Jeremy E Wilusz

List of Publications by Citations

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46
papers
6,781
citations

8,341
ext. papers

8,341
ext. citations

30
h-index
g-index

6.86
L-index

#	Paper	IF	Citations
46	Long noncoding RNAs: functional surprises from the RNA world. <i>Genes and Development</i> , 2009 , 23, 149	94 <u>150</u> 6	1711
45	Short intronic repeat sequences facilitate circular RNA production. <i>Genes and Development</i> , 2014 , 28, 2233-47	12.6	579
44	3Vend processing of a long nuclear-retained noncoding RNA yields a tRNA-like cytoplasmic RNA. <i>Cell</i> , 2008 , 135, 919-32	56.2	497
43	MEN epsilon/beta nuclear-retained non-coding RNAs are up-regulated upon muscle differentiation and are essential components of paraspeckles. <i>Genome Research</i> , 2009 , 19, 347-59	9.7	469
42	Molecular biology. A circuitous route to noncoding RNA. <i>Science</i> , 2013 , 340, 440-1	33.3	346
41	Combinatorial control of Drosophila circular RNA expression by intronic repeats, hnRNPs, and SR proteins. <i>Genes and Development</i> , 2015 , 29, 2168-82	12.6	300
40	A triple helix stabilizes the 3Vends of long noncoding RNAs that lack poly(A) tails. <i>Genes and Development</i> , 2012 , 26, 2392-407	12.6	286
39	A 360🛮 view of circular RNAs: From biogenesis to functions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018 , 9, e1478	9.3	251
38	Sensing Self and Foreign Circular RNAs by Intron Identity. <i>Molecular Cell</i> , 2017 , 67, 228-238.e5	17.6	226
37	The Output of Protein-Coding Genes Shifts to Circular RNAs When the Pre-mRNA Processing Machinery Is Limiting. <i>Molecular Cell</i> , 2017 , 68, 940-954.e3	17.6	213
36	Non-AUG translation: a new start for protein synthesis in eukaryotes. <i>Genes and Development</i> , 2017 , 31, 1717-1731	12.6	174
35	Circular RNA CircFndc3b modulates cardiac repair after myocardial infarction via FUS/VEGF-A axis. <i>Nature Communications</i> , 2019 , 10, 4317	17.4	171
34	High-Resolution Mapping of RNA-Binding Regions in the Nuclear Proteome of Embryonic Stem Cells. <i>Molecular Cell</i> , 2016 , 64, 416-430	17.6	161
33	A length-dependent evolutionarily conserved pathway controls nuclear export of circular RNAs. <i>Genes and Development</i> , 2018 , 32, 639-644	12.6	146
32	Long noncoding RNAs: Re-writing dogmas of RNA processing and stability. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 128-38	6	140
31	Biogenesis and Functions of Circular RNAs Come into Focus. <i>Trends in Cell Biology</i> , 2020 , 30, 226-240	18.3	121
30	tRNAs marked with CCACCA are targeted for degradation. <i>Science</i> , 2011 , 334, 817-21	33.3	111

(2021-2015)

29	A 3VPoly(A) Tract Is Required for LINE-1 Retrotransposition. <i>Molecular Cell</i> , 2015 , 60, 728-741	17.6	87
28	Circular RNAs: Unexpected outputs of many protein-coding genes. RNA Biology, 2017, 14, 1007-1017	4.8	72
27	An improved method for circular RNA purification using RNase R that efficiently removes linear RNAs containing G-quadruplexes or structured 3Vends. <i>Nucleic Acids Research</i> , 2019 , 47, 8755-8769	20.1	67
26	The Integrator Complex Attenuates Promoter-Proximal Transcription at Protein-Coding Genes. <i>Molecular Cell</i> , 2019 , 76, 738-752.e7	17.6	62
25	Tissue-Dependent Expression and Translation of Circular RNAs with Recombinant AAV Vectors In[Vivo. <i>Molecular Therapy - Nucleic Acids</i> , 2018 , 13, 89-98	10.7	56
24	An Unchartered Journey for Ribosomes: Circumnavigating Circular RNAs to Produce Proteins. <i>Molecular Cell</i> , 2017 , 66, 1-2	17.6	54
23	The Integrator complex cleaves nascent mRNAs to attenuate transcription. <i>Genes and Development</i> , 2019 , 33, 1525-1538	12.6	54
22	On-enzyme refolding permits small RNA and tRNA surveillance by the CCA-adding enzyme. <i>Cell</i> , 2015 , 160, 644-658	56.2	52
21	An unexpected ending: noncanonical 3Vend processing mechanisms. <i>Rna</i> , 2010 , 16, 259-66	5.8	49
20	Controlling translation via modulation of tRNA levels. Wiley Interdisciplinary Reviews RNA, 2015 , 6, 453	-79.3	47
20	Controlling translation via modulation of tRNA levels. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015 , 6, 453. Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7	-7 9 .3	47 36
		-7 9 .3 12.6	36
19	Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7 A conserved virus-induced cytoplasmic TRAMP-like complex recruits the exosome to target viral		36
19	Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7 A conserved virus-induced cytoplasmic TRAMP-like complex recruits the exosome to target viral RNA for degradation. <i>Genes and Development</i> , 2016 , 30, 1658-70 Ribosome queuing enables non-AUG translation to be resistant to multiple protein synthesis	12.6	36 35
19 18	Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7 A conserved virus-induced cytoplasmic TRAMP-like complex recruits the exosome to target viral RNA for degradation. <i>Genes and Development</i> , 2016 , 30, 1658-70 Ribosome queuing enables non-AUG translation to be resistant to multiple protein synthesis inhibitors. <i>Genes and Development</i> , 2019 , 33, 871-885 Inducible Expression of Eukaryotic Circular RNAs from Plasmids. <i>Methods in Molecular Biology</i> , 2017	12.6	36 35 32
19 18 17	Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7 A conserved virus-induced cytoplasmic TRAMP-like complex recruits the exosome to target viral RNA for degradation. <i>Genes and Development</i> , 2016 , 30, 1658-70 Ribosome queuing enables non-AUG translation to be resistant to multiple protein synthesis inhibitors. <i>Genes and Development</i> , 2019 , 33, 871-885 Inducible Expression of Eukaryotic Circular RNAs from Plasmids. <i>Methods in Molecular Biology</i> , 2017 , 1648, 143-154 The negative regulator of splicing element of Rous sarcoma virus promotes polyadenylation.	12.6 12.6	36 35 32 22
19 18 17 16	Repetitive elements regulate circular RNA biogenesis. <i>Mobile Genetic Elements</i> , 2015 , 5, 1-7 A conserved virus-induced cytoplasmic TRAMP-like complex recruits the exosome to target viral RNA for degradation. <i>Genes and Development</i> , 2016 , 30, 1658-70 Ribosome queuing enables non-AUG translation to be resistant to multiple protein synthesis inhibitors. <i>Genes and Development</i> , 2019 , 33, 871-885 Inducible Expression of Eukaryotic Circular RNAs from Plasmids. <i>Methods in Molecular Biology</i> , 2017 , 1648, 143-154 The negative regulator of splicing element of Rous sarcoma virus promotes polyadenylation. <i>Journal of Virology</i> , 2006 , 80, 9634-40	12.6 12.6 1.4 6.6	36 35 32 22 21

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The Integrator Complex in Transcription and Development. Trends in Biochemical Sciences, 2020, 45, 923-934 11 Engineering highly efficient backsplicing and translation of synthetic circRNAs. Molecular Therapy -10 10.7 13 Nucleic Acids, 2021, 23, 821-834 Circle the Wagons: Circular RNAs Control Innate Immunity. Cell, 2019, 177, 797-799 56.2 9 12 TET2 chemically modifies tRNAs and regulates tRNA fragment levels. Nature Structural and 17.6 12 Molecular Biology, **2021**, 28, 62-70 The capping enzyme facilitates promoter escape and assembly of a follow-on preinitiation complex for reinitiation. Proceedings of the National Academy of Sciences of the United States of America, 11.5 7 **2019**, 116, 22573-22582 CRISPR/Cas13 effectors have differing extents of off-target effects that limit their utility in 6 20.1 eukaryotic cells.. Nucleic Acids Research, 2022, Nonsense-mediated RNA decay: at the Vautting edgeVof regulated snoRNA production. Genes and 12.6 5 4 Development, 2014, 28, 2447-9 CRISPR/Cas13 effectors have differing extents of off-target effects that limit their utility in eukaryotic cells Attenuation of Eukaryotic Protein-Coding Gene Expression via Premature Transcription 3.9 1 Termination. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 83-93

RNAi Screening to Identify Factors That Control Circular RNA Localization. Methods in Molecular

Use of circular RNAs as markers of readthrough transcription to identify factors regulating

cleavage/polyadenylation events. Methods, 2021, 196, 121-128

Biology, 2021, 2209, 321-332