

Vicent Pelechano

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

5,137
citations

159585

30
h-index

110387

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. Science, 2016, 353, .	12.6	979
2	Gene regulation by antisense transcription. Nature Reviews Genetics, 2013, 14, 880-893.	16.3	556
3	Extensive transcriptional heterogeneity revealed by isoform profiling. Nature, 2013, 497, 127-131.	27.8	408
4	Rapid Detection of COVID-19 Coronavirus Using a Reverse Transcriptional Loop-Mediated Isothermal Amplification (RT-LAMP) Diagnostic Platform. Clinical Chemistry, 2020, 66, 975-977.	3.2	372
5	Polyadenylation site-induced decay of upstream transcripts enforces promoter directionality. Nature Structural and Molecular Biology, 2013, 20, 923-928.	8.2	258
6	Widespread Co-translational RNA Decay Reveals Ribosome Dynamics. Cell, 2015, 161, 1400-1412.	28.9	246
7	Functional consequences of bidirectional promoters. Trends in Genetics, 2011, 27, 267-276.	6.7	194
8	A Complete Set of Nascent Transcription Rates for Yeast Genes. PLoS ONE, 2010, 5, e15442.	2.5	151
9	eIF5A facilitates translation termination globally and promotes the elongation of many non polyproline-specific tripeptide sequences. Nucleic Acids Research, 2017, 45, 7326-7338.	14.5	142
10	System-wide Profiling of RNA-Binding Proteins Uncovers Key Regulators of Virus Infection. Molecular Cell, 2019, 74, 196-211.e11.	9.7	137
11	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. Nature Structural and Molecular Biology, 2014, 21, 560-568.	8.2	100
12	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. Nucleic Acids Research, 2013, 41, e65-e65.	14.5	98
13	Alternative polyadenylation diversifies post-transcriptional regulation by selective <sc>RNA</sc>-protein interactions. Molecular Systems Biology, 2014, 10, 719.	7.2	91
14	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. Nature Genetics, 2016, 48, 984-994.	21.4	75
15	Transcription-driven chromatin repression of Intragenic transcription start sites. PLoS Genetics, 2019, 15, e1007969.	3.5	71
16	Rrp6p Controls mRNA Poly(A) Tail Length and Its Decoration with Poly(A) Binding Proteins. Molecular Cell, 2012, 47, 267-280.	9.7	69
17	A DHODH inhibitor increases p53 synthesis and enhances tumor cell killing by p53 degradation blockage. Nature Communications, 2018, 9, 1107.	12.8	63
18	Regulon-Specific Control of Transcription Elongation across the Yeast Genome. PLoS Genetics, 2009, 5, e1000614.	3.5	59

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19	The transcriptional inhibitor thiolutin blocks mRNA degradation in yeast. <i>Yeast</i> , 2008, 25, 85-92.	1.7	58
20	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , 2014, 9, 1740-1759.	12.0	57
21	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	7.2	52
22	Landscape and Dynamics of Transcription Initiation in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2016, 14, 2463-2475.	6.4	51
23	The Nuclear PolyA-Binding Protein Nab2p Is Essential for mRNA Production. <i>Cell Reports</i> , 2015, 12, 128-139.	6.4	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.	3.3	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.	6.0	47
26	Genome-wide quantification of 5'-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. <i>Nature Protocols</i> , 2016, 11, 359-376.	12.0	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.	14.5	45
28	Transcript isoform sequencing reveals widespread promoter-proximal transcriptional termination in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2020, 11, 2589.	12.8	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.	14.5	40
30	There is a steady-state transcriptome in exponentially growing yeast cells. <i>Yeast</i> , 2010, 27, 413-422.	1.7	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.	6.0	32
32	A high-throughput ChIP-seq for large-scale chromatin studies. <i>Molecular Systems Biology</i> , 2015, 11, 777.	7.2	28
33	Tumor suppressor PNR1 blocks rRNA maturation by recruiting the decapping complex to the nucleolus. <i>EMBO Journal</i> , 2018, 37, .	7.8	28
34	Structural basis for PoxA-mediated resistance to phenicol and oxazolidinone antibiotics. <i>Nature Communications</i> , 2022, 13, 1860.	12.8	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.	3.5	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.	14.5	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.	1.9	23
38	Dynamic remodeling of histone modifications in response to osmotic stress in <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2014, 15, 247.	2.8	22
39	Genome-Wide Polyadenylation Site Mapping. <i>Methods in Enzymology</i> , 2012, 513, 271-296.	1.0	21
40	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , 2019, 29, 1974-1984.	5.5	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.	6.4	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.	8.2	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.	2.9	17
44	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013, 41, 6370-6370.	14.5	17
45	Improved computational analysis of ribosome dynamics from 5â€²P degradome data using fivepseq. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa099.	3.2	14
46	A genomic study of the inter-ORF distances in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2006, 23, 689-699.	1.7	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.	14.5	13
48	The RNA exosome shapes the expression of key protein-coding genes. <i>Nucleic Acids Research</i> , 2020, 48, 8509-8528.	14.5	12
49	High-throughput 5â€²P sequencing enables the study of degradation-associated ribosome stalls. <i>Cell Reports Methods</i> , 2021, 1, 100001.	2.9	12
50	Genomic-Wide Methods to Evaluate Transcription Rates in Yeast. <i>Methods in Molecular Biology</i> , 2011, 734, 25-44.	0.9	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.	3.1	10
52	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, e104-e104.	14.5	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.	0.9	10
54	A genomic view of mRNA turnover in yeast. <i>Comptes Rendus - Biologies</i> , 2011, 334, 647-654.	0.2	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.	3.2	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.	14.5	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.	3.1	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.	0.9	5
59	Application of high-throughput 5â€™P sequencing for the study of co-translational mRNA decay. <i>STAR Protocols</i> , 2021, 2, 100447.	1.2	4
60	From transcriptional complexity to cellular phenotypes: Lessons from yeast. <i>Yeast</i> , 2017, 34, 475-482.	1.7	4
61	Transcriptional mutagenesis dramatically alters genome-wide p53 transactivation landscape. <i>Scientific Reports</i> , 2020, 10, 13513.	3.3	2
62	Using TIF-Seq2 to investigate association between 5â€™ and 3â€™ mRNA ends. <i>Methods in Enzymology</i> , 2021, 655, 85-118.	1.0	2
63	Genome-Wide Identification of Alternative Polyadenylation Events Using 3â€™T-Fill. <i>Methods in Molecular Biology</i> , 2016, 1358, 295-302.	0.9	2
64	OPUSeq simplifies detection of low-frequency DNA variants and uncovers fragmentase-associated artifacts. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	0