

The correlation between rDNA copy number and genom

Genome

46, 48-50

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Comparative Genomics of <i>Pneumocystis carinii</i> with Other Protists: Implications for Life Style1. <i>Journal of Eukaryotic Microbiology</i> , 2004, 51, 30-37.	1.7	19
2	Ribosomal RNA Processing and Ribosome Biogenesis in Eukaryotes. <i>IUBMB Life</i> , 2004, 56, 457-465.	3.4	99
3	Ecology and genetics of tree invasions: from recent introductions to Quaternary migrations. <i>Forest Ecology and Management</i> , 2004, 197, 117-137.	3.2	156
4	Evolution of genome size: multilevel selection, mutation bias or dynamical chaos?. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 620-626.	3.3	64
5	Evolution of Genome Size in Conifers. <i>Silvae Genetica</i> , 2005, 54, 126-137.	0.8	117
6	Mapping of picoeucaryotes in marine ecosystems with quantitative PCR of the 18S rRNA gene. <i>FEMS Microbiology Ecology</i> , 2005, 52, 79-92.	2.7	540
7	Ecotype diversity in the marine picoeukaryote <i>Ostreococcus</i> (Chlorophyta, Prasinophyceae). <i>Environmental Microbiology</i> , 2005, 7, 853-859.	3.8	185
8	Assessing the odd secondary structural properties of nuclear small subunit ribosomal RNA sequences (18S) of the twisted-wing parasites (Insecta: Strepsiptera). <i>Insect Molecular Biology</i> , 2005, 14, 625-643.	2.0	46
9	Toward a stoichiometric framework for evolutionary biology. <i>Oikos</i> , 2005, 109, 6-17.	2.7	95
10	Cytochalasin D can improve heterologous protein productivity in adherent Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2005, 90, 354-364.	3.3	45
11	The relationship between genome size, development rate, and body size in copepods. <i>Hydrobiologia</i> , 2005, 532, 123-137.	2.0	57
12	Genome size of three Brazilian flies from the Sciaridae family. <i>Genetics and Molecular Biology</i> , 2005, 28, 743-748.	1.3	0
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14	Use of a Suspension Array for Rapid Identification of the Varieties and Genotypes of the <i>Cryptococcus neoformans</i> Species Complex. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3662-3672.	3.9	63
15	Genome Size Evolution in Plants. , 2005, , 89-162.		113
16	In Situ Chromosomal Localization of rDNA Sites in "Safed Musli" <i>Chlorophytum Ker-Gawl</i> and Their Physical Measurement by Fiber FISH. <i>Journal of Heredity</i> , 2005, 96, 155-160.	2.4	19
17	Genome Size Evolution in Animals. , 2005, , 3-87.		200
18	The Functional Significance of Ribosomal (r)DNA Variation: Impacts on the Evolutionary Ecology of Organisms. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2005, 36, 219-242.	8.3	137

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19	Microcoding and flow cytometry as a high-throughput fungal identification system for <i>Malassezia</i> species. <i>Journal of Medical Microbiology</i> , 2006, 55, 1197-1209.	1.8	39
20	The genome of <i>Oscheius tipulae</i> : determination of size, complexity, and structure by DNA reassociation using fluorescent dye. <i>Genome</i> , 2006, 49, 1007-1015.	2.0	11
21	Nuclear DNA content and nuclear and cell volume are positively correlated in angiosperms. <i>Cytogenetic and Genome Research</i> , 2006, 114, 77-82.	1.1	135
22	GENETIC DIFFERENCES AMONG NOBLE CRAYFISH (<i>ASTACUS ASTACUS</i>) STOCKS IN FINLAND, SWEDEN AND ESTONIA BASED ON THE ITS1 REGION. <i>Knowledge and Management of Aquatic Ecosystems: an International Journal on Aquatic Ecosystems</i> , 2006, , 965-976.	0.4	12
23	Novel electrochemical identification and semi quantification of bovine constituents in feedstuffs. <i>Science and Technology of Advanced Materials</i> , 2006, 7, 263-269.	6.1	14
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25	Regulation of Growth by Ploidy in <i>Caenorhabditis elegans</i> . <i>Current Biology</i> , 2006, 16, 493-498.	3.9	72
26	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.	5.5	307
27	Molecular Quantification of Symbiotic Dinoflagellate Algae of the Genus <i>Symbiodinium</i> . <i>Biological Bulletin</i> , 2007, 212, 259-268.	1.8	42
28	Karyotype of <i>Araucaria angustifolia</i> and the decondensation/activation mode of its nucleolus organiser region. <i>Australian Journal of Botany</i> , 2007, 55, 165.	0.6	8
29	Finding Repeats in Genome Sequences. , 0, , 197-233.		3
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33	Pan-eukaryote ITS2 homologies revealed by RNA secondary structure. <i>Nucleic Acids Research</i> , 2007, 35, 3322-3329.	14.5	338
34	Physical mapping of 5S and 45S rDNA loci in pufferfishes (Tetraodontiformes). <i>Genetica</i> , 2007, 130, 133-138.	1.1	17
35	A novel real-time polymerase chain reaction method for the qualitative detection of pistachio in food. <i>European Food Research and Technology</i> , 2008, 228, 197-203.	3.3	21
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38	The diversity of small eukaryotic phytoplankton (â‰ƒ3 Î¼m) in marine ecosystems. <i>FEMS Microbiology Reviews</i> , 2008, 32, 795-820.	8.6	363
39	MICROSATELLITE GENOTYPING OF SINGLE CELLS OF THE DINOFLAGELLATE SPECIES <i>LINGULODINIUM POLYEDRUM</i> (DINOPHYCEAE): A NOVEL APPROACH FOR MARINE MICROBIAL POPULATION GENETIC STUDIES¹. <i>Journal of Phycology</i> , 2008, 44, 1116-1125.	2.3	17
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46	Population genomics of domestic and wild yeasts. <i>Nature Precedings</i> , 2008, , .	0.1	1
47	Quantitative Real-Time PCR Assay for QPX (Thraustochytriidae), a Parasite of the Hard Clam () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	3.1	33
48	Massively parallel tag sequencing reveals the complexity of anaerobic marine protistan communities. <i>BMC Biology</i> , 2009, 7, 72.	3.8	180
49	Analysis of Australian fur seal diet by pyrosequencing prey DNA in faeces. <i>Molecular Ecology</i> , 2009, 18, 2022-2038.	3.9	320
50	PCRâ€Based Diversity Estimates of Artificial and Environmental 18S rRNA Gene Libraries. <i>Journal of Eukaryotic Microbiology</i> , 2009, 56, 174-181.	1.7	77
51	Distribution of the uncultured protist MASTâ€4 in the Indian Ocean, Drake Passage and Mediterranean Sea assessed by realâ€time quantitative PCR. <i>Environmental Microbiology</i> , 2009, 11, 397-408.	3.8	34
52	Evidence for lowâ€titre infections in insect symbiosis: <i>Wolbachia</i> in the bark beetle <i>Pityogenes chalcographus</i> (Coleoptera, Scolytinae). <i>Environmental Microbiology</i> , 2009, 11, 1923-1933.	3.8	64
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56	Ribosomal RNA genes in eukaryotic microorganisms: witnesses of phylogeny?. <i>FEMS Microbiology Reviews</i> , 2010, 34, 59-86.	8.6	106
57	Diversity of active marine picoeukaryotes in the Eastern Mediterranean Sea unveiled using photosystem-II <i>psbA</i> transcripts. <i>ISME Journal</i> , 2010, 4, 1044-1052.	9.8	43
58	Effect of environmental variables on eukaryotic microbial community structure of land-fast Arctic sea ice. <i>Environmental Microbiology</i> , 2010, 12, 797-809.	3.8	19
59	Stomatal vs. genome size in angiosperms: the somatic tail wagging the genomic dog?. <i>Annals of Botany</i> , 2010, 105, 573-584.	2.9	121
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69	Quantitative PCR assay for the detection of the parasitic ciliate <i>Cryptocaryon irritans</i> . <i>Fisheries Science</i> , 2011, 77, 607-613.	1.6	22
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71	JAGUC – A SOFTWARE PACKAGE FOR ENVIRONMENTAL DIVERSITY ANALYSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 749-773.	0.8	42
72	Nuclear DNA amounts in angiosperms: targets, trends and tomorrow. <i>Annals of Botany</i> , 2011, 107, 467-590.	2.9	283

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78	Molecular tools for the detection and identification of <i>Ichthyobodo</i> spp. (Kinetoplastida), important fish parasites. <i>Parasitology International</i> , 2012, 61, 675-683.	1.3	27
79	Inter- and intrasporal nuclear ribosomal gene sequence variation within one isolate of arbuscular mycorrhizal fungus, <i>Diversispora</i> sp.. <i>Symbiosis</i> , 2012, 58, 135-147.	2.3	22
80	Nucleoli: Composition, Function, and Dynamics. <i>Plant Physiology</i> , 2012, 158, 44-51.	4.8	109
81	Discovery of multiple IGS haplotypes within genotypes of <i>Puccinia striiformis</i> . <i>Fungal Biology</i> , 2012, 116, 522-528.	2.5	3
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89	QUANTITATIVE REAL-TIME POLYMERASE CHAIN REACTION FOR <i>COCHLODINIUM FULVESCENS</i> (DINOPHYCEAE), A HARMFUL DINOFLAGELLATE FROM CALIFORNIA COASTAL WATERS ¹ . <i>Journal of Phycology</i> , 2012, 48, 384-393.	2.3	27
90	Pyrosequencing of prey DNA in reptile faeces: analysis of earthworm consumption by slow worms. <i>Molecular Ecology Resources</i> , 2012, 12, 259-266.	4.8	66
91	Who is eating what: diet assessment using next generation sequencing. <i>Molecular Ecology</i> , 2012, 21, 1931-1950.	3.9	913

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97	Genome size variation and evolution in the family Asteraceae. <i>Caryologia</i> , 2013, 66, 221-235.	0.3	39
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103	High-throughput amplicon sequencing of rRNA genes requires a copy number correction to accurately reflect the effects of management practices on soil nematode community structure. <i>Molecular Ecology</i> , 2013, 22, 5456-5471.	3.9	62
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109	Protist community composition during early phytoplankton blooms in the naturally iron-fertilized Kerguelen area (Southern Ocean). <i>Biogeosciences</i> , 2014, 11, 5847-5863.	3.3	25

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111	Genomic Characterization of the Mouse Ribosomal DNA Locus. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 243-254.	1.8	39
112	Disparate molecular evolution of two types of repetitive DNAs in the genome of the grasshopper <i>Eyprepocnemis plorans</i> . <i>Heredity</i> , 2014, 112, 531-542.	2.6	22
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