

# Kenneth L McNally

## List of Publications by Year in descending order

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85  
papers

7,480  
citations

87723

38  
h-index

58464

82  
g-index

93  
all docs

93  
docs citations

93  
times ranked

7203  
citing authors

#	ARTICLE	IF	CITATIONS
1	Aus rice root architecture variation contributing to grain yield under drought suggests a key role of nodal root diameter class. <i>Plant, Cell and Environment</i> , 2022, 45, 854-870.	2.8	10
2	State of ex situ conservation of landrace groups of 25 major crops. <i>Nature Plants</i> , 2022, 8, 491-499.	4.7	21
3	Phenotypic response of farmer-selected CWR-derived rice lines to salt stress in the Mekong Delta. <i>Crop Science</i> , 2021, 61, 201-218.	0.8	10
4	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. <i>Crop Science</i> , 2021, 61, 1538-1566.	0.8	26
5	Novel Sources of Pre-Harvest Sprouting Resistance for Japonica Rice Improvement. <i>Plants</i> , 2021, 10, 1709.	1.6	11
6	Editorial: Reproductive Barriers and Gene Introgression in Rice Species. <i>Frontiers in Plant Science</i> , 2021, 12, 699761.	1.7	2
7	Towards a deeper haplotype mining of complex traits in rice with <code>scp&gt;RFGB&lt;/scp&gt; v2.0. <i>Plant Biotechnology Journal</i>, 2020, 18, 14-16.</code>	4.1	78
8	Mass genome sequencing of crops and wild relatives to accelerate crop breeding: the digital rice genebank. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 482, 012005.	0.2	1
9	Advanced Strategic Research to Promote the Use of Rice Genetic Resources. <i>Agronomy</i> , 2020, 10, 1629.	1.3	7
10	Genetic erosion in traditional rice agro-ecosystems in Southern Philippines: drivers and consequences. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 1-10.	0.4	7
11	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	86
12	Upland Rice: Cultural Keystone Species in a Philippine Traditional Agroecosystem. <i>Asian Journal of Agriculture and Development</i> , 2020, 17, 93-105.	0.1	6
13	Variation in seed longevity among diverse Indica rice varieties. <i>Annals of Botany</i> , 2019, 124, 447-460.	1.4	45
14	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	2.4	112
15	Fine Scale Genomic Signals of Admixture and Alien Introgression among Asian Rice Landraces. <i>Genome Biology and Evolution</i> , 2019, 11, 1358-1373.	1.1	32
16	Traditional agro-ecosystems in Southern Philippines. <i>International Journal of Disaster Resilience in the Built Environment</i> , 2019, 10, 289-300.	0.7	3
17	Leaf morphology, rather than plant water status, underlies genetic variation of rice leaf rolling under drought. <i>Plant, Cell and Environment</i> , 2019, 42, 1532-1544.	2.8	67
18	Genetic diversity, linkage disequilibrium, and population structure in a panel of Brazilian rice accessions. <i>Journal of Applied Genetics</i> , 2019, 60, 27-31.	1.0	4

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19	Progress in single-access information systems for wheat and rice crop improvement. Briefings in Bioinformatics, 2019, 20, 565-571.	3.2	4
20	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. Nature, 2018, 557, 43-49.	13.7	1,091
21	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . Nature Genetics, 2018, 50, 285-296.	9.4	413
22	Genome Wide Association Mapping of Grain and Straw Biomass Traits in the Rice Bengal and Assam Aus Panel (BAAP) Grown Under Alternate Wetting and Drying and Permanently Flooded Irrigation. Frontiers in Plant Science, 2018, 9, 1223.	1.7	41
23	An imputation platform to enhance integration of rice genetic resources. Nature Communications, 2018, 9, 3519.	5.8	65
24	Genetic diversity patterns in ex situ collections of <i>Oryza officinalis</i> Wall. ex G. Watt revealed by morphological and microsatellite markers. Genetic Resources and Crop Evolution, 2017, 64, 733-744.	0.8	3
25	Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. Scientific Reports, 2017, 7, 42839.	1.6	74
26	Rice SNP-seek database update: new SNPs, indels, and queries. Nucleic Acids Research, 2017, 45, D1075-D1081.	6.5	290
27	Genetic Loci Governing Grain Yield and Root Development under Variable Rice Cultivation Conditions. Frontiers in Plant Science, 2017, 8, 1763.	1.7	30
28	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . Current Plant Biology, 2016, 7-8, 16-25.	2.3	48
29	Open access resources for genome-wide association mapping in rice. Nature Communications, 2016, 7, 10532.	5.8	371
30	Nucleotide diversity analysis highlights functionally important genomic regions. Scientific Reports, 2016, 6, 35730.	1.6	48
31	Identification of stable QTLs causing chalk in rice grains in nine environments. Theoretical and Applied Genetics, 2016, 129, 141-153.	1.8	54
32	Environmental Response and Genomic Regions Correlated with Rice Root Growth and Yield under Drought in the <i>Oryza</i> SNP Panel across Multiple Study Systems. PLoS ONE, 2015, 10, e0124127.	1.1	24
33	Assessing the genetic diversity of rice originating from Bangladesh, Assam and West Bengal. Rice, 2015, 8, 35.	1.7	63
34	Cell Wall Composition and Bioenergy Potential of Rice Straw Tissues Are Influenced by Environment, Tissue Type, and Genotype. Bioenergy Research, 2015, 8, 1165-1182.	2.2	13
35	SNP-Seek database of SNPs derived from 3000 rice genomes. Nucleic Acids Research, 2015, 43, D1023-D1027.	6.5	357
36	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. Chinese Science Bulletin, 2015, 60, 367-371.	0.4	31

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37	Allele mining and enhanced genetic recombination for rice breeding. <i>Rice</i> , 2015, 8, 34.	1.7	57
38	The 3,000 rice genomes project. <i>GigaScience</i> , 2014, 3, 7.	3.3	451
39	Exploring 'omics' of genetic resources to mitigate the effects of climate change.. , 2014, , 166-189.		0
40	New allelic variants found in key rice salt tolerance genes: an association study. <i>Plant Biotechnology Journal</i> , 2013, 11, 87-100.	4.1	120
41	Screening of rice Genebank germplasm for yield and selection of new drought tolerance donors. <i>Field Crops Research</i> , 2013, 147, 12-22.	2.3	41
42	Crossability patterns within and among <i>Oryza</i> series <i>Sativae</i> species from Asia and Australia. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1899-1914.	0.8	24
43	Ecogeographic Variation in the Morphology of Two Asian Wild Rice Species, <i>Oryza nivara</i> and <i>Oryza rufipogon</i> . <i>International Journal of Plant Sciences</i> , 2013, 174, 896-909.	0.6	13
44	Alternate wetting and drying irrigation for rice in Bangladesh: Is it sustainable and has plant breeding something to offer?. <i>Food and Energy Security</i> , 2013, 2, 120-129.	2.0	74
45	Local differentiation amidst extensive allele sharing in <i>Oryza nivara</i> and <i>Oryza rufipogon</i> . <i>Ecology and Evolution</i> , 2013, 3, 3047-3062.	0.8	14
46	Genomics of gene banks: A case study in rice. <i>American Journal of Botany</i> , 2012, 99, 407-423.	0.8	152
47	High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. <i>Molecular Breeding</i> , 2012, 29, 875-886.	1.0	139
48	Developmental Dynamics and Early Growth Vigour in Rice. Relationship Between Development Rate (1/Phyllochron) and Growth. <i>Journal of Agronomy and Crop Science</i> , 2012, 198, 374-384.	1.7	22
49	Genetic Variation in Biomass Traits among 20 Diverse Rice Varieties. <i>Plant Physiology</i> , 2011, 155, 157-168.	2.3	96
50	Use of EcoTILLING to identify natural allelic variants of rice candidate genes involved in salinity tolerance. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 300-304.	0.4	19
51	Variation in root system architecture and drought response in rice ( <i>Oryza sativa</i> ): Phenotyping of the OryzaSNP panel in rainfed lowland fields. <i>Field Crops Research</i> , 2011, 120, 205-214.	2.3	261
52	Identification of SUB1A alleles from wild rice <i>Oryza rufipogon</i> Griff.. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 1237-1242.	0.8	13
53	Drought Resistance Improvement in Rice: An Integrated Genetic and Resource Management Strategy. <i>Plant Production Science</i> , 2011, 14, 1-14.	0.9	192
54	Structure, allelic diversity and selection of Asr genes, candidate for drought tolerance, in <i>Oryza sativa</i> L. and wild relatives. <i>Theoretical and Applied Genetics</i> , 2010, 121, 769-787.	1.8	68

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55	Development of a Research Platform for Dissecting Phenotype-Genotype Associations in Rice ( <i>Oryza</i> ) Using QTL Mapping and GWAS. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 1116-1125.	1.7	75
56	Migration, isolation and hybridization in island crop populations: the case of Madagascar rice. <i>Molecular Ecology</i> , 2010, 19, 4892-4905.	2.0	47
57	Characterizing genetic diversity and creating novel gene pools in rice for trait dissection and gene function discovery. <i>Nature Precedings</i> , 2010, , .	0.1	0
58	Development of a Core Set from a Large Rice Collection using a Modified Heuristic Algorithm to Retain Maximum Diversity. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 1116-1125.	4.1	16
59	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12273-12278.	3.3	581
60	Improvement of Drought Resistance in Rice. <i>Advances in Agronomy</i> , 2009, , 41-99.	2.4	122
61	Isolation and sequence analysis of DREB2A homologues in three cereal and two legume species. <i>Plant Science</i> , 2009, 177, 460-467.	1.7	33
62	SNP discovery at candidate genes for drought responsiveness in rice. , 2009, , 311-324.		1
63	Revealing sequence variation patterns in rice with machine learning methods. <i>BMC Bioinformatics</i> , 2008, 9, .	1.2	1
64	Rice Molecular Breeding Laboratories in the Genomics Era: Current Status and Future Considerations. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-25.	2.2	68
65	Chemical- and Irradiation-Induced Mutants and TILLING. , 2007, , 148-180.		13
66	Rapid method for detecting SNPs on agarose gels and its application in candidate gene mapping. <i>Molecular Breeding</i> , 2007, 19, 87-101.	1.0	85
67	Fertility in an interspecific rice population and its effect on selection for rhizome length. <i>Field Crops Research</i> , 2006, 95, 30-38.	2.3	7
68	Genetic diversity and phylogenetic relationship in AA <i>Oryza</i> species as revealed by Rim2/Hipa CACTA transposon display. <i>Genes and Genetic Systems</i> , 2006, 81, 93-101.	0.2	28
69	A High-throughput Genomic Tool: Diversity Array Technology Complementary for Rice Genotyping. <i>Journal of Integrative Plant Biology</i> , 2006, 48, 1069-1076.	4.1	25
70	Sequencing Multiple and Diverse Rice Varieties. Connecting Whole-Genome Variation with Phenotypes. <i>Plant Physiology</i> , 2006, 141, 26-31.	2.3	84
71	Linking genotype to phenotype: the International Rice Information System (IRIS). <i>Bioinformatics</i> , 2003, 19, i63-i65.	1.8	38
72	Convergent evolution of perenniality in rice and sorghum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4050-4054.	3.3	196

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73	Evaluation of near-isogenic lines of rice introgressed with QTLs for root depth through marker-aided selection. <i>Theoretical and Applied Genetics</i> , 2001, 103, 75-83.	1.8	192
74	Genetic composition and complexity of virus populations at tungro-endemic and outbreak rice sites. <i>Archives of Virology</i> , 2000, 145, 2643-2657.	0.9	14
75	Genetic diversity of rice tungro spherical virus in tungro-endemic provinces of the Philippines and Indonesia. <i>Archives of Virology</i> , 2000, 145, 1183-1197.	0.9	27
76	Use of introgression lines and zonal mapping to identify RAPD markers linked to QTL. <i>Molecular Breeding</i> , 1997, 3, 203-212.	1.0	10
77	SMALL-SUBUNIT RIBOSOMAL DNA SEQUENCE ANALYSES AND A RECONSTRUCTION OF THE INFERRED PHYLOGENY AMONG SYMBIOTIC DINOFLAGELLATES (PYRRROPHYTA)1. <i>Journal of Phycology</i> , 1994, 30, 316-329.	1.0	93
78	The nucleotide sequence of the small subunit ribosomal RNA gene from <i>Symbiodinium pilosum</i> , a symbiotic dinoflagellate. <i>Current Genetics</i> , 1992, 21, 409-416.	0.8	42
79	Isolation and sequence analysis of the small subunit ribosomal RNA gene from the euryhaline yeast <i>Debaryomyces hansenii</i> . <i>Current Genetics</i> , 1992, 22, 191-195.	0.8	10
80	The complete DNA sequence of the mitochondrial genome of <i>Podospora anserina</i> . <i>Current Genetics</i> , 1990, 17, 375-402.	0.8	215
81	DNA sequence analysis of the mitochondrial ND4L-ND5 gene complex from <i>Podospora anserina</i> . <i>Journal of Molecular Biology</i> , 1990, 212, 269-286.	2.0	24
82	Mitochondrial DNA sequence analysis of the cytochrome oxidase subunit II gene from <i>Podospora anserina</i> . <i>Journal of Molecular Biology</i> , 1990, 212, 287-294.	2.0	5
83	DNA sequence analysis of the 24.5 Kilobase pair cytochrome oxidase subunit I mitochondrial gene from <i>Podospora anserina</i> : a gene with sixteen introns. <i>Current Genetics</i> , 1989, 16, 381-406.	0.8	56
84	DNA sequence analysis of the apocytochrome b gene of <i>Podospora anserina</i> : a new family of intronic open reading frame. <i>Current Genetics</i> , 1989, 16, 407-418.	0.8	31
85	Phenotypic Variation and the Impact of Admixture in the <i>Oryza rufipogon</i> Species Complex (ORSC). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5