

Nevin Dale Young

List of Publications by Year in descending order

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91
papers

10,846
citations

36303

51
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45317

90
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docs citations

94
times ranked

9636
citing authors

#	ARTICLE	IF	CITATIONS
1	Alfalfa (<i>Medicago sativa</i> L.) <i>pho2</i> mutant plants hyperaccumulate phosphate. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	10
2	The antagonistic MYB paralogs <i>RH1</i> and <i>RH2</i> govern anthocyanin leaf markings in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2021, 229, 3330-3344.	7.3	18
3	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	3.8	39
4	Genome-wide association study and genomic selection for tolerance of soybean biomass to soybean cyst nematode infestation. <i>PLoS ONE</i> , 2020, 15, e0235089.	2.5	28
5	A Select and Resequence Approach Reveals Strain-Specific Effects of <i>Medicago</i> Nodule-Specific PLAT-Domain Genes. <i>Plant Physiology</i> , 2020, 182, 463-471.	4.8	13
6	Nodule-specific PLAT domain proteins are expanded in the <i>Medicago</i> lineage and required for nodulation. <i>New Phytologist</i> , 2019, 222, 1538-1550.	7.3	25
7	Genome-wide association study and genomic selection for soybean chlorophyll content associated with soybean cyst nematode tolerance. <i>BMC Genomics</i> , 2019, 20, 904.	2.8	29
8	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
9	Select and resequence reveals relative fitness of bacteria in symbiotic and free-living environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2425-2430.	7.1	88
10	Complete Genome Sequence of <i>Sinorhizobium meliloti</i> Bacteriophage HMSP1-Susan. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
11	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. <i>Plant Physiology</i> , 2017, 173, 921-931.	4.8	71
12	A Guide to Genome-Wide Association Mapping in Plants. <i>Current Protocols in Plant Biology</i> , 2017, 2, 22-38.	2.8	75
13	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. <i>BMC Genomics</i> , 2017, 18, 261.	2.8	87
14	Genome-wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. <i>New Phytologist</i> , 2017, 214, 1597-1613.	7.3	38
15	Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. <i>Molecular Ecology</i> , 2017, 26, 6122-6135.	3.9	40
16	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	2.8	54
17	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
18	Adaptation to climate through flowering phenology: a case study in <i>Medicago truncatula</i> . <i>Molecular Ecology</i> , 2016, 25, 3397-3415.	3.9	36

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19	Exploring structural variants in environmentally sensitive gene families. <i>Current Opinion in Plant Biology</i> , 2016, 30, 19-24.	7.1	9
20	An Alternative Approach to "Identification of Unknowns": Designing a Protocol to Verify the Identities of Nitrogen Fixing Bacteria. <i>Journal of Microbiology and Biology Education</i> , 2015, 16, 247-253.	1.0	12
21	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 269.	3.6	37
22	Association mapping and genomic prediction for resistance to sudden death syndrome in early maturing soybean germplasm. <i>Molecular Breeding</i> , 2015, 35, 128.	2.1	52
23	Genomic Signature of Selective Sweeps Illuminates Adaptation of <i>Medicago truncatula</i> to Root-Associated Microorganisms. <i>Molecular Biology and Evolution</i> , 2015, 32, 2097-2110.	8.9	51
24	Genome-wide association of drought-related and biomass traits with HapMap SNPs in <i>Medicago truncatula</i> . <i>Plant, Cell and Environment</i> , 2015, 38, 1997-2011.	5.7	69
25	Potential of Association Mapping and Genomic Selection to Explore PI 88788 Derived Soybean Cyst Nematode Resistance. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0039.	2.8	63
26	Genomic Characterization of the LEED..PEEDs, a Gene Family Unique to the <i>Medicago</i> Lineage. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2003-2012.	1.8	15
27	Patterns of divergence of a large family of nodule cysteine-rich peptides in accessions of <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2014, 78, 697-705.	5.7	38
28	High-density genome-wide association mapping implicates an <i>F-box</i> encoding gene in <i>Medicago truncatula</i> resistance to <i>Aphanomyces euteiches</i> . <i>New Phytologist</i> , 2014, 201, 1328-1342.	7.3	86
29	Genomic Signature of Adaptation to Climate in <i>Medicago truncatula</i> . <i>Genetics</i> , 2014, 196, 1263-1275.	2.9	160
30	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	9.6	164
31	Selection, genome-wide fitness effects and evolutionary rates in the model legume <i>Medicago truncatula</i> . <i>Molecular Ecology</i> , 2013, 22, 3525-3538.	3.9	54
32	Phylogenetic Signal Variation in the Genomes of <i>Medicago</i> (Fabaceae). <i>Systematic Biology</i> , 2013, 62, 424-438.	5.6	51
33	Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). <i>BMC Bioinformatics</i> , 2013, 14, 335.	2.6	86
34	Estimating heritability using genomic data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 1151-1158.	5.2	54
35	Candidate Genes and Genetic Architecture of Symbiotic and Agronomic Traits Revealed by Whole-Genome, Sequence-Based Association Genetics in <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2013, 8, e65688.	2.5	156
36	Fine-Scale Population Recombination Rates, Hotspots, and Correlates of Recombination in the <i>Medicago truncatula</i> Genome. <i>Genome Biology and Evolution</i> , 2012, 4, 726-737.	2.5	62

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37	Evolution of a Complex Disease Resistance Gene Cluster in Diploid <i>Phaseolus</i> and Tetraploid <i>Glycine</i> . <i>Plant Physiology</i> , 2012, 159, 336-354.	4.8	76
38	Genome-Enabled Insights into Legume Biology. <i>Annual Review of Plant Biology</i> , 2012, 63, 283-305.	18.7	79
39	Population Genomics of the Facultatively Mutualistic Bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002868.	3.5	69
40	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E864-70.	7.1	220
41	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
42	Translating <i>Medicago truncatula</i> genomics to crop legumes. <i>Current Opinion in Plant Biology</i> , 2009, 12, 193-201.	7.1	171
43	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. <i>Theoretical and Applied Genetics</i> , 2008, 116, 945-952.	3.6	210
44	Cross-species EST alignments reveal novel and conserved alternative splicing events in legumes. <i>BMC Plant Biology</i> , 2008, 8, 17.	3.6	49
45	Transcriptional analysis of highly syntenic regions between <i>Medicago truncatula</i> and <i>Glycine max</i> using tiling microarrays. <i>Genome Biology</i> , 2008, 9, R57.	9.6	13
46	Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean. <i>Plant Physiology</i> , 2008, 148, 1740-1759.	4.8	140
47	Replication of Nonautonomous Retroelements in Soybean Appears to Be Both Recent and Common. <i>Plant Physiology</i> , 2008, 148, 1760-1771.	4.8	57
48	Identification and Characterization of Nucleotide-Binding Site-Leucine-Rich Repeat Genes in the Model Plant <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2008, 146, 5-21.	4.8	295
49	Genetic Dissection of Resistance to Anthracnose and Powdery Mildew in <i>Medicago truncatula</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 61-69.	2.6	55
50	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	285
51	Construction, characterization, and preliminary BAC-end sequencing analysis of a bacterial artificial chromosome library of white clover (<i>Trifolium repens</i> L.). <i>Genome</i> , 2007, 50, 412-421.	2.0	18
52	Molecular and cytological responses of <i>Medicago truncatula</i> to <i>Erysiphe pisi</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 307-319.	4.2	58
53	Genome studies and molecular genetics. <i>Current Opinion in Plant Biology</i> , 2006, 9, 95-98.	7.1	9
54	Distribution of Microsatellites in the Genome of <i>Medicago truncatula</i> : A Resource of Genetic Markers That Integrate Genetic and Physical Maps. <i>Genetics</i> , 2006, 172, 2541-2555.	2.9	164

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55	Chromosome-Level Homeology in Paleopolyploid Soybean (<i>Glycine max</i>) Revealed Through Integration of Genetic and Chromosome Maps. <i>Genetics</i> , 2006, 172, 1893-1900.	2.9	68
56	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	7.1	286
57	Highly syntenic regions in the genomes of soybean, <i>Medicago truncatula</i> , and <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2005, 5, 15.	3.6	86
58	Pericentromeric Regions of Soybean (<i>Glycine max</i> L. Merr.) Chromosomes Consist of Retroelements and Tandemly Repeated DNA and Are Structurally and Evolutionarily Labile. <i>Genetics</i> , 2005, 170, 1221-1230.	2.9	53
59	Sequencing the Genespaces of <i>Medicago truncatula</i> and <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2005, 137, 1174-1181.	4.8	243
60	Databases and Information Integration for the <i>Medicago truncatula</i> Genome and Transcriptome. <i>Plant Physiology</i> , 2005, 138, 38-46.	4.8	59
61	Effect of the <i>rhg1</i> gene on penetration, development and reproduction of <i>Heterodera glycines</i> race 3. <i>Nematology</i> , 2004, 6, 729-736.	0.6	11
62	Soybean bacterial artificial chromosome contigs anchored with RFLPs: insights into genome duplication and gene clustering. <i>Genome</i> , 2004, 47, 361-372.	2.0	25
63	Estimating genome conservation between crop and model legume species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15289-15294.	7.1	416
64	The roles of segmental and tandem gene duplication in the evolution of large gene families in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2004, 4, 10.	3.6	1,523
65	Segmental duplications within the <i>Glycine max</i> genome revealed by fluorescence in situ hybridization of bacterial artificial chromosomes. <i>Genome</i> , 2004, 47, 764-768.	2.0	57
66	Comparative Genomics of <i>Glycine max</i> , <i>Medicago truncatula</i> , Other Legumes, and <i>Arabidopsis thaliana</i> . , 2004, , .		0
67	Estimates of conserved microsynteny among the genomes of <i>Glycine max</i> , <i>Medicago truncatula</i> and <i>Arabidopsis thaliana</i> . <i>Theoretical and Applied Genetics</i> , 2003, 106, 1256-1265.	3.6	68
68	Legume genomes: more than peas in a pod. <i>Current Opinion in Plant Biology</i> , 2003, 6, 199-204.	7.1	142
69	OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. <i>BMC Bioinformatics</i> , 2003, 4, 35.	2.6	56
70	DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale homology discovery and visualization. <i>Genome Biology</i> , 2003, 4, R68.	9.6	52
71	MtDB: a database for personalized data mining of the model legume <i>Medicago truncatula</i> transcriptome. <i>Nucleic Acids Research</i> , 2003, 31, 196-201.	14.5	61
72	Genetic and Physical Localization of the Soybean <i>Rpg1-b</i> Disease Resistance Gene Reveals a Complex Locus Containing Several Tightly Linked Families of NBS-LRR Genes. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 817-826.	2.6	77

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73	Phylogeny and Genomic Organization of the TIR and Non-TIR NBS-LRR Resistance Gene Family in <i>Medicago truncatula</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 529-539.	2.6	94
74	Comparative genomic analysis of sequences sampled from a small region on soybean (<i>Glycine</i>) Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50	2.0	43
75	Diversity, Distribution, and Ancient Taxonomic Relationships Within the TIR and Non-TIR NBS-LRR Resistance Gene Subfamilies. <i>Journal of Molecular Evolution</i> , 2002, 54, 548-562.	1.8	126
76	Constructing a plant genetic linkage map with DNA markers. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 31-47.	0.2	5
77	Soybean genomic survey: BAC-end sequences near RFLP and SSR markers. <i>Genome</i> , 2001, 44, 572-581.	2.0	66
78	Differential Regulation of a Family of Apyrase Genes from <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2001, 125, 2104-2119.	4.8	48
79	Differential Expression of Two Soybean Apyrases, One of Which Is an Early Nodulin. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 1053-1070.	2.6	73
80	The genetic architecture of resistance. <i>Current Opinion in Plant Biology</i> , 2000, 3, 285-290.	7.1	162
81	A cautiously optimistic vision for marker-assisted breeding. <i>Molecular Breeding</i> , 1999, 5, 505-510.	2.1	234
82	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. <i>Plant Journal</i> , 1999, 20, 317-332.	5.7	729
83	Genome Mapping of Soybean Cyst Nematode Resistance Genes in "Peking"™, PI 90763, and PI 88788 Using DNA Markers. <i>Crop Science</i> , 1997, 37, 258-264.	1.8	144
84	Constructing a plant genetic linkage map with DNA markers. <i>Advances in Cellular and Molecular Biology of Plants</i> , 1994, , 39-57.	0.2	46
85	Applications of DNA genetic markers to the study of plant growth and development. <i>Plant Growth Regulation</i> , 1993, 12, 229-236.	3.4	4
86	Restriction Fragment Length Polymorphisms (RFLPS) and Crop Improvement. <i>Experimental Agriculture</i> , 1992, 28, 385-398.	0.9	11
87	Potential applications of map-based cloning to plant pathology. <i>Physiological and Molecular Plant Pathology</i> , 1990, 37, 81-94.	2.5	29
88	Pulsed field gel electrophoresis and physical mapping of large DNA fragments in the Tm-2a region of chromosome 9 in tomato. <i>Molecular Genetics and Genomics</i> , 1989, 215, 395-400.	2.4	134
89	Rapid chromosomal assignment of multiple genomic clones in tomato using primary trisomics. <i>Nucleic Acids Research</i> , 1987, 15, 9339-9348.	14.5	50
90	Physiological Control of Arginine Decarboxylase Activity in K-Deficient Oat Shoots. <i>Plant Physiology</i> , 1984, 76, 331-335.	4.8	74

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91	Putrescine and Acid Stress. <i>Plant Physiology</i> , 1983, 71, 767-771.	4.8	158