HYBRID <i>HELIANTHUS</i> SPECIES AND EARLY-GENERATION HYBRIDS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2682-2692.	1.1	74
108	Heterogeneous Selection at Specific Loci in Natural Environments in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2003, 165, 321-329.	1.2	119

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109	Novel Loci Control Variation in Reproductive Timing in <i>Arabidopsis thaliana</i> in Natural Environments. <i>Genetics</i> , 2002, 162, 1875-1884.	1.2	144
110	Empirical test of increasing genetic variation via interpopulation crossing for native plant restoration in variable environments. <i>Restoration Ecology</i> , 0, , .	1.4	1