Meng-Chao Yao

List of Publications by Year
in descending order

73 papers	12,256 citations	87723 38 h-index	88477 70 g-index
76 all docs	76 docs citations	76 times ranked	20901 citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
2	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	4.3	3,122
3	Chapter 16 Isolation of Micro- and Macronuclei of Tetrahymena pyriformis. Methods in Cell Biology, 1975, 9, 311-327.	0.5	357
4	Comparison of the sequences of macro- and micronuclear DNA of Tetrahymena pyriformis. Chromosoma, 1974, 48, 1-18.	1.0	216
5	DNA elimination in tetrahymena: A developmental process involving extensive breakage and rejoining of DNA at defined sites. Cell, 1984, 36, 433-440.	13.5	178
6	A single integrated gene for ribosomal RNA in a eucaryote, tetrahymena pyriformis. Cell, 1977, 12, 121-132.	13.5	176
7	Programmed DNA Deletion As an RNA-Guided System of Genome Defense. Science, 2003, 300, 1581-1584.	6.0	170
8	Pdd1p, A Novel Chromodomain-Containing Protein, Links Heterochromatin Assembly and DNA Elimination in Tetrahymena. Cell, 1996, 87, 75-84.	13.5	163
9	Nongenic, bidirectional transcription precedes and may promote developmental DNA deletion in Tetrahymena thermophila. Genes and Development, 2001, 15, 1287-1298.	2.7	145
10	A Domesticated piggyBac Transposase Plays Key Roles in Heterochromatin Dynamics and DNA Cleavage during Programmed DNA Deletion in Tetrahymena thermophila. Molecular Biology of the Cell, 2010, 21, 1753-1762.	0.9	143
11	GENOME DOWNSIZING DURING CILIATE DEVELOPMENT:Nuclear Division of Labor through Chromosome Restructuring. Annual Review of Genetics, 1996, 30, 557-578.	3.2	138
12	The controlling sequence for site-specific chromosome breakage in tetrahymena. Cell, 1990, 63, 763-772.	13.5	137
13	DNA Elimination in Ciliates: Transposon Domestication and Genome Surveillance. Annual Review of Genetics, 2011, 45, 227-246.	3.2	125
14	A conserved nucleotide sequence at the sites of developmentally regulated chromosomal breakage in tetrahymena. Cell, 1987, 48, 779-788.	13.5	111
15	A programmed site-specific DNA rearrangement in Tetrahymena thermophila requires flanking polypurine tracts. Cell, 1990, 61, 1237-1246.	13.5	109
16	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
17	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
18	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

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19	Induction of Large DNA Palindrome Formation in Yeast: Implications for Gene Amplification and Genome Stability in Eukaryotes. Cell, 1996, 87, 1115-1122.	13.5	93
20	Parental Expression of the Chromodomain Protein Pdd1p Is Required for Completion of Programmed DNA Elimination and Nuclear Differentiation. Molecular Cell, 1999, 4, 865-872.	4.5	93
21	Macronuclear DNA ofTetrahymena thermophilaexists as defined subchromosomal-sized molecules. Nucleic Acids Research, 1985, 13, 5817-5831.	6.5	92
22	TetrahymenaH4 genes: structure, evolution and organization in macro- and micronuclei. Nucleic Acids Research, 1984, 12, 1961-1975.	6.5	89
23	Tandemly repeated hexanucleotide at tetrahymena rDNA free end is generated from a single copy during development. Cell, 1982, 31, 177-182.	13.5	87
24	Palindromic gene amplification â€" an evolutionarily conserved role for DNA inverted repeats in the genome. Nature Reviews Cancer, 2009, 9, 216-224.	12.8	86
25	Ribosomal RNA gene amplification in tetrahymena may be associated with chromosome breakage and DNA elimination. Cell, 1981, 24, 765-774.	13.5	85
26	Programmed DNA deletions in Tetrahymena: mechanisms and implications. Trends in Genetics, 1996, 12, 26-30.	2.9	72
27	Short inverted repeats at a free end signal large palindromic DNA formation in tetrahymena. Cell, 1991, 67, 505-516.	13.5	67
28	Sequence microheterogeneity is generated at junctions of programmed DNA deletions inTetrahymena thermophila. Nucleic Acids Research, 1989, 17, 7263-7272.	6.5	62
29	Alteration of theTetrahymenaGenome During Nuclear Differentiation*â€. Journal of Protozoology, 1979, 26, 10-13.	0.9	60
30	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
31	Elimination of DNA sequences during macronuclear differentiation in Tetrahymena thermophila, as detected by in situ hybridization. Chromosoma, 1982, 85, 11-22.	1.0	55
32	Communication Between Parental and Developing Genomes During Tetrahymena Nuclear Differentiation Is Likely Mediated by Homologous RNAs. Genetics, 2005, 169, 149-160.	1.2	54
33	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
34	Identification of novel chromatin-associated proteins involved in programmed genome rearrangements in Tetrahymena. Journal of Cell Science, 2007, 120, 1978-1989.	1.2	52
35	Role of ATG8 and Autophagy in Programmed Nuclear Degradation in Tetrahymena thermophila. Eukaryotic Cell, 2012, 11, 494-506.	3.4	50
36	Flanking Regulatory Sequences of the Tetrahymena R Deletion Element Determine the Boundaries of DNA Rearrangement. Molecular and Cellular Biology, 1999, 19, 5631-5641.	1.1	47

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37	Induction of Gene Silencing by Hairpin RNA Expression in Tetrahymena thermophila Reveals a Second Small RNAPathway. Molecular and Cellular Biology, 2006, 26, 8731-8742.	1.1	46
38	The piggyBac transposon-derived genes TPB1 and TPB6 mediate essential transposon-like excision during the developmental rearrangement of key genes in Tetrahymena thermophila. Genes and Development, 2016, 30, 2724-2736.	2.7	43
39	An essential role for the DNA breakage-repair protein Ku80 in programmed DNA rearrangements in Tetrahymena thermophila. Molecular Biology of the Cell, 2012, 23, 2213-2225.	0.9	42
40	Detection of circular excised DNA deletion elements in Tetrahymena thermophila during development. Nucleic Acids Research, 1994, 22, 5702-5708.	6.5	36
41	Sequence organization within and flanking clusters of 5S ribosomal RNA genes inTetrahymena. Nucleic Acids Research, 1984, 12, 3003-3021.	6.5	35
42	Role of Histone Deacetylation in Developmentally Programmed DNA Rearrangements in Tetrahymena thermophila. Eukaryotic Cell, 2002, 1, 293-303.	3.4	35
43	Amplification of Ribosomal RNA Genes. , 1986, , 179-201.		35
44	Programmed Genome Rearrangements in Tetrahymena. Microbiology Spectrum, 2014, 2, .	1.2	33
45	Large DNA palindromes as a common form of structural chromosome aberrations in human cancers. Human Cell, 2006, 19, 17-23.	1.2	29
46	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
47	Evolutionary Conservation of Sequences Directing Chromosome Breakage and rDNA Palindrome Formation in Tetrahymenine Ciliates. Genetics, 1996, 144, 1479-1487.	1.2	25
48	Tudor Nuclease Genes and Programmed DNA Rearrangements in Tetrahymena thermophila. Eukaryotic Cell, 2007, 6, 1795-1804.	3.4	22
49	Diversity and Universality of Endosymbiotic Rickettsia in the Fish Parasite Ichthyophthirius multifiliis. Frontiers in Microbiology, 2017, 8, 189.	1.5	21
50	Internal micronuclear DNA regions which include sequences homologous to macronuclear telomeres are deleted during development inTetrahymena. Nucleic Acids Research, 1984, 12, 6103-6116.	6.5	20
51	Sequence characterization ofTetrahymenamacronuclear DNA ends. Nucleic Acids Research, 1986, 14, 2109-2122.	6.5	19
52	Absence of Positive Selection on Centromeric Histones in Tetrahymena Suggests Unsuppressed Centromere-Drive in Lineages Lacking Male Meiosis. Journal of Molecular Evolution, 2011, 72, 510-520.	0.8	19
53	Tetrahymena thermophila JMJD3 Homolog Regulates H3K27 Methylation and Nuclear Differentiation. Eukaryotic Cell, 2012, 11, 601-614.	3.4	18
54	Programmed Minichromosome Elimination as a Mechanism for Somatic Genome Reduction in Tetrahymena thermophila. PLoS Genetics, 2016, 12, e1006403.	1.5	18

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55	The intranuclear organization of normal, hemizygous and excision-deficient rRNA genes during developmental amplification in Tetrahymena thermophila. Chromosoma, 1997, 106, 233-242.	1.0	17
56	Developmentally Regulated Rpd3p Homolog Specific to the Transcriptionally Active Macronucleus of Vegetative Tetrahymena thermophila. Molecular and Cellular Biology, 2000, 20, 8319-8328.	1.1	15
57	Chapter 29 Creation and Use of Antisense Ribosomes in Tetrahymena thermophila. Methods in Cell Biology, 1999, 62, 533-547.	0.5	14
58	Class I Histone Deacetylase Thd1p Affects Nuclear Integrity in Tetrahymena thermophila. Eukaryotic Cell, 2005, 4, 981-990.	3.4	13
59	Dynamic distributions of long double-stranded RNA in Tetrahymena during nuclear development and genome rearrangements. Journal of Cell Science, 2016, 129, 1046-58.	1.2	9
60	Setting boundaries for genome-wide heterochromatic DNA deletions through flanking inverted repeats in Tetrahymena thermophila. Nucleic Acids Research, 2019, 47, 5181-5192.	6.5	8
61	Characterization of the Euplotes crassus Macronuclear rDNA and its Potential as a DNA Transformation Vehicle. Journal of Eukaryotic Microbiology, 1999, 46, 206-216.	0.8	7
62	Chapter 25 Microinjection of Tetrahymena thermophila. Methods in Cell Biology, 1999, 62, 469-484.	0.5	7
63	Selfing mutants link Ku proteins to mating type determination in Tetrahymena. PLoS Biology, 2020, 18, e3000756.	2.6	6
64	Genome-wide analysis of palindrome formation. Nature Genetics, 2010, 42, 279-279.	9.4	5
65	Abundant and diverse Tetrahymena species living in the bladder traps of aquatic carnivorous Utricularia plants. Scientific Reports, 2019, 9, 13669.	1.6	5
66	RNA rules. Nature, 2008, 451, 131-132.	13.7	4
67	DRH1, a p68-related RNA helicase gene, is required for chromosome breakage in Tetrahymena. Biology Open, 2016, 5, 1790-1798.	0.6	3
68	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
69	Antisense in Abundance: The Ribosome as a Vehicle for Antisense RNA. , 1998, 20, 143-151.		2
70	Programmed Genome Rearrangements inTetrahymena. , 0, , 349-367.		1
71	An Intragenic Suppressor of Cold Sensitivity Identifies Potentially Interacting Bases in the Peptidyl Transferase Center of Tetrahymena rRNA. Genetics, 1998, 149, 937-946.	1.2	1
72	Abstract of Symposium. Human Cell, 2005, 18, 29-33.	1.2	0

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73	Introduction for special issue. Journal of Biomedical Science, 2007, 14, 451-451.	2.6	0