

Jeffrey L Boore

List of Publications by Year in descending order

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117
papers

30,586
citations

10979

71
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19169

118
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120
all docs

120
docs citations

120
times ranked

23493
citing authors

#	ARTICLE	IF	CITATIONS
1	Animal mitochondrial genomes. <i>Nucleic Acids Research</i> , 1999, 27, 1767-1780.	6.5	2,950
2	Automatic annotation of organellar genomes with DOGMA. <i>Bioinformatics</i> , 2004, 20, 3252-3255.	1.8	2,922
3	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	6.0	1,712
4	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. <i>Science</i> , 2002, 298, 2157-2167.	6.0	1,539
5	Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate. <i>PLoS Biology</i> , 2005, 3, e314.	2.6	1,280
6	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	6.0	1,086
7	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
8	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	6.0	1,059
9	Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19369-19374.	3.3	1,016
10	Gene translocation links insects and crustaceans. <i>Nature</i> , 1998, 392, 667-668.	13.7	610
11	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
12	Big trees from little genomes: mitochondrial gene order as a phylogenetic tool. <i>Current Opinion in Genetics and Development</i> , 1998, 8, 668-674.	1.5	552
13	The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. <i>Cell</i> , 2011, 147, 1171-1185.	13.5	509
14	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	6.0	492
15	Draft genome sequence and genetic transformation of the oleaginous alga <i>Nannochloropsis gaditana</i> . <i>Nature Communications</i> , 2012, 3, 686.	5.8	438
16	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.	3.5	432
17	Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. <i>Nature</i> , 1995, 376, 163-165.	13.7	414
18	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. <i>Methods in Enzymology</i> , 2005, 395, 348-384.	0.4	410

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19	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
20	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	6.0	371
21	Hexapod Origins: Monophyletic or Paraphyletic?. <i>Science</i> , 2003, 299, 1887-1889.	6.0	349
22	Comparative chloroplast genomics: analyses including new sequences from the angiosperms <i>Nuphar advena</i> and <i>Ranunculus macranthus</i> . <i>BMC Genomics</i> , 2007, 8, 174.	1.2	340
23	Extreme Reconfiguration of Plastid Genomes in the Angiosperm Family Geraniaceae: Rearrangements, Repeats, and Codon Usage. <i>Molecular Biology and Evolution</i> , 2011, 28, 583-600.	3.5	338
24	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1468-1473.	6.0	322
25	Mitochondrial Genomes of Galathealium, Helobdella, and Platynereis: Sequence and Gene Arrangement Comparisons Indicate that Pogonophora Is Not a Phylum and Annelida and Arthropoda Are Not Sister Taxa. <i>Molecular Biology and Evolution</i> , 2000, 17, 87-106.	3.5	295
26	A novel type of RNA editing occurs in the mitochondrial tRNAs of the centipede <i>Lithobius forficatus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13738-13742.	3.3	288
27	A novel mitochondrial genome organization for the blue mussel, <i>Mytilus edulis</i> .. <i>Genetics</i> , 1992, 131, 397-412.	1.2	284
28	Complete mtDNA Sequences of Two Millipedes Suggest a New Model for Mitochondrial Gene Rearrangements: Duplication and Nonrandom Loss. <i>Molecular Biology and Evolution</i> , 2002, 19, 163-169.	3.5	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. <i>American Journal of Botany</i> , 2007, 94, 302-312.	0.8	258
30	Extensive Rearrangements in the Chloroplast Genome of <i>Trachelium caeruleum</i> Are Associated with Repeats and tRNA Genes. <i>Journal of Molecular Evolution</i> , 2008, 66, 350-361.	0.8	257
31	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013, 45, 567-572.	9.4	251
32	Identifying the Basal Angiosperm Node in Chloroplast Genome Phylogenies: Sampling One's Way Out of the Felsenstein Zone. <i>Molecular Biology and Evolution</i> , 2005, 22, 1948-1963.	3.5	242
33	Morphological homoplasy, life history evolution, and historical biogeography of plethodontid salamanders inferred from complete mitochondrial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13820-13825.	3.3	233
34	The use of genome-level characters for phylogenetic reconstruction. <i>Trends in Ecology and Evolution</i> , 2006, 21, 439-446.	4.2	230
35	Phylogenetic position of the Pentastomida and (pan)crustacean relationships. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 537-544.	1.2	222
36	Naked corals: Skeleton loss in Scleractinia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9096-9100.	3.3	221

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37	Extensive Reorganization of the Plastid Genome of <i>Trifolium subterraneum</i> (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. <i>Journal of Molecular Evolution</i> , 2008, 67, 696-704.	0.8	217
38	The Complete Mitochondrial DNA Sequence of the Horseshoe Crab <i>Limulus polyphemus</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 813-824.	3.5	199
39	The Complete Mitochondrial Genome Sequence of the Spider <i>Habronattus oregonensis</i> Reveals Rearranged and Extremely Truncated tRNAs. <i>Molecular Biology and Evolution</i> , 2004, 21, 893-902.	3.5	199
40	Sequencing and Comparing Whole Mitochondrial Genomes of Animals. <i>Methods in Enzymology</i> , 2005, 395, 311-348.	0.4	199
41	Implications of the Plastid Genome Sequence of <i>Typha</i> (Typhaceae, Poales) for Understanding Genome Evolution in Poaceae. <i>Journal of Molecular Evolution</i> , 2010, 70, 149-166.	0.8	196
42	Complete DNA sequence of the mitochondrial genome of the black chiton, <i>Katharina tunicata</i> .. <i>Genetics</i> , 1994, 138, 423-443.	1.2	194
43	Complete plastid genome sequences suggest strong selection for retention of photosynthetic genes in the parasitic plant genus <i>Cuscuta</i> . <i>BMC Plant Biology</i> , 2007, 7, 57.	1.6	162
44	Genome-wide analyses of Geraniaceae plastid DNA reveal unprecedented patterns of increased nucleotide substitutions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18424-18429.	3.3	162
45	Complete sequence of the mitochondrial DNA of the annelid worm <i>Lumbricus terrestris</i> .. <i>Genetics</i> , 1995, 141, 305-319.	1.2	160
46	Phylogenetic and evolutionary implications of complete chloroplast genome sequences of four early-diverging angiosperms: <i>Buxus</i> (Buxaceae), <i>Chloranthus</i> (Chloranthaceae), <i>Dioscorea</i> (Dioscoreaceae), and <i>Illicium</i> (Schisandraceae). <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 547-563.	1.2	154
47	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	1.1	154
48	The Mitochondrial Genome of the Sipunculid <i>Phascolopsis gouldii</i> Supports Its Association with Annelida Rather than Mollusca. <i>Molecular Biology and Evolution</i> , 2002, 19, 127-137.	3.5	142
49	The Duplication/Random Loss Model for Gene Rearrangement Exemplified by Mitochondrial Genomes of Deuterostome Animals. <i>Computational Biology</i> , 2000, , 133-147.	0.1	138
50	Complete Sequences of the Highly Rearranged Molluscan Mitochondrial Genomes of the Scaphopod <i>Graptacme eborea</i> and the Bivalve <i>Mytilus edulis</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1492-1503.	3.5	138
51	Complete plastid genome sequences of <i>Drimys</i> , <i>Liriodendron</i> , and <i>Piper</i> : implications for the phylogenetic relationships of magnoliids. <i>BMC Evolutionary Biology</i> , 2006, 6, 77.	3.2	138
52	Complete Sequence of the Mitochondrial Genome of the Tapeworm <i>Hymenolepis diminuta</i> : Gene Arrangements Indicate that Platyhelminths Are Eutrochozoans. <i>Molecular Biology and Evolution</i> , 2001, 18, 721-730.	3.5	134
53	Evolutionary Conservation of Regulatory Elements in Vertebrate Hox Gene Clusters. <i>Genome Research</i> , 2003, 13, 1111-1122.	2.4	130
54	The mitochondrial genome of <i>Paraspadella gotoi</i> is highly reduced and reveals that chaetognaths are a sister group to protostomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10639-10643.	3.3	122

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55	Molecular Mechanisms of Extensive Mitochondrial Gene Rearrangement in Plethodontid Salamanders. <i>Molecular Biology and Evolution</i> , 2005, 22, 2104-2112.	3.5	120
56	Complete plastome sequences of <i>Equisetum arvense</i> and <i>Isoetes flaccida</i> : implications for phylogeny and plastid genome evolution of early land plant lineages. <i>BMC Evolutionary Biology</i> , 2010, 10, 321.	3.2	120
57	The complete plastid genome sequence of <i>Welwitschia mirabilis</i> : an unusually compact plastome with accelerated divergence rates. <i>BMC Evolutionary Biology</i> , 2008, 8, 130.	3.2	110
58	Functional Gene Losses Occur with Minimal Size Reduction in the Plastid Genome of the Parasitic Liverwort <i>Aneura mirabilis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 393-401.	3.5	108
59	Parallel Evolution of Truncated Transfer RNA Genes in Arachnid Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 949-959.	3.5	108
60	Phylogenetic relationships among amphisbaenian reptiles based on complete mitochondrial genomic sequences. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 22-31.	1.2	102
61	The first complete chloroplast genome sequence of a lycophyte, <i>Huperzia lucidula</i> (Lycopodiaceae). <i>Gene</i> , 2005, 350, 117-128.	1.0	101
62	Systematics and plastid genome evolution of the cryptically photosynthetic parasitic plant genus <i>Cuscuta</i> (Convolvulaceae). <i>BMC Biology</i> , 2007, 5, 55.	1.7	98
63	The Complete Mitochondrial Genome of the Articulate Brachiopod <i>Terebratalia transversa</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1734-1744.	3.5	96
64	Complete Mitochondrial Genome Sequence of the Polychaete Annelid <i>Platynereis dumerilii</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1413-1416.	3.5	94
65	Domestication of olive fly through a multi-regional host shift to cultivated olives: Comparative dating using complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 678-686.	1.2	93
66	Mitochondrial genome data support the basal position of Acoelomorpha and the polyphyly of the Platyhelminthes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 321-332.	1.2	92
67	The complete mitochondrial genome of the enigmatic bigheaded turtle (<i>Platysternon</i>): description of unusual genomic features and the reconciliation of phylogenetic hypotheses based on mitochondrial and nuclear DNA. <i>BMC Evolutionary Biology</i> , 2006, 6, 11.	3.2	90
68	The Mitochondrial Genome of <i>Phoronis architecta</i> —Comparisons Demonstrate that Phoronids Are Lophotrochozoan Protostomes. <i>Molecular Biology and Evolution</i> , 2004, 21, 153-157.	3.5	78
69	Group II Introns Break New Boundaries: Presence in a Bilaterian's Genome. <i>PLoS ONE</i> , 2008, 3, e1488.	1.1	78
70	The phylogeny of Mediterranean tortoises and their close relatives based on complete mitochondrial genome sequences from museum specimens. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 50-64.	1.2	77
71	Comparative phylogenomic analyses of teleost fish Hox gene clusters: lessons from the cichlid fish <i>Astatotilapia burtoni</i> . <i>BMC Genomics</i> , 2007, 8, 317.	1.2	77
72	Arachnid relationships based on mitochondrial genomes: Asymmetric nucleotide and amino acid bias affects phylogenetic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 117-128.	1.2	77

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73	The complete sequence of the mitochondrial genome of <i>Nautilus macromphalus</i> (Mollusca: Tj ETQq1 1 0.784314 192 / Overlock 10 1997)	1.2	75
74	The phylogeny of Nudibranchia (Opisthobranchia, Gastropoda, Mollusca) reconstructed by three molecular markers. <i>Organisms Diversity and Evolution</i> , 2001, 1, 241-256.	0.7	72
75	Complete sequence, gene arrangement, and genetic code of mitochondrial DNA of the cephalochordate <i>Branchiostoma floridae</i> (<i>Amphioxus</i>) [published erratum appears in <i>Mol Biol Evol</i> 1999 Jul;16(7):1010]. <i>Molecular Biology and Evolution</i> , 1999, 16, 410-418.	3.5	70
76	High divergence across the whole mitochondrial genome in the "span-Antarctic" springtail <i>Friesea grisea</i> : Evidence for cryptic species?. <i>Gene</i> , 2010, 449, 30-40.	1.0	65
77	Lophotrochozoan mitochondrial genomes. <i>Integrative and Comparative Biology</i> , 2006, 46, 544-557.	0.9	64
78	Chloroplast genome sequence of the moss <i>Tortula ruralis</i> : gene content, polymorphism, and structural arrangement relative to other green plant chloroplast genomes. <i>BMC Genomics</i> , 2010, 11, 143.	1.2	64
79	Sessile snails, dynamic genomes: gene rearrangements within the mitochondrial genome of a family of caenogastropod molluscs. <i>BMC Genomics</i> , 2010, 11, 440.	1.2	64
80	Molecular Evolution and Recombination in Gender-Associated Mitochondrial DNAs of the Manila Clam <i>Tapes philippinarum</i> . <i>Genetics</i> , 2003, 164, 603-611.	1.2	64
81	Rolling circle amplification of metazoan mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 562-567.	1.2	62
82	Multiple Origins and Rapid Evolution of Duplicated Mitochondrial Genes in Parthenogenetic Geckos (<i>Heteronotia binoei</i> ; Squamata, Gekkonidae). <i>Molecular Biology and Evolution</i> , 2007, 24, 2775-2786.	3.5	59
83	Parallel Loss of Plastid Introns and Their Maturase in the Genus <i>Cuscuta</i> . <i>PLoS ONE</i> , 2009, 4, e5982.	1.1	58
84	A phylogenomic gene cluster resource: the Phylogenetically Inferred Groups (PhIGs) database. <i>BMC Bioinformatics</i> , 2006, 7, 201.	1.2	56
85	Molluscan mitochondrial genomes break the rules. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200159.	1.8	56
86	Genome size, cell size, and the evolution of enucleated erythrocytes in attenuate salamanders. <i>Zoology</i> , 2008, 111, 218-230.	0.6	55
87	Crawling through time: Transition of snails to slugs dating back to the Paleozoic, based on mitochondrial phylogenomics. <i>Marine Genomics</i> , 2011, 4, 51-59.	0.4	52
88	Complete mitochondrial genome sequence of <i>Urechis caupo</i> , a representative of the phylum Echiura. <i>BMC Genomics</i> , 2004, 5, 67.	1.2	51
89	Mitochondrial genome sequences and comparative genomics of <i>Phytophthora ramorum</i> and <i>P. sojae</i> . <i>Current Genetics</i> , 2007, 51, 285-296.	0.8	48
90	Genetic markers in blue crabs (<i>Callinectes sapidus</i>). <i>Journal of Experimental Marine Biology and Ecology</i> , 2005, 319, 15-27.	0.7	44

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91	The Complete Plastid Genome Sequence of <i>Angiopteris evecta</i> (G. Forst.) Hoffm. (Marattiaceae). <i>American Fern Journal</i> , 2007, 97, 95-106.	0.2	44
92	Beyond linear sequence comparisons: the use of genome-level characters for phylogenetic reconstruction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1445-1451.	1.8	41
93	The mitochondrial genome of the entomophagous endoparasite <i>Xenos vesparum</i> (Insecta: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.0	36
94	Divergence in cis-regulatory sequences surrounding the opsin gene arrays of African cichlid fishes. <i>BMC Evolutionary Biology</i> , 2011, 11, 120.	3.2	35
95	Requirements and Standards for Organelle Genome Databases. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 119-126.	1.0	32
96	Evolutionary history of novel genes on the tammar wallaby Y chromosome: Implications for sex chromosome evolution. <i>Genome Research</i> , 2012, 22, 498-507.	2.4	32
97	Genomic evidence for population-specific responses to co-evolving parasites in a New Zealand freshwater snail. <i>Molecular Ecology</i> , 2017, 26, 3663-3675.	2.0	32
98	Genes without frontiers?. <i>Heredity</i> , 2004, 92, 483-489.	1.2	30
99	Using partial genomic fosmid libraries for sequencing complete organellar genomes. <i>BioTechniques</i> , 2006, 41, 69-73.	0.8	29
100	The mitochondrial genomes of <i>Campodea fragilis</i> and <i>Campodea lubbocki</i> (Hexapoda: Diplura): High genetic divergence in a morphologically uniform taxon. <i>Gene</i> , 2006, 381, 49-61.	1.0	28
101	Gene annotation errors are common in the mammalian mitochondrial genomes database. <i>BMC Genomics</i> , 2019, 20, 73.	1.2	28
102	The complete mitochondrial genome of a gecko and the phylogenetic position of the Middle Eastern <i>Teratoscincus keyserlingii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 188-193.	1.2	27
103	Organellar genomes of the four-toothed moss, <i>Tetraphis pellucida</i> . <i>BMC Genomics</i> , 2014, 15, 383.	1.2	27
104	Radical amino acid mutations persist longer in the absence of sex. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 808-824.	1.1	27
105	Analysis of the complete mitochondrial genome sequences of the soybean rust pathogens <i>Phakopsora pachyrhizi</i> and <i>P. meibomia</i> . <i>Mycologia</i> , 2010, 102, 887-897.	0.8	23
106	Relationships between hexapods and crustaceans based on four mitochondrial genes. <i>Crustacean Issues</i> , 2005, , 295-306.	0.9	22
107	Genome Sequence of the Oleaginous Green Alga, <i>Chlorella vulgaris</i> UTEX 395. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 37.	2.0	21
108	Genomic analysis of a sexually-selected character: EST sequencing and microarray analysis of eye-antennal imaginal discs in the stalk-eyed fly <i>Teleopsis dalmanni</i> (Diopsidae). <i>BMC Genomics</i> , 2009, 10, 361.	1.2	20

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109	Response to Comment on "Hexapod Origins: Monophyletic or Paraphyletic?". <i>Science</i> , 2003, 301, 1482e-1482.	6.0	14
110	Colonization history of Galapagos giant tortoises: Insights from mitogenomes support the progression rule. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1262-1275.	0.6	14
111	Development of simple sequence repeat markers for the soybean rust fungus, <i>Phakopsora pachyrhizi</i> . <i>Molecular Ecology Resources</i> , 2008, 8, 1310-1312.	2.2	13
112	Comparative genomic analysis of vertebrate mitochondrial reveals a differential of rearrangements rate between taxonomic class. <i>Scientific Reports</i> , 2022, 12, 5479.	1.6	13
113	Extensive Variation in Nuclear Mitochondrial DNA Content Between the Genomes of <i>Phytophthora sojae</i> and <i>Phytophthora ramorum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1329-1336.	1.4	10
114	Asexuality Associated with Marked Genomic Expansion of Tandemly Repeated rRNA and Histone Genes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3581-3592.	3.5	9
115	Transmission of mitochondrial DNA - playing favorites?. <i>BioEssays</i> , 1997, 19, 751-753.	1.2	8
116	<i>Entamoeba histolytica</i> : a derived, mitochondriate eukaryote?. <i>Trends in Microbiology</i> , 1999, 7, 426-428.	3.5	6
117	DETECTING EVOLUTIONARY TRANSFER OF GENES USING PhIGs ¹ . <i>Journal of Phycology</i> , 2008, 44, 19-22.	1.0	3