

# Nicholas Jarvis Proudfoot

## List of Publications by Year in descending order

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148  
papers

20,714  
citations

9786

73  
h-index

10445

139  
g-index

157  
all docs

157  
docs citations

157  
times ranked

15352  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of lncRNA biogenesis as revealed by nascent transcriptomics. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 389-406.	37.0	151
2	Counteracting chromatin effects of a splicing-correcting antisense oligonucleotide improves its therapeutic efficacy in spinal muscular atrophy. <i>Cell</i> , 2022, 185, 2057-2070.e15.	28.9	28
3	Dual RNA 3' end processing of H2A.X messenger RNA maintains DNA damage repair throughout the cell cycle. <i>Nature Communications</i> , 2021, 12, 359.	12.8	17
4	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. <i>Molecular Cell</i> , 2021, 81, 983-997.e7.	9.7	27
5	POINT technology illuminates the processing of polymerase-associated intact nascent transcripts. <i>Molecular Cell</i> , 2021, 81, 1935-1950.e6.	9.7	52
6	R-Loops Promote Antisense Transcription across the Mammalian Genome. <i>Molecular Cell</i> , 2019, 76, 600-616.e6.	9.7	112
7	Transcriptional Control by Premature Termination: A Forgotten Mechanism. <i>Trends in Genetics</i> , 2019, 35, 553-564.	6.7	112
8	SCAF4 and SCAF8, mRNA Anti-Terminator Proteins. <i>Cell</i> , 2019, 177, 1797-1813.e18.	28.9	85
9	Selective Roles of Vertebrate PCF11 in Premature and Full-Length Transcript Termination. <i>Molecular Cell</i> , 2019, 74, 158-172.e9.	9.7	95
10	R-loop formation during S phase is restricted by PrimPol-mediated repriming. <i>EMBO Journal</i> , 2019, 38, .	7.8	77
11	The SF3B1 K700E Mutation Induces R-Loop Accumulation and Associated DNA Damage. <i>Blood</i> , 2019, 134, 4219-4219.	1.4	4
12	Nuclear fate of yeast snoRNA is determined by co-transcriptional Rnt1 cleavage. <i>Nature Communications</i> , 2018, 9, 1783.	12.8	24
13	Deregulated Expression of Mammalian lncRNA through Loss of SPT6 Induces R-Loop Formation, Replication Stress, and Cellular Senescence. <i>Molecular Cell</i> , 2018, 72, 970-984.e7.	9.7	140
14	RNA Polymerase II Phosphorylated on CTD Serine 5 Interacts with the Spliceosome during Co-transcriptional Splicing. <i>Molecular Cell</i> , 2018, 72, 369-379.e4.	9.7	123
15	Influenza Virus Mounts a Two-Pronged Attack on Host RNA Polymerase II Transcription. <i>Cell Reports</i> , 2018, 23, 2119-2129.e3.	6.4	81
16	Mitochondrial double-stranded RNA triggers antiviral signalling in humans. <i>Nature</i> , 2018, 560, 238-242.	27.8	397
17	RNA Helicase DDX1 Converts RNA G-Quadruplex Structures into R-Loops to Promote IgH Class Switch Recombination. <i>Molecular Cell</i> , 2018, 70, 650-662.e8.	9.7	133
18	Biosynthesis of histone messenger RNA employs a specific 3' end endonuclease. <i>ELife</i> , 2018, 7, .	6.0	14

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19	Distinctive Patterns of Transcription and RNA Processing for Human lincRNAs. <i>Molecular Cell</i> , 2017, 65, 25-38.	9.7	222
20	WNK1 kinase and the termination factor PCF11 connect nuclear mRNA export with transcription. <i>Genes and Development</i> , 2017, 31, 2175-2185.	5.9	15
21	Transcriptional termination in mammals: Stopping the RNA polymerase II juggernaut. <i>Science</i> , 2016, 352, aad9926.	12.6	341
22	Mammalian NET-seq analysis defines nascent RNA profiles and associated RNA processing genome-wide. <i>Nature Protocols</i> , 2016, 11, 413-428.	12.0	86
23	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. <i>Molecular Cell</i> , 2015, 57, 636-647.	9.7	363
24	Microprocessor mediates transcriptional termination of long noncoding RNA transcripts hosting microRNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 319-327.	8.2	120
25	Mammalian NET-Seq Reveals Genome-wide Nascent Transcription Coupled to RNA Processing. <i>Cell</i> , 2015, 161, 526-540.	28.9	466
26	Pcf11 orchestrates transcription termination pathways in yeast. <i>Genes and Development</i> , 2015, 29, 849-861.	5.9	66
27	A double-edged sword: R loops as threats to genome integrity and powerful regulators of gene expression. <i>Genes and Development</i> , 2014, 28, 1384-1396.	5.9	432
28	R-loops induce repressive chromatin marks over mammalian gene terminators. <i>Nature</i> , 2014, 516, 436-439.	27.8	299
29	Human nuclear Dicer restricts the deleterious accumulation of endogenous double-stranded RNA. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 552-559.	8.2	95
30	Terminate and make a loop: regulation of transcriptional directionality. <i>Trends in Biochemical Sciences</i> , 2014, 39, 319-327.	7.5	45
31	Drosha Regulates Gene Expression Independently of RNA Cleavage Function. <i>Cell Reports</i> , 2013, 5, 1499-1510.	6.4	60
32	Definition of RNA Polymerase II CoTC Terminator Elements in the Human Genome. <i>Cell Reports</i> , 2013, 3, 1080-1092.	6.4	28
33	Histone 3 S10 Phosphorylation: "Caught in the R Loop" <i>Molecular Cell</i> , 2013, 52, 470-472.	9.7	3
34	Disengaging polymerase: Terminating RNA polymerase II transcription in budding yeast. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 174-185.	1.9	118
35	Feed backwards model for microRNA processing and splicing in plants. <i>EMBO Reports</i> , 2013, 14, 581-582.	4.5	7
36	R-Loop Stabilization Represses Antisense Transcription at the <i>Arabidopsis FLC</i> Locus. <i>Science</i> , 2013, 340, 619-621.	12.6	326

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37	Genome-wide analysis of poly(A) site selection in <i>Schizosaccharomyces pombe</i> . <i>Rna</i> , 2013, 19, 1617-1631.	3.5	37
38	AT-rich sequence elements promote nascent transcript cleavage leading to RNA polymerase II termination. <i>Nucleic Acids Research</i> , 2013, 41, 1797-1806.	14.5	16
39	Rad51, friend or foe?. <i>ELife</i> , 2013, 2, e00914.	6.0	1
40	Autoregulation of TDP-43 mRNA levels involves interplay between transcription, splicing, and alternative polyA site selection. <i>Genes and Development</i> , 2012, 26, 1679-1684.	5.9	157
41	Gene Loops Enhance Transcriptional Directionality. <i>Science</i> , 2012, 338, 671-675.	12.6	219
42	Convergent transcription induces transcriptional gene silencing in fission yeast and mammalian cells. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1193-1201.	8.2	52
43	Transcription termination between polo and snap, two closely spaced tandem genes of <i>D. melanogaster</i> . <i>Transcription</i> , 2012, 3, 198-212.	3.1	13
44	Ending the message: poly(A) signals then and now. <i>Genes and Development</i> , 2011, 25, 1770-1782.	5.9	490
45	Yeast Sen1 Helicase Protects the Genome from Transcription-Associated Instability. <i>Molecular Cell</i> , 2011, 41, 21-32.	9.7	301
46	Human Senataxin Resolves RNA/DNA Hybrids Formed at Transcriptional Pause Sites to Promote Xrn2-Dependent Termination. <i>Molecular Cell</i> , 2011, 42, 794-805.	9.7	632
47	RNA polymerase II kinetics in <i>polo</i> polyadenylation signal selection. <i>EMBO Journal</i> , 2011, 30, 2431-2444.	7.8	124
48	Autoregulation of convergent RNAi genes in fission yeast. <i>Genes and Development</i> , 2011, 25, 556-568.	5.9	27
49	Co-transcriptional RNA cleavage provides a failsafe termination mechanism for yeast RNA polymerase I. <i>Nucleic Acids Research</i> , 2011, 39, 1439-1448.	14.5	20
50	Role of the RNA/DNA kinase Grc3 in transcription termination by RNA polymerase I. <i>EMBO Reports</i> , 2010, 11, 758-764.	4.5	31
51	Silencing in trans : position matters in fission yeast. <i>EMBO Reports</i> , 2010, 11, 145-146.	4.5	1
52	Transcriptional Activation of the General Amino Acid Permease Gene <i>per1</i> by the Histone Deacetylase <i>Clr6</i> Is Regulated by <i>Oca2</i> Kinase. <i>Molecular and Cellular Biology</i> , 2010, 30, 3396-3410.	2.3	6
53	Coupled RNA Processing and Transcription of Intergenic Primary MicroRNAs. <i>Molecular and Cellular Biology</i> , 2009, 29, 5632-5638.	2.3	101
54	Gene loops function to maintain transcriptional memory through interaction with the nuclear pore complex. <i>Genes and Development</i> , 2009, 23, 2610-2624.	5.9	252

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55	Jmjd6 Catalyses Lysyl-Hydroxylation of U2AF65, a Protein Associated with RNA Splicing. <i>Science</i> , 2009, 325, 90-93.	12.6	356
56	Pre-mRNA Processing Reaches Back to Transcription and Ahead to Translation. <i>Cell</i> , 2009, 136, 688-700.	28.9	754
57	Transcriptional Termination Enhances Protein Expression in Human Cells. <i>Molecular Cell</i> , 2009, 33, 354-364.	9.7	63
58	Fail-Safe Transcriptional Termination for Protein-Coding Genes in <i>S. cerevisiae</i> . <i>Molecular Cell</i> , 2009, 36, 88-98.	9.7	96
59	Primary microRNA transcripts are processed co-transcriptionally. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 902-909.	8.2	335
60	Terminating transcription in yeast: whether to be a 'nerd' or a 'rat'. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 775-776.	8.2	18
61	Transcription-Dependent Gene Looping of the HIV-1 Provirus Is Dictated by Recognition of Pre-mRNA Processing Signals. <i>Molecular Cell</i> , 2008, 29, 56-68.	9.7	96
62	Molecular Dissection of Mammalian RNA Polymerase II Transcriptional Termination. <i>Molecular Cell</i> , 2008, 29, 600-610.	9.7	59
63	Cohesin Complex Promotes Transcriptional Termination between Convergent Genes in <i>S. pombe</i> . <i>Cell</i> , 2008, 132, 983-995.	28.9	186
64	Nuclear Roadblocks for mRNA Export. <i>Cell</i> , 2008, 135, 207-208.	28.9	5
65	An Ungracious Host for an Unwelcome Guest. <i>Cell Host and Microbe</i> , 2008, 4, 89-91.	11.0	4
66	Dynamic interactions between the promoter and terminator regions of the mammalian <i>BRCA1</i> gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5160-5165.	7.1	127
67	Budding yeast RNA polymerases I and II employ parallel mechanisms of transcriptional termination. <i>Genes and Development</i> , 2008, 22, 1082-1092.	5.9	120
68	Human Pcf11 enhances degradation of RNA polymerase II-associated nascent RNA and transcriptional termination. <i>Nucleic Acids Research</i> , 2007, 36, 905-914.	14.5	50
69	Modulating alternative splicing by cotranscriptional cleavage of nascent intronic RNA. <i>Rna</i> , 2007, 14, 359-366.	3.5	20
70	Gene Silencing CUTs Both Ways. <i>Cell</i> , 2007, 131, 649-651.	28.9	5
71	RNA polymerase I in yeast transcribes dynamic nucleosomal rDNA. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 123-130.	8.2	72
72	Adenylation and Exosome-Mediated Degradation of Cotranscriptionally Cleaved Pre-Messenger RNA in Human Cells. <i>Molecular Cell</i> , 2006, 21, 437-443.	9.7	92

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73	Exon Tethering in Transcription by RNA Polymerase II. <i>Molecular Cell</i> , 2006, 21, 849-859.	9.7	122
74	Turnover and Function of Noncoding RNA Polymerase II Transcripts. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006, 71, 275-284.	1.1	3
75	Transcriptional termination sequences in the mouse serum albumin gene. <i>Rna</i> , 2006, 12, 655-665.	3.5	18
76	Homologous gene sequences mediate transcription-domain formation. <i>Journal of Cell Science</i> , 2006, 119, 3876-3887.	2.0	10
77	Pause Sites Promote Transcriptional Termination of Mammalian RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2006, 26, 3986-3996.	2.3	151
78	Strong Polyadenylation and Weak Pausing Combine To Cause Efficient Termination of Transcription in the Human $\hat{\gamma}$ -Globin Gene. <i>Molecular and Cellular Biology</i> , 2005, 25, 3276-3285.	2.3	31
79	Dicer-Dependent Turnover of Intergenic Transcripts from the Human $\hat{\gamma}$ -Globin Gene Cluster. <i>Molecular and Cellular Biology</i> , 2005, 25, 9724-9733.	2.3	69
80	Polypyrimidine Tract Binding Protein Modulates Efficiency of Polyadenylation. <i>Molecular and Cellular Biology</i> , 2004, 24, 4174-4183.	2.3	155
81	Transcriptional termination by RNA polymerase I requires the small subunit Rpa12p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6068-6073.	7.1	72
82	Gene loops juxtapose promoters and terminators in yeast. <i>Nature Genetics</i> , 2004, 36, 1014-1018.	21.4	321
83	Autocatalytic RNA cleavage in the human $\hat{\gamma}$ -globin pre-mRNA promotes transcription termination. <i>Nature</i> , 2004, 432, 526-530.	27.8	103
84	Human 5' cap' 3' exonuclease Xrn2 promotes transcription termination at co-transcriptional cleavage sites. <i>Nature</i> , 2004, 432, 522-525.	27.8	396
85	New perspectives on connecting messenger RNA 3' end formation to transcription. <i>Current Opinion in Cell Biology</i> , 2004, 16, 272-278.	5.4	261
86	Transcription Termination. , 2004, , 369-380.		0
87	Dawdling polymerases allow introns time to splice. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 876-878.	8.2	22
88	Regulation of Elongating RNA Polymerase II by Forkhead Transcription Factors in Yeast. <i>Science</i> , 2003, 300, 492-495.	12.6	62
89	Isw1 Chromatin Remodeling ATPase Coordinates Transcription Elongation and Termination by RNA Polymerase II. <i>Cell</i> , 2003, 115, 425-435.	28.9	160
90	Transcriptional collision between convergent genes in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8796-8801.	7.1	231

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91	Promoter proximal splice sites enhance transcription. <i>Genes and Development</i> , 2002, 16, 2792-2799.	5.9	234
92	Integrating mRNA Processing with Transcription. <i>Cell</i> , 2002, 108, 501-512.	28.9	927
93	Definition of Transcriptional Promoters in the Human $\hat{\beta}^2$ Globin Locus Control Region. <i>Journal of Molecular Biology</i> , 2002, 323, 601-611.	4.2	53
94	A Role for Chromatin Remodeling in Transcriptional Termination by RNA Polymerase II. <i>Molecular Cell</i> , 2002, 10, 1441-1452.	9.7	137
95	Polyadenylation: A tail of two complexes. <i>Current Biology</i> , 2002, 12, R855-R857.	3.9	96
96	U1 snRNA associates with TFIIF and regulates transcriptional initiation. <i>Nature Structural Biology</i> , 2002, 9, 800-5.	9.7	158
97	Transcriptional Termination Factors for RNA Polymerase II in Yeast. <i>Molecular Cell</i> , 2001, 7, 1003-1011.	9.7	56
98	Multiple Transcript Cleavage Precedes Polymerase Release in Termination by RNA Polymerase II. <i>Cell</i> , 2001, 105, 669-681.	28.9	99
99	Genetic dangers in poly(A) signals. <i>EMBO Reports</i> , 2001, 2, 891-892.	4.5	8
100	Intergenic Transcription in the Human $\hat{\beta}^2$ -Globin Gene Cluster. <i>Molecular and Cellular Biology</i> , 2001, 21, 6507-6514.	2.3	84
101	The Retroviruses Human Immunodeficiency Virus Type 1 and Moloney Murine Leukemia Virus Adopt Radically Different Strategies To Regulate Promoter-Proximal Polyadenylation. <i>Journal of Virology</i> , 2001, 75, 11735-11746.	3.4	39
102	Connecting transcription to messenger RNA processing. <i>Trends in Biochemical Sciences</i> , 2000, 25, 290-293.	7.5	155
103	Transcriptional termination and coupled polyadenylation in vitro. <i>EMBO Journal</i> , 2000, 19, 3770-3777.	7.8	71
104	Stem-loop 1 of the U1 snRNP plays a critical role in the suppression of HIV-1 polyadenylation. <i>Rna</i> , 2000, 6, 170-177.	3.5	56
105	Balancing transcriptional interference and initiation on the GAL7 promoter of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 8415-8420.	7.1	72
106	Recruitment of a Basal Polyadenylation Factor by the Upstream Sequence Element of the Human Lamin B2 Polyadenylation Signal. <i>Molecular and Cellular Biology</i> , 2000, 20, 2660-2669.	2.3	40
107	Transcription of the human U2 snRNA genes continues beyond the 3' box in vivo. <i>EMBO Journal</i> , 1999, 18, 2867-2877.	7.8	58
108	Specific Transcriptional Pausing Activates Polyadenylation in a Coupled In Vitro System. <i>Molecular Cell</i> , 1999, 3, 593-600.	9.7	118

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109	Terminal Exon Definition Occurs Cotranscriptionally and Promotes Termination of RNA Polymerase II. <i>Molecular Cell</i> , 1999, 3, 371-378.	9.7	146
110	EM Visualization of Transcription by RNA Polymerase II. <i>Molecular Cell</i> , 1999, 3, 379-387.	9.7	71
111	Definition of Transcriptional Pause Elements in Fission Yeast. <i>Molecular and Cellular Biology</i> , 1999, 19, 1251-1261.	2.3	31
112	Nascent transcription from the nmt1 and nmt2 genes of <i>Schizosaccharomyces pombe</i> overlaps neighbouring genes. <i>EMBO Journal</i> , 1998, 17, 3066-3077.	7.8	32
113	Poly(A) signals control both transcriptional termination and initiation between the tandem GAL10 and GAL7 genes of <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 1998, 17, 4771-4779.	7.8	94
114	Coupling Termination of Transcription to Messenger RNA Maturation in Yeast. <i>Science</i> , 1998, 280, 298-301.	12.6	236
115	Transcriptional interference perturbs the binding of Sp1 to the HIV-1 promoter. <i>Nucleic Acids Research</i> , 1998, 26, 1294-1301.	14.5	104
116	Transcription and polyadenylation in a short human intergenic region. <i>Nucleic Acids Research</i> , 1997, 25, 2326-2335.	14.5	36
117	Transcriptional termination signals for RNA polymerase II in fission yeast. <i>EMBO Journal</i> , 1997, 16, 3633-3643.	7.8	83
118	The HIV-1 5' LTR poly(A) site is inactivated by U1 snRNP interaction with the downstream major splice donor site. <i>EMBO Journal</i> , 1997, 16, 5752-5763.	7.8	105
119	Ending the Message Is Not So Simple. <i>Cell</i> , 1996, 87, 779-781.	28.9	84
120	Activation Domains of Transcription Factors Mediate Replication Dependent Transcription from a Minimal HIV-1 Promoter. <i>Nucleic Acids Research</i> , 1996, 24, 549-557.	14.5	13
121	Proximal promoter elements of the human zeta-globin gene confer embryonic-specific expression on a linked reporter gene in transgenic mice. <i>Nucleic Acids Research</i> , 1996, 24, 4158-4164.	14.5	7
122	Sp1 functions in a chromatin-dependent manner to augment human alpha-globin promoter activity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7237-7241.	7.1	30
123	Expression of the early lymphocyte activation antigen CD69, a C-type lectin, is regulated by mRNA degradation associated with AU-rich sequence motifs. <i>European Journal of Immunology</i> , 1995, 25, 2142-2146.	2.9	43
124	Post-Transcriptional Regulation: Chasing your own poly(A) tail. <i>Current Biology</i> , 1994, 4, 359-361.	3.9	4
125	The primary transcription unit of the human (eqn)a2 globin gene defined by quantitative RT/PCR. <i>Nucleic Acids Research</i> , 1992, 20, 851-858.	14.5	15
126	Poly(A) signals. <i>Cell</i> , 1991, 64, 671-674.	28.9	459



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127	A factor binding GATAAG confers tissue specificity on the promoter of the human $\hat{\gamma}$ -globin gene. <i>Nucleic Acids Research</i> , 1990, 18, 1339-1350.	14.5	52
128	How RNA polymerase II terminates transcription in higher eukaryotes. <i>Trends in Biochemical Sciences</i> , 1989, 14, 105-110.	7.5	284
129	A beginning to the biochemistry of polyadenylation. <i>Trends in Genetics</i> , 1988, 4, 243-245.	6.7	83
130	Position-dependent sequence elements downstream of AAUAAA are required for efficient rabbit $\hat{\gamma}$ -globin mRNA 3' end formation. <i>Cell</i> , 1987, 49, 399-406.	28.9	241
131	The gene for $\hat{\gamma}$ -globin is transcribed in human fetal erythroid tissues. <i>Nature</i> , 1987, 329, 551-554.	27.8	39
132	Molecular biology: Globin gene monkey business. <i>Nature</i> , 1986, 321, 730-731.	27.8	11
133	A sequence downstream of AAUAAA is required for rabbit $\hat{\gamma}$ -globin mRNA 3' end formation. <i>Nature</i> , 1984, 312, 473-474.	27.8	291
134	$\hat{\alpha}$ -Thalassaemia caused by a polyadenylation signal mutation. <i>Nature</i> , 1983, 306, 398-400.	27.8	403
135	A single-base change at a splice site in a $\hat{\alpha}$ -thalassemic gene causes abnormal RNA splicing. <i>Cell</i> , 1982, 29, 903-911.	28.9	375
136	The structure of the human zeta-globin gene and a closely linked, nearly identical pseudogene. <i>Cell</i> , 1982, 31, 553-563.	28.9	331
137	The end of the message. <i>Nature</i> , 1982, 298, 516-517.	27.8	62
138	Structure and in vitro transcription of human globin genes. <i>Science</i> , 1980, 209, 1329-1336.	12.6	247
139	The structure and evolution of the human $\hat{\gamma}$ -globin gene family. <i>Cell</i> , 1980, 21, 653-668.	28.9	1,565
140	The structure of a human $\hat{\alpha}$ -globin pseudogene and its relationship to $\hat{\alpha}$ -globin gene duplication. <i>Cell</i> , 1980, 21, 537-544.	28.9	279
141	Characterization of $\hat{\gamma}$ -globin mRNA in the $\hat{\alpha}$ -thalassemias. <i>Cell</i> , 1978, 14, 289-298.	28.9	45
142	Nucleotide sequence of the 3' terminal third of rabbit $\hat{\alpha}$ -globin messenger RNA: Comparison with human $\hat{\alpha}$ -globin messenger RNA. <i>Cell</i> , 1977, 11, 807-818.	28.9	56
143	Complete 3' noncoding region sequences of rabbit and human $\hat{\gamma}$ -globin messenger RNAs. <i>Cell</i> , 1977, 10, 559-570.	28.9	105
144	The sequence is not enough. <i>Nature</i> , 1977, 265, 499-500.	27.8	1

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145	The 3' terminal sequences of human $\alpha$ and $\beta$ globin messenger RNAs: Comparison with rabbit globin messenger RNA. <i>Cell</i> , 1976, 9, 733-746.	28.9	61
146	Sequence analysis of the 3' non-coding regions of rabbit $\alpha$ - and $\beta$ -globin messenger RNAs. <i>Journal of Molecular Biology</i> , 1976, 107, 491-525.	4.2	48
147	Sequence analysis of immunoglobulin light chain messenger RNA. <i>Nature</i> , 1974, 252, 354-359.	27.8	129
148	Nucleotide sequence adjacent to polyadenylic acid in globin messenger RNA. <i>FEBS Letters</i> , 1974, 38, 179-183.	2.8	26