

Martin PÅevorovskÅ½

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

431
citations

1170033

9
h-index

889612

19
g-index

25
all docs

25
docs citations

25
times ranked

719
citing authors

#	ARTICLE	IF	CITATIONS
1	Repression of a large number of genes requires interplay between homologous recombination and HIRA. <i>Nucleic Acids Research</i> , 2021, 49, 1914-1934.	6.5	2
2	The torpedo effect in <i>Bacillus subtilis</i> : RNase J1 resolves stalled transcription complexes. <i>EMBO Journal</i> , 2020, 39, e102500.	3.5	27
3	Ms1 RNA increases the amount of RNA polymerase in <i>Mycobacterium smegmatis</i> . <i>Molecular Microbiology</i> , 2019, 111, 354-372.	1.2	26
4	Analysis of Lipid Droplet Content in Fission and Budding Yeasts using Automated Image Processing. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	1
5	Mitotic defects in fission yeast lipid metabolism Δcut^{Δ} mutants are suppressed by ammonium chloride. <i>FEMS Yeast Research</i> , 2018, 18, .	1.1	4
6	The phenomenon of lipid metabolism Δcut^{Δ} mutants. <i>Yeast</i> , 2018, 35, 631-637.	0.8	13
7	Introns provide a platform for intergenic regulatory feedback of RPL22 paralogs in yeast. <i>PLoS ONE</i> , 2018, 13, e0190685.	1.1	6
8	Δf^{I} from <i>Bacillus subtilis</i> : Impact on Gene Expression and Characterization of Δf^{I} -Dependent Transcription That Requires New Types of Promoters with Extended ~ 35 and ~ 10 Elements. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	8
9	Nineteen complex-related factor Prp45 is required for the early stages of cotranscriptional spliceosome assembly. <i>Rna</i> , 2017, 23, 1512-1524.	1.6	7
10	Spotsizer: High-throughput quantitative analysis of microbial growth. <i>BioTechniques</i> , 2016, 61, 191-201.	0.8	10
11	Workflow for Genome-Wide Determination of Pre-mRNA Splicing Efficiency from Yeast RNA-seq Data. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	13
12	CSL protein regulates transcription of genes required to prevent catastrophic mitosis in fission yeast. <i>Cell Cycle</i> , 2016, 15, 3082-3093.	1.3	13
13	pREPORT: a multi-readout transcription reporter vector for fission yeast. <i>Yeast</i> , 2015, 32, 327-334.	0.8	1
14	The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015, 47, 235-241.	9.4	174
15	Fission Yeast CSL Transcription Factors: Mapping Their Target Genes and Biological Roles. <i>PLoS ONE</i> , 2015, 10, e0137820.	1.1	19
16	Fission Yeast CSL Proteins Function as Transcription Factors. <i>PLoS ONE</i> , 2013, 8, e59435.	1.1	8
17	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	0.8	29
18	N-Termini of Fungal CSL Transcription Factors Are Disordered, Enriched in Regulatory Motifs and Inhibit DNA Binding in Fission Yeast. <i>PLoS ONE</i> , 2011, 6, e23650.	1.1	8

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19	Cbf11 and Cbf12, the fission yeast CSL proteins, play opposing roles in cell adhesion and coordination of cell and nuclear division. <i>Experimental Cell Research</i> , 2009, 315, 1533-1547.	1.2	27
20	High environmental iron concentrations stimulate adhesion and invasive growth of <i>Schizosaccharomyces pombe</i> . <i>FEMS Microbiology Letters</i> , 2009, 293, 130-134.	0.7	15
21	Fungal CSL transcription factors. <i>BMC Genomics</i> , 2007, 8, 233.	1.2	16
22	A/T-rich inverted DNA repeats are destabilized by chaotrope-containing buffer during purification using silica gel membrane technology. <i>BioTechniques</i> , 2003, 35, 698-702.	0.8	3