Ting-Fang Wang

List of Publications by Year
in descending order

58 papers	7,612 citations	236925 25 h-index	144013 57 g-index
63 all docs	63 docs citations	63 times ranked	16173 citing authors

#	Article	IF	Citations
1	Sexual Crossing, Chromosome-Level Genome Sequences, and Comparative Genomic Analyses for the Medicinal Mushroom <i>Taiwanofungus Camphoratus</i> (Syn. <i>Antrodia Cinnamomea</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.4	4
2	Phase separation and zinc-induced transition modulate synaptic distribution and association of autism-linked CTTNBP2 and SHANK3. Nature Communications, 2022, 13, 2664.	12.8	17
3	Budding yeast Rad51: a paradigm for how phosphorylation and intrinsic structural disorder regulate homologous recombination and protein homeostasis. Current Genetics, 2021, 67, 389-396.	1.7	1
4	<i>Trichoderma reesei</i> Rad51 tolerates mismatches in hybrid meiosis with diverse genome sequences. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
5	Transcriptomic Analysis and C-Terminal Epitope Tagging Reveal Differential Processing and Signaling of Endogenous TLR3 and TLR7. Frontiers in Immunology, 2021, 12, 686060.	4.8	3
6	PacBio Long-Read Sequencing, Assembly, and Funannotate Reannotation of the Complete Genome of Trichoderma reesei QM6a. Methods in Molecular Biology, 2021, 2234, 311-329.	0.9	14
7	TSETA: A Third-Generation Sequencing-Based Computational Tool for Mapping and Visualization of SNPs, Meiotic Recombination Products, and RIP Mutations. Methods in Molecular Biology, 2021, 2234, 331-361.	0.9	2
8	Complete Genome Sequences and Genome-Wide Characterization of <i>Trichoderma</i> Biocontrol Agents Provide New Insights into their Evolution and Variation in Genome Organization, Sexual Development, and Fungal-Plant Interactions. Microbiology Spectrum, 2021, 9, e0066321.	3.0	11
9	Third-generation sequencing-based mapping and visualization of single nucleotide polymorphism, meiotic recombination, illegitimate mutation and repeat-induced point mutation. NAR Genomics and Bioinformatics, 2020, 2, lqaa056.	3.2	5
10	Dual roles of yeast Rad51 N-terminal domain in repairing DNA double-strand breaks. Nucleic Acids Research, 2020, 48, 8474-8489.	14.5	14
11	Repeat-induced point (RIP) mutation in the industrial workhorse fungus Trichoderma reesei. Applied Microbiology and Biotechnology, 2018, 102, 1567-1574.	3.6	14
12	Draft Genome Sequence of Burkholderia sp. Strain WAC0059, a Bacterium Isolated from the Medicinal Fungus Antrodia cinnamomea. Genome Announcements, 2018, 6, .	0.8	2
13	Tlr7 deletion alters expression profiles of genes related to neural function and regulates mouse behaviors and contextual memory. Brain, Behavior, and Immunity, 2018, 72, 101-113.	4.1	30
14	Omics Analyses of Trichoderma reesei CBS999.97 and QM6a Indicate the Relevance of Female Fertility to Carbohydrate-Active Enzyme and Transporter Levels. Applied and Environmental Microbiology, 2017, 83, .	3.1	22
15	Trichoderma reesei complete genome sequence, repeat-induced point mutation, and partitioning of CAZyme gene clusters. Biotechnology for Biofuels, 2017, 10, 170.	6.2	88
16	S. cerevisiaeMre11 recruits conjugated SUMO moieties to facilitate the assembly and function of the Mre11-Rad50-Xrs2 complex. Nucleic Acids Research, 2016, 44, 2199-2213.	14.5	21
17	17 Sexual Development in Trichoderma. , 2016, , 457-474.		7
18	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701

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19	The Genomes of Three Uneven Siblings: Footprints of the Lifestyles of Three Trichoderma Species. Microbiology and Molecular Biology Reviews, 2016, 80, 205-327.	6.6	194
20	Hybrid Infertility: The Dilemma or Opportunity of Applying Sexual Development to Improve Trichoderma reesei Industrial Strains. Fungal Biology, 2016, , 351-359.	0.6	5
21	Trichoderma reesei meiosis generates segmentally aneuploid progeny with higher xylanase-producing capability. Biotechnology for Biofuels, 2015, 8, 30.	6.2	30
22	Interorganelle interactions and inheritance patterns of nuclei and vacuoles in budding yeast meiosis. Autophagy, 2014, 10, 285-295.	9.1	7
23	Genomic and transcriptomic analyses of the medicinal fungus <i>Antrodia cinnamomea</i> for its metabolite biosynthesis and sexual development. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4743-52.	7.1	79
24	Pch2 Prevents Mec1/Tel1-Mediated Hop1 Phosphorylation Occurring Independently of Red1 in Budding Yeast Meiosis. PLoS ONE, 2014, 9, e85687.	2.5	15
25	Three Distinct Modes of Mec1/ATR and Tel1/ATM Activation Illustrate Differential Checkpoint Targeting during Budding Yeast Early Meiosis. Molecular and Cellular Biology, 2013, 33, 3365-3376.	2.3	31
26	Mek1 stabilizes Hop1-Thr318 phosphorylation to promote interhomolog recombination and checkpoint responses during yeast meiosis. Nucleic Acids Research, 2012, 40, 11416-11427.	14.5	63
27	Blue Light Acts as a Double-Edged Sword in Regulating Sexual Development of Hypocrea jecorina (Trichoderma reesei). PLoS ONE, 2012, 7, e44969.	2.5	43
28	Genetic Requirements and Meiotic Function of Phosphorylation of the Yeast Axial Element Protein Red. Molecular and Cellular Biology, 2011, 31, 912-923.	2.3	22
29	Yeast axial-element protein, Red1, binds SUMO chains to promote meiotic interhomologue recombination and chromosome synapsis. EMBO Journal, 2010, 29, 586-596.	7.8	49
30	Three New Structures of Left-Handed RadA Helical Filaments: Structural Flexibility of N-Terminal Domain Is Critical for Recombinase Activity. PLoS ONE, 2009, 4, e4890.	2.5	15
31	The N-terminal domain of Escherichia coli RecA have multiple functions in promoting homologous recombination. Journal of Biomedical Science, 2009, 16, 37.	7.0	17
32	Production of FMDV virus-like particles by a SUMO fusion protein approach in Escherichia coli. Journal of Biomedical Science, 2009, 16, 69.	7.0	35
33	High-throughput screening of soluble recombinant proteins. Protein Science, 2009, 11, 1714-1719.	7.6	145
34	Probing the dynamic differential stiffness of dsDNA interacting with RecA in the enthalpic regime. Optics Express, 2009, 17, 20376.	3.4	10
35	Right or left turn? RecA family protein filaments promote homologous recombination through clockwise axial rotation. BioEssays, 2008, 30, 48-56.	2.5	18
36	Authors' reply to correspondence from Egelman. BioEssays, 2008, 30, 1254-1255.	2.5	2

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37	An improved SUMO fusion protein system for effective production of native proteins. Protein Science, 2008, 17, 1241-1248.	7.6	107
38	Crystal structure of the left-handed archaeal RadA helical filament: identification of a functional motif for controlling quaternary structures and enzymatic functions of RecA family proteins. Nucleic Acids Research, 2007, 35, 1787-1801.	14.5	40
39	Tying SUMO modifications to dynamic behaviors of chromosomes during meiotic prophase of Saccharomyces cerevisiae. Journal of Biomedical Science, 2007, 14, 481-490.	7.0	12
40	Structural and Functional Analyses of Five Conserved Positively Charged Residues in the L1 and N-Terminal DNA Binding Motifs of Archaeal RadA Protein. PLoS ONE, 2007, 2, e858.	2.5	19
41	1P219 Structure of the left-handed archaeal RadA filament : a subunit rotation motif controls homologous DNA strand exchange reaction(7. Nucleic acid binding protein,Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 577 T	0.0	0
42	SUMO modifications control assembly of synaptonemal complex and polycomplex in meiosis of Saccharomyces cerevisiae. Genes and Development, 2006, 20, 2067-2081.	5.9	236
43	Calcium Ion Promotes Yeast Dmc1 Activity via Formation of Long and Fine Helical Filaments with Single-stranded DNA. Journal of Biological Chemistry, 2005, 280, 40980-40984.	3.4	44
44	Molecular Visualization of the Yeast Dmc1 Protein Ring and Dmc1â^'ssDNA Nucleoprotein Complex. Biochemistry, 2005, 44, 6052-6058.	2.5	25
45	Self-cleavage of fusion protein in vivo using TEV protease to yield native protein. Protein Science, 2005, 14, 936-941.	7.6	50
46	Nanoscale Imaging of Biomolecules by Controlled Carbon Nanotube Probes. Japanese Journal of Applied Physics, 2004, 43, 4517-4520.	1.5	8
47	Heterodimeric complexes of Hop2 and Mnd1 function with Dmc1 to promote meiotic homolog juxtaposition and strand assimilation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10572-10577.	7.1	110
48	Identification of Tbr-1/CASK complex target genes in neurons. Journal of Neurochemistry, 2004, 91, 1483-1492.	3.9	80
49	Self-polymerization of archaeal RadA protein into long and fine helical filaments. Biochemical and Biophysical Research Communications, 2004, 323, 845-851.	2.1	16
50	Transcriptional Modification by a CASK-Interacting Nucleosome Assembly Protein. Neuron, 2004, 42, 113-128.	8.1	142
51	pp60 Is a Negative Regulator of Laminin-1-Mediated Neurite Outgrowth in Chick Sensory Neurons. Molecular and Cellular Neurosciences, 2002, 21, 81-93.	2.2	16
52	Supercomplex formation between Mlh1â€"Mlh3 and Sgs1â€"Top3 heterocomplexes in meiotic yeast cells. Biochemical and Biophysical Research Communications, 2002, 296, 949-953.	2.1	40
53	Nuclear translocation and transcription regulation by the membrane-associated guanylate kinase CASK/LIN-2. Nature, 2000, 404, 298-302.	27.8	339
54	Structure and function of ectoapyrase (CD39). Drug Development Research, 1998, 45, 245-252.	2.9	10

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55	Golgi Localization and Functional Expression of Human Uridine Diphosphatase. Journal of Biological Chemistry, 1998, 273, 11392-11399.	3.4	102
56	The Transmembrane Domains of Ectoapyrase (CD39) Affect Its Enzymatic Activity and Quaternary Structure. Journal of Biological Chemistry, 1998, 273, 24814-24821.	3.4	124
57	Characterization of brain ecto-apyrase: evidence for only one ecto-apyrase (CD39) gene. Molecular Brain Research, 1997, 47, 295-302.	2.3	81
58	CD39 Is an Ecto-(Ca2+,Mg2+)-apyrase. Journal of Biological Chemistry, 1996, 271, 9898-9901.	3.4	258