

Juan Mata

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,540
citations

293460

24
h-index

445137

33
g-index

37
all docs

37
docs citations

37
times ranked

4092
citing authors

#	ARTICLE	IF	CITATIONS
1	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	1.2	60
2	Quantitative analysis of protein-RNA interactions in fission yeast. <i>STAR Protocols</i> , 2022, 3, 101373.	0.5	0
3	Ribosome profiling reveals ribosome stalling on tryptophan codons and ribosome queuing upon oxidative stress in fission yeast. <i>Nucleic Acids Research</i> , 2021, 49, 383-399.	6.5	40
4	Proteomic analysis of meiosis and characterization of novel short open reading frames in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Cell Cycle</i> , 2020, 19, 1777-1785.	1.3	8
5	General amino acid control in fission yeast is regulated by a nonconserved transcription factor, with functions analogous to Gcn4/Atf4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1829-E1838.	3.3	48
6	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. <i>Rna</i> , 2018, 24, 1195-1213.	1.6	45
7	A PP2A-B55-Mediated Crosstalk between TORC1 and TORC2 Regulates the Differentiation Response in Fission Yeast. <i>Current Biology</i> , 2017, 27, 175-188.	1.8	32
8	4-Thiouridine Labeling to Analyze mRNA Turnover in <i>Schizosaccharomyces pombe</i> . <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091645.	0.2	2
9	Ribosome Profiling for the Analysis of Translation During Yeast Meiosis. <i>Methods in Molecular Biology</i> , 2017, 1471, 99-122.	0.4	4
10	Effects of cycloheximide on the interpretation of ribosome profiling experiments in <i>Schizosaccharomyces pombe</i> . <i>Scientific Reports</i> , 2017, 7, 10331.	1.6	47
11	Dual RNA Processing Roles of Pat1b via Cytoplasmic Lsm1-7 and Nuclear Lsm2-8 Complexes. <i>Cell Reports</i> , 2017, 20, 1187-1200.	2.9	34
12	Translation Factors Specify Cellular Metabolic State. <i>Cell Reports</i> , 2016, 16, 1787-1788.	2.9	3
13	Role of Ccr4-Not complex in heterochromatin formation at meiotic genes and subtelomeres in fission yeast. <i>Epigenetics and Chromatin</i> , 2015, 8, 28.	1.8	41
14	AnABlast: a new <i>in silico</i> strategy for the genome-wide search of novel genes and fossil regions. <i>DNA Research</i> , 2015, 22, 439-449.	1.5	11
15	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. <i>Genome Research</i> , 2015, 25, 884-896.	2.4	37
16	Systematic Analysis of the Role of RNA-Binding Proteins in the Regulation of RNA Stability. <i>PLoS Genetics</i> , 2014, 10, e1004684.	1.5	67
17	The translational landscape of fission-yeast meiosis and sporulation. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 641-647.	3.6	79
18	Cotranslational protein-RNA associations predict protein-protein interactions. <i>BMC Genomics</i> , 2014, 15, 298.	1.2	14

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19	Genome-wide mapping of polyadenylation sites in fission yeast reveals widespread alternative polyadenylation. <i>RNA Biology</i> , 2013, 10, 1407-1414.	1.5	50
20	Functional characterization of Upf1 targets in <i>Schizosaccharomyces pombe</i> . <i>RNA Biology</i> , 2013, 10, 1057-1065.	1.5	12
21	Widespread Cotranslational Formation of Protein Complexes. <i>PLoS Genetics</i> , 2011, 7, e1002398.	1.5	104
22	Genome-wide mapping of myosin protein-RNA networks suggests the existence of specialized protein production sites. <i>FASEB Journal</i> , 2010, 24, 479-484.	0.2	6
23	Global coordination of transcriptional control and mRNA decay during cellular differentiation. <i>Molecular Systems Biology</i> , 2010, 6, 380.	3.2	61
24	Rng3, a member of the UCS family of myosin co-chaperones, associates with myosin heavy chains cotranslationally. <i>EMBO Reports</i> , 2009, 10, 186-191.	2.0	21
25	urg1: A Uracil-Regulatable Promoter System for Fission Yeast with Short Induction and Repression Times. <i>PLoS ONE</i> , 2008, 3, e1428.	1.1	55
26	A Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast. <i>Molecular Cell</i> , 2007, 26, 145-155.	4.5	184
27	Transcriptional regulatory network for sexual differentiation in fission yeast. <i>Genome Biology</i> , 2007, 8, R217.	13.9	104
28	Global roles of Ste11p, cell type, and pheromone in the control of gene expression during early sexual differentiation in fission yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15517-15522.	3.3	122
29	Post-transcriptional control of gene expression: a genome-wide perspective. <i>Trends in Biochemical Sciences</i> , 2005, 30, 506-514.	3.7	247
30	Periodic gene expression program of the fission yeast cell cycle. <i>Nature Genetics</i> , 2004, 36, 809-817.	9.4	472
31	Whole-genome microarrays of fission yeast: characteristics, accuracy, reproducibility, and processing of array data. <i>BMC Genomics</i> , 2003, 4, 27.	1.2	190
32	Global Transcriptional Responses of Fission Yeast to Environmental Stress. <i>Molecular Biology of the Cell</i> , 2003, 14, 214-229.	0.9	726
33	The transcriptional program of meiosis and sporulation in fission yeast. <i>Nature Genetics</i> , 2002, 32, 143-147.	9.4	451
34	Tea2p Is a Kinesin-like Protein Required to Generate Polarized Growth in Fission Yeast. <i>Journal of Cell Biology</i> , 2000, 151, 15-28.	2.3	132