Maria Rodriguez-Lopez

List of Publications by Year in descending order

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623734 794594 22 552 14 19 citations g-index h-index papers 33 33 33 691 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Functional profiling of long intergenic non-coding RNAs in fission yeast. ELife, 2022, 11, .	6.0	7
2	Barcode sequencing and a high-throughput assay for chronological lifespan uncover ageing-associated genes in fission yeast. Microbial Cell, 2021, 8, 146-160.	3.2	19
3	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. PLoS Genetics, 2021, 17, e1009784.	3.5	2
4	Recombination and biased segregation of mitochondrial genomes during crossing and meiosis of different strains. MicroPublication Biology, 2021, 2021, .	0.1	0
5	The GATA Transcription Factor Gaf1 Represses tRNAs, Inhibits Growth, and Extends Chronological Lifespan Downstream of Fission Yeast TORC1. Cell Reports, 2020, 30, 3240-3249.e4.	6.4	33
6	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. Molecular Systems Biology, 2020, 16, e9270.	7.2	27
7	Pyphe, a python toolbox for assessing microbial growth and cell viability in high-throughput colony screens. ELife, 2020, 9, .	6.0	37
8	Longevity is determined by ETS transcription factors in multiple tissues and diverse species. PLoS Genetics, 2019, 15, e1008212.	3.5	23
9	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	8.9	12
10	General amino acid control in fission yeast is regulated by a nonconserved transcription factor, with functions analogous to Gcn4/Atf4. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1829-E1838.	7.1	48
11	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. Genetics, 2018, 210, 733-744.	2.9	8
12	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. Rna, 2018, 24, 1195-1213.	3.5	45
13	The copper transport-associated protein Ctr4 can form prion-like epigenetic determinants in Schizosaccharomyces pombe. Microbial Cell, 2017, 4, 16-28.	3.2	16
14	Functional and regulatory profiling of energy metabolism in fission yeast. Genome Biology, 2016, 17, 240.	8.8	44
15	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 2016, 1, 19.	1.8	27
16	Role of Ccr4-Not complex in heterochromatin formation at meiotic genes and subtelomeres in fission yeast. Epigenetics and Chromatin, 2015, 8, 28.	3.9	41
17	Ace2 receives helping hand for cell-cycle transcription. Cell Cycle, 2015, 14, 3351-3352.	2.6	2
18	Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence. G3: Genes, Genomes, Genetics, 2015, 5, 145-155.	1.8	38

#	Article	IF	CITATIONS
19	Natural genetic variation impacts expression levels of coding, nonâ€coding, and antisense transcripts in fission yeast. Molecular Systems Biology, 2014, 10, 764.	7.2	65
20	The fission yeast rDNA-binding protein Reb1 regulates G1 phase under nutritional stress. Journal of Cell Science, 2011, 124, 25-34.	2.0	22
21	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 0, 1, 19.	1.8	18
22	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 0, 1, 19.	1.8	5