

Peter G Foster

List of Publications by Year in descending order

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79
papers

8,434
citations

71004

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79
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81
all docs

81
docs citations

81
times ranked

9056
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
2	Phylogeny and temporal diversification of mosquitoes (Diptera: Culicidae) with an emphasis on the Neotropical fauna. <i>Systematic Entomology</i> , 2021, 46, 798-811.	1.7	20
3	<i>Anopheles darlingi</i> versus <i>Nyssorhynchus darlingi</i> , the discussion continues. <i>Trends in Parasitology</i> , 2021, 37, 847-848.	1.5	3
4	Phylogenomics provides robust support for a two-domains tree of life. <i>Nature Ecology and Evolution</i> , 2020, 4, 138-147.	3.4	159
5	The Chloroplast Land Plant Phylogeny: Analyses Employing Better-Fitting Tree- and Site-Heterogeneous Composition Models. <i>Frontiers in Plant Science</i> , 2020, 11, 1062.	1.7	19
6	The mitochondrial phylogeny of land plants shows support for Setaphyta under composition-heterogeneous substitution models. <i>PeerJ</i> , 2020, 8, e8995.	0.9	18
7	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. <i>ISME Journal</i> , 2019, 13, 2150-2161.	4.4	108
8	Environment-dependent fitness gains can be driven by horizontal gene transfer of transporter-encoding genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5613-5622.	3.3	37
9	Nuclear protein phylogenies support the monophyly of the three bryophyte groups (Bryophyta) Tj ETQq1 1 0.784314 rgBT /Overlock 3.5 84		
10	Curious bivalves: Systematic utility and unusual properties of anomalodesmatan mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 60-72.	1.2	24
11	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4602-E4611.	3.3	232
12	Phylogeny of Anophelinae using mitochondrial protein coding genes. <i>Royal Society Open Science</i> , 2017, 4, 170758.	1.1	83
13	Can quartet analyses combining maximum likelihood estimation and Hennigian logic overcome long branch attraction in phylogenomic sequence data?. <i>PLoS ONE</i> , 2017, 12, e0183393.	1.1	4
14	Mitochondrial Genomes of <i>Anopheles</i> (<i>Kerteszia</i>) (Diptera: Culicidae) From the Atlantic Forest, Brazil. <i>Journal of Medical Entomology</i> , 2016, 53, 790-797.	0.9	17
15	Family-Level Sampling of Mitochondrial Genomes in Coleoptera: Compositional Heterogeneity and Phylogenetics. <i>Genome Biology and Evolution</i> , 2016, 8, 161-175.	1.1	157
16	Next-Generation Mitogenomics: A Comparison of Approaches Applied to Caecilian Amphibian Phylogeny. <i>PLoS ONE</i> , 2016, 11, e0156757.	1.1	13
17	Implementing and testing Bayesian and maximum-likelihood supertree methods in phylogenetics. <i>Royal Society Open Science</i> , 2015, 2, 140436.	1.1	49
18	Mitochondrial genomes and comparative analyses of <i>Culex camposi</i> , <i>Culex coronator</i> , <i>Culex usquat</i> and <i>Culex usquatissimus</i> (Diptera:Culicidae), members of the coronator group. <i>BMC Genomics</i> , 2015, 16, 831.	1.2	35

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19	The complete mitochondrial genome of <i>Limnoria quadripunctata</i> Holthuis (Isopoda: Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	0.6	10
20	Horizontal gene flow from Eubacteria to Archaeobacteria and what it means for our understanding of eukaryogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140337.	1.8	23
21	Compositional Biases among Synonymous Substitutions Cause Conflict between Gene and Protein Trees for Plastid Origins. <i>Molecular Biology and Evolution</i> , 2014, 31, 1697-1709.	3.5	49
22	Reduced Glycemic Variability in Diazoxide-Responsive Children with Congenital Hyperinsulinism Using Supplemental Omega-3-Polyunsaturated Fatty Acids; A Pilot Trial with MaxEPAR. <i>Frontiers in Endocrinology</i> , 2014, 5, 31.	1.5	9
23	Analyses of Charophyte Chloroplast Genomes Help Characterize the Ancestral Chloroplast Genome of Land Plants. <i>Genome Biology and Evolution</i> , 2014, 6, 897-911.	1.1	62
24	The mitochondrial genome of <i>Parascaris univalens</i> - implications for a "forgotten" parasite. <i>Parasites and Vectors</i> , 2014, 7, 428.	1.0	30
25	Case-Deletion Diagnostics for Linear Mixed Models. <i>Technometrics</i> , 2014, 56, 269-281.	1.3	16
26	Development of anonymous nuclear markers from Illumina paired-end data for Seychelles caecilian amphibians (Gymnophiona: Indotyphlidae). <i>Conservation Genetics Resources</i> , 2014, 6, 289-291.	0.4	6
27	The complete mitochondrial genome of a turbinid vetigastropod from MiSeq Illumina sequencing of genomic DNA and steps towards a resolved gastropod phylogeny. <i>Gene</i> , 2014, 533, 38-47.	1.0	86
28	Conflicting Phylogenies for Early Land Plants are Caused by Composition Biases among Synonymous Substitutions. <i>Systematic Biology</i> , 2014, 63, 272-279.	2.7	172
29	Patterns of prokaryotic lateral gene transfers affecting parasitic microbial eukaryotes. <i>Genome Biology</i> , 2013, 14, R19.	13.9	80
30	Reduction and Expansion in Microsporidian Genome Evolution: New Insights from Comparative Genomics. <i>Genome Biology and Evolution</i> , 2013, 5, 2285-2303.	1.1	114
31	An archaeal origin of eukaryotes supports only two primary domains of life. <i>Nature</i> , 2013, 504, 231-236.	13.7	456
32	A 20-state empirical amino-acid substitution model for green plant chloroplasts. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 218-220.	1.2	21
33	Whole-community DNA barcoding reveals a spatio-temporal continuum of biodiversity at species and genetic levels. <i>Nature Communications</i> , 2013, 4, 1892.	5.8	71
34	Heterogeneous Models Place the Root of the Placental Mammal Phylogeny. <i>Molecular Biology and Evolution</i> , 2013, 30, 2145-2156.	3.5	115
35	Phylogenetic Analysis and DNA-based Species Confirmation in <i>Anopheles</i> (<i>Nyssorhynchus</i>). <i>PLoS ONE</i> , 2013, 8, e54063.	1.1	78
36	A congruent phylogenomic signal places eukaryotes within the Archaea. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4870-4879.	1.2	126

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37	Next generation sequencing and comparative analyses of <i>Xenopus</i> mitogenomes. <i>BMC Genomics</i> , 2012, 13, 496.	1.2	23
38	Horizontal gene transfer facilitated the evolution of plant parasitic mechanisms in the oomycetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15258-15263.	3.3	225
39	Detection of a new yellow fever virus lineage within the South American genotype I in Brazil. <i>Journal of Medical Virology</i> , 2010, 82, 175-185.	2.5	68
40	Resurrection of Two Species From Synonymy of <i>Anopheles</i> (<i>Nyssorhynchus </i>) <i>strodei Root, and Characterization of a Distinct Morphological Form From the Strodei Complex (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2010, 47, 504-526.	0.9	11
41	Resurrection of Two Species From Synonymy of <i>Anopheles</i> (<i>Nyssorhynchus</i>) <i>strodei</i> Root, and Characterization of a Distinct Morphological Form From the Strodei Complex (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2010, 47, 504-526.	0.9	17
42	Phylogenetic relationships among species of <i>Anopheles</i> (<i>Nyssorhynchus</i>) (Diptera, Culicidae) based on nuclear and mitochondrial gene sequences. <i>Acta Tropica</i> , 2010, 114, 88-96.	0.9	32
43	Phylogenomic Analysis Demonstrates a Pattern of Rare and Ancient Horizontal Gene Transfer between Plants and Fungi. <i>Plant Cell</i> , 2009, 21, 1897-1911.	3.1	162
44	The primary divisions of life: a phylogenomic approach employing composition-heterogeneous methods. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2197-2207.	1.8	103
45	Horizontal Gene Transfer in Eukaryotic Parasites: A Case Study of <i>Entamoeba histolytica</i> and <i>Trichomonas vaginalis</i> . <i>Methods in Molecular Biology</i> , 2009, 532, 489-500.	0.4	48
46	Detection of a new mumps virus genotype during parotitis epidemic of 2006-2007 in the State of São Paulo, Brazil. <i>Journal of Medical Virology</i> , 2008, 80, 323-329.	2.5	25
47	The archaeobacterial origin of eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20356-20361.	3.3	306
48	Resurrection of <i>Anopheles goeldii</i> from synonymy with <i>Anopheles nuneztovari</i> (Diptera, Culicidae) and a new record for <i>Anopheles dunhami</i> in the Brazilian Amazon. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2008, 103, 791-799.	0.8	28
49	Phylogeny of the <i>Leucosphyrus</i> Group of <i>Anopheles</i> (<i>Cellia</i>) (Diptera: Culicidae) Based on Mitochondrial Gene Sequences. <i>Annals of the Entomological Society of America</i> , 2007, 100, 27-35.	1.3	27
50	Of clades and clans: terms for phylogenetic relationships in unrooted trees. <i>Trends in Ecology and Evolution</i> , 2007, 22, 114-115.	4.2	145
51	Structure and Content of the <i>Entamoeba histolytica</i> Genome. <i>Advances in Parasitology</i> , 2007, 65, 51-190.	1.4	188
52	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
53	VNTR analysis of selected outbreaks of <i>Burkholderia pseudomallei</i> in Australia. <i>Infection, Genetics and Evolution</i> , 2007, 7, 416-423.	1.0	32
54	The nematode?arthropod clade revisited: phylogenomic analyses from ribosomal protein genes misled by shared evolutionary biases. <i>Cladistics</i> , 2007, 23, 130-144.	1.5	12

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55	Evolution of four gene families with patchy phylogenetic distributions: influx of genes into protist genomes. <i>BMC Evolutionary Biology</i> , 2006, 6, 27.	3.2	94
56	Evolutionary Origins of the Eukaryotic Shikimate Pathway: Gene Fusions, Horizontal Gene Transfer, and Endosymbiotic Replacements. <i>Eukaryotic Cell</i> , 2006, 5, 1517-1531.	3.4	170
57	Dense Taxonomic EST Sampling and Its Applications for Molecular Systematics of the Coleoptera (Beetles). <i>Molecular Biology and Evolution</i> , 2006, 23, 268-278.	3.5	86
58	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005, 433, 865-868.	13.7	783
59	Inference of the Phylogenetic Position of Oxymonads Based on Nine Genes: Support for Metamonada and Excavata. <i>Molecular Biology and Evolution</i> , 2005, 22, 2508-2518.	3.5	66
60	Molecular Phylogeny of Neotropical <i>Anopheles</i> (<i>Nyssorhynchus</i>) <i>albitarsis</i> Species Complex (Diptera: Culicidae). <i>Annals of the Entomological Society of America</i> , 2005, 98, 918-925.	1.3	42
61	Behavioral and Physical Masculinization Are Related to Genotype in Girls with Congenital Adrenal Hyperplasia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2004, 89, 419-424.	1.8	98
62	Modeling Compositional Heterogeneity. <i>Systematic Biology</i> , 2004, 53, 485-495.	2.7	438
63	<i>Trichomonas</i> hydrogenosomes contain the NADH dehydrogenase module of mitochondrial complex I. <i>Nature</i> , 2004, 432, 618-622.	13.7	247
64	Molecular analysis of the dengue virus type 1 and 2 in Brazil based on sequences of the genomic envelope-nonstructural protein 1 junction region. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2004, 46, 145-152.	0.5	5
65	Hydrogenosomes, Mitochondria and Early Eukaryotic Evolution. <i>IUBMB Life</i> , 2003, 55, 387-395.	1.5	151
66	An ultrastructural and molecular study of <i>Hyperamoeba dachnaya</i> , n. sp., and its relationship to the mycetozoan slime moulds. <i>European Journal of Protistology</i> , 2003, 39, 319-336.	0.5	29
67	Mitochondria and hydrogenosomes are two forms of the same fundamental organelle. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2003, 358, 191-203.	1.8	138
68	Type 1 Error Rates of the Parsimony Permutation Tail Probability Test. <i>Systematic Biology</i> , 2002, 51, 524-527.	2.7	13
69	Phylogeny of Anophelinae (Diptera: Culicidae) based on nuclear ribosomal and mitochondrial DNA sequences. <i>Systematic Entomology</i> , 2002, 27, 361-382.	1.7	120
70	Comparison of EST libraries from seven beetle species: towards a framework for phylogenomics of the Coleoptera. <i>Insect Molecular Biology</i> , 2002, 11, 467-475.	1.0	37
71	Bias in Phylogenetic Estimation and Its Relevance to the Choice between Parsimony and Likelihood Methods. <i>Systematic Biology</i> , 2001, 50, 525-539.	2.7	190
72	Bias in Phylogenetic Estimation and Its Relevance to the Choice between Parsimony and Likelihood Methods. <i>Systematic Biology</i> , 2001, 50, 525-539.	2.7	309

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73	Iron Hydrogenases and the Evolution of Anaerobic Eukaryotes. <i>Molecular Biology and Evolution</i> , 2000, 17, 1695-1709.	3.5	128
74	Compositional Bias May Affect Both DNA-Based and Protein-Based Phylogenetic Reconstructions. <i>Journal of Molecular Evolution</i> , 1999, 48, 284-290.	0.8	301
75	Nucleotide Composition Bias Affects Amino Acid Content in Proteins Coded by Animal Mitochondria. <i>Journal of Molecular Evolution</i> , 1997, 44, 282-288.	0.8	170
76	Unbiased Estimation of Symmetrical Directional Mutation Pressure from Protein-Coding DNA. <i>Journal of Molecular Evolution</i> , 1997, 44, 468-468.	0.8	7
77	Unbiased estimation of symmetrical directional mutation pressure from protein-coding DNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 476-480.	0.8	13
78	Unbiased Estimation of Symmetrical Directional Mutation Pressure from Protein-Coding DNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 476-480.	0.8	1
79	High-throughput multiplexed mitogenomics for Metazoa: prospects and limitations. , 0, , 84-100.		0