

Domenico Libri

List of Publications by Year in descending order

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75
papers

5,370
citations

87888

38
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88630

70
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88
all docs

88
docs citations

88
times ranked

4004
citing authors

#	ARTICLE	IF	CITATIONS
1	A Modified Cross-Linking Analysis of cDNAs (CRAC) Protocol for Detecting RNA-Protein Interactions and Transcription at Single-Nucleotide Resolution. <i>Methods in Molecular Biology</i> , 2022, 2477, 35-55.	0.9	1
2	An integrated model for termination of RNA polymerase III transcription. <i>Science Advances</i> , 2022, 8, .	10.3	14
3	Sen1 is a key regulator of transcription-driven conflicts. <i>Molecular Cell</i> , 2022, 82, 2952-2966.e6.	9.7	14
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	Data from crosslinking and analysis of cDNAs (CRAC) of Nab3 in yeast cells expressing a circular ncRNA decoy. <i>Data in Brief</i> , 2021, 35, 106951.	1.0	1
6	Degradation of Non-coding RNAs Promotes Recycling of Termination Factors at Sites of Transcription. <i>Cell Reports</i> , 2020, 32, 107942.	6.4	19
7	Sen1 Is Recruited to Replication Forks via Ctf4 and Mrc1 and Promotes Genome Stability. <i>Cell Reports</i> , 2020, 30, 2094-2105.e9.	6.4	26
8	Termination of non-coding transcription in yeast relies on both an RNA Pol II CTD interaction domain and a CTD-mimicking region in Sen1. <i>EMBO Journal</i> , 2020, 39, e101548.	7.8	23
9	Opposing chromatin remodelers control transcription initiation frequency and start site selection. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 744-754.	8.2	93
10	Single-molecule characterization of extrinsic transcription termination by Sen1 helicase. <i>Nature Communications</i> , 2019, 10, 1545.	12.8	13
11	High-resolution transcription maps reveal the widespread impact of roadblock termination in yeast. <i>EMBO Journal</i> , 2018, 37, .	7.8	60
12	General Regulatory Factors Control the Fidelity of Transcription by Restricting Non-coding and Ectopic Initiation. <i>Molecular Cell</i> , 2018, 72, 955-969.e7.	9.7	52
13	Pervasive transcription fine-tunes replication origin activity. <i>ELife</i> , 2018, 7, .	6.0	21
14	Sen1 has unique structural features grafted on the architecture of the Upf1-like helicase family. <i>EMBO Journal</i> , 2017, 36, 1590-1604.	7.8	45
15	Biochemical characterization of the helicase Sen1 provides new insights into the mechanisms of non-coding transcription termination. <i>Nucleic Acids Research</i> , 2017, 45, 1355-1370.	14.5	52
16	Transcription Termination: Variations on Common Themes. <i>Trends in Genetics</i> , 2016, 32, 508-522.	6.7	94
17	Sleeping Beauty and the Beast (of pervasive transcription). <i>Rna</i> , 2015, 21, 678-679.	3.5	10
18	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. <i>Nucleic Acids Research</i> , 2015, 43, 3358-3372.	14.5	43

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19	Transcription termination and the control of the transcriptome: why, where and how to stop. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 190-202.	37.0	246
20	Non-coding transcription by RNA polymerase II in yeast: Hasard or necessity?. <i>Biochimie</i> , 2015, 117, 28-36.	2.6	21
21	Endless Quarrels at the End of Genes. <i>Molecular Cell</i> , 2015, 60, 192-194.	9.7	10
22	Characterization of the Mechanisms of Transcription Termination by the Helicase Sen1. <i>Methods in Molecular Biology</i> , 2015, 1259, 313-331.	0.9	9
23	Roadblock Termination by Reb1p Restricts Cryptic and Readthrough Transcription. <i>Molecular Cell</i> , 2014, 56, 667-680.	9.7	53
24	Molecular Basis for Coordinating Transcription Termination with Noncoding RNA Degradation. <i>Molecular Cell</i> , 2014, 55, 467-481.	9.7	99
25	A bacterial-like mechanism for transcription termination by the Sen1p helicase in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 884-891.	8.2	102
26	High-Frequency Promoter Firing Links THO Complex Function to Heavy Chromatin Formation. <i>Cell Reports</i> , 2013, 5, 1082-1094.	6.4	14
27	Dealing with Pervasive Transcription. <i>Molecular Cell</i> , 2013, 52, 473-484.	9.7	250
28	RNA quality control in the nucleus: The Angels' share of RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 604-611.	1.9	42
29	The Role of Ctk1 Kinase in Termination of Small Non-Coding RNAs. <i>PLoS ONE</i> , 2013, 8, e80495.	2.5	15
30	Ers1 links HP1 to RNAi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11258-11263.	7.1	27
31	<i>In vivo</i> SELEX reveals novel sequence and structural determinants of Nrd1-Nab3-Sen1-dependent transcription termination. <i>EMBO Journal</i> , 2012, 31, 3935-3948.	7.8	67
32	Extensive Degradation of RNA Precursors by the Exosome in Wild-Type Cells. <i>Molecular Cell</i> , 2012, 48, 409-421.	9.7	218
33	Implication of Ccr4-Not complex function in mRNA quality control in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2011, 17, 1788-1794.	3.5	17
34	Nuclear mRNA quality control in yeast is mediated by Nrd1 co-transcriptional recruitment, as revealed by the targeting of Rho-induced aberrant transcripts. <i>Nucleic Acids Research</i> , 2011, 39, 2809-2820.	14.5	27
35	Gcn4 misregulation reveals a direct role for the evolutionary conserved EKC/KEOPS in the t6A modification of tRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 6148-6160.	14.5	79
36	Sex matters in the birth of genes. <i>Cell Research</i> , 2010, 20, 499-501.	12.0	0

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37	Nuclear Poly(A)-Binding Proteins and Nuclear Degradation: Take the mRNA and Run?. <i>Molecular Cell</i> , 2010, 37, 3-5.	9.7	17
38	Structure of the archaeal Kae1/Bud32 fusion protein MJ1130: a model for the eukaryotic EKC/KEOPS subcomplex. <i>EMBO Journal</i> , 2008, 27, 2340-2351.	7.8	62
39	Phosphorylation of the RNA polymerase II C-terminal domain dictates transcription termination choice. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 786-794.	8.2	130
40	mRNA journey to the cytoplasm: attire required. <i>Biology of the Cell</i> , 2008, 100, 327-342.	2.0	30
41	Futile Cycle of Transcription Initiation and Termination Modulates the Response to Nucleotide Shortage in <i>S. cerevisiae</i> . <i>Molecular Cell</i> , 2008, 31, 671-682.	9.7	93
42	THO/Sub2p Functions to Coordinate 3' End Processing with Gene-Nuclear Pore Association. <i>Cell</i> , 2008, 135, 308-321.	28.9	129
43	Exonucleolysis is required for nuclear mRNA quality control in yeast THO mutants. <i>Rna</i> , 2008, 14, 2305-2313.	3.5	48
44	Binding of an aptamer to the N-terminal fragment of VCAM-1. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 6119-6122.	2.2	12
45	Dissecting mechanisms of nuclear mRNA surveillance in THO/sub2 complex mutants. <i>EMBO Journal</i> , 2007, 26, 2317-2326.	7.8	114
46	Transcription Termination and Nuclear Degradation of Cryptic Unstable Transcripts: A Role for the Nrd1-Nab3 Pathway in Genome Surveillance. <i>Molecular Cell</i> , 2006, 23, 853-864.	9.7	209
47	Yeast homolog of a cancer-testis antigen defines a new transcription complex. <i>EMBO Journal</i> , 2006, 25, 3576-3585.	7.8	122
48	An Autocrine Loop Involving Ret and Glial Cell-Derived Neurotrophic Factor Mediates Retinoic Acid-Induced Neuroblastoma Cell Differentiation. <i>Molecular Cancer Research</i> , 2006, 4, 481-488.	3.4	30
49	Neutralizing Aptamers from Whole-Cell SELEX Inhibit the RET Receptor Tyrosine Kinase. <i>PLoS Biology</i> , 2005, 3, e123.	5.6	228
50	A Link between Transcription and mRNP Quality in <i>Saccharomyces cerevisiae</i> . <i>RNA Biology</i> , 2005, 2, 45-48.	3.1	6
51	Cryptic Pol II Transcripts Are Degraded by a Nuclear Quality Control Pathway Involving a New Poly(A) Polymerase. <i>Cell</i> , 2005, 121, 725-737.	28.9	764
52	The DECD box Putative ATPase Sub2p Is an Early mRNA Export Factor. <i>Current Biology</i> , 2004, 14, 447.	3.9	1
53	Modulation of Transcription Affects mRNP Quality. <i>Molecular Cell</i> , 2004, 16, 235-244.	9.7	57
54	Early Formation of mRNP. <i>Molecular Cell</i> , 2003, 11, 1129-1138.	9.7	106

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55	Localization of nuclear retained mRNAs in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2003, 9, 1049-1057.	3.5	62
56	Interactions between mRNA Export Commitment, 3' End Quality Control, and Nuclear Degradation. <i>Molecular and Cellular Biology</i> , 2002, 22, 8254-8266.	2.3	223
57	A Role for the 5' U Mismatch in the Recognition of the 5' Splice Site of Yeast Introns by the U1 Small Nuclear Ribonucleoprotein Particle. <i>Journal of Biological Chemistry</i> , 2002, 277, 18173-18181.	3.4	16
58	Nucleic acid aptamers in cancer medicine. <i>FEBS Letters</i> , 2002, 528, 12-16.	2.8	99
59	The DECD box putative ATPase Sub2p is an early mRNA export factor. <i>Current Biology</i> , 2001, 11, 1711-1715.	3.9	142
60	Multiple roles for the yeast SUB2/yUAP56 gene in splicing. <i>Genes and Development</i> , 2001, 15, 36-41.	5.9	111
61	Splicing enhancement in the yeast rp51b intron. <i>Rna</i> , 2000, 6, 352-368.	3.5	7
62	RNA structural patterns and splicing: molecular basis for an RNA-based enhancer. <i>Rna</i> , 1995, 1, 425-36.	3.5	44
63	Splicing of the alternative exons of the chicken, rat, and <i>Xenopus</i> beta tropomyosin transcripts requires class-specific elements. <i>Journal of Biological Chemistry</i> , 1994, 269, 19675-8.	3.4	9
64	Pre-mRNA secondary structure and the regulation of splicing. <i>BioEssays</i> , 1993, 15, 165-169.	2.5	96
65	Intronic sequence with both negative and positive effects on the regulation of alternative transcripts of the chicken β^2 tropomyosin transcripts. <i>Nucleic Acids Research</i> , 1992, 20, 3987-3992.	14.5	41
66	In Vivo Splicing of the β^2 Tropomyosin Pre-mRNA: A Role for Branch Point and Donor Site Competition. <i>Molecular and Cellular Biology</i> , 1992, 12, 3204-3215.	2.3	24
67	Cis regulating elements which control in vivo alternative splicing of the chicken beta tropomyosin primary transcript. <i>Symposia of the Society for Experimental Biology</i> , 1992, 46, 355-62.	0.0	0
68	The chicken gene encoding the β^1 isoform of tropomyosin of fast-twitch muscle fibers: organization, expression and identification of the major proteins synthesized. <i>Gene</i> , 1991, 107, 229-240.	2.2	45
69	Tissue-Specific Splicing in Vivo of the β^2 -Tropomyosin Gene: Dependence on an RNA Secondary Structure. <i>Science</i> , 1991, 252, 1842-1845.	12.6	167
70	Exon as well as Intron Sequences Are cis-Regulating Elements for the Mutually Exclusive Alternative Splicing of the β^2 Tropomyosin Gene. <i>Molecular and Cellular Biology</i> , 1990, 10, 5036-5046.	2.3	70
71	In vitro splicing of mutually exclusive exons from the chicken beta-tropomyosin gene: role of the branch point location and very long pyrimidine stretch. <i>EMBO Journal</i> , 1990, 9, 241-9.	7.8	41
72	A nonmuscle tropomyosin is encoded by the smooth/skeletal beta-tropomyosin gene and its RNA is transcribed from an internal promoter. <i>Journal of Biological Chemistry</i> , 1990, 265, 3471-3.	3.4	19

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73	Chick β -tropomyosin gene contains three sets of mutually exclusive alternatively spliced exons. Nucleic Acids Research, 1989, 17, 5400-5400.	14.5	6
74	Tissue-specific transcriptional control of β - and β^2 -tropomyosins in chicken muscle development. Developmental Biology, 1989, 131, 430-438.	2.0	20
75	A single gene codes for the beta subunits of smooth and skeletal muscle tropomyosin in the chicken. Journal of Biological Chemistry, 1989, 264, 2935-44.	3.4	61