

# John P Hamilton

## List of Publications by Year in Descending Order

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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.

66

papers

6,063

citations

36

h-index

73

g-index

73

ext. papers

7,975

ext. citations

7.3

avg, IF

5.27

L-index

#	Paper	IF	Citations
66	Phased, chromosome-scale genome assemblies of tetraploid potato reveals a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity.. <i>Molecular Plant</i> , <b>2022</b> ,	14.4	2
65	Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels.. <i>Plant Genome</i> , <b>2022</b> , e20197	4.4	0
64	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , <b>2021</b> , 33, 882-900	11.6	3
63	High-resolution genome-wide association study pinpoints metal transporter and chelator genes involved in the genetic control of element levels in maize grain. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	3
62	The <i>Mitragyna speciosa</i> (Kratom) Genome: a resource for data-mining potent pharmaceuticals that impact human health. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	4
61	Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
60	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , <b>2021</b> , 12, 2638	17.4	6
59	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , <b>2021</b> , 14, e20114	4.4	1
58	The evolutionary origins of the cat attractant nepetalactone in catnip. <i>Science Advances</i> , <b>2020</b> , 6, eaba0721	21.3	22
57	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , <b>2020</b> , 52, 1018-1023	30.3	40
56	Construction of a chromosome-scale long-read reference genome assembly for potato. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	36
55	Genome assembly of <i>Chiococca alba</i> uncovers key enzymes involved in the biosynthesis of unusual terpenoids. <i>DNA Research</i> , <b>2020</b> , 27,	4.5	1
54	Genome sequencing of four culinary herbs reveals terpenoid genes underlying chemodiversity in the Nepetoideae. <i>DNA Research</i> , <b>2020</b> , 27,	4.5	6
53	Generation of a chromosome-scale genome assembly of the insect-repellent terpenoid-producing Lamiaceae species, <i>Callicarpa americana</i> . <i>GigaScience</i> , <b>2020</b> , 9,	7.6	4
52	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated $\beta$ -carotene and starch content in hexaploid sweetpotato [ <i>Ipomoea batatas</i> (L.) Lam.]. <i>Theoretical and Applied Genetics</i> , <b>2020</b> , 133, 23-36	6	33
51	A chromosomal-scale genome assembly of <i>Tectona grandis</i> reveals the importance of tandem gene duplication and enables discovery of genes in natural product biosynthetic pathways. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	25
50	Genome-wide Inference of Somatic Translocation Events During Potato Dihaploid Production. <i>Plant Genome</i> , <b>2019</b> , 12, 180079	4.4	7

49	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , <b>2019</b> , 12, 180069	4.4	10
48	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , <b>2019</b> , 97, 1154-1167	6.9	54
47	Gene Discovery in Gelsemium Highlights Conserved Gene Clusters in Monoterpene Indole Alkaloid Biosynthesis. <i>ChemBioChem</i> , <b>2019</b> , 20, 83-87	3.8	33
46	Genome sequence of M6, a diploid inbred clone of the high-glycoalkaloid-producing tuber-bearing potato species <i>Solanum chacoense</i> , reveals residual heterozygosity. <i>Plant Journal</i> , <b>2018</b> , 94, 562-570	6.9	69
45	The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 2380-2397	20.1	9
44	Reply to Huang et al.: Avoiding "one-size-fits-all" approaches to variant discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E6394-E6395	11.5	2
43	Genome Assembly and Annotation of the Medicinal Plant , a Producer of Anticancer and Antimalarial Cardenolides. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 385-391	3.2	17
42	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , <b>2018</b> , 9, 4580	17.4	86
41	Characterization of the <i>Xanthomonas translucens</i> Complex Using Draft Genomes, Comparative Genomics, Phylogenetic Analysis, and Diagnostic LAMP Assays. <i>Phytopathology</i> , <b>2017</b> , 107, 519-527	3.8	31
40	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 203-219	3.2	27
39	Genome diversity of tuber-bearing uncovers complex evolutionary history and targets of domestication in the cultivated potato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E9999-E10008	11.5	164
38	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , <b>2017</b> , 29, 2374-2392	11.6	57
37	De novo genome assembly of <i>Camptotheca acuminata</i> , a natural source of the anti-cancer compound camptothecin. <i>GigaScience</i> , <b>2017</b> , 6, 1-7	7.6	39
36	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i> . <i>Plant Cell</i> , <b>2016</b> , 28, 388-405	11.6	126
35	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. <i>PLoS ONE</i> , <b>2016</b> , 11, e0147229	3.7	25
34	Gene amplification of 5-enol-pyruvylshikimate-3-phosphate synthase in glyphosate-resistant <i>Kochia scoparia</i> . <i>Planta</i> , <b>2015</b> , 241, 463-74	4.7	95
33	Genome-guided investigation of plant natural product biosynthesis. <i>Plant Journal</i> , <b>2015</b> , 82, 680-92	6.9	128
32	A root-expressed L-phenylalanine:4-hydroxyphenylpyruvate aminotransferase is required for tropane alkaloid biosynthesis in <i>Atropa belladonna</i> . <i>Plant Cell</i> , <b>2014</b> , 26, 3745-62	11.6	48

31	Timber! Felling the loblolly pine genome. <i>Genome Biology</i> , <b>2014</b> , 15, 111	18.3	0
30	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. <i>Plant Genome</i> , <b>2014</b> , 7, plantgenome2013.12.0042	4.4	66
29	Comparative analysis of two emerging rice seed bacterial pathogens. <i>Phytopathology</i> , <b>2014</b> , 104, 436-443.8	3.8	31
28	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , <b>2013</b> , 6, 4	5.8	1110
27	Construction of reference chromosome-scale pseudomolecules for potato: integrating the potato genome with genetic and physical maps. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 2031-47	3.2	172
26	Carbohydrate-active enzymes in pythium and their role in plant cell wall and storage polysaccharide degradation. <i>PLoS ONE</i> , <b>2013</b> , 8, e72572	3.7	52
25	Comparative genomics reveals insight into virulence strategies of plant pathogenic oomycetes. <i>PLoS ONE</i> , <b>2013</b> , 8, e75072	3.7	100
24	Advances in plant genome sequencing. <i>Plant Journal</i> , <b>2012</b> , 70, 177-90	6.9	128
23	Expression profiling of <i>Cucumis sativus</i> in response to infection by <i>Pseudoperonospora cubensis</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e34954	3.7	43
22	mRNA-Seq analysis of the <i>Pseudoperonospora cubensis</i> transcriptome during cucumber ( <i>Cucumis sativus</i> L.) infection. <i>PLoS ONE</i> , <b>2012</b> , 7, e35796	3.7	47
21	Integration of two diploid potato linkage maps with the potato genome sequence. <i>PLoS ONE</i> , <b>2012</b> , 7, e36347	3.7	160
20	Development of transcriptomic resources for interrogating the biosynthesis of monoterpene indole alkaloids in medicinal plant species. <i>PLoS ONE</i> , <b>2012</b> , 7, e52506	3.7	121
19	Single Nucleotide Polymorphism Discovery in Cultivated Tomato via Sequencing by Synthesis. <i>Plant Genome</i> , <b>2012</b> , 5,	4.4	70
18	Alternative splicing of a multi-drug transporter from <i>Pseudoperonospora cubensis</i> generates an RXLR effector protein that elicits a rapid cell death. <i>PLoS ONE</i> , <b>2012</b> , 7, e34701	3.7	36
17	Development of a large SNP genotyping array and generation of high-density genetic maps in tomato. <i>PLoS ONE</i> , <b>2012</b> , 7, e40563	3.7	217
16	Single nucleotide polymorphism discovery in elite North American potato germplasm. <i>BMC Genomics</i> , <b>2011</b> , 12, 302	4.5	167
15	Genomic analysis of <i>Xanthomonas oryzae</i> isolates from rice grown in the United States reveals substantial divergence from known <i>X. oryzae</i> pathovars. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 3930-7	4.8	59
14	The Comprehensive Phytopathogen Genomics Resource: a web-based resource for data-mining plant pathogen genomes. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2011</b> , 2011, bar053 <sup>5</sup>		21

13	A stereoselective hydroxylation step of alkaloid biosynthesis by a unique cytochrome P450 in <i>Catharanthus roseus</i> . <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 16751-7	5.4	98
12	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , <b>2010</b> , 11, R73	18.3	280
11	Genomics-Based Diagnostic Marker Development for <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> and <i>X. oryzae</i> pv. <i>oryzicola</i> . <i>Plant Disease</i> , <b>2010</b> , 94, 311-319	1.5	76
10	Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. <i>BMC Genomics</i> , <b>2008</b> , 9, 542	4.5	66
9	EuCAP, a Eukaryotic Community Annotation Package, and its application to the rice genome. <i>BMC Genomics</i> , <b>2007</b> , 8, 388	4.5	6
8	Identification and characterization of lineage-specific genes within the Poaceae. <i>Plant Physiology</i> , <b>2007</b> , 145, 1311-22	6.6	52
7	The TIGR Plant Transcript Assemblies database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D846-51	20.1	168
6	The TIGR Rice Genome Annotation Resource: improvements and new features. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D883-7	20.1	846
5	Comprehensive analysis of alternative splicing in rice and comparative analyses with <i>Arabidopsis</i> . <i>BMC Genomics</i> , <b>2006</b> , 7, 327	4.5	262
4	Expressed sequence tags from loblolly pine embryos reveal similarities with angiosperm embryogenesis. <i>Plant Molecular Biology</i> , <b>2006</b> , 62, 485-501	4.6	62
3	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , <b>2005</b> , 3, 20	7.3	139
2	The institute for genomic research Osa1 rice genome annotation database. <i>Plant Physiology</i> , <b>2005</b> , 138, 18-26	6.6	188
1	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2