

Meng-Chao Yao

List of Publications by Year in descending order

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73
papers

12,256
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87723

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88477

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all docs

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docs citations

76
times ranked

20901
citing authors

#	ARTICLE	IF	CITATIONS
1	Selfing mutants link Ku proteins to mating type determination in <i>Tetrahymena</i> . <i>PLoS Biology</i> , 2020, 18, e3000756.	2.6	6
2	Abundant and diverse <i>Tetrahymena</i> species living in the bladder traps of aquatic carnivorous <i>Utricularia</i> plants. <i>Scientific Reports</i> , 2019, 9, 13669.	1.6	5
3	Setting boundaries for genome-wide heterochromatic DNA deletions through flanking inverted repeats in <i>Tetrahymena thermophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, 5181-5192.	6.5	8
4	Diversity and Universality of Endosymbiotic <i>Rickettsia</i> in the Fish Parasite <i>Ichthyophthirius multifiliis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 189.	1.5	21
5	The piggyBac transposon-derived genes <i>TPB1</i> and <i>TPB6</i> mediate essential transposon-like excision during the developmental rearrangement of key genes in <i>Tetrahymena thermophila</i> . <i>Genes and Development</i> , 2016, 30, 2724-2736.	2.7	43
6	<i>DRH1</i> , a p68-related RNA helicase gene, is required for chromosome breakage in <i>Tetrahymena</i> . <i>Biology Open</i> , 2016, 5, 1790-1798.	0.6	3
7	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
8	Dynamic distributions of long double-stranded RNA in <i>Tetrahymena</i> during nuclear development and genome rearrangements. <i>Journal of Cell Science</i> , 2016, 129, 1046-58.	1.2	9
9	Programmed Minichromosome Elimination as a Mechanism for Somatic Genome Reduction in <i>Tetrahymena thermophila</i> . <i>PLoS Genetics</i> , 2016, 12, e1006403.	1.5	18
10	Programmed Genome Rearrangements in <i>Tetrahymena</i> . <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	33
11	<i>Tetrahymena thermophila</i> JMJD3 Homolog Regulates H3K27 Methylation and Nuclear Differentiation. <i>Eukaryotic Cell</i> , 2012, 11, 601-614.	3.4	18
12	Role of ATG8 and Autophagy in Programmed Nuclear Degradation in <i>Tetrahymena thermophila</i> . <i>Eukaryotic Cell</i> , 2012, 11, 494-506.	3.4	50
13	An essential role for the DNA breakage-repair protein Ku80 in programmed DNA rearrangements in <i>Tetrahymena thermophila</i> . <i>Molecular Biology of the Cell</i> , 2012, 23, 2213-2225.	0.9	42
14	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544.	4.3	3,122
15	DNA Elimination in Ciliates: Transposon Domestication and Genome Surveillance. <i>Annual Review of Genetics</i> , 2011, 45, 227-246.	3.2	125
16	Absence of Positive Selection on Centromeric Histones in <i>Tetrahymena</i> Suggests Unsuppressed Centromere-Drive in Lineages Lacking Male Meiosis. <i>Journal of Molecular Evolution</i> , 2011, 72, 510-520.	0.8	19
17	Genome-wide analysis of palindrome formation. <i>Nature Genetics</i> , 2010, 42, 279-279.	9.4	5
18	A Domesticated piggyBac Transposase Plays Key Roles in Heterochromatin Dynamics and DNA Cleavage during Programmed DNA Deletion in <i>Tetrahymena thermophila</i> . <i>Molecular Biology of the Cell</i> , 2010, 21, 1753-1762.	0.9	143

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19	Modulating somatic DNA copy number through maternal RNA. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21951-21952.	3.3	2
20	Palindromic gene amplification – an evolutionarily conserved role for DNA inverted repeats in the genome. Nature Reviews Cancer, 2009, 9, 216-224.	12.8	86
21	RNA rules. Nature, 2008, 451, 131-132.	13.7	4
22	Intrastrand Annealing Leads to the Formation of a Large DNA Palindrome and Determines the Boundaries of Genomic Amplification in Human Cancer. Molecular and Cellular Biology, 2007, 27, 1993-2002.	1.1	57
23	Identification of novel chromatin-associated proteins involved in programmed genome rearrangements in Tetrahymena. Journal of Cell Science, 2007, 120, 1978-1989.	1.2	52
24	Tudor Nuclease Genes and Programmed DNA Rearrangements in Tetrahymena thermophila. Eukaryotic Cell, 2007, 6, 1795-1804.	3.4	22
25	Introduction for special issue. Journal of Biomedical Science, 2007, 14, 451-451.	2.6	0
26	Large DNA palindromes as a common form of structural chromosome aberrations in human cancers. Human Cell, 2006, 19, 17-23.	1.2	29
27	The Condensin Complex Is Essential for Amitotic Segregation of Bulk Chromosomes, but Not Nucleoli, in the Ciliate Tetrahymena thermophila. Molecular and Cellular Biology, 2006, 26, 4690-4700.	1.1	26
28	The CNA1 Histone of the Ciliate Tetrahymena thermophila Is Essential for Chromosome Segregation in the Germline Micronucleus. Molecular Biology of the Cell, 2006, 17, 485-497.	0.9	53
29	Induction of Gene Silencing by Hairpin RNA Expression in Tetrahymena thermophila Reveals a Second Small RNA Pathway. Molecular and Cellular Biology, 2006, 26, 8731-8742.	1.1	46
30	Widespread and nonrandom distribution of DNA palindromes in cancer cells provides a structural platform for subsequent gene amplification. Nature Genetics, 2005, 37, 320-327.	9.4	95
31	Communication Between Parental and Developing Genomes During Tetrahymena Nuclear Differentiation Is Likely Mediated by Homologous RNAs. Genetics, 2005, 169, 149-160.	1.2	54
32	Class I Histone Deacetylase Thd1p Affects Nuclear Integrity in Tetrahymena thermophila. Eukaryotic Cell, 2005, 4, 981-990.	3.4	13
33	RNA-Guided DNA Deletion in Tetrahymena: An RNAi-Based Mechanism for Programmed Genome Rearrangements. Annual Review of Genetics, 2005, 39, 537-559.	3.2	104
34	Abstract of Symposium. Human Cell, 2005, 18, 29-33.	1.2	0
35	Programmed DNA Deletion As an RNA-Guided System of Genome Defense. Science, 2003, 300, 1581-1584.	6.0	170
36	Short inverted repeats initiate gene amplification through the formation of a large DNA palindrome in mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8772-8777.	3.3	105

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37	Role of Histone Deacetylation in Developmentally Programmed DNA Rearrangements in <i>Tetrahymena thermophila</i> . <i>Eukaryotic Cell</i> , 2002, 1, 293-303.	3.4	35
38	Nongenic, bidirectional transcription precedes and may promote developmental DNA deletion in <i>Tetrahymena thermophila</i> . <i>Genes and Development</i> , 2001, 15, 1287-1298.	2.7	145
39	Developmentally Regulated Rpd3p Homolog Specific to the Transcriptionally Active Macronucleus of Vegetative <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Biology</i> , 2000, 20, 8319-8328.	1.1	15
40	Characterization of the <i>Euplotes crassus</i> Macronuclear rDNA and its Potential as a DNA Transformation Vehicle. <i>Journal of Eukaryotic Microbiology</i> , 1999, 46, 206-216.	0.8	7
41	Parental Expression of the Chromodomain Protein Pdd1p Is Required for Completion of Programmed DNA Elimination and Nuclear Differentiation. <i>Molecular Cell</i> , 1999, 4, 865-872.	4.5	93
42	Chapter 25 Microinjection of <i>Tetrahymena thermophila</i> . <i>Methods in Cell Biology</i> , 1999, 62, 469-484.	0.5	7
43	Chapter 29 Creation and Use of Antisense Ribosomes in <i>Tetrahymena thermophila</i> . <i>Methods in Cell Biology</i> , 1999, 62, 533-547.	0.5	14
44	Flanking Regulatory Sequences of the <i>Tetrahymena</i> R Deletion Element Determine the Boundaries of DNA Rearrangement. <i>Molecular and Cellular Biology</i> , 1999, 19, 5631-5641.	1.1	47
45	Antisense in Abundance: The Ribosome as a Vehicle for Antisense RNA. , 1998, 20, 143-151.		2
46	An Intragenic Suppressor of Cold Sensitivity Identifies Potentially Interacting Bases in the Peptidyl Transferase Center of <i>Tetrahymena</i> rRNA. <i>Genetics</i> , 1998, 149, 937-946.	1.2	1
47	The intranuclear organization of normal, hemizygous and excision-deficient rRNA genes during developmental amplification in <i>Tetrahymena thermophila</i> . <i>Chromosoma</i> , 1997, 106, 233-242.	1.0	17
48	Pdd1p, A Novel Chromodomain-Containing Protein, Links Heterochromatin Assembly and DNA Elimination in <i>Tetrahymena</i> . <i>Cell</i> , 1996, 87, 75-84.	13.5	163
49	Induction of Large DNA Palindrome Formation in Yeast: Implications for Gene Amplification and Genome Stability in Eukaryotes. <i>Cell</i> , 1996, 87, 1115-1122.	13.5	93
50	Programmed DNA deletions in <i>Tetrahymena</i> : mechanisms and implications. <i>Trends in Genetics</i> , 1996, 12, 26-30.	2.9	72
51	GENOME DOWNSIZING DURING CILIATE DEVELOPMENT:Nuclear Division of Labor through Chromosome Restructuring. <i>Annual Review of Genetics</i> , 1996, 30, 557-578.	3.2	138
52	Evolutionary Conservation of Sequences Directing Chromosome Breakage and rDNA Palindrome Formation in Tetrahymenine Ciliates. <i>Genetics</i> , 1996, 144, 1479-1487.	1.2	25
53	Detection of circular excised DNA deletion elements in <i>Tetrahymena thermophila</i> during development. <i>Nucleic Acids Research</i> , 1994, 22, 5702-5708.	6.5	36
54	Short inverted repeats at a free end signal large palindromic DNA formation in tetrahymena. <i>Cell</i> , 1991, 67, 505-516.	13.5	67

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55	The controlling sequence for site-specific chromosome breakage in tetrahymena. <i>Cell</i> , 1990, 63, 763-772.	13.5	137
56	A programmed site-specific DNA rearrangement in <i>Tetrahymena thermophila</i> requires flanking polypurine tracts. <i>Cell</i> , 1990, 61, 1237-1246.	13.5	109
57	Sequence microheterogeneity is generated at junctions of programmed DNA deletions in <i>Tetrahymena thermophila</i> . <i>Nucleic Acids Research</i> , 1989, 17, 7263-7272.	6.5	62
58	A conserved nucleotide sequence at the sites of developmentally regulated chromosomal breakage in tetrahymena. <i>Cell</i> , 1987, 48, 779-788.	13.5	111
59	Sequence characterization of <i>Tetrahymena</i> macronuclear DNA ends. <i>Nucleic Acids Research</i> , 1986, 14, 2109-2122.	6.5	19
60	Amplification of Ribosomal RNA Genes. , 1986, , 179-201.		35
61	Macronuclear DNA of <i>Tetrahymena thermophila</i> exists as defined subchromosomal-sized molecules. <i>Nucleic Acids Research</i> , 1985, 13, 5817-5831.	6.5	92
62	Internal micronuclear DNA regions which include sequences homologous to macronuclear telomeres are deleted during development in <i>Tetrahymena</i> . <i>Nucleic Acids Research</i> , 1984, 12, 6103-6116.	6.5	20
63	Sequence organization within and flanking clusters of 5S ribosomal RNA genes in <i>Tetrahymena</i> . <i>Nucleic Acids Research</i> , 1984, 12, 3003-3021.	6.5	35
64	<i>Tetrahymena</i> H4 genes: structure, evolution and organization in macro- and micronuclei. <i>Nucleic Acids Research</i> , 1984, 12, 1961-1975.	6.5	89
65	DNA elimination in tetrahymena: A developmental process involving extensive breakage and rejoining of DNA at defined sites. <i>Cell</i> , 1984, 36, 433-440.	13.5	178
66	Tandemly repeated hexanucleotide at tetrahymena rDNA free end is generated from a single copy during development. <i>Cell</i> , 1982, 31, 177-182.	13.5	87
67	Elimination of DNA sequences during macronuclear differentiation in <i>Tetrahymena thermophila</i> , as detected by in situ hybridization. <i>Chromosoma</i> , 1982, 85, 11-22.	1.0	55
68	Ribosomal RNA gene amplification in tetrahymena may be associated with chromosome breakage and DNA elimination. <i>Cell</i> , 1981, 24, 765-774.	13.5	85
69	Alteration of the <i>Tetrahymena</i> Genome During Nuclear Differentiation*â€€. <i>Journal of Protozoology</i> , 1979, 26, 10-13.	0.9	60
70	A single integrated gene for ribosomal RNA in a eucaryote, tetrahymena pyriformis. <i>Cell</i> , 1977, 12, 121-132.	13.5	176
71	Chapter 16 Isolation of Micro- and Macronuclei of <i>Tetrahymena pyriformis</i> . <i>Methods in Cell Biology</i> , 1975, 9, 311-327.	0.5	357
72	Comparison of the sequences of macro- and micronuclear DNA of <i>Tetrahymena pyriformis</i> . <i>Chromosoma</i> , 1974, 48, 1-18.	1.0	216

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73	Programmed Genome Rearrangements inTetrahymena. , 0, , 349-367.		1