Robert K Jansen

List of Publications by Year
in descending order

104 papers	7,696 citations	61984 43 h-index	54911 84 g-index
108 all docs	108 docs citations	108 times ranked	4612 citing authors

#	Article	IF	Citations
1	Born in the mitochondrion and raised in the nucleus: Evolution of a novel tandem repeat family in Medicago polymorpha (Fabaceae). Plant Journal, 2022, , .	5.7	5
2	Genotype-specific patterns of physiological and antioxidative responses in barley under salinity stress. Cereal Research Communications, 2022, 50, 851-863.	1.6	6
3	Highly Resolved Papilionoid Legume Phylogeny Based on Plastid Phylogenomics. Frontiers in Plant Science, 2022, 13, 823190.	3.6	25
4	Effects of Salt Stress on Transcriptional and Physiological Responses in Barley Leaves with Contrasting Salt Tolerance. International Journal of Molecular Sciences, 2022, 23, 5006.	4.1	6
5	Extensive variation in nucleotide substitution rate and gene/intron loss in mitochondrial genomes of Pelargonium. Molecular Phylogenetics and Evolution, 2021, 155, 106986.	2.7	12
6	Differential expression of genes contributing to PCD triggered by exogenous oxalic acid in tomato (Solanum lycopersicum). Plant Biosystems, 2021, 155, 871-877.	1.6	2
7	Plastid Genomes of Flowering Plants: Essential Principles. Methods in Molecular Biology, 2021, 2317, 3-47.	0.9	16
8	Clade-Specific Plastid Inheritance Patterns Including Frequent Biparental Inheritance in Passiflora Interspecific Crosses. International Journal of Molecular Sciences, 2021, 22, 2278.	4.1	9
9	Transcriptional analysis of Rhazya stricta in response to jasmonic acid. Electronic Journal of Biotechnology, 2021, 50, 68-76.	2.2	0
10	The evolutionary fate of rpl32 and rps16 losses in the Euphorbia schimperi (Euphorbiaceae) plastome. Scientific Reports, 2021, 11, 7466.	3.3	15
11	The chicken or the egg? Plastome evolution and an independent loss of the inverted repeat in papilionoid legumes. Plant Journal, 2021, 107, 861-875.	5.7	29
12	Evaluating the contribution of osmotic and oxidative stress components on barley growth under salt stress. AoB PLANTS, 2021, 13, plab034.	2.3	19
13	Transcriptomic Analysis of Salt-Stress-Responsive Genes in Barley Roots and Leaves. International Journal of Molecular Sciences, 2021, 22, 8155.	4.1	23
14	In and out: Evolution of viral sequences in the mitochondrial genomes of legumes (Fabaceae). Molecular Phylogenetics and Evolution, 2021, 163, 107236.	2.7	9
15	Caught in the Act: Variation in plastid genome inverted repeat expansion within and between populations of <i>Medicago minima</i>. Ecology and Evolution, 2020, 10, 12129-12137.	1.9	12
16	Nucleotide substitution rates of diatom plastid encoded protein genes are positively correlated with genome architecture. Scientific Reports, 2020, 10, 14358.	3.3	7
17	Unprecedented Intraindividual Structural Heteroplasmy in Eleocharis (Cyperaceae, Poales) Plastomes. Genome Biology and Evolution, 2020, 12, 641-655.	2.5	22
18	Rampant Nuclear Transfer and Substitutions of Plastid Genes in Passiflora. Genome Biology and Evolution, 2020, 12, 1313-1329.	2.5	15

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19	Comparative Mitogenome Analysis of the Genus Trifolium Reveals Independent Gene Fission of ccmFn and Intracellular Gene Transfers in Fabaceae. International Journal of Molecular Sciences, 2020, 21, 1959.	4.1	17
20	Historical biogeography of Vochysiaceae reveals an unexpected perspective of plant evolution in the Neotropics. American Journal of Botany, 2020, 107, 1004-1020.	1.7	13
21	Under the rug: Abandoning persistent misconceptions that obfuscate organelle evolution. Molecular Phylogenetics and Evolution, 2020, 151, 106903.	2.7	42
22	Billie Lee Turner â€“ February 22, 1925 â€“ May 27, 2020. Lundellia, 2020, 23, .	0.1	0
23	Title is missing!. , 2020, 15, e0228400.		0
24	Title is missing!. , 2020, 15, e0228400.		0
25	Title is missing!. , 2020, 15, e0228400.		0
26	Title is missing!. , 2020, 15, e0228400.		0
27	<i>Passiflora</i> plastome sequencing reveals widespread genomic rearrangements. Journal of Systematics and Evolution, 2019, 57, 1-14.	3.1	61
28	Fluctuations in Fabaceae mitochondrial genome size and content are both ancient and recent. BMC Plant Biology, 2019, 19, 448.	3.6	32
29	Highly accelerated rates of genomic rearrangements and nucleotide substitutions in plastid genomes of Passiflora subgenus Decaloba. Molecular Phylogenetics and Evolution, 2019, 138, 53-64.	2.7	53
30	Incongruence between gene trees and species trees and phylogenetic signal variation in plastid genes. Molecular Phylogenetics and Evolution, 2019, 138, 219-232.	2.7	124
31	Lost and Found: Return of the Inverted Repeat in the Legume Clade Defined by Its Absence. Genome Biology and Evolution, 2019, 11, 1321-1333.	2.5	67
32	Plastome based phylogenetics and younger crown node age in Pelargonium. Molecular Phylogenetics and Evolution, 2019, 137, 33-43.	2.7	19
33	<i>ACE</i> insertion/deletion genetic polymorphism, serum <i>ACE</i> levels and high dietary salt intake influence the risk of obesity development among the Saudi adult population. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2019, 20, 147032031987094.	1.7	9
34	Aberration or Analogy? The Atypical Plastomes of Geraniaceae. Advances in Botanical Research, 2018, , 223-262.	1.1	32
35	Phylogenetic analysis and a review of the history of the accidental phytoplankter, Phaeodactylum tricornutum Bohlin (Bacillariophyta). PLoS ONE, 2018, 13, e0196744.	2.5	17
36	Recombinationâ€dependent replication and gene conversion homogenize repeat sequences and diversify plastid genome structure. American Journal of Botany, 2017, 104, 559-572.	1.7	86

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37	Plastome-Wide Nucleotide Substitution Rates Reveal Accelerated Rates in Papilionoideae and Correlations with Genome Features Across Legume Subfamilies. Journal of Molecular Evolution, 2017, 84, 187-203.	1.8	45
38	Expansion of inverted repeat does not decrease substitution rates in <i>Pelargonium</i> plastid genomes. New Phytologist, 2017, 214, 842-851.	7.3	99
39	Statistical hybrid detection and the inference of ancestral distribution areas in Tolpis (Asteraceae). Biological Journal of the Linnean Society, 2017, 121, 133-149.	1.6	6
40	Plastome Sequencing of Ten Nonmodel Crop Species Uncovers a Large Insertion of Mitochondrial DNA in Cashew. Plant Genome, 2017, 10, plantgenome2017.03.0020.	2.8	56
41	Molecular and Morphological Investigations of the Stauros-bearing, Raphid Pennate Diatoms (Bacillariophyceae): Craspedostauros E.J. Cox, and Staurotropis T.B.B. Paddock, and their Relationship to the Rest of the Mastogloiales. Protist, 2017, 168, 48-70.	1.5	30
42	Contrasting Patterns of Nucleotide Substitution Rates Provide Insight into Dynamic Evolution of Plastid and Mitochondrial Genomes of Geranium. Genome Biology and Evolution, 2017, 9, 1766-1780.	2.5	62
43	Transcriptomic and metabolic responses of Calotropis procera to salt and drought stress. BMC Plant Biology, 2017, 17, 231.	3.6	30
44	Transcriptomic analysis of salt stress responsive genes in Rhazya stricta. PLoS ONE, 2017, 12, e0177589.	2.5	27
45	Divergence of RNA polymerase Î± subunits in angiosperm plastid genomes is mediated by genomic rearrangement. Scientific Reports, 2016, 6, 24595.	3.3	47
46	Analysis of transcriptional response to heat stress in Rhazya stricta. BMC Plant Biology, 2016, 16, 252.	3.6	39
47	Multigene Assessment of Biodiversity of Diatom(Bacillariophyceae) Assemblages from the Littoral Zone of the Bohai and Yellow Seas in Yantai Region of Northeast China with some Remarks on Ubiquitous Taxa. Journal of Coastal Research, 2016, 74, 166-195.	0.3	32
48	The nuclear genome of Rhazya stricta and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. Scientific Reports, 2016, 6, 33782.	3.3	26
49	Variable presence of the inverted repeat and plastome stability in<i>Erodium</i>. Annals of Botany, 2016, 117, 1209-1220.	2.9	94
50	Coevolution between Nuclear-Encoded DNA Replication, Recombination, and Repair Genes and Plastid Genome Complexity. Genome Biology and Evolution, 2016, 8, 622-634.	2.5	51
51	Plastidâ€"Nuclear Interaction and Accelerated Coevolution in Plastid Ribosomal Genes in Geraniaceae. Genome Biology and Evolution, 2016, 8, 1824-1838.	2.5	68
52	Plastid genome sequences of legumes reveal parallel inversions and multiple losses of <i>rps16</i> in papilionoids. Journal of Systematics and Evolution, 2015, 53, 458-468.	3.1	125
53	Mimosoid legume plastome evolution: IR expansion, tandem repeat expansions and accelerated rate of evolution in clpP. Scientific Reports, 2015, 5, 16958.	3.3	125
54	Dynamic evolution of <i>Geranium</i> mitochondrial genomes through multiple horizontal and intracellular gene transfers. New Phytologist, 2015, 208, 570-583.	7.3	84

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55	Metabolomic Profiling of 13 Diatom Cultures and Their Adaptation to Nitrate-Limited Growth Conditions. PLoS ONE, 2015, 10, e0138965.	2.5	41
56	NDH expression marks major transitions in plant evolution and reveals coordinate intracellular gene loss. BMC Plant Biology, 2015, 15, 100.	3.6	89
57	Sources of inversion variation in the small single copy (SSC) region of chloroplast genomes. American Journal of Botany, 2015, 102, 1751-1752.	1.7	84
58	Coordinated Rates of Evolution between Interacting Plastid and Nuclear Genes in Geraniaceae. Plant Cell, 2015, 27, 563-573.	6.6	57
59	RNA-Seq analysis of the wild barley (H.Âspontaneum) leaf transcriptome under salt stress. Comptes Rendus - Biologies, 2015, 338, 285-297.	0.2	76
60	Complete plastome sequence of Thalictrum coreanum (Ranunculaceae) and transfer of the rpl32 gene to the nucleus in the ancestor of the subfamily Thalictroideae. BMC Plant Biology, 2015, 15, 40.	3.6	71
61	Dissecting signal and noise in diatom chloroplast protein encoding genes with phylogenetic information profiling. Molecular Phylogenetics and Evolution, 2015, 89, 28-36.	2.7	81
62	New Insights into Plagiogrammaceae (Bacillariophyta) Based on Multigene Phylogenies and Morphological Characteristics with the Description of a New Genus and Three New Species. PLoS ONE, 2015, 10, e0139300.	2.5	29
63	Conserved Gene Order and Expanded Inverted Repeats Characterize Plastid Genomes of Thalassiosirales. PLoS ONE, 2014, 9, e107854.	2.5	44
64	Retrotransposon-based molecular markers for assessment of genomic diversity. Functional Plant Biology, 2014, 41, 781.	2.1	13
65	Evolutionary and biotechnology implications of plastid genome variation in the invertedâ€repeatâ€lacking clade of legumes. Plant Biotechnology Journal, 2014, 12, 743-754.	8.3	146
66	The Plastid Genomes of Flowering Plants. Methods in Molecular Biology, 2014, 1132, 3-38.	0.9	151
67	Characterization of ten date palm (Phoenix dactylifera L.) cultivars from Saudi Arabia using AFLP and ISSR markers. Comptes Rendus - Biologies, 2014, 337, 6-18.	0.2	25
68	Reconstruction of the Ancestral Plastid Genome in Geraniaceae Reveals a Correlation between Genome Rearrangements, Repeats, and Nucleotide Substitution Rates. Molecular Biology and Evolution, 2014, 31, 645-659.	8.9	306
69	Corrected sequence of the wheat plastid genome. Comptes Rendus - Biologies, 2014, 337, 499-502.	0.2	6
70	Environmental stress activation of plant long-terminal repeat retrotransposons. Functional Plant Biology, 2014, 41, 557.	2.1	32
71	Complete sequences of organelle genomes from the medicinal plant Rhazya stricta(Apocynaceae) and contrasting patterns of mitochondrial genome evolution across asterids. BMC Genomics, 2014, 15, 405.	2.8	73
72	Whole Mitochondrial and Plastid Genome SNP Analysis of Nine Date Palm Cultivars Reveals Plastid Heteroplasmy and Close Phylogenetic Relationships among Cultivars. PLoS ONE, 2014, 9, e94158.	2.5	58

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73	Comparative analyses of two Geraniaceae transcriptomes using next-generation sequencing. BMC Plant Biology, 2013, 13, 228.	3.6	38
74	Phylogenetic analyses of <i>Tolpis</i> Adans. (Asteraceae) reveal patterns of adaptive radiation, multiple colonization and interspecific hybridization. Cladistics, 2013, 29, 416-434.	3.3	28
75	Phylogeny, rate variation, and genome size evolution of Pelargonium (Geraniaceae). Molecular Phylogenetics and Evolution, 2012, 64, 654-670.	2.7	55
76	Plastid Genomes of Seed Plants. Advances in Photosynthesis and Respiration, 2012, , 103-126.	1.0	268
77	Recent loss of plastid-encoded ndh genes within Erodium (Geraniaceae). Plant Molecular Biology, 2011, 76, 263-272.	3.9	140
78	Extreme Reconfiguration of Plastid Genomes in the Angiosperm Family Geraniaceae: Rearrangements, Repeats, and Codon Usage. Molecular Biology and Evolution, 2011, 28, 583-600.	8.9	338
79	Complete Plastid Genome Sequences of Three Rosids (Castanea, Prunus, Theobroma): Evidence for At Least Two Independent Transfers of rpl22 to the Nucleus. Molecular Biology and Evolution, 2011, 28, 835-847.	8.9	203
80	Taxonomic and biogeographic implications of a phylogenetic analysis of the Campanulaceae based on three chloroplast genes. Taxon, 2009, 58, 715-734.	0.7	72
81	Extensive Reorganization of the Plastid Genome of Trifolium subterraneum (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. Journal of Molecular Evolution, 2008, 67, 696-704.	1.8	217
82	Complete plastid genome sequence of the chickpea (Cicer arietinum) and the phylogenetic distribution of rps12 and clpP intron losses among legumes (Leguminosae). Molecular Phylogenetics and Evolution, 2008, 48, 1204-1217.	2.7	214
83	Genome-wide analyses of Geraniaceae plastid DNA reveal unprecedented patterns of increased nucleotide substitutions. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18424-18429.	7.1	162
84	Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19369-19374.	7.1	1,016
85	A Phylogeny of Euphorbieae Subtribe Euphorbiinae (Euphorbiaceae) Based on Molecular Data. Journal of Plant Biology, 2007, 50, 644-649.	2.1	34
86	Pollen Morphology and Ultrastructure of Calyceraceae. Lundellia, 2007, 10, 32-48.	0.1	9
87	Molecular systematics of <i>Descurainia</i> (Brassicaceae) in the Canary Islands: biogeographic and taxonomic implications. Taxon, 2006, 55, 671-682.	0.7	55
88	Phylogenetic analyses of Vitis (Vitaceae) based on complete chloroplast genome sequences: effects of taxon sampling and phylogenetic methods on resolving relationships among rosids. BMC Evolutionary Biology, 2006, 6, 32.	3.2	230
89	The Complete Chloroplast Genome Sequence of Pelargonium Ã— 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
90	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. Methods in Enzymology, 2005, 395, 348-384.	1.0	410

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91	Using molecular phylogenies to test phytogeographical links between East/South Africaâ€"Southern Arabia and the Macaronesian islandsâ€"a review, and the case of <i>Vierea</i> and <i>Pulicaria</i> section <i>Vieraeopsis</i> (Asteraceae). Taxon, 2004, 53, 333-346.	0.7	54
92	Origin and evolution of the endemic genera of Gonosperminae (Asteraceae: Anthemideae) from the Canary Islands: evidence from nucleotide sequences of the internal transcribed spacers of the nuclear ribosomal DNA. American Journal of Botany, 2001, 88, 161-169.	1.7	85
93	Origin and evolution of the endemic Macaronesian Inuleae (Asteraceae): evidence from the internal transcribed spacers of nuclear ribosomal DNA. Biological Journal of the Linnean Society, 2001, 72, 77-97.	1.6	3
94	Fast Phylogenetic Methods for the Analysis of Genome Rearrangement Data: An Empirical Study. , 2001, , .		14
95	Phylogenetic Implications of Pollen Morphology and Ultrastructure in The Barnadesioideae (Asteraceae). Lundellia, 2000, 3, 26-40.	0.1	21
96	Polemoniaceae phylogeny and classification: implications of sequence data from the chloroplast gene ndhF. American Journal of Botany, 2000, 87, 1300-1308.	1.7	25
97	Natural hybridization between an outcrossing and a selfingPhlox (Polemoniaceae): The maternal species of F1 hybrids. Plant Systematics and Evolution, 1999, 218, 153-158.	0.9	28
98	Molecular evidence for the phylogenetic position ofHanabusaya asiatica Nakai (Campanulaceae), an endemic species in Korea. Journal of Plant Biology, 1999, 42, 168-173.	2.1	8
99	Taxonomy and Phylogeny of a Gulf Coast Disjunct Group ofSpigelia(Loganiaceae Sensu Lato). Lundellia, 1999, 2, 1-13.	0.1	8
100	A chloroplast DNA phylogeny of lilacs (Syringa , Oleaceae): plastome groups show a strong correlation with crossing groups. American Journal of Botany, 1998, 85, 1338-1351.	1.7	32
101	Chloroplast DNA restriction site variation and phylogeny of the Berberidaceae. American Journal of Botany, 1998, 85, 1766-1778.	1.7	56
102	The highly rearranged chloroplast genome of Trachelium caeruleum (Campanulaceae): multiple inversions, inverted repeat expansion and contraction, transposition, insertions/deletions, and several repeat families. Current Genetics, 1997, 31, 419-429.	1.7	153
103	Systematic implications of chloroplast DNA VARIATION IN J altomata and selected physaloid genera (Solanaceae). American Journal of Botany, 1994, 81, 912-918.	1.7	19
104	Systematic Implications of Chloroplast DNA Variation in Jaltomata and Selected Physaloid Genera (Solanaceae). American Journal of Botany, 1994, 81, 912.	1.7	16