

Vicent Pelechano

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

5,137
citations

159358

30
h-index

110170

64
g-index

78
all docs

78
docs citations

78
times ranked

9060
citing authors

#	ARTICLE	IF	CITATIONS
1	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
2	Gene regulation by antisense transcription. <i>Nature Reviews Genetics</i> , 2013, 14, 880-893.	7.7	556
3	Extensive transcriptional heterogeneity revealed by isoform profiling. <i>Nature</i> , 2013, 497, 127-131.	13.7	408
4	Rapid Detection of COVID-19 Coronavirus Using a Reverse Transcriptional Loop-Mediated Isothermal Amplification (RT-LAMP) Diagnostic Platform. <i>Clinical Chemistry</i> , 2020, 66, 975-977.	1.5	372
5	Polyadenylation site-induced decay of upstream transcripts enforces promoter directionality. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 923-928.	3.6	258
6	Widespread Co-translational RNA Decay Reveals Ribosome Dynamics. <i>Cell</i> , 2015, 161, 1400-1412.	13.5	246
7	Functional consequences of bidirectional promoters. <i>Trends in Genetics</i> , 2011, 27, 267-276.	2.9	194
8	A Complete Set of Nascent Transcription Rates for Yeast Genes. <i>PLoS ONE</i> , 2010, 5, e15442.	1.1	151
9	eIF5A facilitates translation termination globally and promotes the elongation of many non polyproline-specific tripeptide sequences. <i>Nucleic Acids Research</i> , 2017, 45, 7326-7338.	6.5	142
10	System-wide Profiling of RNA-Binding Proteins Uncovers Key Regulators of Virus Infection. <i>Molecular Cell</i> , 2019, 74, 196-211.e11.	4.5	137
11	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 560-568.	3.6	100
12	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013, 41, e65-e65.	6.5	98
13	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , 2014, 10, 719.	3.2	91
14	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. <i>Nature Genetics</i> , 2016, 48, 984-994.	9.4	75
15	Transcription-driven chromatin repression of Intragenic transcription start sites. <i>PLoS Genetics</i> , 2019, 15, e1007969.	1.5	71
16	Rrp6p Controls mRNA Poly(A) Tail Length and Its Decoration with Poly(A) Binding Proteins. <i>Molecular Cell</i> , 2012, 47, 267-280.	4.5	69
17	A DHODH inhibitor increases p53 synthesis and enhances tumor cell killing by p53 degradation blockage. <i>Nature Communications</i> , 2018, 9, 1107.	5.8	63
18	Regulon-Specific Control of Transcription Elongation across the Yeast Genome. <i>PLoS Genetics</i> , 2009, 5, e1000614.	1.5	59

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19	The transcriptional inhibitor thiolutin blocks mRNA degradation in yeast. <i>Yeast</i> , 2008, 25, 85-92.	0.8	58
20	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , 2014, 9, 1740-1759.	5.5	57
21	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	3.2	52
22	Landscape and Dynamics of Transcription Initiation in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2016, 14, 2463-2475.	2.9	51
23	The Nuclear PolyA-Binding Protein Nab2p Is Essential for mRNA Production. <i>Cell Reports</i> , 2015, 12, 128-139.	2.9	47
24	Direct detection of SARS-CoV-2 using non-commercial RT-LAMP reagents on heat-inactivated samples. <i>Scientific Reports</i> , 2021, 11, 1820.	1.6	47
25	Sample-to-answer COVID-19 nucleic acid testing using a low-cost centrifugal microfluidic platform with bead-based signal enhancement and smartphone read-out. <i>Lab on A Chip</i> , 2021, 21, 2932-2944.	3.1	47
26	Genome-wide quantification of 5'-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. <i>Nature Protocols</i> , 2016, 11, 359-376.	5.5	45
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.	6.5	45
28	Transcript isoform sequencing reveals widespread promoter-proximal transcriptional termination in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2020, 11, 2589.	5.8	42
29	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.	6.5	40
30	There is a steady-state transcriptome in exponentially growing yeast cells. <i>Yeast</i> , 2010, 27, 413-422.	0.8	36
31	Recommendations for accurate genotyping of SARS-CoV-2 using amplicon-based sequencing of clinical samples. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1036.e1-1036.e8.	2.8	32
32	A high-throughput ChIP-seq protocol for large-scale chromatin studies. <i>Molecular Systems Biology</i> , 2015, 11, 777.	3.2	28
33	Tumor suppressor PNR1 blocks rRNA maturation by recruiting the decapping complex to the nucleolus. <i>EMBO Journal</i> , 2018, 37, .	3.5	28
34	Structural basis for PoxA-mediated resistance to phenicol and oxazolidinone antibiotics. <i>Nature Communications</i> , 2022, 13, 1860.	5.8	25
35	The Lsm1-7/Pat1 complex binds to stress-activated mRNAs and modulates the response to hyperosmotic shock. <i>PLoS Genetics</i> , 2018, 14, e1007563.	1.5	24
36	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. <i>Nucleic Acids Research</i> , 2015, 43, 787-802.	6.5	23

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37	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.	0.9	23
38	Dynamic remodeling of histone modifications in response to osmotic stress in <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2014, 15, 247.	1.2	22
39	Genome-Wide Polyadenylation Site Mapping. <i>Methods in Enzymology</i> , 2012, 513, 271-296.	0.4	21
40	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , 2019, 29, 1974-1984.	2.4	20
41	Not4 and Not5 modulate translation elongation by Rps7A ubiquitination, Rli1 moonlighting, and condensates that exclude eIF5A. <i>Cell Reports</i> , 2021, 36, 109633.	2.9	20
42	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 580-589.	3.6	19
43	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.	1.2	17
44	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013, 41, 6370-6370.	6.5	17
45	Improved computational analysis of ribosome dynamics from 5â€²P degradome data using fivepseq. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa099.	1.5	14
46	A genomic study of the inter-ORF distances in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2006, 23, 689-699.	0.8	13
47	The ribosome assembly gene network is controlled by the feedback regulation of transcription elongation. <i>Nucleic Acids Research</i> , 2017, 45, 9302-9318.	6.5	13
48	The RNA exosome shapes the expression of key protein-coding genes. <i>Nucleic Acids Research</i> , 2020, 48, 8509-8528.	6.5	12
49	High-throughput 5â€²P sequencing enables the study of degradation-associated ribosome stalls. <i>Cell Reports Methods</i> , 2021, 1, 100001.	1.4	12
50	Genomic-Wide Methods to Evaluate Transcription Rates in Yeast. <i>Methods in Molecular Biology</i> , 2011, 734, 25-44.	0.4	11
51	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.	1.5	10
52	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, e104-e104.	6.5	10
53	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.	0.4	10
54	A genomic view of mRNA turnover in yeast. <i>Comptes Rendus - Biologies</i> , 2011, 334, 647-654.	0.1	6

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55	Simultaneous detection of SARS-CoV-2 and pandemic (H1N1) 2009 virus with real-time isothermal platform. <i>Heliyon</i> , 2021, 7, e07584.	1.4	6
56	A functional connection between translation elongation and protein folding at the ribosome exit tunnel in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2021, 49, 206-220.	6.5	6
57	The relative importance of transcription rate, cryptic transcription and mRNA stability on shaping stress responses in yeast. <i>Transcription</i> , 2012, 3, 39-44.	1.7	5
58	Multiplexed CHIP-Seq Using Direct Nucleosome Barcoding: A Tool for High-Throughput Chromatin Analysis. <i>Methods in Molecular Biology</i> , 2018, 1689, 177-194.	0.4	5
59	Application of high-throughput 5'UTR sequencing for the study of co-translational mRNA decay. <i>STAR Protocols</i> , 2021, 2, 100447.	0.5	4
60	From transcriptional complexity to cellular phenotypes: Lessons from yeast. <i>Yeast</i> , 2017, 34, 475-482.	0.8	4
61	Transcriptional mutagenesis dramatically alters genome-wide p53 transactivation landscape. <i>Scientific Reports</i> , 2020, 10, 13513.	1.6	2
62	Using TIF-Seq2 to investigate association between 5' and 3' mRNA ends. <i>Methods in Enzymology</i> , 2021, 655, 85-118.	0.4	2
63	Genome-Wide Identification of Alternative Polyadenylation Events Using 3'UTR-Fill. <i>Methods in Molecular Biology</i> , 2016, 1358, 295-302.	0.4	2
64	OPUSeq simplifies detection of low-frequency DNA variants and uncovers fragmentase-associated artifacts. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	0