Nevin Dale Young

List of Publications by Year
in descending order

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91 papers	10,846 citations	36203 51 h-index	45213 90 g-index
94 all docs	94 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. G3: Genes, Genomes, Genetics, 2022, , .	0.8	10
2	The antagonistic MYB paralogs <i>RH1</i> and <i>RH2</i> govern anthocyanin leaf markings in <i>Medicago truncatula</i>. New Phytologist, 2021, 229, 3330-3344.	3.5	18
3	The genome of a wild Medicago species provides insights into the tolerant mechanisms of legume forage to environmental stress. BMC Biology, 2021, 19, 96.	1.7	39
4	Genome-wide association study and genomic selection for tolerance of soybean biomass to soybean cyst nematode infestation. PLoS ONE, 2020, 15, e0235089.	1.1	28
5	A Select and Resequence Approach Reveals Strain-Specific Effects of <i>Medicago</i> Nodule-Specific PLAT-Domain Genes. Plant Physiology, 2020, 182, 463-471.	2.3	13
6	Noduleâ€specific PLAT domain proteins are expanded in the <i>Medicago</i> lineage and required for nodulation. New Phytologist, 2019, 222, 1538-1550.	3.5	25
7	Genome-wide association study and genomic selection for soybean chlorophyll content associated with soybean cyst nematode tolerance. BMC Genomics, 2019, 20, 904.	1.2	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. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2425-2430.	3.3	88
10	Complete Genome Sequence of Sinorhizobium meliloti Bacteriophage HMSP1-Susan. Genome Announcements, 2018, 6, .	0.8	2
11	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. Plant Physiology, 2017, 173, 921-931.	2.3	71
12	A Guide to Genomeâ€Wide Association Mapping in Plants. Current Protocols in Plant Biology, 2017, 2, 22-38.	2.8	75
13	Exploring structural variation and gene family architecture with De Novo assemblies of 15 Medicago genomes. BMC Genomics, 2017, 18, 261.	1.2	87
14	Genomeâ€wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. New Phytologist, 2017, 214, 1597-1613.	3.5	38
15	Transcriptomic basis of genome by genome variation in a legumeâ€rhizobia mutualism. Molecular Ecology, 2017, 26, 6122-6135.	2.0	40
16	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, Medicago truncatula. BMC Genomics, 2017, 18, 578.	1.2	54
17	Hybrid assembly with long and short reads improves discovery of gene family expansions. BMC Genomics, 2017, 18, 541.	1.2	51
18	Adaptation to climate through flowering phenology: a case study in <i>Medicago truncatula</i>. Molecular Ecology, 2016, 25, 3397-3415.	2.0	36

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19	Exploring structural variants in environmentally sensitive gene families. Current Opinion in Plant Biology, 2016, 30, 19-24.	3.5	9
20	An Alternative Approach to â€œIdentification of Unknownsâ€: Designing a Protocol to Verify the Identities of Nitrogen Fixing Bacteria. Journal of Microbiology and Biology Education, 2015, 16, 247-253.	0.5	12
21	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. Frontiers in Plant Science, 2015, 6, 269.	1.7	37
22	Association mapping and genomic prediction for resistance to sudden death syndrome in early maturing soybean germplasm. Molecular Breeding, 2015, 35, 128.	1.0	52
23	Genomic Signature of Selective Sweeps Illuminates Adaptation of<i>Medicago truncatula</i>to Root-Associated Microorganisms. Molecular Biology and Evolution, 2015, 32, 2097-2110.	3.5	51
24	Genomeâ€wide association of droughtâ€related and biomass traits with HapMap SNPs in <i>Medicago truncatula</i>. Plant, Cell and Environment, 2015, 38, 1997-2011.	2.8	69
25	Potential of Association Mapping and Genomic Selection to Explore PI 88788 Derived Soybean Cyst Nematode Resistance. Plant Genome, 2014, 7, plantgenome2013.11.0039.	1.6	63
26	Genomic Characterization of the LEED..PEEDs, a Gene Family Unique to the <i>Medicago</i> Lineage. G3: Genes, Genomes, Genetics, 2014, 4, 2003-2012.	0.8	15
27	Patterns of divergence of a large family of nodule cysteineâ€rich peptides in accessions of <i><scp>M</scp>edicago truncatula</i>. Plant Journal, 2014, 78, 697-705.	2.8	38
28	Highâ€density genomeâ€wide association mapping implicates an <scp>F</scp>â€box encoding gene in <i><scp>M</scp>edicago truncatula</i> resistance to <i><scp>A</scp>phanomyces euteiches</i>. New Phytologist, 2014, 201, 1328-1342.	3.5	86
29	Genomic Signature of Adaptation to Climate in <i>Medicago truncatula</i>. Genetics, 2014, 196, 1263-1275.	1.2	160
30	Comparative genomics of the core and accessory genomes of 48 Sinorhizobium strains comprising five genospecies. Genome Biology, 2013, 14, R17.	13.9	164
31	Selection, genomeâ€wide fitness effects and evolutionary rates in the model legume <i><scp>M</scp>edicago truncatula</i>. Molecular Ecology, 2013, 22, 3525-3538.	2.0	54
32	Phylogenetic Signal Variation in the Genomes of Medicago (Fabaceae). Systematic Biology, 2013, 62, 424-438.	2.7	51
33	Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). BMC Bioinformatics, 2013, 14, 335.	1.2	86
34	Estimating heritability using genomic data. Methods in Ecology and Evolution, 2013, 4, 1151-1158.	2.2	54
35	Candidate Genes and Genetic Architecture of Symbiotic and Agronomic Traits Revealed by Whole-Genome, Sequence-Based Association Genetics in Medicago truncatula. PLoS ONE, 2013, 8, e65688.	1.1	156
36	Fine-Scale Population Recombination Rates, Hotspots, and Correlates of Recombination in the Medicago truncatula Genome. Genome Biology and Evolution, 2012, 4, 726-737.	1.1	62

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37	Evolution of a Complex Disease Resistance Gene Cluster in Diploid<i>Phaseolus</i>and Tetraploid<i>Glycine</i>Â Â Â. Plant Physiology, 2012, 159, 336-354.	2.3	76
38	Genome-Enabled Insights into Legume Biology. Annual Review of Plant Biology, 2012, 63, 283-305.	8.6	79
39	Population Genomics of the Facultatively Mutualistic Bacteria Sinorhizobium meliloti and S. medicae. PLoS Genetics, 2012, 8, e1002868.	1.5	69
40	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E864-70.	3.3	220
41	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	13.7	1,166
42	Translating Medicago truncatula genomics to crop legumes. Current Opinion in Plant Biology, 2009, 12, 193-201.	3.5	171
43	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. Theoretical and Applied Genetics, 2008, 116, 945-952.	1.8	210
44	Cross-species EST alignments reveal novel and conserved alternative splicing events in legumes. BMC Plant Biology, 2008, 8, 17.	1.6	49
45	Transcriptional analysis of highly syntenic regions between Medicago truncatula and Glycine max using tiling microarrays. Genome Biology, 2008, 9, R57.	13.9	13
46	Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean Â. Plant Physiology, 2008, 148, 1740-1759.	2.3	140
47	Replication of Nonautonomous Retroelements in Soybean Appears to Be Both Recent and Common Â. Plant Physiology, 2008, 148, 1760-1771.	2.3	57
48	Identification and Characterization of Nucleotide-Binding Site-Leucine-Rich Repeat Genes in the Model Plant <i>Medicago truncatula</i> Â. Plant Physiology, 2008, 146, 5-21.	2.3	295
49	Genetic Dissection of Resistance to Anthracnose and Powdery Mildew in <i>Medicago truncatula</i>. Molecular Plant-Microbe Interactions, 2008, 21, 61-69.	1.4	55
50	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. Genetics, 2007, 176, 685-696.	1.2	285
51	Construction, characterization, and preliminary BAC-end sequencing analysis of a bacterial artificial chromosome library of white clover (Trifolium repens L.). Genome, 2007, 50, 412-421.	0.9	18
52	Molecular and cytological responses of Medicago truncatula to Erysiphe pisi. Molecular Plant Pathology, 2007, 8, 307-319.	2.0	58
53	Genome studies and molecular genetics. Current Opinion in Plant Biology, 2006, 9, 95-98.	3.5	9
54	Distribution of Microsatellites in the Genome of Medicago truncatula: A Resource of Genetic Markers That Integrate Genetic and Physical Maps. Genetics, 2006, 172, 2541-2555.	1.2	164

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55	Chromosome-Level Homeology in Paleopolyploid Soybean (Glycine max) Revealed Through Integration of Genetic and Chromosome Maps. Genetics, 2006, 172, 1893-1900.	1.2	68
56	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	3.3	286
57	Highly syntenic regions in the genomes of soybean, Medicago truncatula, and Arabidopsis thaliana. BMC Plant Biology, 2005, 5, 15.	1.6	86
58	Pericentromeric Regions of Soybean (Glycine max L. Merr.) Chromosomes Consist of Retroelements and Tandemly Repeated DNA and Are Structurally and Evolutionarily Labile. Genetics, 2005, 170, 1221-1230.	1.2	53
59	Sequencing the Genespaces of Medicago truncatula and Lotus japonicus: Figure 1.. Plant Physiology, 2005, 137, 1174-1181.	2.3	243
60	Databases and Information Integration for the Medicago truncatula Genome and Transcriptome. Plant Physiology, 2005, 138, 38-46.	2.3	59
61	Effect of the rhg1 gene on penetration, development and reproduction of Heterodera glycines race 3. Nematology, 2004, 6, 729-736.	0.2	11
62	Soybean bacterial artificial chromosome contigs anchored with RFLPs: insights into genome duplication and gene clustering. Genome, 2004, 47, 361-372.	0.9	25
63	Estimating genome conservation between crop and model legume species. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15289-15294.	3.3	416
64	The roles of segmental and tandem gene duplication in the evolution of large gene families in Arabidopsis thaliana. BMC Plant Biology, 2004, 4, 10.	1.6	1,523
65	Segmental duplications within the Glycine max genome revealed by fluorescence in situ hybridization of bacterial artificial chromosomes. Genome, 2004, 47, 764-768.	0.9	57
66	Comparative Genomics of Glycine max, Medicago truncatula, Other Legumes, and Arabidopsis thaliana. , 2004, , .		0
67	Estimates of conserved microsynteny among the genomes of Glycine max, Medicago truncatula and Arabidopsis thaliana. Theoretical and Applied Genetics, 2003, 106, 1256-1265.	1.8	68
68	Legume genomes: more than peas in a pod. Current Opinion in Plant Biology, 2003, 6, 199-204.	3.5	142
69	OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. BMC Bioinformatics, 2003, 4, 35.	1.2	56
70	DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale homology discovery and visualization. Genome Biology, 2003, 4, R68.	13.9	52
71	MtDB: a database for personalized data mining of the model legume Medicago truncatula transcriptome. Nucleic Acids Research, 2003, 31, 196-201.	6.5	61
72	Genetic and Physical Localization of the Soybean Rpg1-b Disease Resistance Gene Reveals a Complex Locus Containing Several Tightly Linked Families of NBS-LRR Genes. Molecular Plant-Microbe Interactions, 2003, 16, 817-826.	1.4	77

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73	Phylogeny and Genomic Organization of the TIR and Non-TIR NBS-LRR Resistance Gene Family in Medicago truncatul. Molecular Plant-Microbe Interactions, 2002, 15, 529-539.	1.4	94
74	Comparative genomic analysis of sequences sampled from a small region on soybean (Glycine max) molecular linkage group G. Genome, 2002, 45, 634-645.	0.9	43
75	Diversity, Distribution, and Ancient Taxonomic Relationships Within the TIR and Non-TIR NBS-LRR Resistance Gene Subfamilies. Journal of Molecular Evolution, 2002, 54, 548-562.	0.8	126
76	Constructing a plant genetic linkage map with DNA markers. Advances in Cellular and Molecular Biology of Plants, 2001, , 31-47.	0.2	5
77	Soybean genomic survey: BAC-end sequences near RFLP and SSR markers. Genome, 2001, 44, 572-581.	0.9	66
78	Differential Regulation of a Family of Apyrase Genes fromMedicago truncatula. Plant Physiology, 2001, 125, 2104-2119.	2.3	48
79	Differential Expression of Two Soybean Apyrases, One of Which Is an Early Nodulin. Molecular Plant-Microbe Interactions, 2000, 13, 1053-1070.	1.4	73
80	The genetic architecture of resistance. Current Opinion in Plant Biology, 2000, 3, 285-290.	3.5	162
81	A cautiously optimistic vision for marker-assisted breeding. Molecular Breeding, 1999, 5, 505-510.	1.0	234
82	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. Plant Journal, 1999, 20, 317-332.	2.8	729
83	Genome Mapping of Soybean Cyst Nematode Resistance Genes in â€˜Pekingâ€™, PI 90763, and PI 88788 Using DNA Markers. Crop Science, 1997, 37, 258-264.	0.8	144
84	Constructing a plant genetic linkage map with DNA markers. Advances in Cellular and Molecular Biology of Plants, 1994, , 39-57.	0.2	46
85	Applications of DNA genetic markers to the study of plant growth and development. Plant Growth Regulation, 1993, 12, 229-236.	1.8	4
86	Restriction Fragment Length Polymorphisms (RFLPS) and Crop Improvement. Experimental Agriculture, 1992, 28, 385-398.	0.4	11
87	Potential applications of map-based cloning to plant pathology. Physiological and Molecular Plant Pathology, 1990, 37, 81-94.	1.3	29
88	Pulsed field gel electrophoresis and physical mapping of large DNA fragments in the Tm-2a region of chromosome 9 in tomato. Molecular Genetics and Genomics, 1989, 215, 395-400.	2.4	134
89	Rapid chromosomal assignment of mulilpie genomic clones in tomato using primary trisomics. Nucleic Acids Research, 1987, 15, 9339-9348.	6.5	50
90	Physiological Control of Arginine Decarboxylase Activity in K-Deficient Oat Shoots. Plant Physiology, 1984, 76, 331-335.	2.3	74

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91	Putrescine and Acid Stress. Plant Physiology, 1983, 71, 767-771.	2.3	158