

JosÃ© E PÃ©rez-OrtÃ­n

List of Publications by Year in descending order

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119
papers

5,544
citations

87888

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95266

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all docs

130
docs citations

130
times ranked

5840
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Deep Sequencing of Nascent Transcription in Yeast with BioGRO-seq. <i>Methods in Molecular Biology</i> , 2022, 2477, 57-70.	0.9	0
2	Recruitment of Xrn1 to stress-induced genes allows efficient transcription by controlling RNA polymerase II backtracking. <i>RNA Biology</i> , 2021, 18, 1458-1474.	3.1	5
3	Rpb4 and Puf3 imprint and post-transcriptionally control the stability of a common set of mRNAs in yeast. <i>RNA Biology</i> , 2021, 18, 1206-1220.	3.1	10
4	Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. <i>RNA Biology</i> , 2021, 18, 1310-1323.	3.1	12
5	A Trans-Omics Comparison Reveals Common Gene Expression Strategies in Four Model Organisms and Exposes Similarities and Differences between Them. <i>Cells</i> , 2021, 10, 334.	4.1	4
6	Eukaryotic RNA Polymerases: The Many Ways to Transcribe a Gene. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 663209.	3.5	19
7	Cell volume homeostatically controls the rDNA repeat copy number and rRNA synthesis rate in yeast. <i>PLoS Genetics</i> , 2021, 17, e1009520.	3.5	14
8	The total mRNA concentration buffering system in yeast is global rather than gene-specific. <i>Rna</i> , 2021, 27, 1281-1290.	3.5	11
9	A genome-wide transcriptional study reveals that iron deficiency inhibits the yeast TORC1 pathway. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194414.	1.9	19
10	Homeostasis in the Central Dogma of molecular biology: the importance of mRNA instability. <i>RNA Biology</i> , 2019, 16, 1659-1666.	3.1	26
11	The mRNA degradation factor Xrn1 regulates transcription elongation in parallel to Ccr4. <i>Nucleic Acids Research</i> , 2019, 47, 9524-9541.	14.5	26
12	Measuring RNA polymerase activity genome-wide with high-resolution run-on-based methods. <i>Methods</i> , 2019, 159-160, 177-182.	3.8	14
13	The telomeric Cdc13â€“Stn1â€“Ten1 complex regulates RNA polymerase II transcription. <i>Nucleic Acids Research</i> , 2019, 47, 6250-6268.	14.5	8
14	The exonuclease Xrn1 activates transcription and translation of mRNAs encoding membrane proteins. <i>Nature Communications</i> , 2019, 10, 1298.	12.8	36
15	The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally. <i>Epigenetics and Chromatin</i> , 2018, 11, 13.	3.9	19
16	A role for Mog1 in H2Bub1 and H3K4me3 regulation affecting RNAPII transcription and mRNA export. <i>EMBO Reports</i> , 2018, 19, .	4.5	11
17	Modulation of protein synthesis and degradation maintains proteostasis during yeast growth at different temperatures. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 794-802.	1.9	9
18	Asymmetric cell division requires specific mechanisms for adjusting global transcription. <i>Nucleic Acids Research</i> , 2017, 45, 12401-12412.	14.5	30

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19	Functional Genomics in Wine Yeast: DNA Arrays and Next Generation Sequencing. , 2017, , 573-604.		1
20	The ribosome assembly gene network is controlled by the feedback regulation of transcription elongation. <i>Nucleic Acids Research</i> , 2017, 45, 9302-9318.	14.5	13
21	Subtracting the sequence bias from partially digested MNase-seq data reveals a general contribution of TFIS to nucleosome positioning. <i>Epigenetics and Chromatin</i> , 2017, 10, 58.	3.9	17
22	The importance of controlling mRNA turnover during cell proliferation. <i>Current Genetics</i> , 2016, 62, 701-710.	1.7	23
23	Growth rate controls mRNA turnover in steady and non-steady states. <i>RNA Biology</i> , 2016, 13, 1175-1181.	3.1	21
24	Defects in the NC2 repressor affect both canonical and non-coding RNA polymerase II transcription initiation in yeast. <i>BMC Genomics</i> , 2016, 17, 183.	2.8	9
25	Rpb1 foot mutations demonstrate a major role of Rpb4 in mRNA stability during stress situations in yeast. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 731-743.	1.9	23
26	The mRNA cap-binding protein Cbc1 is required for high and timely expression of genes by promoting the accumulation of gene-specific activators at promoters. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 405-419.	1.9	10
27	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. <i>Nucleic Acids Research</i> , 2016, 44, 3643-3658.	14.5	45
28	Biotin-Genomic Run-On (Bio-GRO): A High-Resolution Method for the Analysis of Nascent Transcription in Yeast. <i>Methods in Molecular Biology</i> , 2016, 1361, 125-139.	0.9	10
29	Comparative Transcriptomic Analysis Reveals Similarities and Dissimilarities in <i>Saccharomyces cerevisiae</i> Wine Strains Response to Nitrogen Availability. <i>PLoS ONE</i> , 2015, 10, e0122709.	2.5	49
30	Impact of high pH stress on yeast gene expression: A comprehensive analysis of mRNA turnover during stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 653-664.	1.9	44
31	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. <i>Nucleic Acids Research</i> , 2015, 43, 787-802.	14.5	23
32	A web application for the unspecific detection of differentially expressed DNA regions in strand-specific expression data: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 3228-3230.	4.1	0
33	Cytoplasmic 5â€²-3â€² exonuclease Xrn1p is also a genome-wide transcription factor in yeast. <i>Frontiers in Genetics</i> , 2014, 5, 1.	2.3	427
34	What do you mean by transcription rate?. <i>BioEssays</i> , 2013, 35, 1056-1062.	2.5	19
35	External conditions inversely change the RNA polymerase II elongation rate and density in yeast. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 1248-1255.	1.9	17
36	Eukaryotic mRNA Decay: Methodologies, Pathways, and Links to Other Stages of Gene Expression. <i>Journal of Molecular Biology</i> , 2013, 425, 3750-3775.	4.2	125

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37	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	28.9	311
38	mRNASTab—a web application for mRNA stability analysis. <i>Bioinformatics</i> , 2013, 29, 813-814.	4.1	1
39	Topoisomerase II regulates yeast genes with singular chromatin architectures. <i>Nucleic Acids Research</i> , 2013, 41, 9243-9256.	14.5	14
40	Nonsense-Mediated mRNA Decay Controls the Changes in Yeast Ribosomal Protein Pre-mRNAs Levels upon Osmotic Stress. <i>PLoS ONE</i> , 2013, 8, e61240.	2.5	24
41	The relative importance of transcription rate, cryptic transcription and mRNA stability on shaping stress responses in yeast. <i>Transcription</i> , 2012, 3, 39-44.	3.1	5
42	Genome-wide studies of mRNA synthesis and degradation in eukaryotes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 604-615.	1.9	31
43	Genomic-Wide Methods to Evaluate Transcription Rates in Yeast. <i>Methods in Molecular Biology</i> , 2011, 734, 25-44.	0.9	11
44	Global Estimation of mRNA Stability in Yeast. <i>Methods in Molecular Biology</i> , 2011, 734, 3-23.	0.9	8
45	A genomic view of mRNA turnover in yeast. <i>Comptes Rendus - Biologies</i> , 2011, 334, 647-654.	0.2	6
46	Genomic and Proteomic Analysis of Wine Yeasts. , 2011, , 143-168.		0
47	Genomic Insights into the Different Layers of Gene Regulation in Yeast. <i>Genetics Research International</i> , 2011, 2011, 1-12.	2.0	2
48	The Conserved Foot Domain of RNA Pol II Associates with Proteins Involved in Transcriptional Initiation and/or Early Elongation. <i>Genetics</i> , 2011, 189, 1235-1248.	2.9	17
49	Heat Shock Response in Yeast Involves Changes in Both Transcription Rates and mRNA Stabilities. <i>PLoS ONE</i> , 2011, 6, e17272.	2.5	82
50	There is a steady-state transcriptome in exponentially growing yeast cells. <i>Yeast</i> , 2010, 27, 413-422.	1.7	36
51	A method for genome-wide analysis of DNA helical tension by means of psoralen—DNA photobinding. <i>Nucleic Acids Research</i> , 2010, 38, e182-e182.	14.5	65
52	The distribution of active RNA polymerase II along the transcribed region is gene-specific and controlled by elongation factors. <i>Nucleic Acids Research</i> , 2010, 38, 4651-4664.	14.5	40
53	A Complete Set of Nascent Transcription Rates for Yeast Genes. <i>PLoS ONE</i> , 2010, 5, e15442.	2.5	151
54	Regulon-Specific Control of Transcription Elongation across the Yeast Genome. <i>PLoS Genetics</i> , 2009, 5, e1000614.	3.5	59

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55	Chimeric Genomes of Natural Hybrids of <i>Saccharomyces cerevisiae</i> and <i>Saccharomyces kudriavzevii</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 2534-2544.	3.1	83
56	Specific and global regulation of mRNA stability during osmotic stress in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2009, 15, 1110-1120.	3.5	133
57	DNA Arrays. , 2009, , 469-488.		0
58	Mechanism-based Clustering of Genome-wide RNA Levels: Roles of Transcription and Transcript-Degradation Rates. , 2009, , 237-255.		10
59	The transcriptional inhibitor thiolutin blocks mRNA degradation in yeast. <i>Yeast</i> , 2008, 25, 85-92.	1.7	58
60	Mitochondrial inheritance and fermentative : oxidative balance in hybrids between <i>Saccharomyces cerevisiae</i> and <i>Saccharomyces uvarum</i> . <i>Yeast</i> , 2008, 25, 485-500.	1.7	44
61	Comprehensive Transcriptional Analysis of the Oxidative Response in Yeast. <i>Journal of Biological Chemistry</i> , 2008, 283, 17908-17918.	3.4	69
62	Genomics of mRNA turnover. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 6, 282-291.	3.8	23
63	The inner nuclear membrane protein Src1 associates with subtelomeric genes and alters their regulated gene expression. <i>Journal of Cell Biology</i> , 2008, 182, 897-910.	5.2	100
64	<i>Saccharomyces cerevisiae</i> Signature Genes for Predicting Nitrogen Deficiency during Alcoholic Fermentation. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5363-5369.	3.1	25
65	Transcriptional Response of <i>Saccharomyces cerevisiae</i> to Different Nitrogen Concentrations during Alcoholic Fermentation. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3049-3060.	3.1	96
66	Common gene expression strategies revealed by genome-wide analysis in yeast. <i>Genome Biology</i> , 2007, 8, R222.	9.6	33
67	The Sas3p and Gcn5p histone acetyltransferases are recruited to similar genes. <i>Genome Biology</i> , 2007, 8, R119.	9.6	43
68	A novel approach for the improvement of stress resistance in wine yeasts. <i>International Journal of Food Microbiology</i> , 2007, 114, 83-91.	4.7	73
69	Genomics and gene transcription kinetics in yeast. <i>Trends in Genetics</i> , 2007, 23, 250-257.	6.7	105
70	A genomic study of the inter-ORF distances in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2006, 23, 689-699.	1.7	13
71	Yeast HAT1 and HAT2 deletions have different life-span and transcriptome phenotypes. <i>FEBS Letters</i> , 2005, 579, 4063-4068.	2.8	14
72	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2004, 33, D364-D368.	14.5	288

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73	Saccharomyces cerevisiae Glutaredoxin 5-deficient Cells Subjected to Continuous Oxidizing Conditions Are Affected in the Expression of Specific Sets of Genes. Journal of Biological Chemistry, 2004, 279, 12386-12395.	3.4	60
74	Genomic Run-On Evaluates Transcription Rates for All Yeast Genes and Identifies Gene Regulatory Mechanisms. Molecular Cell, 2004, 15, 303-313.	9.7	233
75	Sus1, a Functional Component of the SAGA Histone Acetylase Complex and the Nuclear Pore-Associated mRNA Export Machinery. Cell, 2004, 116, 75-86.	28.9	330
76	A new set of DNA macrochips for the yeast Saccharomyces cerevisiae: features and uses. International Microbiology, 2004, 7, 199-206.	2.4	56
77	Arginase Activity is a Useful Marker of Nitrogen Limitation During Alcoholic Fermentations. Systematic and Applied Microbiology, 2003, 26, 471-479.	2.8	31
78	Structural characterization of chromosome I size variants from a natural yeast strain. Yeast, 2003, 20, 171-183.	1.7	28
79	Molecular Characterization of a Chromosomal Rearrangement Involved in the Adaptive Evolution of Yeast Strains. Genome Research, 2002, 12, 1533-1539.	5.5	243
80	DNA chips for yeast biotechnology. The case of wine yeasts. Journal of Biotechnology, 2002, 98, 227-241.	3.8	59
81	Study of the First Hours of Microvinification by the Use of Osmotic Stress-response Genes as Probes. Systematic and Applied Microbiology, 2002, 25, 153-161.	2.8	39
82	SRC1: an intron-containing yeast gene involved in sister chromatid segregation. Yeast, 2002, 19, 43-54.	1.7	45
83	Functional analysis of yeast gene families involved in metabolism of vitamins B1 and B6. Yeast, 2002, 19, 1261-1276.	1.7	89
84	Bromodomain factor 1 (Bdf1) protein interacts with histones. FEBS Letters, 2001, 496, 31-35.	2.8	35
85	Whole Genome Analysis of a Wine Yeast Strain. Comparative and Functional Genomics, 2001, 2, 69-79.	2.0	58
86	Stress response and expression patterns in wine fermentations of yeast genes induced at the diauxic shift. Yeast, 2000, 16, 139-148.	1.7	88
87	Expression Levels and Patterns of Glycolytic Yeast Genes During Wine Fermentation. Systematic and Applied Microbiology, 2000, 23, 300-303.	2.8	26
88	Statistical analysis of yeast genomic downstream sequences reveals putative polyadenylation signals. Nucleic Acids Research, 2000, 28, 1000-1010.	14.5	120
89	Mitotic Recombination and Genetic Changes in Saccharomyces cerevisiae during Wine Fermentation. Applied and Environmental Microbiology, 2000, 66, 2057-2061.	3.1	95
90	Stress response and expression patterns in wine fermentations of yeast genes induced at the diauxic shift. Yeast, 2000, 16, 139-148.	1.7	4

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91	Title is missing!. Biotechnology Letters, 1999, 21, 271-274.	2.2	14
92	News & Notes: Stochastic Nucleosome Positioning in a Yeast Chromatin Region Is Not Dependent on Histone H1. Current Microbiology, 1999, 39, 168-172.	2.2	16
93	Transcriptional and Structural Study of a Region of Two Convergent Overlapping Yeast Genes. Current Microbiology, 1999, 39, 369-373.	2.2	18
94	An inverse correlation between stress resistance and stuck fermentations in wine yeasts. A molecular study. , 1999, 64, 698-708.		94
95	Functional analysis of 12 ORFs from Saccharomyces cerevisiae chromosome II. , 1999, 15, 913-919.		6
96	Detection of Non-B-DNA Secondary Structures by S1 Nuclease Digestion. Journal of Chemical Education, 1998, 75, 762.	2.3	2
97	Optimized Method To Obtain Stable Food-Safe Recombinant Wine Yeast Strains. Journal of Agricultural and Food Chemistry, 1998, 46, 1689-1693.	5.2	46
98	The yeast FBP1 poly(A) signal functions in both orientations and overlaps with a gene promoter. Nucleic Acids Research, 1998, 26, 4588-4596.	14.5	9
99	HAT1 and HAT2 Proteins Are Components of a Yeast Nuclear Histone Acetyltransferase Enzyme Specific for Free Histone H4. Journal of Biological Chemistry, 1998, 273, 12599-12605.	3.4	88
100	Making your own gene library. Biochemical Education, 1997, 25, 237-242.	0.1	20
101	Analysis of the Structure of a Natural Alternating d(TA) _n Sequence in Yeast Chromatin. , 1997, 13, 313-326.		23
102	Chromatin structure of the yeast FBP1 gene: Transcription-dependent changes in the regulatory and coding regions. Yeast, 1993, 9, 1229-1240.	1.7	9
103	A Natural A/T-Rich Sequence from the Yeast FBP1 Gene Exists as a Cruciform in Escherichia coli Cells. Plasmid, 1993, 29, 222-232.	1.4	6
104	The role of histones and their modifications in the informative content of chromatin. Experientia, 1993, 49, 780-788.	1.2	37
105	Chromatin structure of the yeast SUC2 promoter in regulatory mutants. Molecular Genetics and Genomics, 1992, 231, 395-400.	2.4	59
106	The POT1 gene for yeast peroxisomal thiolase is subject to three different mechanisms of regulation. Molecular Microbiology, 1992, 6, 1867-1875.	2.5	29
107	A new glucose-repressible gene identified from the analysis of chromatin structure in deletion mutants of yeast SUC2 locus. Yeast, 1991, 7, 379-389.	1.7	52
108	Chromatin structure of the 5' flanking region of the yeast LEU2 gene. Molecular Genetics and Genomics, 1989, 217, 464-470.	2.4	9

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109	Chromatin structure of yeast genes. <i>Yeast</i> , 1989, 5, 219-238.	1.7	28
110	Chromatin structure of transposon Tn903 cloned into a yeast plasmid. <i>Plasmid</i> , 1989, 22, 143-150.	1.4	3
111	In vivo assembly of chromatin on pBR322 sequences cloned into yeast plasmids. <i>Plasmid</i> , 1989, 21, 113-119.	1.4	4
112	A rapid method for the screening of plasmids in transformed yeast strains. <i>Current Microbiology</i> , 1988, 17, 19-22.	2.2	5
113	Analysis of chromatin structure and composition. <i>Biochemical Education</i> , 1988, 16, 45-47.	0.1	2
114	Presence of nucleosomes in <i>Penicillium chrysogenum</i> . <i>Current Microbiology</i> , 1987, 15, 151-154.	2.2	1
115	On the presence of HMG proteins in yeast. <i>FEBS Letters</i> , 1986, 197, 179-182.	2.8	5
116	Rapid plasmid isolation. A laboratory experiment for intermediate and advanced students. <i>Biochemical Education</i> , 1986, 14, 142-144.	0.1	5
117	DNase I sensitivity of the chromatin of the yeast SUC2 gene for invertase. <i>Molecular Genetics and Genomics</i> , 1986, 205, 422-427.	2.4	18
118	Isolation and Characterization of an Fe(III)-Chelating Compound Produced by <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 1986, 52, 157-160.	3.1	40
119	Partial purification and properties of two histone acetyltransferases from the yeast, <i>Saccharomyces cerevisiae</i> . <i>Archives of Biochemistry and Biophysics</i> , 1985, 239, 184-190.	3.0	28