Hisao Moriya

List of Publications by Year in descending order

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

#	Article	IF	Citations
1	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
2	Genetic Profiling of Resource Overload. Seibutsu Butsuri, 2022, 62, 134-136.	0.1	0
3	Identification of uncharacterized proteins potentially localized to mitochondria (UPMs) in <scp> Saccharomyces cerevisiae </scp> using a fluorescent protein unstable in the cytoplasm. Yeast, 2021, , .	1.7	2
4	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
5	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
6	Development of an experimental method of systematically estimating protein expression limits in HEK293 cells. Scientific Reports, 2020, 10, 4798.	3.3	20
7	Exploring the Complexity of Protein-Level Dosage Compensation that Fine-Tunes Stoichiometry of Multiprotein Complexes. PLoS Genetics, 2020, 16, e1009091.	3.5	3
8	Genetic profiling of protein burden and nuclear export overload. ELife, 2020, 9, .	6.0	8
9	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
10	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
11	Genetic Analysis of Signal Generation by the Rgt2 Glucose Sensor of Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2018, 8, 2685-2696.	1.8	13
12	Estimating the protein burden limit of yeast cells by measuring the expression limits of glycolytic proteins. ELife, 2018, 7, .	6.0	46
13	Assessing phagotrophy in the mixotrophic ciliate Paramecium bursaria using GFP-expressing yeast cells. FEMS Microbiology Letters, 2017, 364, .	1.8	9
14	Post-Translational Dosage Compensation Buffers Genetic Perturbations to Stoichiometry of Protein Complexes. PLoS Genetics, 2017, 13, e1006554.	3.5	67
15	Cellular growth defects triggered by an overload of protein localization processes. Scientific Reports, 2016, 6, 31774.	3.3	47
16	Quantitative nature of overexpression experiments. Molecular Biology of the Cell, 2015, 26, 3932-3939.	2.1	120
17	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
18	Small Toxic Protein Encoded on Chromosome VII of Saccharomyces cerevisiae. PLoS ONE, 2015, 10, e0120678.	2.5	4

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19	Completing SBGN-AF Networks by Logic-Based Hypothesis Finding. Lecture Notes in Computer Science, 2014, , 165-179.	1.3	2
20	Evaluation of the lower protein limit in the budding yeast Saccharomyces cerevisiae using TIPI-gTOW. BMC Systems Biology, 2014, 8, 2.	3.0	7
21	Distinct mechanisms for spiro-carbon formation reveal biosynthetic pathway crosstalk. Nature Chemical Biology, 2013, 9, 818-825.	8.0	123
22	A Genome-Wide Activity Assessment of Terminator Regions in Saccharomyces cerevisiae Provides a â€³Terminatomeâ€³ Toolbox. ACS Synthetic Biology, 2013, 2, 337-347.	3.8	117
23	Identification of dosage-sensitive genes in Saccharomyces cerevisiae using the genetic tug-of-war method. Genome Research, 2013, 23, 300-311.	5.5	125
24	Parallel Real-Time PCR on a Chip for Genetic Tug-of-War (gTOW) Method. Analytical Sciences, 2013, 29, 367-371.	1.6	2
25	Relationships between Cell Cycle Regulator Gene Copy Numbers and Protein Expression Levels in Schizosaccharomyces pombe. PLoS ONE, 2013, 8, e73319.	2.5	4
26	Cell Cycle Analysis, Systematic Gene Overexpression. , 2013, , 247-249.		0
27	Measuring the Copy Number Limits of All Genes in Yeast. Seibutsu Butsuri, 2013, 53, 323-325.	0.1	0
28	Robustness analysis of cellular systems using the genetic tug-of-war method. Molecular BioSystems, 2012, 8, 2513.	2.9	22
29	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
30	Overexpression limits of fission yeast cellâ€cycle regulators in vivo and in silico. Molecular Systems Biology, 2011, 7, 556.	7.2	14
31	Fragilities Caused by Dosage Imbalance in Regulation of the Budding Yeast Cell Cycle. PLoS Genetics, 2010, 6, e1000919.	3.5	33
32	A comprehensive molecular interaction map of the budding yeast cell cycle. Molecular Systems Biology, 2010, 6, 415.	7.2	62
33	Plasmid Construction Using Recombination Activity in the Fission Yeast Schizosaccharomyces pombe. PLoS ONE, 2010, 5, e9652.	2.5	27
34	In Vivo Robustness Analysis of Cell Division Cycle Genes in Saccharomyces cerevisiae. PLoS Genetics, 2006, 2, e111.	3.5	94
35	Integration of Transcriptional and Posttranslational Regulation in a Glucose Signal Transduction Pathway in Saccharomyces cerevisiae. Eukaryotic Cell, 2006, 5, 167-173.	3.4	81
36	A robustness analysis of eukaryotic cell cycle concerning Cdc25 and wee1 proteins. , 2006, , .		4

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37	A Robustness Analysis of Eukaryotic Cell Cycle concerning Cdc25 and Wee1 Proteins. , 2006, , .		5
38	Inhibition of nuclear factor ÎºB by IÎºB superrepressor gene transfer ameliorates ischemia-reperfusion injury after experimental lung transplantation. Journal of Thoracic and Cardiovascular Surgery, 2005, 130, 194-201.	0.8	54
39	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
40	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
41	Analysis of genetic interactions betweenDHH1,SSD1 andELM1 indicates their involvement in cellular morphology determination inSaccharomyces cerevisiae. , 1999, 15, 481-496.		42
42	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