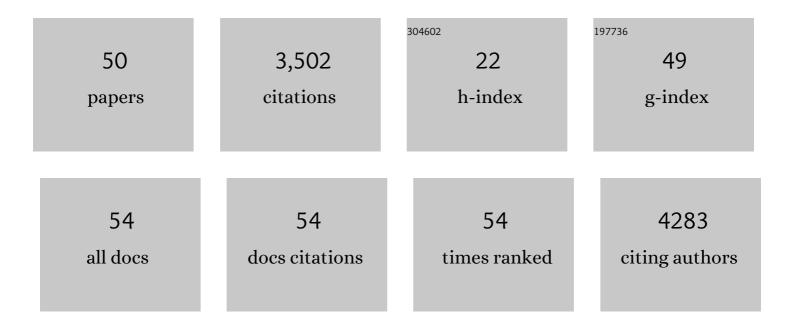
Stephen P Ficklin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Addressing noise in co-expression network construction. Briefings in Bioinformatics, 2022, 23, .	3.2	4
2	GEMmaker: process massive RNA-seq datasets on heterogeneous computational infrastructure. BMC Bioinformatics, 2022, 23, 156.	1.2	2
3	Identification of condition-specific regulatory mechanisms in normal and cancerous human lung tissue. BMC Genomics, 2022, 23, 350.	1.2	0
4	Named Data Networking for Genomics Data Management and Integrated Workflows. Frontiers in Big Data, 2021, 4, 582468.	1.8	3
5	Transcriptomics of Differential Ripening in â€~d'Anjou' Pear (Pyrus communis L.). Frontiers in Plant Science, 2021, 12, 609684.	1.7	7
6	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
7	Tripal and Galaxy: supporting reproducible scientific workflows for community biological databases. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
8	"A reference genome assembly and adaptive trait analysis of Castanea mollissima †Vanuxem,' a source of resistance to chestnut blight in restoration breeding― Tree Genetics and Genomes, 2020, 16, 1.	0.6	14
9	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
10	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
11	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
12	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
13	Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. Methods in Molecular Biology, 2019, 1962, 29-51.	0.4	66
14	GPU Implementation of Pairwise Gaussian Mixture Models for Multi-Modal Gene Co-Expression Networks. IEEE Access, 2019, 7, 160845-160857.	2.6	7
15	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
16	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic Acids Research, 2019, 47, D1137-D1145.	6.5	285
17	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
18	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

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19	High-density multi-population consensus genetic linkage map for peach. PLoS ONE, 2018, 13, e0207724.	1.1	19
20	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
21	Growing and cultivating the forest genomics database, TreeGenes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-11.	1.4	40
22	Discovery and validation of a glioblastoma co-expressed gene module. Oncotarget, 2018, 9, 10995-11008.	0.8	15
23	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	1.6	44
24	blend4php: a PHP API for galaxy. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw154.	1.4	5
25	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
26	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
27	Understanding Software Platforms for In-Memory Scientific Data Analysis: A Case Study of the Spark System. , 2016, , .		1
28	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
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	Development and preliminary evaluation of a 90ÂK Axiom® SNP array for the allo-octoploid cultivated strawberry Fragaria × ananassa. BMC Genomics, 2015, 16, 155.	1.2	179
31	The Genome Database for Rosaceae (GDR): year 10 update. Nucleic Acids Research, 2014, 42, D1237-D1244.	6.5	195
32	CottonGen: a genomics, genetics and breeding database for cotton research. Nucleic Acids Research, 2014, 42, D1229-D1236.	6.5	304
33	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
34	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
35	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
36	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

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37	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
38	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. PLoS ONE, 2013, 8, e55871.	1.1	49
39	Chestnut resistance to the blight disease: insights from transcriptome analysis. BMC Plant Biology, 2012, 12, 38.	1.6	68
40	Uniform standards for genome databases in forest and fruit trees. Tree Genetics and Genomes, 2012, 8, 549-557.	0.6	20
41	Conserved Non-Coding Regulatory Signatures in Arabidopsis Co-Expressed Gene Modules. PLoS ONE, 2012, 7, e45041.	1.1	7
42	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
43	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
44	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
45	A genetically anchored physical framework for Theobroma cacao cv. Matina 1-6. BMC Genomics, 2011, 12, 413.	1.2	13
46	Tripal: a construction toolkit for online genome databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar044-bar044.	1.4	60
47	Gene Coexpression Network Alignment and Conservation of Gene Modules between Two Grass Species: Maize and Rice Â. Plant Physiology, 2011, 156, 1244-1256.	2.3	141
48	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks Â. Plant Physiology, 2010, 154, 13-24.	2.3	93
49	CMD: a Cotton Microsatellite Database resource for Gossypium genomics. BMC Genomics, 2006, 7, 132.	1.2	102
50	GDR (Genome Database for Rosaceae): integrated web resources for Rosaceae genomics and genetics research. BMC Bioinformatics, 2004, 5, 130.	1.2	82