Jeffrey L Boore

List of Publications by Year
in descending order

117 papers	30,586 citations	10986 71 h-index	19190 118 g-index
120 all docs	120 docs citations	120 times ranked	23493 citing authors

#	Article	IF	Citations
1	Animal mitochondrial genomes. Nucleic Acids Research, 1999, 27, 1767-1780.	14.5	2,950
2	Automatic annotation of organellar genomes with DOGMA. Bioinformatics, 2004, 20, 3252-3255.	4.1	2,922
3	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
4	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167.	12.6	1,539
5	Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate. PLoS Biology, 2005, 3, e314.	5.6	1,280
6	The Ecoresponsive Genome of <i>Daphnia pulex</i>. Science, 2011, 331, 555-561.	12.6	1,086
7	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	17.5	1,069
8	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. Science, 2006, 313, 1261-1266.	12.6	1,059
9	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
10	Gene translocation links insects and crustaceans. Nature, 1998, 392, 667-668.	27.8	610
11	Insights into bilaterian evolution from three spiralian genomes. Nature, 2013, 493, 526-531.	27.8	564
12	Big trees from little genomes: mitochondrial gene order as a phylogenetic tool. Current Opinion in Genetics and Development, 1998, 8, 668-674.	3.3	552
13	The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. Cell, 2011, 147, 1171-1185.	28.9	509
14	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. Science, 2010, 330, 1549-1551.	12.6	492
15	Draft genome sequence and genetic transformation of the oleaginous alga Nannochloropsis gaditana. Nature Communications, 2012, 3, 686.	12.8	438
16	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
17	Deducing the pattern of arthropod phytogeny from mitochondrial DNA rearrangements. Nature, 1995, 376, 163-165.	27.8	414
18	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. Methods in Enzymology, 2005, 395, 348-384.	1.0	410

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19	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	9.6	391
20	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	12.6	371
21	Hexapod Origins: Monophyletic or Paraphyletic?. Science, 2003, 299, 1887-1889.	12.6	349
22	Comparative chloroplast genomics: analyses including new sequences from the angiosperms Nuphar advena and Ranunculus macranthus. BMC Genomics, 2007, 8, 174.	2.8	340
23	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
24	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i>. Science, 2013, 342, 1468-1473.	12.6	322
25	Mitochondrial Genomes of Galathealinum, Helobdella, and Platynereis: Sequence and Gene Arrangement Comparisons Indicate that Pogonophora Is Not a Phylum and Annelida and Arthropoda Are Not Sister Taxa. Molecular Biology and Evolution, 2000, 17, 87-106.	8.9	295
26	A novel type of RNA editing occurs in the mitochondrial tRNAs of the centipede Lithobius forficatus. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13738-13742.	7.1	288
27	A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.. Genetics, 1992, 131, 397-412.	2.9	284
28	Complete mtDNA Sequences of Two Millipedes Suggest a New Model for Mitochondrial Gene Rearrangements: Duplication and Nonrandom Loss. Molecular Biology and Evolution, 2002, 19, 163-169.	8.9	266
29	A comparative analysis of the <i>Lactuca</i> and <i>Helianthus</i> (Asteraceae) plastid genomes: identification of divergent regions and categorization of shared repeats. American Journal of Botany, 2007, 94, 302-312.	1.7	258
30	Extensive Rearrangements in the Chloroplast Genome of Trachelium caeruleum Are Associated with Repeats and tRNA Genes. Journal of Molecular Evolution, 2008, 66, 350-361.	1.8	257
31	The genome of the platyfish, Xiphophorus maculatus, provides insights into evolutionary adaptation and several complex traits. Nature Genetics, 2013, 45, 567-572.	21.4	251
32	Identifying the Basal Angiosperm Node in Chloroplast Genome Phylogenies: Sampling One's Way Out of the Felsenstein Zone. Molecular Biology and Evolution, 2005, 22, 1948-1963.	8.9	242
33	Morphological homoplasy, life history evolution, and historical biogeography of plethodontid salamanders inferred from complete mitochondrial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13820-13825.	7.1	233
34	The use of genome-level characters for phylogenetic reconstruction. Trends in Ecology and Evolution, 2006, 21, 439-446.	8.7	230
35	Phylogenetic position of the Pentastomida and (pan)crustacean relationships. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 537-544.	2.6	222
36	Naked corals: Skeleton loss in Scleractinia. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9096-9100.	7.1	221

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37	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
38	The Complete Mitochondrial DNA Sequence of the Horseshoe Crab Limulus polyphemus. Molecular Biology and Evolution, 2000, 17, 813-824.	8.9	199
39	The Complete Mitochondrial Genome Sequence of the Spider Habronattus oregonensis Reveals Rearranged and Extremely Truncated tRNAs. Molecular Biology and Evolution, 2004, 21, 893-902.	8.9	199
40	Sequencing and Comparing Whole Mitochondrial Genomes of Animals. Methods in Enzymology, 2005, 395, 311-348.	1.0	199
41	Implications of the Plastid Genome Sequence of Typha (Typhaceae, Poales) for Understanding Genome Evolution in Poaceae. Journal of Molecular Evolution, 2010, 70, 149-166.	1.8	196
42	Complete DNA sequence of the mitochondrial genome of the black chiton, Katharina tunicata.. Genetics, 1994, 138, 423-443.	2.9	194
43	Complete plastid genome sequences suggest strong selection for retention of photosynthetic genes in the parasitic plant genus Cuscuta. BMC Plant Biology, 2007, 7, 57.	3.6	162
44	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
45	Complete sequence of the mitochondrial DNA of the annelid worm Lumbricus terrestris.. Genetics, 1995, 141, 305-319.	2.9	160
46	Phylogenetic and evolutionary implications of complete chloroplast genome sequences of four early-diverging angiosperms: Buxus (Buxaceae), Chloranthus (Chloranthaceae), Dioscorea (Dioscoreaceae), and Illicium (Schisandraceae). Molecular Phylogenetics and Evolution, 2007, 45, 547-563.	2.7	154
47	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. Genome Biology and Evolution, 2010, 2, 425-440.	2.5	154
48	The Mitochondrial Genome of the Sipunculid Phascolopsis gouldii Supports Its Association with Annelida Rather than Mollusca. Molecular Biology and Evolution, 2002, 19, 127-137.	8.9	142
49	The Duplication/Random Loss Model for Gene Rearrangement Exemplified by Mitochondrial Genomes of Deuterostome Animals. Computational Biology, 2000, , 133-147.	0.2	138
50	Complete Sequences of the Highly Rearranged Molluscan Mitochondrial Genomes of the Scaphopod Graptacme eborea and the Bivalve Mytilus edulis. Molecular Biology and Evolution, 2004, 21, 1492-1503.	8.9	138
51	Complete plastid genome sequences of Drimys, Liriodendron, and Piper: implications for the phylogenetic relationships of magnoliids. BMC Evolutionary Biology, 2006, 6, 77.	3.2	138
52	Complete Sequence of the Mitochondrial Genome of the Tapeworm Hymenolepis diminuta: Gene Arrangements Indicate that Platyhelminths Are Eutrochozoans. Molecular Biology and Evolution, 2001, 18, 721-730.	8.9	134
53	Evolutionary Conservation of Regulatory Elements in Vertebrate <i>Hox</i> Gene Clusters. Genome Research, 2003, 13, 1111-1122.	5.5	130
54	The mitochondrial genome of Paraspadella gotoi is highly reduced and reveals that chaetognaths are a sister group to protostomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10639-10643.	7.1	122

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55	Molecular Mechanisms of Extensive Mitochondrial Gene Rearrangement in Plethodontid Salamanders. Molecular Biology and Evolution, 2005, 22, 2104-2112.	8.9	120
56	Complete plastome sequences of Equisetum arvense and Isoetes flaccida: implications for phylogeny and plastid genome evolution of early land plant lineages. BMC Evolutionary Biology, 2010, 10, 321.	3.2	120
57	The complete plastid genome sequence of Welwitschia mirabilis: an unusually compact plastome with accelerated divergence rates. BMC Evolutionary Biology, 2008, 8, 130.	3.2	110
58	Functional Gene Losses Occur with Minimal Size Reduction in the Plastid Genome of the Parasitic Liverwort Aneura mirabilis. Molecular Biology and Evolution, 2008, 25, 393-401.	8.9	108
59	Parallel Evolution of Truncated Transfer RNA Genes in Arachnid Mitochondrial Genomes. Molecular Biology and Evolution, 2008, 25, 949-959.	8.9	108
60	Phylogenetic relationships among amphisbaenian reptiles based on complete mitochondrial genomic sequences. Molecular Phylogenetics and Evolution, 2004, 33, 22-31.	2.7	102
61	The first complete chloroplast genome sequence of a lycophyte, Huperzia lucidula (Lycopodiaceae). Gene, 2005, 350, 117-128.	2.2	101
62	Systematics and plastid genome evolution of the cryptically photosynthetic parasitic plant genus Cuscuta(Convolvulaceae). BMC Biology, 2007, 5, 55.	3.8	98
63	The Complete Mitochondrial Genome of the Articulate Brachiopod Terebratalia transversa. Molecular Biology and Evolution, 2001, 18, 1734-1744.	8.9	96
64	Complete Mitochondrial Genome Sequence of the Polychaete Annelid Platynereis dumerilii. Molecular Biology and Evolution, 2001, 18, 1413-1416.	8.9	94
65	Domestication of olive fly through a multi-regional host shift to cultivated olives: Comparative dating using complete mitochondrial genomes. Molecular Phylogenetics and Evolution, 2010, 57, 678-686.	2.7	93
66	Mitochondrial genome data support the basal position of Acoelomorpha and the polyphyly of the Platyhelminthes. Molecular Phylogenetics and Evolution, 2004, 33, 321-332.	2.7	92
67	The complete mitochondrial genome of the enigmatic bigheaded turtle (Platysternon): description of unusual genomic features and the reconciliation of phylogenetic hypotheses based on mitochondrial and nuclear DNA. BMC Evolutionary Biology, 2006, 6, 11.	3.2	90
68	The Mitochondrial Genome of Phoronis architectaâ€"Comparisons Demonstrate that Phoronids Are Lophotrochozoan Protostomes. Molecular Biology and Evolution, 2004, 21, 153-157.	8.9	78
69	Group II Introns Break New Boundaries: Presence in a Bilaterian's Genome. PLoS ONE, 2008, 3, e1488.	2.5	78
70	The phylogeny of Mediterranean tortoises and their close relatives based on complete mitochondrial genome sequences from museum specimens. Molecular Phylogenetics and Evolution, 2006, 38, 50-64.	2.7	77
71	Comparative phylogenomic analyses of teleost fish Hox gene clusters: lessons from the cichlid fish Astatotilapia burtoni. BMC Genomics, 2007, 8, 317.	2.8	77
72	Arachnid relationships based on mitochondrial genomes: Asymmetric nucleotide and amino acid bias affects phylogenetic analyses. Molecular Phylogenetics and Evolution, 2009, 50, 117-128.	2.7	77

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73	The complete sequence of the mitochondrial genome of Nautilus macromphalus (Mollusca:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.8	75
74	The phylogeny of Nudibranchia (Opisthobranchia, Gastropoda, Mollusca) reconstructed by three molecular markers. Organisms Diversity and Evolution, 2001, 1, 241-256.	1.6	72
75	Complete sequence, gene arrangement, and genetic code of mitochondrial DNA of the cephalochordate Branchiostoma floridae (Amphioxus) [published erratum appears in Mol Biol Evol 1999 Jul;16(7):1010]. Molecular Biology and Evolution, 1999, 16, 410-418.	8.9	70
76	High divergence across the whole mitochondrial genome in the â€œpan-Antarcticâ€•springtail Friesea grisea: Evidence for cryptic species?. Gene, 2010, 449, 30-40.	2.2	65
77	Lophotrochozoan mitochondrial genomes. Integrative and Comparative Biology, 2006, 46, 544-557.	2.0	64
78	Chloroplast genome sequence of the moss Tortula ruralis: gene content, polymorphism, and structural arrangement relative to other green plant chloroplast genomes. BMC Genomics, 2010, 11, 143.	2.8	64
79	Sessile snails, dynamic genomes: gene rearrangements within the mitochondrial genome of a family of caenogastropod molluscs. BMC Genomics, 2010, 11, 440.	2.8	64
80	Molecular Evolution and Recombination in Gender-Associated Mitochondrial DNAs of the Manila Clam Tapes philippinarum. Genetics, 2003, 164, 603-611.	2.9	64
81	Rolling circle amplification of metazoan mitochondrial genomes. Molecular Phylogenetics and Evolution, 2006, 39, 562-567.	2.7	62
82	Multiple Origins and Rapid Evolution of Duplicated Mitochondrial Genes in Parthenogenetic Geckos (Heteronotia binoei; Squamata, Gekkonidae). Molecular Biology and Evolution, 2007, 24, 2775-2786.	8.9	59
83	Parallel Loss of Plastid Introns and Their Maturase in the Genus Cuscuta. PLoS ONE, 2009, 4, e5982.	2.5	58
84	A phylogenomic gene cluster resource: the Phylogenetically Inferred Groups (PhIGs) database. BMC Bioinformatics, 2006, 7, 201.	2.6	56
85	Molluscan mitochondrial genomes break the rules. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200159.	4.0	56
86	Genome size, cell size, and the evolution of enucleated erythrocytes in attenuate salamanders. Zoology, 2008, 111, 218-230.	1.2	55
87	Crawling through time: Transition of snails to slugs dating back to the Paleozoic, based on mitochondrial phylogenomics. Marine Genomics, 2011, 4, 51-59.	1.1	52
88	Complete mitochondrial genome sequence of Urechis caupo, a representative of the phylum Echiura. BMC Genomics, 2004, 5, 67.	2.8	51
89	Mitochondrial genome sequences and comparative genomics of Phytophthora ramorum and P. sojae. Current Genetics, 2007, 51, 285-296.	1.7	48
90	Genetic markers in blue crabs (Callinectes sapidus). Journal of Experimental Marine Biology and Ecology, 2005, 319, 15-27.	1.5	44

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91	The Complete Plastid Genome Sequence of Angiopteris evecta (G. Forst.) Hoffm. (Marattiaceae). American Fern Journal, 2007, 97, 95-106.	0.3	44
92	Beyond linear sequence comparisons: the use of genome-level characters for phylogenetic reconstruction. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 1445-1451.	4.0	41
93	The mitochondrial genome of the entomophagous endoparasite Xenos vesparum (Insecta:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.2	36
94	Divergence in cis-regulatory sequences surrounding the opsin gene arrays of African cichlid fishes. BMC Evolutionary Biology, 2011, 11, 120.	3.2	35
95	Requirements and Standards for Organelle Genome Databases. OMICS A Journal of Integrative Biology, 2006, 10, 119-126.	2.0	32
96	Evolutionary history of novel genes on the tammar wallaby Y chromosome: Implications for sex chromosome evolution. Genome Research, 2012, 22, 498-507.	5.5	32
97	Genomic evidence for populationâ€specific responses to coâ€evolving parasites in a New Zealand freshwater snail. Molecular Ecology, 2017, 26, 3663-3675.	3.9	32
98	Genes without frontiers?. Heredity, 2004, 92, 483-489.	2.6	30
99	Using partial genomic fosmid libraries for sequencing complete organellar genomes. BioTechniques, 2006, 41, 69-73.	1.8	29
100	The mitochondrial genomes of Campodea fragilis and Campodea lubbocki (Hexapoda: Diplura): High genetic divergence in a morphologically uniform taxon. Gene, 2006, 381, 49-61.	2.2	28
101	Gene annotation errors are common in the mammalian mitochondrial genomes database. BMC Genomics, 2019, 20, 73.	2.8	28
102	The complete mitochondrial genome of a gecko and the phylogenetic position of the Middle Eastern Teratoscincus keyserlingii. Molecular Phylogenetics and Evolution, 2005, 36, 188-193.	2.7	27
103	Organellar genomes of the four-toothed moss, Tetraphis pellucida. BMC Genomics, 2014, 15, 383.	2.8	27
104	Radical amino acid mutations persist longer in the absence of sex. Evolution; International Journal of Organic Evolution, 2018, 72, 808-824.	2.3	27
105	Analysis of the complete mitochondrial genome sequences of the soybean rust pathogens<i>Phakopsora pachyrhizi</i>and<i>P. meibomiae</i>. Mycologia, 2010, 102, 887-897.	1.9	23
106	Relationships between hexapods and crustaceans based on four mitochondrial genes. Crustacean Issues, 2005, , 295-306.	0.9	22
107	Genome Sequence of the Oleaginous Green Alga, Chlorella vulgaris UTEX 395. Frontiers in Bioengineering and Biotechnology, 2018, 6, 37.	4.1	21
108	Genomic analysis of a sexually-selected character: EST sequencing and microarray analysis of eye-antennal imaginal discs in the stalk-eyed fly Teleopsis dalmanni (Diopsidae). BMC Genomics, 2009, 10, 361.	2.8	20

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109	Response to Comment on "Hexapod Origins: Monophyletic or Paraphyletic?". Science, 2003, 301, 1482e-1482.	12.6	14
110	Colonization history of Galapagos giant tortoises: Insights from mitogenomes support the progression rule. Journal of Zoological Systematics and Evolutionary Research, 2020, 58, 1262-1275.	1.4	14
111	Development of simple sequence repeat markers for the soybean rust fungus, <i>Phakopsora pachyrhizi</i>. Molecular Ecology Resources, 2008, 8, 1310-1312.	4.8	13
112	Comparative genomic analysis of vertebrate mitochondrial reveals a differential of rearrangements rate between taxonomic class. Scientific Reports, 2022, 12, 5479.	3.3	13
113	Extensive Variation in Nuclear Mitochondrial DNA Content Between the Genomes of Phytophthora sojae and Phytophthora ramorum. Molecular Plant-Microbe Interactions, 2006, 19, 1329-1336.	2.6	10
114	Asexuality Associated with Marked Genomic Expansion of Tandemly Repeated rRNA and Histone Genes. Molecular Biology and Evolution, 2021, 38, 3581-3592.	8.9	9
115	Transmission of mitochondrial DNA - playing favorites?. BioEssays, 1997, 19, 751-753.	2.5	8
116	Entamoeba histolytica: a derived, mitochondriate eukaryote?. Trends in Microbiology, 1999, 7, 426-428.	7.7	6
117	DETECTING EVOLUTIONARY TRANSFER OF GENES USING PhIGs¹. Journal of Phycology, 2008, 44, 19-22.	2.3	3