Nevin Dale Young

List of Publications by Year
in descending order

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	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
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	13.7	1,166
3	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
4	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
5	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
6	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
7	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. Genetics, 2007, 176, 685-696.	1.2	285
8	Sequencing the Genespaces of Medicago truncatula and Lotus japonicus: Figure 1.. Plant Physiology, 2005, 137, 1174-1181.	2.3	243
9	A cautiously optimistic vision for marker-assisted breeding. Molecular Breeding, 1999, 5, 505-510.	1.0	234
10	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
11	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. Theoretical and Applied Genetics, 2008, 116, 945-952.	1.8	210
12	Translating Medicago truncatula genomics to crop legumes. Current Opinion in Plant Biology, 2009, 12, 193-201.	3.5	171
13	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
14	Comparative genomics of the core and accessory genomes of 48 Sinorhizobium strains comprising five genospecies. Genome Biology, 2013, 14, R17.	13.9	164
15	The genetic architecture of resistance. Current Opinion in Plant Biology, 2000, 3, 285-290.	3.5	162
16	Genomic Signature of Adaptation to Climate in <i>Medicago truncatula</i>. Genetics, 2014, 196, 1263-1275.	1.2	160
17	Putrescine and Acid Stress. Plant Physiology, 1983, 71, 767-771.	2.3	158
18	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

#	Article	IF	Citations
19	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
20	Legume genomes: more than peas in a pod. Current Opinion in Plant Biology, 2003, 6, 199-204.	3.5	142
21	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
22	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
23	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
24	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
25	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
26	Exploring structural variation and gene family architecture with De Novo assemblies of 15 Medicago genomes. BMC Genomics, 2017, 18, 261.	1.2	87
27	Highly syntenic regions in the genomes of soybean, Medicago truncatula, and Arabidopsis thaliana. BMC Plant Biology, 2005, 5, 15.	1.6	86
28	Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). BMC Bioinformatics, 2013, 14, 335.	1.2	86
29	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
30	Genome-Enabled Insights into Legume Biology. Annual Review of Plant Biology, 2012, 63, 283-305.	8.6	79
31	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
32	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
33	A Guide to Genomeâ€Wide Association Mapping in Plants. Current Protocols in Plant Biology, 2017, 2, 22-38.	2.8	75
34	Physiological Control of Arginine Decarboxylase Activity in K-Deficient Oat Shoots. Plant Physiology, 1984, 76, 331-335.	2.3	74
35	Differential Expression of Two Soybean Apyrases, One of Which Is an Early Nodulin. Molecular Plant-Microbe Interactions, 2000, 13, 1053-1070.	1.4	73
36	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. Plant Physiology, 2017, 173, 921-931.	2.3	71

#	ARTICLE	IF	CITATIONS
37	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
38	Population Genomics of the Facultatively Mutualistic Bacteria Sinorhizobium meliloti and S. medicae. PLoS Genetics, 2012, 8, e1002868.	1.5	69
39	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
40	Chromosome-Level Homeology in Paleopolyploid Soybean (Glycine max) Revealed Through Integration of Genetic and Chromosome Maps. Genetics, 2006, 172, 1893-1900.	1.2	68
41	Soybean genomic survey: BAC-end sequences near RFLP and SSR markers. Genome, 2001, 44, 572-581.	0.9	66
42	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
43	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
44	MtDB: a database for personalized data mining of the model legume Medicago truncatula transcriptome. Nucleic Acids Research, 2003, 31, 196-201.	6.5	61
45	Databases and Information Integration for the Medicago truncatula Genome and Transcriptome. Plant Physiology, 2005, 138, 38-46.	2.3	59
46	Molecular and cytological responses of Medicago truncatula to Erysiphe pisi. Molecular Plant Pathology, 2007, 8, 307-319.	2.0	58
47	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
48	Replication of Nonautonomous Retroelements in Soybean Appears to Be Both Recent and Common Â. Plant Physiology, 2008, 148, 1760-1771.	2.3	57
49	OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. BMC Bioinformatics, 2003, 4, 35.	1.2	56
50	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
51	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
52	Estimating heritability using genomic data. Methods in Ecology and Evolution, 2013, 4, 1151-1158.	2.2	54
53	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
54	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

#	Article	IF	Citations
55	DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale homology discovery and visualization. Genome Biology, 2003, 4, R68.	13.9	52
56	Association mapping and genomic prediction for resistance to sudden death syndrome in early maturing soybean germplasm. Molecular Breeding, 2015, 35, 128.	1.0	52
57	Phylogenetic Signal Variation in the Genomes of Medicago (Fabaceae). Systematic Biology, 2013, 62, 424-438.	2.7	51
58	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
59	Hybrid assembly with long and short reads improves discovery of gene family expansions. BMC Genomics, 2017, 18, 541.	1.2	51
60	Rapid chromosomal assignment of mulilpie genomic clones in tomato using primary trisomics. Nucleic Acids Research, 1987, 15, 9339-9348.	6.5	50
61	Cross-species EST alignments reveal novel and conserved alternative splicing events in legumes. BMC Plant Biology, 2008, 8, 17.	1.6	49
62	Differential Regulation of a Family of Apyrase Genes fromMedicago truncatula. Plant Physiology, 2001, 125, 2104-2119.	2.3	48
63	Constructing a plant genetic linkage map with DNA markers. Advances in Cellular and Molecular Biology of Plants, 1994, , 39-57.	0.2	46
64	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
65	Transcriptomic basis of genome by genome variation in a legumeâ€rhizobia mutualism. Molecular Ecology, 2017, 26, 6122-6135.	2.0	40
66	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
67	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
68	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
69	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. Frontiers in Plant Science, 2015, 6, 269.	1.7	37
70	Adaptation to climate through flowering phenology: a case study in <i>Medicago truncatula</i>. Molecular Ecology, 2016, 25, 3397-3415.	2.0	36
71	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
72	Potential applications of map-based cloning to plant pathology. Physiological and Molecular Plant Pathology, 1990, 37, 81-94.	1.3	29

#	Article	IF	Citations
73	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
74	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
75	Soybean bacterial artificial chromosome contigs anchored with RFLPs: insights into genome duplication and gene clustering. Genome, 2004, 47, 361-372.	0.9	25
76	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
77	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
78	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
79	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
80	Transcriptional analysis of highly syntenic regions between Medicago truncatula and Glycine max using tiling microarrays. Genome Biology, 2008, 9, R57.	13.9	13
81	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
82	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
83	Restriction Fragment Length Polymorphisms (RFLPS) and Crop Improvement. Experimental Agriculture, 1992, 28, 385-398.	0.4	11
84	Effect of the rhg1 gene on penetration, development and reproduction of Heterodera glycines race 3. Nematology, 2004, 6, 729-736.	0.2	11
85	Alfalfa (<i>Medicago sativa</i>L.)<i>pho2</i>mutant plants hyperaccumulate phosphate. G3: Genes, Genomes, Genetics, 2022, , .	0.8	10
86	Genome studies and molecular genetics. Current Opinion in Plant Biology, 2006, 9, 95-98.	3.5	9
87	Exploring structural variants in environmentally sensitive gene families. Current Opinion in Plant Biology, 2016, 30, 19-24.	3.5	9
88	Constructing a plant genetic linkage map with DNA markers. Advances in Cellular and Molecular Biology of Plants, 2001, , 31-47.	0.2	5
89	Applications of DNA genetic markers to the study of plant growth and development. Plant Growth Regulation, 1993, 12, 229-236.	1.8	4
90	Complete Genome Sequence of Sinorhizobium meliloti Bacteriophage HMSP1-Susan. Genome Announcements, 2018, 6, .	0.8	2

#	Article	IF	Citations
91	Comparative Genomics of Glycine max, Medicago truncatula, Other Legumes, and Arabidopsis thaliana. , 2004, , .		0