Jun-Yi Leu

List of Publications by Year
in descending order

48 papers	2,057 citations	304743 22 h-index	265206 42 g-index
52 all docs	52 docs citations	52 times ranked	2517 citing authors

#	Article	IF	Citations
1	Incompatibility of Nuclear and Mitochondrial Genomes Causes Hybrid Sterility between Two Yeast Species. Cell, 2008, 135, 1065-1073.	28.9	326
2	The Meiosis-Specific Hop2 Protein of S. cerevisiae Ensures Synapsis between Homologous Chromosomes. Cell, 1998, 94, 375-386.	28.9	190
3	Multiple Molecular Mechanisms Cause Reproductive Isolation between Three Yeast Species. PLoS Biology, 2010, 8, e1000432.	5.6	131
4	Clusters of Nucleotide Substitutions and Insertion/Deletion Mutations Are Associated with Repeat Sequences. PLoS Biology, 2011, 9, e1000622.	5.6	106
5	Dynamic Large-Scale Chromosomal Rearrangements Fuel Rapid Adaptation in Yeast Populations. PLoS Genetics, 2013, 9, e1003232.	3.5	106
6	Speciation through cytonuclear incompatibility: Insights from yeast and implications for higher eukaryotes. BioEssays, 2010, 32, 401-411.	2.5	98
7	The Pachytene Checkpoint in S. cerevisiae Depends on Swe1-Mediated Phosphorylation of the Cyclin-Dependent Kinase Cdc28. Molecular Cell, 1999, 4, 805-814.	9.7	80
8	On the Nature and Evolutionary Impact of Phenotypic Robustness Mechanisms. Annual Review of Ecology, Evolution, and Systematics, 2014, 45, 495-517.	8.3	77
9	High-Resolution Mutation Mapping Reveals Parallel Experimental Evolution in Yeast. PLoS Biology, 2006, 4, e256.	5.6	73
10	Characterization of Chromosome Stability in Diploid, Polyploid and Hybrid Yeast Cells. PLoS ONE, 2013, 8, e68094.	2.5	71
11	Experimental Evolution of Mating Discrimination in Budding Yeast. Current Biology, 2006, 16, 280-286.	3.9	60
12	Natural history of budding yeast. Current Biology, 2009, 19, R886-R890.	3.9	53
13	The histone deacetylase Hos2 forms an Hsp42-dependent cytoplasmic granule in quiescent yeast cells. Molecular Biology of the Cell, 2012, 23, 1231-1242.	2.1	51
14	The Evolution of Low Mutation Rates in Experimental Mutator Populations of Saccharomyces cerevisiae. Current Biology, 2012, 22, 1235-1240.	3.9	49
15	Heterothallism inSaccharomyces cerevisiaeisolates from nature: effect ofHOlocus on the mode of reproduction. Molecular Ecology, 2010, 19, 121-131.	3.9	46
16	The Red Queen in mitochondria: cyto-nuclear co-evolution, hybrid breakdown and human disease. Frontiers in Genetics, 2015, 6, 187.	2.3	46
17	Mitochondrialâ€“nuclear coâ€evolution leads to hybrid incompatibility through pentatricopeptide repeat proteins. EMBO Reports, 2017, 18, 87-101.	4.5	41
18	Hsp90 Regulates Nongenetic Variation in Response to Environmental Stress. Molecular Cell, 2013, 50, 82-92.	9.7	37

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19	A Comprehensive Analysis of Transcript-Supported De Novo Genes in Saccharomyces sensu stricto Yeasts. Molecular Biology and Evolution, 2017, 34, 2823-2838.	8.9	28
20	Breaking a species barrier by enabling hybrid recombination. Current Biology, 2021, 31, R180-R181.	3.9	28
21	The Hsp90-Dependent Proteome Is Conserved and Enriched for Hub Proteins with High Levels of Proteinâ€“Protein Connectivity. Genome Biology and Evolution, 2014, 6, 2851-2865.	2.5	27
22	A Tradeoff Drives the Evolution of Reduced Metal Resistance in Natural Populations of Yeast. PLoS Genetics, 2011, 7, e1002034.	3.5	27
23	A population study of killer viruses reveals different evolutionary histories of two closely related <scp>S</scp>accharomyces sensu stricto yeasts. Molecular Ecology, 2015, 24, 4312-4322.	3.9	26
24	The evolutionary dynamics of tRNA-gene copy number and codon-use in E. coli.. BMC Evolutionary Biology, 2015, 15, 163.	3.2	26
25	Coevolution with bacteria drives the evolution of aerobic fermentation in Lachancea kluyveri. PLoS ONE, 2017, 12, e0173318.	2.5	25
26	Experimental Evolution Reveals Interplay between Sch9 and Polyploid Stability in Yeast. PLoS Genetics, 2016, 12, e1006409.	3.5	24
27	Heterologous Hsp90 promotes phenotypic diversity through network evolution. PLoS Biology, 2018, 16, e2006450.	5.6	24
28	Differentiated cytoplasmic granule formation in quiescent and non-quiescent cells upon chronological aging. Microbial Cell, 2016, 3, 109-119.	3.2	22
29	Sex alters molecular evolution in diploid experimental populations of S. cerevisiae. Nature Ecology and Evolution, 2020, 4, 453-460.	7.8	20
30	Splicing of the Meiosis-Specific HOP2 Transcript Utilizes a Unique 5â€² Splice Site. Molecular and Cellular Biology, 1999, 19, 7933-7943.	2.3	18
31	Genome plasticity in Paramecium bursaria revealed by population genomics. BMC Biology, 2020, 18, 180.	3.8	16
32	Misfolding-prone proteins are reversibly sequestered to an Hsp42-associated granule upon chronological aging. Journal of Cell Science, 2018, 131, .	2.0	13
33	Protein Complexes Form a Basis for Complex Hybrid Incompatibility. Frontiers in Genetics, 2021, 12, 609766.	2.3	13
34	A maize cryptic Ac-homologous sequence derived from an Activator transposable element does not transpose. Molecular Genetics and Genomics, 1992, 233, 411-418.	2.4	12
35	Hsp90 Maintains Proteostasis of the Galactose Utilization Pathway To Prevent Cell Lethality. Molecular and Cellular Biology, 2016, 36, 1412-1424.	2.3	10
36	Plastic Rewiring of Sef1 Transcriptional Networks and the Potential of Nonfunctional Transcription Factor Binding in Facilitating Adaptive Evolution. Molecular Biology and Evolution, 2021, 38, 4732-4747.	8.9	9

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37	Mutation at a distance caused by homopolymeric guanine repeats in Saccharomyces cerevisiae. Science Advances, 2016, 2, e1501033.	10.3	8
38	Hsp90 mediates the crosstalk between galactose metabolism and cell morphology pathways in yeast. Current Genetics, 2017, 63, 23-27.	1.7	8
39	The evolution of germâ€“soma nuclear differentiation in eukaryotic unicells. Current Biology, 2020, 30, R502-R510.	3.9	8
40	Experimental evolution reveals a general role for the methyltransferase Hmt1 in noise buffering. PLoS Biology, 2019, 17, e3000433.	5.6	7
41	Experimental evolution improves mitochondrial genome quality control in Saccharomyces cerevisiae and extends its replicative lifespan. Current Biology, 2021, 31, 3663-3670.e4.	3.9	5
42	iTARGEX analysis of yeast deletome reveals novel regulators of transcriptional buffering in S phase and protein turnover. Nucleic Acids Research, 2021, 49, 7318-7329.	14.5	2
43	Making Sense of Noise. , 2020, , 379-391.		2
44	Multiple Intermolecular Interactions Facilitate Rapid Evolution of Essential Genes. SSRN Electronic Journal, 0, , .	0.4	1
45	Experimental evolution reveals a general role for the methyltransferase Hmt1 in noise buffering. , 2019, 17, e3000433.		0
46	Experimental evolution reveals a general role for the methyltransferase Hmt1 in noise buffering. , 2019, 17, e3000433.		0
47	Experimental evolution reveals a general role for the methyltransferase Hmt1 in noise buffering. , 2019, 17, e3000433.		0
48	Experimental evolution reveals a general role for the methyltransferase Hmt1 in noise buffering. , 2019, 17, e3000433.		0