Daniel C. Jeffares

List of Publications by Year in descending order

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42 papers

3,808 citations

236612 25 h-index 42 g-index

55 all docs 55 docs citations

55 times ranked 5715 citing authors

#	Article	IF	CITATIONS
1	Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nature Genetics, 2007, 39, 839-847.	9.4	648
2	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. Nature Communications, 2017, 8, 14061.	5 . 8	472
3	Rapidly regulated genes are intron poor. Trends in Genetics, 2008, 24, 375-378.	2.9	340
4	The biology of intron gain and loss. Trends in Genetics, 2006, 22, 16-22.	2.9	238
5	The Path from the RNA World. Journal of Molecular Evolution, 1998, 46, 1-17.	0.8	235
6	Relics from the RNA World. Journal of Molecular Evolution, 1998, 46, 18-36.	0.8	212
7	Genome variation and evolution of the malaria parasite Plasmodium falciparum. Nature Genetics, 2007, 39, 120-125.	9.4	184
8	Eukaryotic Intron Loss. Science, 2003, 300, 1393-1393.	6.0	180
9	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
10	Early evolution: prokaryotes, the new kids on the block. BioEssays, 1999, 21, 880-889.	1.2	156
11	A Beginners Guide to Estimating the Non-synonymous to Synonymous Rate Ratio of all Protein-Coding Genes in a Genome. Methods in Molecular Biology, 2015, 1201, 65-90.	0.4	105
12	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> Genome Research, 2008, 18, 281-292.	2.4	81
13	Selected Schizosaccharomyces pombe Strains Have Characteristics That Are Beneficial for Winemaking. PLoS ONE, 2016, 11, e0151102.	1.1	81
14	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. Genome Research, 2014, 24, 1169-1179.	2.4	64
15	PCR amplification of the fasâ€1 gene for the detection of virulent strains of Rhodococcus fascians. Plant Pathology, 1996, 45, 407-417.	1.2	62
16	A Leishmania infantum genetic marker associated with miltefosine treatment failure for visceral leishmaniasis. EBioMedicine, 2018, 36, 83-91.	2.7	56
17	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. Molecular Biology and Evolution, 2019, 36, 1975-1989.	3.5	50
18	Direct isolation of poly(A)+ RNA from 4 M guanidine thiocyanate-lysed cell extracts using locked nucleic acid-oligo(T) capture. Nucleic Acids Research, 2004, 32, e64-e64.	6.5	43

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19	An Overview of the Introns-First Theory. Journal of Molecular Evolution, 2009, 69, 527-540.	0.8	43
20	Evolutionarily Stable Association of Intronic snoRNAs and microRNAs with Their Host Genes. Genome Biology and Evolution, 2009, 1 , 420-428.	1.1	42
21	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. PLoS ONE, 2011, 6, e15292.	1.1	38
22	Diversification of Genes Encoding Mei2-Like RNA Binding Proteins in Plants. Plant Molecular Biology, 2004, 54, 653-670.	2.0	36
23	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. PLoS Genetics, 2010, 6, e1001099.	1.5	30
24	The natural diversity and ecology of fission yeast. Yeast, 2018, 35, 253-260.	0.8	28
25	Comparative structural and evolutionary analyses predict functional sites in the artemisinin resistance malaria protein K13. Scientific Reports, 2019, 9, 10675.	1.6	28
26	A description of the Mei2-like protein family; structure, phylogenetic distribution and biological context. Development Genes and Evolution, 2004, 214, 149-158.	0.4	27
27	Temperature-dependence of carbon acquisition and demand in relation to shoot growth of kiwifruit (Actinidia deliciosa) vines grown in controlled environments. Functional Plant Biology, 1998, 25, 843.	1.1	26
28	The genome of the zoonotic malaria parasite Plasmodium simium reveals adaptations to host switching. BMC Biology, 2021, 19, 219.	1.7	21
29	Outsourcing the Nucleus: Nuclear Pore Complex Genes are no Longer Encoded in Nucleomorph Genomes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	12
30	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	3.5	12
31	Candidates for Balancing Selection in Leishmania donovani Complex Parasites. Genome Biology and Evolution, 2021, 13, .	1.1	11
32	Spotsizer: High-throughput quantitative analysis of microbial growth. BioTechniques, 2016, 61, 191-201.	0.8	10
33	Pre-rRNA processing and the path from the RNA world. Trends in Biochemical Sciences, 1995, 20, 298-299.	3.7	8
34	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. Genetics, 2018, 210, 733-744.	1.2	8
35	Reconstruction of Microbial Haplotypes by Integration of Statistical and Physical Linkage in Scaffolding. Molecular Biology and Evolution, 2021, 38, 2660-2672.	3.5	8
36	Experimental Selection of Paromomycin Resistance in Leishmania donovani Amastigotes Induces Variable Genomic Polymorphisms. Microorganisms, 2021, 9, 1546.	1.6	7

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37	Differences in non-LTR retrotransposons within C. elegans and C. briggsae genomes. Gene, 2004, 330, 61-66.	1.0	6
38	Does the Ribosome Challenge our Understanding of the RNA World?. Journal of Molecular Evolution, 2016, 82, 1-4.	0.8	6
39	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. PLoS Genetics, 2021, 17, e1009784.	1.5	2
40	Identification of individual root-knot nematodes using low coverage long-read sequencing. PLoS ONE, 2021, 16, e0253248.	1.1	2
41	Does the Ribosome Challenge our Understanding of the RNA World?. Journal of Molecular Evolution, 2016, 82, 1-4.	0.8	1
42	Variables Influencing Differences in Sequence Conservation in the Fission Yeast Schizosaccharomyces pombe. Journal of Molecular Evolution, 2021, 89, 601-610.	0.8	0