Hisao Moriya

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1263183/publications.pdf

Version: 2024-02-01

394421 330143 1,671 42 19 37 citations g-index h-index papers 48 48 48 2391 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Glucose sensing and signaling in Saccharomyces cerevisiae through the Rgt2 glucose sensor and casein kinase I. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1572-1577.	7.1	208
2	Yak1p, a DYRK family kinase, translocates to the nucleus and phosphorylates yeast Pop2p in response to a glucose signal. Genes and Development, 2001, 15, 1217-1228.	5.9	138
3	Identification of dosage-sensitive genes in <i>Saccharomyces cerevisiae</i> using the genetic tug-of-war method. Genome Research, 2013, 23, 300-311.	5 . 5	125
4	Distinct mechanisms for spiro-carbon formation reveal biosynthetic pathway crosstalk. Nature Chemical Biology, 2013, 9, 818-825.	8.0	123
5	Quantitative nature of overexpression experiments. Molecular Biology of the Cell, 2015, 26, 3932-3939.	2.1	120
6	A Genome-Wide Activity Assessment of Terminator Regions in <i>Saccharomyces cerevisiae</i> Provides a ″Terminatome″ Toolbox. ACS Synthetic Biology, 2013, 2, 337-347.	3.8	117
7	In Vivo Robustness Analysis of Cell Division Cycle Genes in Saccharomyces cerevisiae. PLoS Genetics, 2006, 2, e111.	3.5	94
8	Integration of Transcriptional and Posttranslational Regulation in a Glucose Signal Transduction Pathway in Saccharomyces cerevisiae. Eukaryotic Cell, 2006, 5, 167-173.	3.4	81
9	Post-Translational Dosage Compensation Buffers Genetic Perturbations to Stoichiometry of Protein Complexes. PLoS Genetics, 2017, 13, e1006554.	3.5	67
10	Establishing a New Methodology for Genome Mining and Biosynthesis of Polyketides and Peptides through Yeast Molecular Genetics. ChemBioChem, 2012, 13, 846-854.	2.6	65
11	A comprehensive molecular interaction map of the budding yeast cell cycle. Molecular Systems Biology, 2010, 6, 415.	7.2	62
12	Aneuploid proliferation defects in yeast are not driven by copy number changes of a few dosage-sensitive genes. Genes and Development, 2015, 29, 898-903.	5.9	55
13	Inhibition of nuclear factor κB by IκB superrepressor gene transfer ameliorates ischemia-reperfusion injury after experimental lung transplantation. Journal of Thoracic and Cardiovascular Surgery, 2005, 130, 194-201.	0.8	54
14	Cellular growth defects triggered by an overload of protein localization processes. Scientific Reports, 2016, 6, 31774.	3.3	47
15	Estimating the protein burden limit of yeast cells by measuring the expression limits of glycolytic proteins. ELife, 2018, 7, .	6.0	46
16	Analysis of genetic interactions between DHH1, SSD1 and ELM1 indicates their involvement in cellular morphology determination in Saccharomyces cerevisiae., 1999, 15, 481-496.		42
17	Fragilities Caused by Dosage Imbalance in Regulation of the Budding Yeast Cell Cycle. PLoS Genetics, 2010, 6, e1000919.	3.5	33
18	Plasmid Construction Using Recombination Activity in the Fission Yeast Schizosaccharomyces pombe. PLoS ONE, 2010, 5, e9652.	2.5	27

#	Article	IF	Citations
19	Robustness analysis of cellular systems using the genetic tug-of-war method. Molecular BioSystems, 2012, 8, 2513.	2.9	22
20	Cloning and characterization of thehrpAgene in theterCregion ofEscherichia coilthat is highly similar to the DEAH family RNA helicase genes ofSaccharomyces cerevisiae. Nucleic Acids Research, 1995, 23, 595-598.	14.5	21
21	Development of an experimental method of systematically estimating protein expression limits in HEK293 cells. Scientific Reports, 2020, 10, 4798.	3.3	20
22	Overexpression limits of fission yeast cell ycle regulators <i>in vivo</i> and <i>in silico</i> . Molecular Systems Biology, 2011, 7, 556.	7.2	14
23	Genetic Analysis of Signal Generation by the Rgt2 Glucose Sensor of <i>Saccharomyces cerevisiae</i> G3: Genes, Genomes, Genetics, 2018, 8, 2685-2696.	1.8	13
24	Assessing phagotrophy in the mixotrophic ciliate Paramecium bursaria using GFP-expressing yeast cells. FEMS Microbiology Letters, 2017, 364, .	1.8	9
25	Genetic profiling of protein burden and nuclear export overload. ELife, 2020, 9, .	6.0	8
26	Evaluation of the lower protein limit in the budding yeast Saccharomyces cerevisiae using TIPI-gTOW. BMC Systems Biology, 2014, 8, 2.	3.0	7
27	Comparative Gene Analysis Focused on Silica Cell Wall Formation: Identification of Diatom-Specific SET Domain Protein Methyltransferases. Marine Biotechnology, 2020, 22, 551-563.	2.4	7
28	Yeast screening system reveals the inhibitory mechanism of cancer cell proliferation by benzyl isothiocyanate through down-regulation of Mis12. Scientific Reports, 2019, 9, 8866.	3.3	5
29	N-terminal deletion of Swi3 created by the deletion of a dubious ORF YJL175W mitigates protein burden effect in S. cerevisiae. Scientific Reports, 2020, 10, 9500.	3.3	5
30	A Robustness Analysis of Eukaryotic Cell Cycle concerning Cdc25 and Wee1 Proteins., 2006,,.		5
31	Massive expression of cysteine-containing proteins causes abnormal elongation of yeast cells by perturbing the proteasome. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	5
32	A robustness analysis of eukaryotic cell cycle concerning Cdc25 and wee1 proteins., 2006,,.		4
33	Relationships between Cell Cycle Regulator Gene Copy Numbers and Protein Expression Levels in Schizosaccharomyces pombe. PLoS ONE, 2013, 8, e73319.	2.5	4
34	Small Toxic Protein Encoded on Chromosome VII of Saccharomyces cerevisiae. PLoS ONE, 2015, 10, e0120678.	2.5	4
35	Exploring the Complexity of Protein-Level Dosage Compensation that Fine-Tunes Stoichiometry of Multiprotein Complexes. PLoS Genetics, 2020, 16, e1009091.	3.5	3
36	The expression level and cytotoxicity of green fluorescent protein are modulated by an additional N-terminal sequence. AIMS Biophysics, 2020, 7, 121-132.	0.6	3

#	Article	IF	Citations
37	Parallel Real-Time PCR on a Chip for Genetic Tug-of-War (gTOW) Method. Analytical Sciences, 2013, 29, 367-371.	1.6	2
38	Completing SBGN-AF Networks by Logic-Based Hypothesis Finding. Lecture Notes in Computer Science, 2014, , 165-179.	1.3	2
39	Identification of uncharacterized proteins potentially localized to mitochondria (UPMs) in <scp> <i>Saccharomyces cerevisiae</i> </scp> using a fluorescent protein unstable in the cytoplasm. Yeast, 2021, , .	1.7	2
40	Cell Cycle Analysis, Systematic Gene Overexpression. , 2013, , 247-249.		0
41	Measuring the Copy Number Limits of All Genes in Yeast. Seibutsu Butsuri, 2013, 53, 323-325.	0.1	0
42	Genetic Profiling of Resource Overload. Seibutsu Butsuri, 2022, 62, 134-136.	0.1	O