Stephen P Ficklin

List of Publications by Year
in descending order

50 papers	3,502 citations	304602 22 h-index	197736 49 g-index
54 all docs	54 docs citations	54 times ranked	4283 citing authors

#	ARTICLE	IF	CITATIONS
1	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	9.4	1,031
2	CottonGen: a genomics, genetics and breeding database for cotton research. Nucleic Acids Research, 2014, 42, D1229-D1236.	6.5	304
3	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic Acids Research, 2019, 47, D1137-D1145.	6.5	285
4	The Genome Database for Rosaceae (GDR): year 10 update. Nucleic Acids Research, 2014, 42, D1237-D1244.	6.5	195
5	Development and preliminary evaluation of a 90ÂK AxiomÂ® SNP array for the allo-octoploid cultivated strawberry Fragaria Ã— ananassa. BMC Genomics, 2015, 16, 155.	1.2	179
6	Gene Coexpression Network Alignment and Conservation of Gene Modules between Two Grass Species: Maize and Rice Â Â. Plant Physiology, 2011, 156, 1244-1256.	2.3	141
7	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. PLoS ONE, 2011, 6, e28150.	1.1	139
8	Development and Evaluation of a Genome-Wide 6K SNP Array for Diploid Sweet Cherry and Tetraploid Sour Cherry. PLoS ONE, 2012, 7, e48305.	1.1	109
9	CMD: a Cotton Microsatellite Database resource for Gossypium genomics. BMC Genomics, 2006, 7, 132.	1.2	102
10	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks Â Â Â. Plant Physiology, 2010, 154, 13-24.	2.3	93
11	GDR (Genome Database for Rosaceae): integrated web resources for Rosaceae genomics and genetics research. BMC Bioinformatics, 2004, 5, 130.	1.2	82
12	Chestnut resistance to the blight disease: insights from transcriptome analysis. BMC Plant Biology, 2012, 12, 38.	1.6	68
13	Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. Methods in Molecular Biology, 2019, 1962, 29-51.	0.4	66
14	Tripal: a construction toolkit for online genome databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar044-bar044.	1.4	60
15	Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat075.	1.4	52
16	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
17	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. PLoS ONE, 2013, 8, e55871.	1.1	49
18	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	1.6	44

#	Article	IF	Citations
19	Growing and cultivating the forest genomics database, TreeGenes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-11.	1.4	40
20	A physical map of the Chinese chestnut (Castanea mollissima) genome and its integration with the genetic map. Tree Genetics and Genomes, 2013, 9, 525-537.	0.6	36
21	Dissecting the Genetic Architecture of Aphanomyces Root Rot Resistance in Lentil by QTL Mapping and Genome-Wide Association Study. International Journal of Molecular Sciences, 2020, 21, 2129.	1.8	28
22	A Systems-Genetics Approach and Data Mining Tool to Assist in the Discovery of Genes Underlying Complex Traits in Oryza sativa. PLoS ONE, 2013, 8, e68551.	1.1	26
23	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. Frontiers in Plant Science, 2019, 10, 813.	1.7	24
24	Maximizing capture of gene co-expression relationships through pre-clustering of input expression samples: an Arabidopsis case study. BMC Systems Biology, 2013, 7, 44.	3.0	22
25	Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	22
26	Sequencing of a QTL-rich region of the Theobroma cacao genome using pooled BACs and the identification of trait specific candidate genes. BMC Genomics, 2011, 12, 379.	1.2	20
27	Uniform standards for genome databases in forest and fruit trees. Tree Genetics and Genomes, 2012, 8, 549-557.	0.6	20
28	High-density multi-population consensus genetic linkage map for peach. PLoS ONE, 2018, 13, e0207724.	1.1	19
29	Large-Scale Gene Relocations following an Ancient Genome Triplication Associated with the Diversification of Core Eudicots. PLoS ONE, 2016, 11, e0155637.	1.1	19
30	Co-expression networks provide insights into molecular mechanisms of postharvest temperature modulation of apple fruit to reduce superficial scald. Postharvest Biology and Technology, 2019, 149, 27-41.	2.9	18
31	New extension software modules to enhance searching and display of transcriptome data in Tripal databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	15
32	Discovery and validation of a glioblastoma co-expressed gene module. Oncotarget, 2018, 9, 10995-11008.	0.8	15
33	â€œA reference genome assembly and adaptive trait analysis of Castanea mollissima â€˜Vanuxem,â€™ a source of resistance to chestnut blight in restoration breedingâ€• Tree Genetics and Genomes, 2020, 16, 1.	0.6	14
34	A genetically anchored physical framework for Theobroma cacao cv. Matina 1-6. BMC Genomics, 2011, 12, 413.	1.2	13
35	Chado use case: storing genomic, genetic and breeding data of Rosaceae and Gossypium crops in Chado. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw010.	1.4	11
36	Making sense of performance in in-memory computing frameworks for scientific data analysis: A case study of the spark system. Journal of Parallel and Distributed Computing, 2018, 120, 369-382.	2.7	11

#	Article	IF	Citations
37	A Fixed Cohort Field Study of Gene Expression in Circulating Leukocytes From Dairy Cows With and Without Mastitis. Frontiers in Veterinary Science, 2020, 7, 559279.	0.9	8
38	Extension modules for storage, visualization and querying of genomic, genetic and breeding data in Tripal databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	7
39	GPU Implementation of Pairwise Gaussian Mixture Models for Multi-Modal Gene Co-Expression Networks. IEEE Access, 2019, 7, 160845-160857.	2.6	7
40	Transcriptomics of Differential Ripening in â€˜dâ€™Anjouâ€™ Pear (Pyrus communis L.). Frontiers in Plant Science, 2021, 12, 609684.	1.7	7
41	Conserved Non-Coding Regulatory Signatures in Arabidopsis Co-Expressed Gene Modules. PLoS ONE, 2012, 7, e45041.	1.1	7
42	Tripal, a community update after 10Âyears of supporting open source, standards-based genetic, genomic and breeding databases. Briefings in Bioinformatics, 2021, 22, .	3.2	6
43	blend4php: a PHP API for galaxy. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw154.	1.4	5
44	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
45	Addressing noise in co-expression network construction. Briefings in Bioinformatics, 2022, 23, .	3.2	4
46	Named Data Networking for Genomics Data Management and Integrated Workflows. Frontiers in Big Data, 2021, 4, 582468.	1.8	3
47	GEMmaker: process massive RNA-seq datasets on heterogeneous computational infrastructure. BMC Bioinformatics, 2022, 23, 156.	1.2	2
48	Understanding Software Platforms for In-Memory Scientific Data Analysis: A Case Study of the Spark System. , 2016, , .		1
49	Tripal and Galaxy: supporting reproducible scientific workflows for community biological databases. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
50	Identification of condition-specific regulatory mechanisms in normal and cancerous human lung tissue. BMC Genomics, 2022, 23, 350.	1.2	0