

Jeffrey P Mower

List of Publications by Year in descending order

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58
papers

5,653
citations

126907

33
h-index

138484

58
g-index

60
all docs

60
docs citations

60
times ranked

4891
citing authors

#	ARTICLE	IF	CITATIONS
1	RNAi in Budding Yeast. <i>Science</i> , 2009, 326, 544-550.	12.6	480
2	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	21.4	469
3	The Complete Chloroplast Genome Sequence of <i>Pelargonium Ã— hortorum</i> : Organization and Evolution of the Largest and Most Highly Rearranged Chloroplast Genome of Land Plants. <i>Molecular Biology and Evolution</i> , 2006, 23, 2175-2190.	8.9	432
4	Evolutionary dynamics of the plastid inverted repeat: the effects of expansion, contraction, and loss on substitution rates. <i>New Phytologist</i> , 2016, 209, 1747-1756.	7.3	352
5	The PREP suite: predictive RNA editors for plant mitochondrial genes, chloroplast genes and user-defined alignments. <i>Nucleic Acids Research</i> , 2009, 37, W253-W259.	14.5	302
6	Mitochondrial substitution rates are extraordinarily elevated and variable in a genus of flowering plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17741-17746.	7.1	246
7	Gene transfer from parasitic to host plants. <i>Nature</i> , 2004, 432, 165-166.	27.8	237
8	Extensive variation in synonymous substitution rates in mitochondrial genes of seed plants. <i>BMC Evolutionary Biology</i> , 2007, 7, 135.	3.2	219
9	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (<i>Fragaria vesca</i>) with chromosome-scale contiguity. <i>GigaScience</i> , 2018, 7, 1-7.	6.4	209
10	Plant Mitochondrial Genome Diversity: The Genomics Revolution. , 2012, , 123-144.		151
11	<i>Ginkgo</i> and <i>Welwitschia</i> Mitogenomes Reveal Extreme Contrasts in Gymnosperm Mitochondrial Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1448-1460.	8.9	151
12	Multiple major increases and decreases in mitochondrial substitution rates in the plant family Geraniaceae. <i>BMC Evolutionary Biology</i> , 2005, 5, 73.	3.2	141
13	Frequent, Phylogenetically Local Horizontal Transfer of the <i>cox1</i> Group I Intron in Flowering Plant Mitochondria. <i>Molecular Biology and Evolution</i> , 2008, 25, 1762-1777.	8.9	137
14	PREP-Mt: predictive RNA editor for plant mitochondrial genes. <i>BMC Bioinformatics</i> , 2005, 6, 96.	2.6	121
15	Horizontal acquisition of multiple mitochondrial genes from a parasitic plant followed by gene conversion with host mitochondrial genes. <i>BMC Biology</i> , 2010, 8, 150.	3.8	104
16	Evidence against Equimolarity of Large Repeat Arrangements and a Predominant Master Circle Structure of the Mitochondrial Genome from a Monkeyflower (<i>Mimulus guttatus</i>) Lineage with Cryptic CMS. <i>Genome Biology and Evolution</i> , 2012, 4, 670-686.	2.5	104
17	Unprecedented Heterogeneity in the Synonymous Substitution Rate within a Plant Genome. <i>Molecular Biology and Evolution</i> , 2014, 31, 1228-1236.	8.9	103
18	Structural Diversity Among Plastid Genomes of Land Plants. <i>Advances in Botanical Research</i> , 2018, 85, 263-292.	1.1	101

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19	Patterns of partial RNA editing in mitochondrial genes of <i>Beta vulgaris</i> . <i>Molecular Genetics and Genomics</i> , 2006, 276, 285-293.	2.1	94
20	Variable presence of the inverted repeat and plastome stability in <i>Erodium</i> . <i>Annals of Botany</i> , 2016, 117, 1209-1220.	2.9	94
21	Complete plastid genomes from <i>Ophioglossum californicum</i> , <i>Psilotum nudum</i> , and <i>Equisetum hyemale</i> reveal an ancestral land plant genome structure and resolve the position of Equisetales among monilophytes. <i>BMC Evolutionary Biology</i> , 2013, 13, 8.	3.2	91
22	Predominant and Substoichiometric Isomers of the Plastid Genome Coexist within Juniperus Plants and Have Shifted Multiple Times during Cupressophyte Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 580-590.	2.5	91
23	The Reverse Transcriptase/RNA Maturase Protein MatR Is Required for the Splicing of Various Group II Introns in Brassicaceae Mitochondria. <i>Plant Cell</i> , 2016, 28, 2805-2829.	6.6	91
24	Molecular Evolution of Bat Color Vision Genes. <i>Molecular Biology and Evolution</i> , 2003, 21, 295-302.	8.9	86
25	Dynamic evolution of <i>Geranium</i> mitochondrial genomes through multiple horizontal and intracellular gene transfers. <i>New Phytologist</i> , 2015, 208, 570-583.	7.3	84
26	Complete mitochondrial genomes from the ferns <i>Ophioglossum californicum</i> and <i>Psilotum nudum</i> are highly repetitive with the largest organellar introns. <i>New Phytologist</i> , 2017, 213, 391-403.	7.3	83
27	Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of <i>Brassica oleracea</i> . <i>Mitochondrion</i> , 2014, 19, 135-143.	3.4	81
28	Variation in protein gene and intron content among land plant mitogenomes. <i>Mitochondrion</i> , 2020, 53, 203-213.	3.4	64
29	High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 2773-2785.	8.9	60
30	Variable Frequency of Plastid RNA Editing among Ferns and Repeated Loss of Uridine-to-Cytidine Editing from Vascular Plants. <i>PLoS ONE</i> , 2015, 10, e0117075.	2.5	58
31	Lycophyte plastid genomics: extreme variation in $\langle \text{GC} \rangle$, gene and intron content and multiple inversions between a direct and inverted orientation of the $\langle \text{rRNA} \rangle$ repeat. <i>New Phytologist</i> , 2019, 222, 1061-1075.	7.3	51
32	Loss of Two Introns from the <i>Magnolia tripetala</i> Mitochondrial <i>cox2</i> Gene Implicates Horizontal Gene Transfer and Gene Conversion as a Novel Mechanism of Intron Loss. <i>Molecular Biology and Evolution</i> , 2012, 29, 3111-3120.	8.9	46
33	Evolution of Plant Mitochondrial Intron-Encoded Maturases: Frequent Lineage-Specific Loss and Recurrent Intracellular Transfer to the Nucleus. <i>Journal of Molecular Evolution</i> , 2013, 77, 43-54.	1.8	39
34	Comparative analyses of two Geraniaceae transcriptomes using next-generation sequencing. <i>BMC Plant Biology</i> , 2013, 13, 228.	3.6	38
35	Modeling Sites of RNA Editing as a Fifth Nucleotide State Reveals Progressive Loss of Edited Sites from Angiosperm Mitochondria. <i>Molecular Biology and Evolution</i> , 2008, 25, 52-61.	8.9	35
36	Ribosomal protein L10 is encoded in the mitochondrial genome of many land plants and green algae. <i>BMC Evolutionary Biology</i> , 2009, 9, 265.	3.2	33

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37	Limited mitogenomic degradation in response to a parasitic lifestyle in Orobanchaceae. <i>Scientific Reports</i> , 2016, 6, 36285.	3.3	33
38	Extensive Shifts from <i>Cis</i> - to <i>Trans</i> -splicing of Gymnosperm Mitochondrial Introns. <i>Molecular Biology and Evolution</i> , 2020, 37, 1615-1620.	8.9	32
39	Extreme Features of the <i>Galdieria sulphuraria</i> Organellar Genomes: A Consequence of Polyextremophily?. <i>Genome Biology and Evolution</i> , 2015, 7, 367-380.	2.5	31
40	The minicircular and extremely heteroplasmic mitogenome of the holoparasitic plant <i>Rhopalocnemis phalloides</i> . <i>Current Biology</i> , 2022, 32, 470-479.e5.	3.9	28
41	The Role of Horizontal Transfer in Shaping the Plant Mitochondrial Genome. <i>Advances in Botanical Research</i> , 2012, 63, 41-69.	1.1	25
42	Mobile Elements Shape Plastome Evolution in Ferns. <i>Genome Biology and Evolution</i> , 2018, 10, 2558-2571.	2.5	25
43	Plastomes from tribe Plantagineae (Plantaginaceae) reveal infrageneric structural synapomorphies and localized hypermutation for <i>Plantago</i> and functional loss of <i>ndh</i> genes from <i>Littorella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107217.	2.7	23
44	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> . <i>Genome Biology and Evolution</i> , 2016, 8, 3193-3201.	2.5	22
45	Complete loss of RNA editing from the plastid genome and most highly expressed mitochondrial genes of <i>Welwitschia mirabilis</i> . <i>Science China Life Sciences</i> , 2019, 62, 498-506.	4.9	19
46	Multiple origins of endosymbionts in <i>Chlorellaceae</i> with no reductive effects on the plastid or mitochondrial genomes. <i>Scientific Reports</i> , 2017, 7, 10101.	3.3	17
47	Phylogenomic evidence for ancient recombination between plastid genomes of the <i>Cupressus-Juniperus-Xanthocyparis</i> complex (Cupressaceae). <i>BMC Evolutionary Biology</i> , 2018, 18, 137.	3.2	17
48	<i>Fragaria</i> mitogenomes evolve rapidly in structure but slowly in sequence and incur frequent multinucleotide mutations mediated by microinversions. <i>New Phytologist</i> , 2022, 236, 745-759.	7.3	16
49	Assessing Anthocyanin Biosynthesis in Solanaceae as a Model Pathway for Secondary Metabolism. <i>Genes</i> , 2019, 10, 559.	2.4	14
50	Independent Evolution of Acetolactate Synthase-inhibiting Herbicide Resistance in Weedy <i>Sorghum</i> Populations across Common Geographic Regions. <i>Weed Science</i> , 2017, 65, 164-176.	1.5	13
51	Episodic and guanine-cytosine-biased bursts of intragenomic and interspecific synonymous divergence in <i>Ajugoideae</i> (Lamiaceae) mitogenomes. <i>New Phytologist</i> , 2020, 228, 1107-1114.	7.3	13
52	Complete chloroplast genome sequencing of vetiver grass (<i>Chrysopogon zizanioides</i>) identifies markers that distinguish the non-fertile "Sunshine"™ cultivar from other accessions. <i>Industrial Crops and Products</i> , 2017, 108, 629-635.	5.2	11
53	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. <i>Journal of Experimental Botany</i> , 2020, 71, 3361-3373.	4.8	9
54	Plastid and mitochondrial phylogenomics reveal correlated substitution rate variation in <i>Koenigia</i> (Polygonoideae, Polygonaceae) and a reduced plastome for <i>Koenigia delicatula</i> including loss of all <i>ndh</i> genes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107544.	2.7	5

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55	The OXA2a Insertase of Arabidopsis Is Required for Cytochrome <i>c</i> Maturation. <i>Plant Physiology</i> , 2020, 184, 1042-1055.	4.8	4
56	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. <i>Nature Communications</i> , 2022, 13, 820.	12.8	4
57	The Mitochondrial Genome of <i>Eleusine indica</i> and Characterization of Gene Content Within Poaceae. <i>Genome Biology and Evolution</i> , 2019, 12, 3684-3697.	2.5	3
58	Complete Mitogenomes of Two <i>Aragoa</i> Species and Phylogeny of Plantagineae (Plantaginaceae.) <i>Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50 6</i>	3.5	3