

Alan M Lambowitz

List of Publications by Year in descending order

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109
papers

5,837
citations

101543
36
h-index

168389
53
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121
all docs

121
docs citations

121
times ranked

5446
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for template switching by a group II intron-encoded non-LTR-retroelement reverse transcriptase. <i>Journal of Biological Chemistry</i> , 2021, 297, 100971.	3.4	13
2	TGIRT-seq Protocol for the Comprehensive Profiling of Coding and Non-coding RNA Biotypes in Cellular, Extracellular Vesicle, and Plasma RNAs. <i>Bio-protocol</i> , 2021, 11, e4239.	0.4	4
3	Identification of protein-protected mRNA fragments and structured excised intron RNAs in human plasma by TGIRT-seq peak calling. <i>ELife</i> , 2020, 9, .	6.0	20
4	BCDIN3D regulates tRNAHis 3â€™ fragment processing. <i>PLoS Genetics</i> , 2019, 15, e1008273.	3.5	24
5	Improved TGIRT-seq methods for comprehensive transcriptome profiling with decreased adapter dimer formation and bias correction. <i>Scientific Reports</i> , 2019, 9, 7953.	3.3	56
6	Group II Intron RNPs and Reverse Transcriptases: From Retroelements to Research Tools. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032375.	5.5	26
7	Template-switching mechanism of a group II intron-encoded reverse transcriptase and its implications for biological function and RNA-Seq. <i>Journal of Biological Chemistry</i> , 2019, 294, 19764-19784.	3.4	18
8	Distinct mechanisms of microRNA sorting into cancer cell-derived extracellular vesicle subtypes. <i>ELife</i> , 2019, 8, .	6.0	164
9	Simultaneous sequencing of coding and noncoding RNA reveals a human transcriptome dominated by a small number of highly expressed noncoding genes. <i>Rna</i> , 2018, 24, 950-965.	3.5	61
10	Detection of expanded RNA repeats using thermostable group II intron reverse transcriptase. <i>Nucleic Acids Research</i> , 2018, 46, e1-e1.	14.5	14
11	A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition. <i>Molecular Cell</i> , 2018, 72, 700-714.e8.	9.7	25
12	Limitations of alignment-free tools in total RNA-seq quantification. <i>BMC Genomics</i> , 2018, 19, 510.	2.8	64
13	A Highly Proliferative Group IIC Intron from <i>Geobacillus stearothermophilus</i> Reveals New Features of Group II Intron Mobility and Splicing. <i>Journal of Molecular Biology</i> , 2018, 430, 2760-2783.	4.2	14
14	Broad role for YBX1 in defining the small noncoding RNA composition of exosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8987-E8995.	7.1	250
15	Facile single-stranded DNA sequencing of human plasma DNA via thermostable group II intron reverse transcriptase template switching. <i>Scientific Reports</i> , 2017, 7, 8421.	3.3	28
16	Structure of a Thermostable Group II Intron Reverse Transcriptase with Template-Primer and Its Functional and Evolutionary Implications. <i>Molecular Cell</i> , 2017, 68, 926-939.e4.	9.7	61
17	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	4.1	52
18	DMS-MaPseq for genome-wide or targeted RNA structure probing <i>in vivo</i> . <i>Nature Methods</i> , 2017, 14, 75-82.	19.0	309

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19	Structural Divergence of the Group I Intron Binding Surface in Fungal Mitochondrial Tyrosyl-tRNA Synthetases That Function in RNA Splicing. <i>Journal of Biological Chemistry</i> , 2016, 291, 11911-11927.	3.4	3
20	DUSP11 activity on triphosphorylated transcripts promotes Argonaute association with noncanonical viral microRNAs and regulates steady-state levels of cellular noncoding RNAs. <i>Genes and Development</i> , 2016, 30, 2076-2092.	5.9	46
21	RNA-seq of human reference RNA samples using a thermostable group II intron reverse transcriptase. <i>Rna</i> , 2016, 22, 597-613.	3.5	80
22	High-throughput sequencing of human plasma RNA by using thermostable group II intron reverse transcriptases. <i>Rna</i> , 2016, 22, 111-128.	3.5	101
23	Direct CRISPR spacer acquisition from RNA by a natural reverse transcriptase–Cas1 fusion protein. <i>Science</i> , 2016, 351, aad4234.	12.6	170
24	Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution. <i>Microbiology Spectrum</i> , 2015, 3, MDNA3-0050-2014.	3.0	119
25	piggyBac Transposons. , 2015, , 873-890.		6
26	Integration, Regulation, and Long-Term Stability of R2 Retrotransposons. , 2015, , 1125-1146.		4
27	Retroviral Integrase Structure and DNA Recombination Mechanism. , 2015, , 1011-1033.		0
28	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of <i>Schizosaccharomyces pombe</i> . , 2015, , 997-1010.		2
29	Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3. , 2015, , 289-309.		1
30	Mammalian Endogenous Retroviruses. , 2015, , 1079-1100.		10
31	Mobile DNA in the Pathogenic <i>Neisseria</i> . , 2015, , 451-469.		3
32	vlsAntigenic Variation Systems of Lyme Disease Borrelia: Eluding Host Immunity through both Random, Segmental Gene Conversion and Framework Heterogeneity. , 2015, , 471-489.		4
33	Site-specific non-LTR retrotransposons. , 2015, , 1147-1163.		1
34	Mobile Bacterial Group II Introns at the Crux of Eukaryotic Evolution. , 2015, , 1209-1236.		12
35	Retrohoming of a Mobile Group II Intron in Human Cells Suggests How Eukaryotes Limit Group II Intron Proliferation. <i>PLoS Genetics</i> , 2015, 11, e1005422.	3.5	11
36	The IS200/IS605 Family and “Peel and Paste” Single-strand Transposition Mechanism. , 2015, , 609-630.		5

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37	Rqc2p and 60 <i>S</i> ribosomal subunits mediate mRNA-independent elongation of nascent chains. <i>Science</i> , 2015, 347, 75-78.	12.6	245
38	Efficient and quantitative high-throughput tRNA sequencing. <i>Nature Methods</i> , 2015, 12, 835-837.	19.0	426
39	Lester Reed: A “complex” man who loved science. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6247-6247.	7.1	2
40	Evolution of RNA-Protein Interactions: Non-Specific Binding Led to RNA Splicing Activity of Fungal Mitochondrial Tyrosyl-tRNA Synthetases. <i>PLoS Biology</i> , 2014, 12, e1002028.	5.6	11
41	Biotechnological applications of mobile group II introns and their reverse transcriptases: gene targeting, RNA-seq, and non-coding RNA analysis. <i>Mobile DNA</i> , 2014, 5, 2.	3.6	66
42	Broad and adaptable RNA structure recognition by the human interferon-induced tetratricopeptide repeat protein IFIT5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12025-12030.	7.1	76
43	The contribution of cellulosomal scaffoldins to cellulose hydrolysis by <i>Clostridium thermocellum</i> analyzed by using thermotargetrons. <i>Biotechnology for Biofuels</i> , 2014, 7, 80.	6.2	46
44	Molecular insights into RNA and DNA helicase evolution from the determinants of specificity for a DEAD-box RNA helicase. <i>ELife</i> , 2014, 3, e04630.	6.0	33
45	Thermostable group II intron reverse transcriptase fusion proteins and their use in cDNA synthesis and next-generation RNA sequencing. <i>Rna</i> , 2013, 19, 958-970.	3.5	175
46	The Retrohoming of Linear Group II Intron RNAs in <i>Drosophila melanogaster</i> Occurs by Both DNA Ligase 4-Dependent and -Independent Mechanisms. <i>PLoS Genetics</i> , 2012, 8, e1002534.	3.5	23
47	Group II Introns: Mobile Ribozymes that Invade DNA. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a003616-a003616.	5.5	357
48	Mobile Group II Introns: Site-Specific DNA Integration and Applications in Gene Targeting. <i>FASEB Journal</i> , 2011, 25, 202.3.	0.5	0
49	Genetic identification of potential RNA-binding regions in a group II intron-encoded reverse transcriptase. <i>Rna</i> , 2010, 16, 732-747.	3.5	24
50	Mechanisms Used for Genomic Proliferation by Thermophilic Group II Introns. <i>PLoS Biology</i> , 2010, 8, e1000391.	5.6	45
51	Gene Targeting in Gram-Negative Bacteria by Use of a Mobile Group II Intron (“Targetron”) Expressed from a Broad-Host-Range Vector. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2735-2743.	3.1	49
52	Domain structure and three-dimensional model of a group II intron-encoded reverse transcriptase. <i>Rna</i> , 2005, 11, 14-28.	3.5	85
53	Mobile Group II Introns. <i>Annual Review of Genetics</i> , 2004, 38, 1-35.	7.6	421
54	Characterization of the C-Terminal DNA-binding/DNA Endonuclease Region of a Group II Intron-encoded Protein. <i>Journal of Molecular Biology</i> , 2002, 324, 933-951.	4.2	85

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55	Group II introns as controllable gene targeting vectors for genetic manipulation of bacteria. <i>Nature Biotechnology</i> , 2001, 19, 1162-1167.	17.5	193
56	Group II Introns Designed to Insert into Therapeutically Relevant DNA Target Sites in Human Cells. <i>Science</i> , 2000, 289, 452-457.	12.6	203
57	RNA and Protein Catalysis in Group II Intron Splicing and Mobility Reactions Using Purified Components. <i>Biochemistry</i> , 1999, 38, 9069-9083.	2.5	144
58	De novo and DNA primer-mediated initiation of cDNA synthesis by the mauriceville retroplasmid reverse transcriptase involve recognition of a 3â€² CCA sequence 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 271, 311-332.	4.2	47
59	Efficient integration of an intron RNA into double-stranded DNA by reverse splicing. <i>Nature</i> , 1996, 381, 332-335.	27.8	165
60	A tyrosyl-tRNA synthetase can function similarly to an RNA structure in the Tetrahymena ribozyme. <i>Nature</i> , 1994, 370, 147-150.	27.8	122
61	The mauriceville plasmid reverse transcriptase can initiate cDNA synthesis de novo and may be related to reverse transcriptase and DNA polymerase progenitor. <i>Cell</i> , 1993, 75, 1071-1081.	28.9	106
62	Group I and group II introns.. <i>FASEB Journal</i> , 1993, 7, 15-24.	0.5	268
63	A novel reverse transcriptase activity associated with mitochondrial plasmids of neurospora. <i>Cell</i> , 1988, 55, 693-704.	28.9	109
64	Mitochondrial plasmids of neurospora: Integration into mitochondrial DNA and evidence for reverse transcription in mitochondria. <i>Cell</i> , 1986, 47, 505-516.	28.9	139
65	Characterization of a novel plasmid DNA found in mitochondria of N. crassa. <i>Cell</i> , 1981, 24, 443-452.	28.9	136
66	Adeno-associated Virus as a Mammalian DNA Vector. , 0, , 827-849.	4	
67	The Î» Integrase Site-specific Recombination Pathway. , 0, , 91-118.	2	
68	<i>Sleeping Beauty</i> Transposition. , 0, , 851-872.	2	
69	Cre Recombinase. , 0, , 119-138.	7	
70	Mechanisms of DNA Transposition. , 0, , 529-553.	11	
71	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.	12	
72	P Transposable Elements in <i>Drosophila</i> and other Eukaryotic Organisms. , 0, , 727-752.	6	

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73	Tyrosine Recombinase Retrotransposons and Transposons. , 0, , 1271-1291.	5	
74	The Tn <i><3></i> -family of Replicative Transposons. , 0, , 693-726.	14	
75	The Influence of LINE-1 and SINE Retrotransposons on Mammalian Genomes. , 0, , 1165-1208.	25	
76	Tn7. , 0, , 647-667.	13	
77	An Unexplored Diversity of Reverse Transcriptases in Bacteria. , 0, , 1253-1269.	2	
78	A Moveable Feast: An Introduction to Mobile DNA. , 0, , 1-39.	6	
79	Serine Resolvases. , 0, , 237-252.	1	
80	Phage-encoded Serine Integrases and Other Large Serine Recombinases. , 0, , 253-272.	14	
81	V(D)J Recombination: Mechanism, Errors, and Fidelity. , 0, , 311-324.	4	
82	Programmed Genome Rearrangements in Tetrahymena. , 0, , 349-367.	1	
83	Programmed Rearrangement in Ciliates: <i><3>Paramecium</i> . , 0, , 369-388.	2	
84	Recombination and Diversification of the Variant Antigen Encoding Genes in the Malaria Parasite Plasmodium falciparum. , 0, , 437-449.	1	
85	Copy-out-Paste-in Transposition of IS911: A Major Transposition Pathway. , 0, , 591-607.	30	
86	Transposons Tn <i><10></i> and Tn <i><5></i> . , 0, , 631-645.	2	
87	The Serine Recombinases. , 0, , 73-89.	5	
88	Transposable Phage Mu. , 0, , 669-691.	6	
89	Mariner and the ITm Superfamily of Transposons. , 0, , 753-772.	2	
90	<i><3>Mutator</i> and <i><3>MULE</i> Transposons. , 0, , 801-826.	2	

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91	<i>Helitrons</i>, the Eukaryotic Rolling-circle Transposable Elements. , 0, , 891-924.	8	
92	Ty3, a Position-specific Retrotransposon in Budding Yeast. , 0, , 965-996.	5	
93	Host Factors in Retroviral Integration and the Selection of Integration Target Sites. , 0, , 1035-1050.	2	
94	Diversity-generating Retroelements in Phage and Bacterial Genomes. , 0, , 1237-1252.	8	
95	The Integron: Adaptation On Demand. , 0, , 139-161.	7	
96	Site-specific DNA Inversion by Serine Recombinases. , 0, , 199-236.	2	
97	<i>hAT</i> Transposable Elements. , 0, , 773-800.	2	
98	Programmed Genome Rearrangements in the CiliateOxytricha. , 0, , 389-407.	1	
99	DNA Recombination Strategies During Antigenic Variation in the African Trypanosome. , 0, , 409-435.	2	
100	Retroviral DNA Transposition: Themes and Variations. , 0, , 1101-1123.	0	
101	The Integration and Excision of CTnDOT. , 0, , 183-198.	0	
102	An Overview of Tyrosine Site-specific Recombination: From an Flp Perspective. , 0, , 41-71.	24	
103	Hairpin Telomere Resolvases. , 0, , 273-287.	0	
104	Related Mechanisms of Antibody Somatic Hypermutation and Class Switch Recombination. , 0, , 325-348.	3	
105	Reverse Transcription of Retroviruses and LTR Retrotransposons. , 0, , 1051-1077.	4	
106	Mating-type Gene Switching in <i>Saccharomyces cerevisiae</i>. , 0, , 491-514.	0	
107	A Unique DNA Recombination Mechanism of the Mating/Cell-type Switching of Fission Yeasts: a Review. , 0, , 515-528.	2	
108	The Ty1 LTR-Retrotransposon of Budding Yeast,<i>Saccharomyces cerevisiae</i>. , 0, , 925-964.	1	

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- 109 Xer Site-Specific Recombination: Promoting Vertical and Horizontal Transmission of Genetic Information. , 0, , 163-182. 3