Daniel C. Jeffares

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1110372/publications.pdf

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42	3,808	236612	264894
papers	citations	25	42
		h-index	g-index

55	55	55	5715
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reconstruction of Microbial Haplotypes by Integration of Statistical and Physical Linkage in Scaffolding. Molecular Biology and Evolution, 2021, 38, 2660-2672.	3.5	8
2	Experimental Selection of Paromomycin Resistance in Leishmania donovani Amastigotes Induces Variable Genomic Polymorphisms. Microorganisms, 2021, 9, 1546.	1.6	7
3	Variables Influencing Differences in Sequence Conservation in the Fission Yeast Schizosaccharomyces pombe. Journal of Molecular Evolution, 2021, 89, 601-610.	0.8	0
4	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
5	The genome of the zoonotic malaria parasite Plasmodium simium reveals adaptations to host switching. BMC Biology, 2021, 19, 219.	1.7	21
6	Identification of individual root-knot nematodes using low coverage long-read sequencing. PLoS ONE, 2021, 16, e0253248.	1.1	2
7	Candidates for Balancing Selection in Leishmania donovani Complex Parasites. Genome Biology and Evolution, 2021, 13, .	1.1	11
8	Comparative structural and evolutionary analyses predict functional sites in the artemisinin resistance malaria protein K13. Scientific Reports, 2019, 9, 10675.	1.6	28
9	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. Molecular Biology and Evolution, 2019, 36, 1975-1989.	3.5	50
10	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	3.5	12
11	The natural diversity and ecology of fission yeast. Yeast, 2018, 35, 253-260.	0.8	28
12	A Leishmania infantum genetic marker associated with miltefosine treatment failure for visceral leishmaniasis. EBioMedicine, 2018, 36, 83-91.	2.7	56
13	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. Genetics, 2018, 210, 733-744.	1.2	8
14	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. Nature Communications, 2017, 8, 14061.	5.8	472
15	Spotsizer: High-throughput quantitative analysis of microbial growth. BioTechniques, 2016, 61, 191-201.	0.8	10
16	Selected Schizosaccharomyces pombe Strains Have Characteristics That Are Beneficial for Winemaking. PLoS ONE, 2016, 11, e0151102.	1.1	81
17	Does the Ribosome Challenge our Understanding of the RNA World?. Journal of Molecular Evolution, 2016, 82, 1-4.	0.8	6
18	Does the Ribosome Challenge our Understanding of the RNA World?. Journal of Molecular Evolution, 2016, 82, 1-4.	0.8	1

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19	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
20	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
21	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
22	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. PLoS ONE, 2011, 6, e15292.	1.1	38
23	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. PLoS Genetics, 2010, 6, e1001099.	1.5	30
24	Evolutionarily Stable Association of Intronic snoRNAs and microRNAs with Their Host Genes. Genome Biology and Evolution, 2009, 1, 420-428.	1.1	42
25	An Overview of the Introns-First Theory. Journal of Molecular Evolution, 2009, 69, 527-540.	0.8	43
26	Rapidly regulated genes are intron poor. Trends in Genetics, 2008, 24, 375-378.	2.9	340
27	Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. Genome Research, 2008, 18, 281-292.	2.4	81
28	Genome variation and evolution of the malaria parasite Plasmodium falciparum. Nature Genetics, 2007, 39, 120-125.	9.4	184
29	Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nature Genetics, 2007, 39, 839-847.	9.4	648
30	Outsourcing the Nucleus: Nuclear Pore Complex Genes are no Longer Encoded in Nucleomorph Genomes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	12
31	The biology of intron gain and loss. Trends in Genetics, 2006, 22, 16-22.	2.9	238
32	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
33	Diversification of Genes Encoding Mei2-Like RNA Binding Proteins in Plants. Plant Molecular Biology, 2004, 54, 653-670.	2.0	36
34	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
35	Differences in non-LTR retrotransposons within C. elegans and C. briggsae genomes. Gene, 2004, 330, 61-66.	1.0	6
36	Eukaryotic Intron Loss. Science, 2003, 300, 1393-1393.	6.0	180

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37	Early evolution: prokaryotes, the new kids on the block. BioEssays, 1999, 21, 880-889.	1.2	156
38	The Path from the RNA World. Journal of Molecular Evolution, 1998, 46, 1-17.	0.8	235
39	Relics from the RNA World. Journal of Molecular Evolution, 1998, 46, 18-36.	0.8	212
40	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
41	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
42	Pre-rRNA processing and the path from the RNA world. Trends in Biochemical Sciences, 1995, 20, 298-299.	3.7	8