## Ning Ye

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59	846	17	27
papers	citations	h-index	g-index
76 ext. papers	1,177 ext. citations	4.3 avg, IF	4.26 L-index

#	Paper	IF	Citations
59	The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , <b>2014</b> , 24, 1274-7	24.7	104
58	L1-Norm Distance Linear Discriminant Analysis Based on an Effective Iterative Algorithm. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , <b>2018</b> , 28, 114-129	6.4	63
57	Different autosomes evolved into sex chromosomes in the sister genera of Salix and Populus. <i>Scientific Reports</i> , <b>2015</b> , 5, 9076	4.9	60
56	A weighted one-class support vector machine. <i>Neurocomputing</i> , <b>2016</b> , 189, 1-10	5.4	45
55	Organellar genome assembly methods and comparative analysis of horticultural plants. <i>Horticulture Research</i> , <b>2018</b> , 5, 3	7:7	44
54	Transcriptome analysis of the differentially expressed genes in the male and female shrub willows (Salix suchowensis). <i>PLoS ONE</i> , <b>2013</b> , 8, e60181	3.7	32
53	TA-CNN: Two-way attention models in deep convolutional neural network for plant recognition. <i>Neurocomputing</i> , <b>2019</b> , 365, 191-200	5.4	27
52	Analysis of the Complete Mitochondrial Genome Sequence of the Diploid Cotton by Comparative Genomics Approaches. <i>BioMed Research International</i> , <b>2016</b> , 2016, 5040598	3	25
51	Genome-wide identification and characterization of WRKY gene family in Salix suchowensis. <i>PeerJ</i> , <b>2016</b> , 4, e2437	3.1	25
50	Robust capped L1-norm twin support vector machine. <i>Neural Networks</i> , <b>2019</b> , 114, 47-59	9.1	25
49	Neighborhood linear discriminant analysis. <i>Pattern Recognition</i> , <b>2021</b> , 123, 108422	7:7	24
48	Assembly and comparative analysis of complete mitochondrial genome sequence of an economic plant. <i>PeerJ</i> , <b>2017</b> , 5, e3148	3.1	23
47	Major Chromosomal Rearrangements Distinguish Willow and Poplar After the Ancestral "Salicoid" Genome Duplication. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1868-75	3.9	22
46	Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , <b>2014</b> , 33, 205-224	5.6	22
45	Collaborative Filtering Recommendation Algorithm Based on Item Clustering and Global Similarity <b>2012</b> ,		21
44	Complete chloroplast genome sequence of a major economic species, Ziziphus jujuba (Rhamnaceae). <i>Current Genetics</i> , <b>2017</b> , 63, 117-129	2.9	20
43	A supervoxel approach to the segmentation of individual trees from LiDAR point clouds. <i>Remote Sensing Letters</i> , <b>2018</b> , 9, 515-523	2.3	17

42	Item-Based Collaborative Filtering Recommendation Algorithm Combining Item Category with Interestingness Measure <b>2012</b> ,		15	
41	Locality preserving multimodal discriminative learning for supervised feature selection. <i>Knowledge and Information Systems</i> , <b>2011</b> , 27, 473-490	2.4	14	
40	VGSC: A Web-Based Vector Graph Toolkit of Genome Synteny and Collinearity. <i>BioMed Research International</i> , <b>2016</b> , 2016, 7823429	3	14	
39	Fast orthogonal linear discriminant analysis with application to image classification. <i>Neurocomputing</i> , <b>2015</b> , 158, 216-224	5.4	13	
38	Learning a tensor subspace for semi-supervised dimensionality reduction. Soft Computing, 2011, 15, 383	3395	12	
37	The complete mitochondrial genome of. <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 592-593	0.5	11	
36	Learning Cascade Attention for fine-grained image classification. <i>Neural Networks</i> , <b>2020</b> , 122, 174-182	9.1	11	
35	Individual stem detection in residential environments with MLS data. <i>Remote Sensing Letters</i> , <b>2018</b> , 9, 51-60	2.3	10	
34	Assembly and analysis of the complete L. (Salicaceae) mitochondrial genome sequence. <i>SpringerPlus</i> , <b>2016</b> , 5, 1894		10	
33	Differential retention and expansion of the ancestral genes associated with the paleopolyploidies in modern rosid plants, as revealed by analysis of the extensins super-gene family. <i>BMC Genomics</i> , <b>2014</b> , 15, 612	4.5	10	
32	A feature selection method for nonparallel plane support vector machine classification. <i>Optimization Methods and Software</i> , <b>2012</b> , 27, 431-443	1.3	10	
31	Relative density degree induced boundary detection for one-class SVM. <i>Soft Computing</i> , <b>2016</b> , 20, 4473	-4485	9	
30	Identification of alternatively spliced gene isoforms and novel noncoding RNAs by single-molecule long-read sequencing in. <i>RNA Biology</i> , <b>2020</b> , 17, 966-976	4.8	7	
29	The complete mitochondrial genome of. Mitochondrial DNA Part B: Resources, 2016, 1, 122-123	0.5	7	
28	Least squares twin support vector machine classification via maximum one-class within class variance. <i>Optimization Methods and Software</i> , <b>2012</b> , 27, 53-69	1.3	7	
27	ASCENT: Active Supervision for Semi-Supervised Learning. <i>IEEE Transactions on Knowledge and Data Engineering</i> , <b>2020</b> , 32, 868-882	4.2	7	
26	Comparative genomics analysis reveals gene family expansion and changes of expression patterns associated with natural adaptations of flowering time and secondary metabolism in yellow Camellia. <i>Functional and Integrative Genomics</i> , <b>2018</b> , 18, 659-671	3.8	6	
25	Genome-wide identification and characterization of the MADS-box gene family in. <i>PeerJ</i> , <b>2019</b> , 7, e8019	3.1	6	

24	Enhanced Adaptive Locality Preserving Projections for Face Recognition 2017,		5
23	Incorporating neighborsdistribution knowledge into support vector machines. <i>Soft Computing</i> , <b>2017</b> , 21, 6407-6420	3.5	5
22	Genome-wide detection of genetic loci triggering uneven descending of gametes from a natural hybrid pine. <i>Tree Genetics and Genomes</i> , <b>2012</b> , 8, 1371-1377	2.1	5
21	Localized Multi-plane TWSVM Classifier via Manifold Regularization 2010,		5
20	Genome-wide identification and characterization of WUSCHEL-related homeobox (WOX) genes in Salix suchowensis. <i>Journal of Forestry Research</i> , <b>2019</b> , 30, 1811-1822	2	4
19	The complete chloroplast genome sequence of an economic plant. <i>Mitochondrial DNA Part B: Resources</i> , <b>2017</b> , 2, 483-485	0.5	4
18	Density-based weighting multi-surface least squares classification with its applications. <i>Knowledge and Information Systems</i> , <b>2012</b> , 33, 289-308	2.4	4
17	Transcriptome and Degradome Profiling Reveals a Role of miR530 in the Circadian Regulation of Gene Expression in. <i>Cells</i> , <b>2021</b> , 10,	7.9	4
16	VGSC2: Second generation vector graph toolkit of genome synteny and collinearity. <i>Genomics</i> , <b>2020</b> , 112, 286-288	4.3	4
15	Wood Defect Recognition Based on Affinity Propagation Clustering 2010,		3
14	The Whole Genome Assembly and Comparative Genomic Research of Thellungiella parvula (Extremophile Crucifer) Mitochondrion. <i>International Journal of Genomics</i> , <b>2016</b> , 2016, 5283628	2.5	3
13	A new method for shoreline extraction from airborne LiDAR point clouds. <i>Remote Sensing Letters</i> , <b>2019</b> , 10, 496-505	2.3	3
12			
	Iterative support vector machine with guaranteed accuracy and run time. Expert Systems, 2010, 27, 338-	348	2
11	Support vector machine with guaranteed accuracy and run time. <i>Expert Systems</i> , <b>2010</b> , 27, 338-	348	2
10		<b>348</b> 18.3	
	Support vector machine with orthogonal Chebyshev kernel 2006,  The genome of oil-Camellia and population genomics analysis provide insights into seed oil		2
10	Support vector machine with orthogonal Chebyshev kernel <b>2006</b> ,  The genome of oil-Camellia and population genomics analysis provide insights into seed oil domestication <i>Genome Biology</i> , <b>2022</b> , 23, 14  Detecting the Candidate Gender Determinants by Bioinformatic Prediction of miRNAs and Their Targets from Transcriptome Sequences of the Male and Female Flowers in. <i>BioMed Research</i>	18.3	2

## LIST OF PUBLICATIONS

6	Incremental Support Vector Machine Learning: An Angle Approach <b>2011</b> ,		1	
5	Support vectors classification and incremental learning 2011,		1	
4	Automatic Wood Defects Recognition Comparative Research 2008,		1	
3	GEsture: an online hand-drawing tool for gene expression pattern search. <i>PeerJ</i> , <b>2018</b> , 6, e4927	3.1	1	
2	Alternative Polyadenylation in response to temperature stress contributes to gene regulation in Populus trichocarpa. <i>BMC Genomics</i> , <b>2021</b> , 22, 53	4.5	1	
1	Feel the inside: A haptic interface for navigating stress distribution inside objects. <i>Visual Computer</i> , <b>2020</b> , 36, 2445-2456	2.3		