Jeffrey P Mower

List of Publications by Year in descending order

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		126907	138484	
58	5,653	33	58	
papers	citations	h-index	g-index	
60	60	60	4891	
all docs	docs citations	times ranked	citing authors	

#	Article	IF	CITATIONS
1	The minicircular and extremely heteroplasmic mitogenome of the holoparasitic plant Rhopalocnemis phalloides. Current Biology, 2022, 32, 470-479.e5.	3.9	28
2	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. Nature Communications, 2022, 13, 820.	12.8	4
3	<i>Fragaria</i> mitogenomes evolve rapidly in structure but slowly in sequence and incur frequent multinucleotide mutations mediated by microinversions. New Phytologist, 2022, 236, 745-759.	7.3	16
4	Plastid and mitochondrial phylogenomics reveal correlated substitution rate variation in Koenigia (Polygonoideae, Polygonaceae) and a reduced plastome for Koenigia delicatula including loss of all ndh genes. Molecular Phylogenetics and Evolution, 2022, 174, 107544.	2.7	5
5	Plastomes from tribe Plantagineae (Plantaginaceae) reveal infrageneric structural synapormorphies and localized hypermutation for Plantago and functional loss of ndh genes from Littorella. Molecular Phylogenetics and Evolution, 2021, 162, 107217.	2.7	23
6	Complete Mitogenomes of Two Aragoa Species and Phylogeny of Plantagineae (Plantaginaceae,) Tj ETQq0 0 0 rş	gBT ₃ /Overl	ock 10 Tf 50 5
7	The OXA2a Insertase of Arabidopsis Is Required for Cytochrome <i>c</i> Maturation. Plant Physiology, 2020, 184, 1042-1055.	4.8	4
8	Variation in protein gene and intron content among land plant mitogenomes. Mitochondrion, 2020, 53, 203-213.	3.4	64
9	Episodic and guanine–cytosineâ€biased bursts of intragenomic and interspecific synonymous divergence in Ajugoideae (Lamiaceae) mitogenomes. New Phytologist, 2020, 228, 1107-1114.	7.3	13
10	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. Journal of Experimental Botany, 2020, 71, 3361-3373.	4.8	9
11	Extensive ShiftsÂfrom <i>Cis</i> -to <i>Trans</i> -splicing of Gymnosperm Mitochondrial Introns. Molecular Biology and Evolution, 2020, 37, 1615-1620.	8.9	32
12	Assessing Anthocyanin Biosynthesis in Solanaceae as a Model Pathway for Secondary Metabolism. Genes, 2019, 10, 559.	2.4	14
13	Complete loss of RNA editing from the plastid genome and most highly expressed mitochondrial genes of Welwitschia mirabilis. Science China Life Sciences, 2019, 62, 498-506.	4.9	19
14	Origin and evolution of the octoploid strawberry genome. Nature Genetics, 2019, 51, 541-547.	21.4	469
15	The Mitochondrial Genome of Eleusine indica and Characterization of Gene Content Within Poaceae. Genome Biology and Evolution, 2019, 12, 3684-3697.	2.5	3
16	Lycophyte plastid genomics: extreme variation in <scp>GC</scp> , gene and intron content and multiple inversions between a direct and inverted orientation of the <scp>rRNA</scp> repeat. New Phytologist, 2019, 222, 1061-1075.	7.3	51
17	Structural Diversity Among Plastid Genomes of Land Plants. Advances in Botanical Research, 2018, 85, 263-292.	1.1	101
18	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (Fragaria vesca) with chromosome-scale contiguity. GigaScience, 2018, 7, 1-7.	6.4	209

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19	Phylogenomic evidence for ancient recombination between plastid genomes of the Cupressus-Juniperus-Xanthocyparis complex (Cupressaceae). BMC Evolutionary Biology, 2018, 18, 137.	3.2	17
20	High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. Molecular Biology and Evolution, 2018, 35, 2773-2785.	8.9	60
21	Mobile Elements Shape Plastome Evolution in Ferns. Genome Biology and Evolution, 2018, 10, 2558-2571.	2.5	25
22	Multiple origins of endosymbionts in Chlorellaceae with no reductive effects on the plastid or mitochondrial genomes. Scientific Reports, 2017, 7, 10101.	3.3	17
23	Complete chloroplast genome sequencing of vetiver grass (Chrysopogon zizanioides) identifies markers that distinguish the non-fertile †Sunshine†cultivar from other accessions. Industrial Crops and Products, 2017, 108, 629-635.	5.2	11
24	Complete mitochondrial genomes from the ferns <i>Ophioglossum californicum</i> and <i>Psilotum nudum</i> are highly repetitive with the largest organellar introns. New Phytologist, 2017, 213, 391-403.	7.3	83
25	Independent Evolution of Acetolactate Synthase–inhibiting Herbicide Resistance in WeedySorghumPopulations across Common Geographic Regions. Weed Science, 2017, 65, 164-176.	1.5	13
26	Limited mitogenomic degradation in response to a parasitic lifestyle in Orobanchaceae. Scientific Reports, 2016, 6, 36285.	3.3	33
27	Variable presence of the inverted repeat and plastome stability in <i>Erodium</i> . Annals of Botany, 2016, 117, 1209-1220.	2.9	94
28	Loss of a <i>Trans-</i> Splicing <i>nad1</i> Intron from Geraniaceae and Transfer of the Maturase Gene <i>matR</i> to the Nucleus in <i>Pelargonium</i> . Genome Biology and Evolution, 2016, 8, 3193-3201.	2.5	22
29	The Reverse Transcriptase/RNA Maturase Protein MatR Is Required for the Splicing of Various Group II Introns in Brassicaceae Mitochondria. Plant Cell, 2016, 28, 2805-2829.	6.6	91
30	Evolutionary dynamics of the plastid inverted repeat: the effects of expansion, contraction, and loss on substitution rates. New Phytologist, 2016, 209, 1747-1756.	7.3	352
31	<i>Ginkgo</i> and <i>Welwitschia</i> Mitogenomes Reveal Extreme Contrasts in Gymnosperm Mitochondrial Evolution. Molecular Biology and Evolution, 2016, 33, 1448-1460.	8.9	151
32	Dynamic evolution of <i>Geranium</i> mitochondrial genomes through multiple horizontal and intracellular gene transfers. New Phytologist, 2015, 208, 570-583.	7.3	84
33	Extreme Features of the Galdieria sulphuraria Organellar Genomes: A Consequence of Polyextremophily?. Genome Biology and Evolution, 2015, 7, 367-380.	2.5	31
34	Variable Frequency of Plastid RNA Editing among Ferns and Repeated Loss of Uridine-to-Cytidine Editing from Vascular Plants. PLoS ONE, 2015, 10, e0117075.	2.5	58
35	Predominant and Substoichiometric Isomers of the Plastid Genome Coexist within Juniperus Plants and Have Shifted Multiple Times during Cupressophyte Evolution. Genome Biology and Evolution, 2014, 6, 580-590.	2.5	91
36	Unprecedented Heterogeneity in the Synonymous Substitution Rate within a Plant Genome. Molecular Biology and Evolution, 2014, 31, 1228-1236.	8.9	103

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37	Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of Brassica oleracea. Mitochondrion, 2014, 19, 135-143.	3.4	81
38	Evolution of Plant Mitochondrial Intron-Encoded Maturases: Frequent Lineage-Specific Loss and Recurrent Intracellular Transfer to the Nucleus. Journal of Molecular Evolution, 2013, 77, 43-54.	1.8	39
39	Comparative analyses of two Geraniaceae transcriptomes using next-generation sequencing. BMC Plant Biology, 2013, 13, 228.	3.6	38
40	Complete plastid genomes from Ophioglossum californicum, Psilotum nudum, and Equisetum hyemale reveal an ancestral land plant genome structure and resolve the position of Equisetales among monilophytes. BMC Evolutionary Biology, 2013, 13, 8.	3.2	91
41	Evidence against Equimolarity of Large Repeat Arrangements and a Predominant Master Circle Structure of the Mitochondrial Genome from a Monkeyflower (Mimulus guttatus) Lineage with Cryptic CMS. Genome Biology and Evolution, 2012, 4, 670-686.	2.5	104
42	Loss of Two Introns from the Magnolia tripetala Mitochondrial cox2 Gene Implicates Horizontal Gene Transfer and Gene Conversion as a Novel Mechanism of Intron Loss. Molecular Biology and Evolution, 2012, 29, 3111-3120.	8.9	46
43	The Role of Horizontal Transfer in Shaping the Plant Mitochondrial Genome. Advances in Botanical Research, 2012, 63, 41-69.	1.1	25
44	Plant Mitochondrial Genome Diversity: The Genomics Revolution. , 2012, , 123-144.		151
45	Horizontal acquisition of multiple mitochondrial genes from a parasitic plant followed by gene conversion with host mitochondrial genes. BMC Biology, 2010, 8, 150.	3.8	104
46	The PREP suite: predictive RNA editors for plant mitochondrial genes, chloroplast genes and user-defined alignments. Nucleic Acids Research, 2009, 37, W253-W259.	14.5	302
47	Ribosomal protein L10 is encoded in the mitochondrial genome of many land plants and green algae. BMC Evolutionary Biology, 2009, 9, 265.	3.2	33
48	RNAi in Budding Yeast. Science, 2009, 326, 544-550.	12.6	480
49	Modeling Sites of RNA Editing as a Fifth Nucleotide State Reveals Progressive Loss of Edited Sites from Angiosperm Mitochondria. Molecular Biology and Evolution, 2008, 25, 52-61.	8.9	35
50	Frequent, Phylogenetically Local Horizontal Transfer of the cox1 Group I Intron in Flowering Plant Mitochondria. Molecular Biology and Evolution, 2008, 25, 1762-1777.	8.9	137
51	Extensive variation in synonymous substitution rates in mitochondrial genes of seed plants. BMC Evolutionary Biology, 2007, 7, 135.	3.2	219
52	Patterns of partial RNA editing in mitochondrial genes of Beta vulgaris. Molecular Genetics and Genomics, 2006, 276, 285-293.	2.1	94
53	The Complete Chloroplast Genome Sequence of Pelargonium \tilde{A} — hortorum: Organization and Evolution of the Largest and Most Highly Rearranged Chloroplast Genome of Land Plants. Molecular Biology and Evolution, 2006, 23, 2175-2190.	8.9	432
54	PREP-Mt: predictive RNA editor for plant mitochondrial genes. BMC Bioinformatics, 2005, 6, 96.	2.6	121

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55	Multiple major increases and decreases in mitochondrial substitution rates in the plant family Geraniaceae. BMC Evolutionary Biology, 2005, 5, 73.	3.2	141
56	Mitochondrial substitution rates are extraordinarily elevated and variable in a genus of flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17741-17746.	7.1	246
57	Gene transfer from parasitic to host plants. Nature, 2004, 432, 165-166.	27.8	237
58	Molecular Evolution of Bat Color Vision Genes. Molecular Biology and Evolution, 2003, 21, 295-302.	8.9	86