

Austen R D Ganley

List of Publications by Year in descending order

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39
papers

2,448
citations

304602

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37
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all docs

44
docs citations

44
times ranked

3573
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly efficient concerted evolution in the ribosomal DNA repeats: Total rDNA repeat variation revealed by whole-genome shotgun sequence data. <i>Genome Research</i> , 2007, 17, 184-191.	2.4	307
2	Recombination Regulation by Transcription-Induced Cohesin Dissociation in rDNA Repeats. <i>Science</i> , 2005, 309, 1581-1584.	6.0	283
3	Multilocus sequence typing suggests the chytrid pathogen of amphibians is a recently emerged clone. <i>Molecular Ecology</i> , 2003, 12, 395-403.	2.0	244
4	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	1.5	226
5	Resolving Arthropod Phylogeny: Exploring Phylogenetic Signal within 41 kb of Protein-Coding Nuclear Gene Sequence. <i>Systematic Biology</i> , 2008, 57, 920-938.	2.7	178
6	The Effect of Replication Initiation on Gene Amplification in the rDNA and Its Relationship to Aging. <i>Molecular Cell</i> , 2009, 35, 683-693.	4.5	132
7	The shared genomic architecture of human nucleolar organizer regions. <i>Genome Research</i> , 2013, 23, 2003-2012.	2.4	107
8	Cellular Senescence in Yeast Is Regulated by rDNA Noncoding Transcription. <i>Current Biology</i> , 2013, 23, 1794-1798.	1.8	99
9	Ribosomal DNA and cellular senescence: new evidence supporting the connection between rDNA and aging. <i>FEMS Yeast Research</i> , 2014, 14, 49-59.	1.1	98
10	Repeat elements organise 3D genome structure and mediate transcription in the filamentous fungus <i>Epichloa festucae</i> . <i>PLoS Genetics</i> , 2018, 14, e1007467.	1.5	79
11	An Interspecific Fungal Hybrid Reveals Cross-Kingdom Rules for Allopolyploid Gene Expression Patterns. <i>PLoS Genetics</i> , 2014, 10, e1004180.	1.5	68
12	Monitoring the Rate and Dynamics of Concerted Evolution in the Ribosomal DNA Repeats of <i>Saccharomyces cerevisiae</i> Using Experimental Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 2883-2891.	3.5	55
13	Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. <i>New Phytologist</i> , 2013, 198, 525-535.	3.5	55
14	The conservation landscape of the human ribosomal RNA gene repeats. <i>PLoS ONE</i> , 2018, 13, e0207531.	1.1	55
15	Extraordinary Ribosomal Spacer Length Heterogeneity in a <i>Neotyphodium</i> Endophyte Hybrid: Implications for Concerted Evolution. <i>Genetics</i> , 1998, 150, 1625-1637.	1.2	48
16	Biochar in Co-Contaminated Soil Manipulates Arsenic Solubility and Microbiological Community Structure, and Promotes Organochlorine Degradation. <i>PLoS ONE</i> , 2015, 10, e0125393.	1.1	45
17	<i>Epichloa hybrida</i> , sp. nov., an emerging model system for investigating fungal allopolyploidy. <i>Mycologia</i> , 2017, 109, 1-15.	0.8	43
18	Identifying gene-independent noncoding functional elements in the yeast ribosomal DNA by phylogenetic footprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11787-11792.	3.3	42

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19	The Case of the Missing Ancient Fungal Polyploids. <i>American Naturalist</i> , 2016, 188, 602-614.	1.0	38
20	Changes in long-range rDNA-genomic interactions associate with altered RNA polymerase II gene programs during malignant transformation. <i>Communications Biology</i> , 2019, 2, 39.	2.0	33
21	Comparison of Illumina de novo assembled and Sanger sequenced viral genomes: A case study for RNA viruses recovered from the plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>Virus Research</i> , 2016, 219, 51-57.	1.1	28
22	Concerted Evolution in the Ribosomal RNA Genes of an <i>Epichloa</i> Endophyte Hybrid: Comparison between Tandemly Arranged rDNA and Dispersed 5S rrrn Genes. <i>Fungal Genetics and Biology</i> , 2002, 35, 39-51.	0.9	25
23	HyLiTE: accurate and flexible analysis of gene expression in hybrid and allopolyploid species. <i>BMC Bioinformatics</i> , 2015, 16, 8.	1.2	25
24	The nucleolus: a raft adrift in the nuclear sea or the keystone in nuclear structure?. <i>Biomolecular Concepts</i> , 2013, 4, 277-286.	1.0	24
25	Yeast hypertrophy: cause or consequence of aging? Reply to Bilinski et al. <i>FEMS Yeast Research</i> , 2012, 12, 267-268.	1.1	22
26	A positive role for yeast extrachromosomal rDNA circles?. <i>BioEssays</i> , 2012, 34, 725-729.	1.2	18
27	The Nucleolus and Ribosomal Genes in Aging and Senescence. , 0, , .		16
28	Complete Sequence Construction of the Highly Repetitive Ribosomal RNA Gene Repeats in Eukaryotes Using Whole Genome Sequence Data. <i>Methods in Molecular Biology</i> , 2016, 1455, 161-181.	0.4	11
29	Phylogenetic Footprinting to Find Functional DNA Elements. <i>Methods in Molecular Biology</i> , 2007, 395, 367-379.	0.4	8
30	A Sequence-Specific Interaction between the <i>Saccharomyces cerevisiae</i> rRNA Gene Repeats and a Locus Encoding an RNA Polymerase I Subunit Affects Ribosomal DNA Stability. <i>Molecular and Cellular Biology</i> , 2015, 35, 544-554.	1.1	7
31	Contrasting patterns of coding and flanking region evolution in mammalian keratin associated protein-1 genes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 352-361.	1.2	5
32	Yeast cell aging and death. <i>FEMS Yeast Research</i> , 2014, 14, 1-1.	1.1	4
33	Striving for clarity about the "Lamarckian" nature of CRISPR-Cas systems. <i>Biology and Philosophy</i> , 2019, 34, 1.	0.7	4
34	A de novo <i>ACTB</i> gene pathogenic variant in identical twins with phenotypic variation for hydrops and jejunal atresia. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 1299-1306.	0.7	3
35	Creeping yeast: a simple, cheap and robust protocol for the identification of mating type in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2022, 22, .	1.1	2
36	Cross-kingdom transcriptomic trends in the evolution of hybrid gene expression. <i>Journal of Evolutionary Biology</i> , 2022, 35, 1126-1137.	0.8	2

#	ARTICLE	IF	CITATIONS
37	Aerial warfare: An inducible production of volatile bioactive metabolites in a novel species of <i>Scytinostroma</i> sp.. <i>Fungal Genetics and Biology</i> , 2022, 158, 103646.	0.9	1
38	Phylogenetic Footprinting to Find Functional DNA Elements. , 0, , 367-380.		0
39	Telomere-to-Telomere Genome Sequences across a Single Genus Reveal Highly Variable Chromosome Rearrangement Rates but Absolute Stasis of Chromosome Number. <i>Journal of Fungi (Basel,)</i> Tj ETQq1 1 0.784314 rjBT /Overlock 10 T		