

Frank A Feltus

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

7,619
citations

159585

30
h-index

56724

83
g-index

95
all docs

95
docs citations

95
times ranked

9759
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
2	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
3	Molecular Biology of the 3 β -Hydroxysteroid Dehydrogenase/5 β - Δ^4 Isomerase Gene Family. <i>Endocrine Reviews</i> , 2005, 26, 525-582.	20.1	502
4	An SNP Resource for Rice Genetics and Breeding Based on Subspecies <i>Indica</i> and <i>Japonica</i> Genome Alignments. <i>Genome Research</i> , 2004, 14, 1812-1819.	5.5	318
5	Sequencing papaya X and Y chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	7.1	264
6	Meta-analysis of Polyploid Cotton QTL Shows Unequal Contributions of Subgenomes to a Complex Network of Genes and Gene Clusters Implicated in Lint Fiber Development. <i>Genetics</i> , 2007, 176, 2577-2588.	2.9	240
7	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	8.8	225
8	Many gene and domain families have convergent fates following independent whole-genome duplication events in <i>Arabidopsis</i> , <i>Oryza</i> , <i>Saccharomyces</i> and <i>Tetraodon</i> . <i>Trends in Genetics</i> , 2006, 22, 597-602.	6.7	181
9	Buffering of crucial functions by paleologous duplicated genes may contribute cyclicity to angiosperm genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2730-2735.	7.1	168
10	Gene Coexpression Network Alignment and Conservation of Gene Modules between Two Grass Species: Maize and Rice. <i>Plant Physiology</i> , 2011, 156, 1244-1256.	4.8	141
11	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. <i>PLoS ONE</i> , 2011, 6, e28150.	2.5	139
12	The repetitive landscape of the chicken genome. <i>Genome Research</i> , 2004, 15, 126-136.	5.5	108
13	Paracrine Regulation of Matrix Metalloproteinase Expression in the Normal Human Endometrium. <i>Gynecologic and Obstetric Investigation</i> , 1999, 48, 2-13.	1.6	100
14	DNA motifs associated with aberrant CpG island methylation. <i>Genomics</i> , 2006, 87, 572-579.	2.9	95
15	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks. <i>Plant Physiology</i> , 2010, 154, 13-24.	4.8	93
16	Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. <i>Genetics</i> , 2007, 177, 1753-1763.	2.9	85
17	Low X/Y divergence in four pairs of papaya sex-linked genes. <i>Plant Journal</i> , 2008, 53, 124-132.	5.7	78
18	Chromosomal location and gene paucity of the male specific region on papaya Y chromosome. <i>Molecular Genetics and Genomics</i> , 2007, 278, 177-185.	2.1	73

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19	The first genome-level transcriptome of the wood-degrading fungus <i>Phanerochaete chrysosporium</i> grown on red oak. <i>Current Genetics</i> , 2009, 55, 273-286.	1.7	53
20	Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits. <i>Biotechnology for Biofuels</i> , 2012, 5, 80.	6.2	53
21	scRNA-seq analyses of <i>Arabidopsis thaliana</i> seedlings after exposure to blue-light phototropic stimuli in microgravity. <i>American Journal of Botany</i> , 2019, 106, 1466-1476.	1.7	53
22	Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat075.	3.0	52
23	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. <i>PLoS ONE</i> , 2013, 8, e55871.	2.5	49
24	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. <i>Scientific Reports</i> , 2017, 7, 8617.	3.3	44
25	Comparative Genomics of Grasses Promises a Bountiful Harvest. <i>Plant Physiology</i> , 2009, 149, 125-131.	4.8	42
26	RNAseq Analysis of the Response of <i>Arabidopsis thaliana</i> to Fractional Gravity Under Blue-Light Stimulation During Spaceflight. <i>Frontiers in Plant Science</i> , 2019, 10, 1529.	3.6	42
27	Growing and cultivating the forest genomics database, TreeGenes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-11.	3.0	40
28	Construction of physical maps for the sex-specific regions of papaya sex chromosomes. <i>BMC Genomics</i> , 2012, 13, 176.	2.8	39
29	Analysis of Crystallinity Index and Hydrolysis Rates in the Bioenergy Crop <i>Sorghum bicolor</i> . <i>Bioenergy Research</i> , 2012, 5, 387-397.	3.9	37
30	Systems genetics: A paradigm to improve discovery of candidate genes and mechanisms underlying complex traits. <i>Plant Science</i> , 2014, 223, 45-48.	3.6	37
31	Glucocorticoids enhance activation of the human type II 3 β -hydroxysteroid dehydrogenase/5 α - Δ^4 isomerase gene. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2002, 82, 55-63.	2.5	31
32	The Evolution of an Invasive Plant, <i>Sorghum halepense</i> L. (Johnsongrass™). <i>Frontiers in Genetics</i> , 2020, 11, 317.	2.3	30
33	Comparative Analysis and Functional Annotation of a Large Expressed Sequence Tag Collection of Apple. <i>Plant Genome</i> , 2009, 2, .	2.8	28
34	A sorghum diversity panel biofuel feedstock screen for genotypes with high hydrolysis yield potential. <i>Industrial Crops and Products</i> , 2010, 31, 444-448.	5.2	28
35	A Systems-Genetics Approach and Data Mining Tool to Assist in the Discovery of Genes Underlying Complex Traits in <i>Oryza sativa</i> . <i>PLoS ONE</i> , 2013, 8, e68551.	2.5	26
36	Identification and mapping of conserved ortholog set (COS) II sequences of cacao and their conversion to SNP markers for marker-assisted selection in <i>Theobroma cacao</i> and comparative genomics studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 97-111.	1.6	25

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37	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
38	Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	22
39	A Larger Chocolate Chip—Development of a 15K Theobroma cacao L. SNP Array to Create High-Density Linkage Maps. Frontiers in Plant Science, 2017, 8, 2008.	3.6	21
40	Novel nuclear intron-spanning primers for Arecaceae evolutionary biology. Molecular Ecology Resources, 2008, 8, 211-214.	4.8	20
41	Transcriptome analysis of leaf tissue from Bermudagrass (Cynodon dactylon) using a normalised cDNA library. Functional Plant Biology, 2008, 35, 585.	2.1	20
42	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.	2.8	20
43	Large-Scale Gene Relocations following an Ancient Genome Triplication Associated with the Diversification of Core Eudicots. PLoS ONE, 2016, 11, e0155637.	2.5	19
44	OSG-GEM: Gene Expression Matrix Construction Using the Open Science Grid. Bioinformatics and Biology Insights, 2016, 10, BBI.S38193.	2.0	18
45	Epidermal Growth Factor Increases Cortisol Production and Type II 3 β -Hydroxysteroid Dehydrogenase/5 α - β 4-Isomerase Expression in Human Adrenocortical Carcinoma Cells: Evidence for a Stat5-Dependent Mechanism. Endocrinology, 2003, 144, 1847-1853.	2.8	16
46	New genomic resources for switchgrass: a BAC library and comparative analysis of homoeologous genomic regions harboring bioenergy traits. BMC Genomics, 2011, 12, 369.	2.8	15
47	Widespread Genotype-Phenotype Correlations in Intellectual Disability. Frontiers in Psychiatry, 2018, 9, 535.	2.6	15
48	Uncovering biomarker genes with enriched classification potential from Hallmark gene sets. Scientific Reports, 2019, 9, 9747.	3.3	15
49	A genetically anchored physical framework for Theobroma cacao cv. Matina 1-6. BMC Genomics, 2011, 12, 413.	2.8	13
50	Evidence of function for conserved noncoding sequences in <i>Arabidopsis thaliana</i> . New Phytologist, 2012, 193, 241-252.	7.3	13
51	Identification of bioconversion quantitative trait loci in the interspecific cross Sorghum bicolor—Sorghum propinquum. Theoretical and Applied Genetics, 2013, 126, 2367-2380.	3.6	13
52	Ergot alkaloid exposure during gestation alters: 3. Fetal growth, muscle fiber development, and miRNA transcriptome. Journal of Animal Science, 2019, 97, 3153-3168.	0.5	13
53	Linking Binary Gene Relationships to Drivers of Renal Cell Carcinoma Reveals Convergent Function in Alternate Tumor Progression Paths. Scientific Reports, 2019, 9, 2899.	3.3	13
54	Assessing pooled BAC and whole genome shotgun strategies for assembly of complex genomes. BMC Genomics, 2011, 12, 194.	2.8	12

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55	The Widening Gulf between Genomics Data Generation and Consumption: A Practical Guide to Big Data Transfer Technology. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28988.	2.0	12
56	A scalable, open-source implementation of a large-scale mechanistic model for single cell proliferation and death signaling. <i>Nature Communications</i> , 2022, 13, .	12.8	12
57	Autism risk genes are evolutionarily ancient and maintain a unique feature landscape that echoes their function. <i>Autism Research</i> , 2019, 12, 860-869.	3.8	10
58	Plant stress biomarkers from biosimulations: the Transcriptomeâ€”Metabolome^{â„¢} (<scp>TTM</scp>^{â„¢}) technology â€” effects of drought stress on rice. <i>Plant Biology</i> , 2015, 17, 63-73.	3.8	9
59	Maximizing the performance of scientific data transfer by optimizing the interface between parallel file systems and advanced research networks. <i>Future Generation Computer Systems</i> , 2018, 79, 190-198.	7.5	9
60	Cellular State Transformations Using Deep Learning for Precision Medicine Applications. <i>Patterns</i> , 2020, 1, 100087.	5.9	9
61	Sorting Five Human Tumor Types Reveals Specific Biomarkers and Background Classification Genes. <i>Scientific Reports</i> , 2018, 8, 8180.	3.3	8
62	Tissue specific analysis of bioconversion traits in the bioenergy grass <i>Sorghum bicolor</i> . <i>Industrial Crops and Products</i> , 2013, 50, 118-130.	5.2	7
63	Cancer cell redirection biomarker discovery using a mutual information approach. <i>PLoS ONE</i> , 2017, 12, e0179265.	2.5	7
64	Integrity Protection for Scientific Workflow Data. , 2019, , .		7
65	Identifying Temporally Regulated Root Nodulation Biomarkers Using Time Series Gene Co-Expression Network Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1409.	3.6	7
66	GPU Implementation of Pairwise Gaussian Mixture Models for Multi-Modal Gene Co-Expression Networks. <i>IEEE Access</i> , 2019, 7, 160845-160857.	4.2	7
67	Conserved Non-Coding Regulatory Signatures in Arabidopsis Co-Expressed Gene Modules. <i>PLoS ONE</i> , 2012, 7, e45041.	2.5	7
68	Identifying differentially expressed genes in cancer patients using a nonâ€”parameter Ising model. <i>Proteomics</i> , 2011, 11, 3845-3852.	2.2	6
69	Quantitative models of hydrolysis conversion efficiency and biomass crystallinity index for plant breeding. <i>Plant Breeding</i> , 2013, 132, 252-258.	1.9	6
70	Big Data Smart Socket (BDSS): a system that abstracts data transfer habits from end users. <i>Bioinformatics</i> , 2017, 33, 627-628.	4.1	6
71	OSG-KINC: High-throughput gene co-expression network construction using the open science grid. , 2017, , .		6
72	BAC Sequencing Using Pooled Methods. <i>Methods in Molecular Biology</i> , 2015, 1227, 55-67.	0.9	6

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73	RNA Expression Profiling Reveals Differentially Regulated Growth Factor and Receptor Expression in Redirected Cancer Cells. <i>Stem Cells and Development</i> , 2017, 26, 646-655.	2.1	5
74	Time Series Transcriptome Analysis in <i>Medicago truncatula</i> Shoot and Root Tissue During Early Nodulation. <i>Frontiers in Plant Science</i> , 2022, 13, 861639.	3.6	5
75	Experimental validation of inter-subspecific genetic diversity in rice represented by the differences between the DNA sequences of "Nipponbare"™ and "93-11"™. <i>Science Bulletin</i> , 2007, 52, 1327-1337.	1.7	4
76	Exploration into biomarker potential of region-specific brain gene co-expression networks. <i>Scientific Reports</i> , 2020, 10, 17089.	3.3	4
77	Addressing noise in co-expression network construction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
78	Named Data Networking for Genomics Data Management and Integrated Workflows. <i>Frontiers in Big Data</i> , 2021, 4, 582468.	2.9	3
79	Conserved Non-Coding Sequences are Associated with Rates of mRNA Decay in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 129.	3.6	2
80	Moving Just Enough Deep Sequencing Data to Get the Job Done. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221985635.	2.0	2
81	EdgeScaping: Mapping the spatial distribution of pairwise gene expression intensities. <i>PLoS ONE</i> , 2019, 14, e0220279.	2.5	2
82	NetExtractor: Extracting a Cerebellar Tissue Gene Regulatory Network Using Differentially Expressed High Mutual Information Binary RNA Profiles. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2953-2963.	1.8	2
83	Discovery of eQTL Alleles Associated with Autism Spectrum Disorder: A Case-Control Study. <i>Journal of Autism and Developmental Disorders</i> , 0, , .	2.7	2
84	A non-parameter Ising model for network-based identification of differentially expressed genes in recurrent breast cancer patients. , 2010, , .		1
85	Exploring Lossy Compression of Gene Expression Matrices. , 2019, , .		1
86	TriPal and Galaxy: supporting reproducible scientific workflows for community biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	1
87	Identification of condition-specific biomarker systems in uterine cancer. <i>G3: Genes, Genomes, Genetics</i> , 2021, , .	1.8	1
88	<i>Saccharinae</i> Bioinformatics Resources. , 2013, , 303-330.		0
89	EdgeCrafting: mining embedded, latent, nonlinear patterns to construct gene relationship networks. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	0
90	Intelligent Resource Provisioning for Scientific Workflows and HPC. , 2021, , .		0

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91	Identification of condition-specific regulatory mechanisms in normal and cancerous human lung tissue. BMC Genomics, 2022, 23, 350.	2.8	0
92	Simulating the restoration of normal gene expression from different thyroid cancer stages using deep learning. BMC Cancer, 2022, 22, .	2.6	0