

# Alain T Laederach

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4832054/publications.pdf>

Version: 2024-02-01

88  
papers

4,574  
citations

117625

34  
h-index

110387

64  
g-index

96  
all docs

96  
docs citations

96  
times ranked

6875  
citing authors

#	ARTICLE	IF	CITATIONS
1	Disease-associated human genetic variation through the lens of precursor and mature RNA structure. <i>Human Genetics</i> , 2022, 141, 1659-1672.	3.8	10
2	A novel algorithm for ranking RNA structure candidates. <i>Biophysical Journal</i> , 2022, 121, 7-10.	0.5	5
3	Sequence and tissue targeting specificity of ZFP36L2 reveals <i>Elavl2</i> as a novel target with co-regulation potential. <i>Nucleic Acids Research</i> , 2022, , .	14.5	3
4	Distinct responses to rare codons in select <i>Drosophila</i> tissues. <i>ELife</i> , 2022, 11, .	6.0	11
5	Direct Mapping of Higher-Order RNA Interactions by SHAPE-JuMP. <i>Biochemistry</i> , 2021, 60, 1971-1982.	2.5	24
6	To Knot or Not to Knot: Multiple Conformations of the SARS-CoV-2 Frameshifting RNA Element. <i>Journal of the American Chemical Society</i> , 2021, 143, 11404-11422.	13.7	35
7	<i>In vivo</i> architecture of the telomerase RNA catalytic core in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2021, 49, 12445-12466.	14.5	8
8	Cigarette smoking-associated isoform switching and 3' UTR lengthening via alternative polyadenylation. <i>Genomics</i> , 2021, 113, 4184-4195.	2.9	3
9	Alternative poly-adenylation modulates $\alpha 1$ -antitrypsin expression in chronic obstructive pulmonary disease. <i>PLoS Genetics</i> , 2021, 17, e1009912.	3.5	3
10	Identifying proximal RNA interactions from cDNA-encoded crosslinks with ShapeJumper. <i>PLoS Computational Biology</i> , 2021, 17, e1009632.	3.2	3
11	The Effects of Rare <i>SERPINA1</i> Variants on Lung Function and Emphysema in SPIROMICS. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 540-554.	5.6	38
12	Using SHAPE-MaP To Model RNA Secondary Structure and Identify 3' UTR Variation in Chikungunya Virus. <i>Journal of Virology</i> , 2020, 94, .	3.4	22
13	The structure of the influenza A virus genome. <i>Nature Microbiology</i> , 2019, 4, 1781-1789.	13.3	157
14	Towards an understanding of RNA structural modalities: a riboswitch case study. <i>Computational and Mathematical Biophysics</i> , 2019, 7, 48-63.	1.1	1
15	The role of RNA-RNA interactions in the assembly and reassortment of influenza A viruses. <i>Access Microbiology</i> , 2019, 1, .	0.5	0
16	Allele-specific SHAPE-MaP assessment of the effects of somatic variation and protein binding on mRNA structure. <i>Rna</i> , 2018, 24, 513-528.	3.5	20
17	Structural divergence creates new functional features in alphavirus genomes. <i>Nucleic Acids Research</i> , 2018, 46, 3657-3670.	14.5	45
18	A pipeline for computational design of novel RNA-like topologies. <i>Nucleic Acids Research</i> , 2018, 46, 7040-7051.	14.5	25

#	ARTICLE	IF	CITATIONS
19	A Functional riboSNitch in the 3' Untranslated Region of FKBP5 Alters MicroRNA-320a Binding Efficiency and Mediates Vulnerability to Chronic Post-Traumatic Pain. <i>Journal of Neuroscience</i> , 2018, 38, 8407-8420.	3.6	52
20	Messenger RNA Structure Regulates Translation Initiation: A Mechanism Exploited from Bacteria to Humans. <i>Biochemistry</i> , 2018, 57, 3537-3539.	2.5	48
21	Impact of RNA structure on ZFP36L2 interaction with luteinizing hormone receptor mRNA. <i>Rna</i> , 2017, 23, 1209-1223.	3.5	10
22	Comparative Visualization of the RNA Suboptimal Conformational Ensemble In Vivo. <i>Biophysical Journal</i> , 2017, 113, 290-301.	0.5	35
23	Transcending the prediction paradigm: novel applications of SHAPE to RNA function and evolution. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1374.	6.4	41
24	An RNA structure-mediated, posttranscriptional model of human Î±-1-antitrypsin expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10244-E10253.	7.1	52
25	Classification of RNA structure change by gazing at experimental data. <i>Bioinformatics</i> , 2017, 33, 1647-1655.	4.1	20
26	Structure-Function Model for Kissing Loop Interactions That Initiate Dimerization of Ty1 RNA. <i>Viruses</i> , 2017, 9, 93.	3.3	7
27	Primary and Secondary Sequence Structure Requirements for Recognition and Discrimination of Target RNAs by <i>Pseudomonas aeruginosa</i> RsmA and RsmF. <i>Journal of Bacteriology</i> , 2016, 198, 2458-2469.	2.2	46
28	A unified analytic framework for prioritization of non-coding variants of uncertain significance in heritable breast and ovarian cancer. <i>BMC Medical Genomics</i> , 2016, 9, 19.	1.5	28
29	Selecting against accidental RNA interactions. <i>ELife</i> , 2016, 5, .	6.0	1
30	REGULATORY RNA. , 2016, , .		0
31	The potential of the riboSNitch in personalized medicine. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 517-532.	6.4	42
32	Multiple conformations are a conserved and regulatory feature of the RB1 5' UTR. <i>Rna</i> , 2015, 21, 1274-1285.	3.5	60
33	Detecting riboSNitches with RNA folding algorithms: a genome-wide benchmark. <i>Nucleic Acids Research</i> , 2015, 43, 1859-1868.	14.5	43
34	Single Molecule Cluster Analysis dissects splicing pathway conformational dynamics. <i>Nature Methods</i> , 2015, 12, 1077-1084.	19.0	34
35	A clear path to RNA catalysis. <i>Nature Chemical Biology</i> , 2015, 11, 906-908.	8.0	1
36	Increased Transcript Complexity in Genes Associated with Chronic Obstructive Pulmonary Disease. <i>PLoS ONE</i> , 2015, 10, e0140885.	2.5	18

#	ARTICLE	IF	CITATIONS
37	Mapping the Kinetic Barriers of a Large RNA Molecule's Folding Landscape. PLoS ONE, 2014, 9, e85041.	2.5	7
38	A second layer of information in RNA. Nature, 2014, 505, 621-622.	27.8	13
39	Small RNAs derived from lncRNA RNase MRP have gene-silencing activity relevant to human cartilage hair hypoplasia. Human Molecular Genetics, 2014, 23, 368-382.	2.9	83
40	Understanding the Role of Three-Dimensional Topology in Determining the Folding Intermediates of Group I Introns. Biophysical Journal, 2013, 104, 1326-1337.	0.5	11
41	Evolutionary Evidence for Alternative Structure in RNA Sequence Co-variation. PLoS Computational Biology, 2013, 9, e1003152.	3.2	40
42	Structural effects of linkage disequilibrium on the transcriptome. Rna, 2012, 18, 77-87.	3.5	49
43	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	21.4	362
44	Evaluating our ability to predict the structural disruption of RNA by SNPs. BMC Genomics, 2012, 13, S6.	2.8	51
45	Modeling RNA Folding Pathways and Intermediates Using Time-Resolved Hydroxyl Radical Footprinting Data. Nucleic Acids and Molecular Biology, 2012, , 319-334.	0.2	0
46	A novel application of pattern recognition for accurate SNP and indel discovery from high-throughput data: Targeted resequencing of the glucocorticoid receptor co-chaperone FKBP5 in a Caucasian population. Molecular Genetics and Metabolism, 2011, 104, 457-469.	1.1	16
47	Meeting report of the RNA Ontology Consortium January 8-9, 2011. Standards in Genomic Sciences, 2011, 4, 252-256.	1.5	1
48	Membrane RNAs in bacteria. Molecular Microbiology, 2011, 79, 1-2.	2.5	2
49	Strategies for Articulated Multibody-Based Adaptive Coarse Grain Simulation of RNA. Methods in Enzymology, 2011, 487, 73-98.	1.0	39
50	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	3.5	28
51	RNA molecules with conserved catalytic cores but variable peripheries fold along unique energetically optimized pathways. Rna, 2011, 17, 1589-1603.	3.5	21
52	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. Nature Genetics, 2010, 42, 781-785.	21.4	692
53	Evaluation of the information content of RNA structure mapping data for secondary structure prediction. Rna, 2010, 16, 1108-1117.	3.5	52
54	Disease-Associated Mutations That Alter the RNA Structural Ensemble. PLoS Genetics, 2010, 6, e1001074.	3.5	292

#	ARTICLE	IF	CITATIONS
55	Exhaustive Enumeration of Kinetic Model Topologies for the Analysis of Time-Resolved RNA Folding. <i>Algorithms</i> , 2009, 2, 200-214.	2.1	10
56	Rapid Quantification and Analysis of Kinetic $\text{H}^{\bullet}\text{OH}$ Radical Footprinting Data Using SAFA. <i>Methods in Enzymology</i> , 2009, 468, 47-66.	1.0	4
57	Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters. <i>Rna</i> , 2009, 15, 189-199.	3.5	300
58	On Adaptivity in Coarse Grain Molecular Dynamics. , 2009, , .		0
59	Energy barriers, pathways, and dynamics during folding of large, multidomain RNAs. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 655-666.	6.1	53
60	Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments. <i>Nature Protocols</i> , 2008, 3, 1395-1401.	12.0	70
61	Structural inference of native and partially folded RNA by high-throughput contact mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4144-4149.	7.1	79
62	High-throughput single-nucleotide structural mapping by capillary automated footprinting analysis. <i>Nucleic Acids Research</i> , 2008, 36, e63-e63.	14.5	89
63	Distinct contribution of electrostatics, initial conformational ensemble, and macromolecular stability in RNA folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7045-7050.	7.1	56
64	Local RNA structural changes induced by crystallization are revealed by SHAPE. <i>Rna</i> , 2007, 13, 536-548.	3.5	51
65	Informatics challenges in structured RNA. <i>Briefings in Bioinformatics</i> , 2007, 8, 294-303.	6.5	13
66	Coplanar and coaxial orientations of RNA bases and helices. <i>Rna</i> , 2007, 13, 643-650.	3.5	19
67	Local Kinetic Measures of Macromolecular Structure Reveal Partitioning among Multiple Parallel Pathways from the Earliest Steps in the Folding of a Large RNA Molecule. <i>Journal of Molecular Biology</i> , 2006, 358, 1179-1190.	4.2	46
68	The Paradoxical Behavior of a Highly Structured Misfolded Intermediate in RNA Folding. <i>Journal of Molecular Biology</i> , 2006, 363, 531-544.	4.2	92
69	Docking Carbohydrates to Proteins: Empirical Free Energy Functions. <i>ACS Symposium Series</i> , 2006, , 258-270.	0.5	0
70	Modeling protein recognition of carbohydrates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 591-597.	2.6	53
71	SAFA: Semi-automated footprinting analysis software for high-throughput quantification of nucleic acid footprinting experiments. <i>Rna</i> , 2005, 11, 344-354.	3.5	299
72	Arg343 in human surfactant protein D governs discrimination between glucose and N-acetylglucosamine ligands. <i>Glycobiology</i> , 2004, 14, 693-700.	2.5	19

#	ARTICLE	IF	CITATIONS
73	Visualizing complexes of phospholipids with Streptomyces phospholipase D by automated docking. Proteins: Structure, Function and Bioinformatics, 2004, 57, 27-35.	2.6	12
74	Computational functional genomics. IEEE Signal Processing Magazine, 2004, 21, 62-69.	5.6	5
75	Specific empirical free energy function for automated docking of carbohydrates to proteins. Journal of Computational Chemistry, 2003, 24, 1748-1757.	3.3	47
76	Determinants of Intra versus Intermolecular Self-association Within the Regulatory Domains of Rlk and Itk. Journal of Molecular Biology, 2003, 329, 1011-1020.	4.2	31
77	Ligand Specificity Modulated by Prolyl Imide Bond Cis/Trans Isomerization in the Itk SH2 Domain: A Quantitative NMR Study. Journal of the American Chemical Society, 2003, 125, 15706-15707.	13.7	40
78	Solution and Micelle-Bound Structures of Tachyplesin I and Its Active Aromatic Linear Derivatives. Biochemistry, 2002, 41, 12359-12368.	2.5	98
79	Competing modes of self-association in the regulatory domains of Bruton's tyrosine kinase: Intramolecular contact versus asymmetric homodimerization. Protein Science, 2002, 11, 36-57.	7.6	24
80	Competing modes of self-association in the regulatory domains of Bruton's tyrosine kinase: Intramolecular contact versus asymmetric homodimerization. Protein Science, 2002, 11, 36-57.	7.6	30
81	Polysaccharide Recognition by Surfactant Protein D: A Novel Interactions of a C-Type Lectin with Nonterminal Glucosyl Residues. Biochemistry, 2001, 40, 7789-7798.	2.5	50
82	The Role of Cation- $\pi$ Interactions in Biomolecular Association. Design of Peptides Favoring Interactions between Cationic and Aromatic Amino Acid Side Chains. Journal of the American Chemical Society, 2001, 123, 6232-6245.	13.7	122
83	Automated docking of $\alpha$ -(1 $\rightarrow$ 4)- and $\alpha$ -(1 $\rightarrow$ 6)-linked glucosyl trisaccharides and maltopentaose into the soybean $\alpha$ -amylase active site. , 2000, 40, 299-309.		25
84	Automated docking of maltose, 2-deoxymaltose, and maltotetraose into the soybean $\alpha$ -amylase active site. , 1999, 37, 166-175.		30
85	On the characterization of industrial carbon blacks by physico-chemical and by empirical parameters. Carbon, 1996, 34, 135-137.	10.3	2
86	On the characterization of carbon blacks by various techniques. Carbon, 1994, 32, 1359-1362.	10.3	30
87	Water adsorption in carbons described by the dubinin $\pi$ -astakhov and dubinin $\pi$ -serpinski equations. Journal of the Chemical Society, Faraday Transactions, 1994, 90, 3689-3691.	1.7	41
88	Quantitative prediction of variant effects on alternative splicing in MAPT using endogenous pre-messenger RNA structure probing. ELife, 0, 11, .	6.0	6