Ann E Loraine

List of Publications by Year
in descending order

45 papers	3,726 citations	236925 25 h-index	265206 42 g-index
50 all docs	50 docs citations	50 times ranked	6867 citing authors

#	Article	IF	Citations
1	The Integrated Genome Browser: free software for distribution and exploration of genome-scale datasets. Bioinformatics, 2009, 25, 2730-2731.	4.1	558
2	NetAffx: Affymetrix probesets and annotations. Nucleic Acids Research, 2003, 31, 82-86.	14.5	438
3	Integrated genome browser: visual analytics platform for genomics. Bioinformatics, 2016, 32, 2089-2095.	4.1	347
4	Identification of Cytokinin-Responsive Genes Using Microarray Meta-Analysis and RNA-Seq in Arabidopsis Â Â Â. Plant Physiology, 2013, 162, 272-294.	4.8	230
5	RNA-Seq of Arabidopsis Pollen Uncovers Novel Transcription and Alternative Splicing Â Â Â. Plant Physiology, 2013, 162, 1092-1109.	4.8	195
6	Transcriptional Coordination of the Metabolic Network in Arabidopsis. Plant Physiology, 2006, 142, 762-774.	4.8	178
7	Assembly of an Interactive Correlation Network for the Arabidopsis Genome Using a Novel Heuristic Clustering Algorithm Â. Plant Physiology, 2009, 152, 29-43.	4.8	174
8	Cytokinin induces genome-wide binding of the type-B response regulator ARR10 to regulate growth and development in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5995-E6004.	7.1	154
9	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. GigaScience, 2015, 4, 5.	6.4	138
10	Large€scale transposon mutagenesis of<i>Mycoplasma pulmonis</i>. Molecular Microbiology, 2008, 69, 67-76.	2.5	117
11	A regulon conserved in monocot and dicot plants defines a functional module in antifungal plant immunity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21896-21901.	7.1	110
12	CressExpress: A Tool For Large-Scale Mining of Expression Data from Arabidopsis Â Â. Plant Physiology, 2008, 147, 1004-1016.	4.8	103
13	Comparisons of computational methods for differential alternative splicing detection using RNA-seq in plant systems. BMC Bioinformatics, 2014, 15, 364.	2.6	91
14	Efficient Quantification of the Health-Relevant Anthocyanin and Phenolic Acid Profiles in Commercial Cultivars and Breeding Selections of Blueberries (Vaccinium spp.). Journal of Agricultural and Food Chemistry, 2013, 61, 4806-4815.	5.2	88
15	Coordination of Chloroplast Development through the Action of the GNC and GLK Transcription Factor Families. Plant Physiology, 2018, 178, 130-147.	4.8	85
16	COBRA-LIKE2, a Member of the Glycosylphosphatidylinositol-Anchored COBRA-LIKE Family, Plays a Role in Cellulose Deposition in Arabidopsis Seed Coat Mucilage Secretory Cells Â, Â Â. Plant Physiology, 2015, 167, 711-724.	4.8	82
17	Analysis and Visualization of RNA-Seq Expression Data Using RStudio, Bioconductor, and Integrated Genome Browser. Methods in Molecular Biology, 2015, 1284, 481-501.	0.9	69
18	RNA-Seq Links the Transcription Factors AINTEGUMENTA and AINTEGUMENTA-LIKE6 to Cell Wall Remodeling and Plant Defense Pathways. Plant Physiology, 2016, 171, 2069-2084.	4.8	57

#	Article	IF	Citations
19	Mining *Arabidopsis thaliana* RNA‐seq data with Integrated Genome Browser reveals stress‐induced alternative splicing of the putative splicing regulator SR45a. American Journal of Botany, 2012, 99, 219-231.	1.7	50
20	The Arabidopsis transcription factor AINTEGUMENTA orchestrates patterning genes and auxin signaling in the establishment of floral growth and form. Plant Journal, 2020, 103, 752-768.	5.7	42
21	An 'eFP‐Seq Browser' for visualizing and exploring RNA sequencing data. Plant Journal, 2019, 100, 641-654.	5.7	41
22	Characterization of the cytokinin-responsive transcriptome in rice. BMC Plant Biology, 2016, 16, 260.	3.6	38
23	Prevalence of alternative splicing choices in Arabidopsis thaliana. BMC Plant Biology, 2010, 10, 102.	3.6	34
24	Genome of *Mycoplasma arthritidis*. Infection and Immunity, 2008, 76, 4000-4008.	2.2	33
25	Genome‐wide characterization of differential transcript usage in *Arabidopsis thaliana*. Plant Journal, 2017, 92, 1218-1231.	5.7	31
26	Visualizing the genome: techniques for presenting human genome data and annotations. BMC Bioinformatics, 2002, 3, 19.	2.6	30
27	BioViews: Java-Based Tools for Genomic Data‰Visualization. Genome Research, 1998, 8, 291-305.	5.5	28
28	Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies €. Nucleic Acids Research, 2008, 36, e26-e26.	14.5	24
29	Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild relative of sweet potato. Scientific Reports, 2017, 7, 9624.	3.3	22
30	AINTEGUMENTA and AINTEGUMENTA-LIKE6 directly regulate floral homeotic, growth, and vascular development genes in young Arabidopsis flowers. Journal of Experimental Botany, 2021, 72, 5478-5493.	4.8	21
31	Consistency Analysis of Redundant Probe Sets on Affymetrix Three-Prime Expression Arrays and Applications to Differential mRNA Processing. PLoS ONE, 2009, 4, e4229.	2.5	20
32	MARA: a novel approach for highly multiplexed locus-specific SNP genotyping using high-density DNA oligonucleotide arrays. Nucleic Acids Research, 2004, 32, e181-e181.	14.5	18
33	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct, 2019, 3, e00109.	1.9	14
34	ProtAnnot: an App for Integrated Genome Browser to display how alternative splicing and transcription affect proteins. Bioinformatics, 2016, 32, 2499-2501.	4.1	12
35	Analysis of pollen-specific alternative splicing in *Arabidopsis thaliana* via semi-quantitative PCR. PeerJ, 2015, 3, e919.	2.0	11
36	Anno genominis XX: 20 years of Arabidopsis genomics. Plant Cell, 2021, 33, 832-845.	6.6	11

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37	Exploring Alternative Transcript Structure in the Human Genome Using BLOCKS and InterPro. Journal of Bioinformatics and Computational Biology, 2003, 01, 289-306.	0.8	10
38	A Protocol for Visual Analysis of Alternative Splicing in RNA-Seq Data Using Integrated Genome Browser. Methods in Molecular Biology, 2014, 1158, 123-137.	0.9	5
39	Global correlation analysis between redundant probe sets using a large collection of Arabidopsis ath1 expression profiling data. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2006, , 223-6.	0.4	5
40	GLOBAL CORRELATION ANALYSIS BETWEEN REDUNDANT PROBE SETS USING A LARGE COLLECTION OF ARABIDOPSIS ATH1 EXPRESSION PROFILING DATA. , 2006, , .		4
41	Protein-based analysis of alternative splicing in the human genome. Proceedings, 2002, 1, 118-24.	0.1	3
42	Many rice genes are differentially spliced between roots and shoots but cytokinin has minimal effect on splicing. Plant Direct, 2019, 3, e00136.	1.9	2
43	Cell-specific cis-natural antisense transcripts (cis-NATs) in the sperm and the pollen vegetative cells of Arabidopsis thaliana. F1000Research, 2018, 7, 93.	1.6	2
44	Integrated Genome Browser App Store. Bioinformatics, 2022, , .	4.1	0
45	BioViz Connect: Web Application Linking CyVerse Cloud Resources to Genomic Visualization in the Integrated Genome Browser. Frontiers in Bioinformatics, 2022, 2, .	2.1	0