

Daniel Gautheret

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3117845/publications.pdf>

Version: 2024-02-01

86
papers

7,273
citations

76196

40
h-index

60497

81
g-index

95
all docs

95
docs citations

95
times ranked

10095
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-omics prediction in melanoma immunotherapy: A new brick in the wall. <i>Cancer Cell</i> , 2022, 40, 14-16.	7.7	3
2	The contribution of uncharted RNA sequences to tumor identity in lung adenocarcinoma. <i>NAR Cancer</i> , 2022, 4, zcac001.	1.6	2
3	Accurate characterization of <i>Escherichia coli</i> tRNA modifications with a simple method of deep-sequencing library preparation. <i>RNA Biology</i> , 2021, 18, 33-46.	1.5	11
4	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	6.5	475
5	Identification of RNAs bound by Hfq reveals widespread RNA partners and a sporulation regulator in the human pathogen <i>Clostridioides difficile</i> . <i>RNA Biology</i> , 2021, 18, 1931-1952.	1.5	13
6	Reference-free transcriptome signatures for prostate cancer prognosis. <i>BMC Cancer</i> , 2021, 21, 394.	1.1	6
7	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021, 149, 193-210.	1.3	62
8	2-kupl: mapping-free variant detection from DNA-seq data of matched samples. <i>BMC Bioinformatics</i> , 2021, 22, 304.	1.2	1
9	Kmerator Suite: design of specific <i>k</i> -mer signatures and automatic metadata discovery in large RNA-seq datasets. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab058.	1.5	2
10	Landscape of the Noncoding Transcriptome Response of Two Arabidopsis Ecotypes to Phosphate Starvation. <i>Plant Physiology</i> , 2020, 183, 1058-1072.	2.3	23
11	Bridging the gap between reference and real transcriptomes. <i>Genome Biology</i> , 2019, 20, 112.	3.8	38
12	Reference-free transcriptome exploration reveals novel RNAs for prostate cancer diagnosis. <i>Life Science Alliance</i> , 2019, 2, e201900449.	1.3	12
13	A benchmark study of scoring methods for non-coding mutations. <i>Bioinformatics</i> , 2018, 34, 1635-1641.	1.8	21
14	Native elongating transcript sequencing reveals global anti-correlation between sense and antisense nascent transcription in fission yeast. <i>Rna</i> , 2018, 24, 196-208.	1.6	43
15	CRISPRCasFinder, an update of CRISRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. <i>Nucleic Acids Research</i> , 2018, 46, W246-W251.	6.5	985
16	The conserved regulatory RNA RsaE down-regulates the arginine degradation pathway in <i>Staphylococcus aureus</i> . <i>Nucleic Acids Research</i> , 2018, 46, 8803-8816.	6.5	34
17	DE-kupl: exhaustive capture of biological variation in RNA-seq data through <i>k</i> -mer decomposition. <i>Genome Biology</i> , 2017, 18, 243.	3.8	33
18	The Non-Coding RNA Journal Club: Highlights on Recent Papers 4. <i>Non-coding RNA</i> , 2016, 2, 9.	1.3	1

#	ARTICLE	IF	CITATIONS
19	Detection of generic differential RNA processing events from RNA-seq data. <i>RNA Biology</i> , 2016, 13, 59-67.	1.5	27
20	Nonsense-Mediated Decay Restricts LncRNA Levels in Yeast Unless Blocked by Double-Stranded RNA Structure. <i>Molecular Cell</i> , 2016, 61, 379-392.	4.5	101
21	VING: a software for visualization of deep sequencing signals. <i>BMC Research Notes</i> , 2015, 8, 419.	0.6	18
22	The Non-Coding RNA Journal Club: Highlights on Recent Papers. <i>Non-coding RNA</i> , 2015, 1, 87-93.	1.3	3
23	A Dual Model for Prioritizing Cancer Mutations in the Non-coding Genome Based on Germline and Somatic Events. <i>PLoS Computational Biology</i> , 2015, 11, e1004583.	1.5	17
24	Revisiting the structure/function relationships of H/ACA(-like) RNAs: a unified model for Euryarchaea and Crenarchaea. <i>Nucleic Acids Research</i> , 2015, 43, 7744-7761.	6.5	5
25	In plants, decapping prevents RDR6-dependent production of small interfering RNAs from endogenous mRNAs. <i>Nucleic Acids Research</i> , 2015, 43, 2902-2913.	6.5	107
26	An assessment of bacterial small RNA target prediction programs. <i>RNA Biology</i> , 2015, 12, 509-513.	1.5	74
27	Mining the coding and non-coding genome for cancer drivers. <i>Cancer Letters</i> , 2015, 369, 307-315.	3.2	15
28	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. <i>Cancer Discovery</i> , 2014, 4, 1088-1101.	7.7	213
29	Detection of non-coding RNA in bacteria and archaea using the DETRâ€™™PROK Galaxy pipeline. <i>Methods</i> , 2013, 63, 60-65.	1.9	21
30	Zinc-mediated RNA fragmentation allows robust transcript reassembly upon whole transcriptome RNA-Seq. <i>Methods</i> , 2013, 63, 25-31.	1.9	27
31	A universal RNA structural motif docking the elbow of tRNA in the ribosome, RNase P and T-box leaders. <i>Nucleic Acids Research</i> , 2013, 41, 5494-5502.	6.5	39
32	RNA at 92Â°C. <i>RNA Biology</i> , 2013, 10, 1211-1220.	1.5	53
33	NAPP: the Nucleic Acid Phylogenetic Profile Database. <i>Nucleic Acids Research</i> , 2012, 40, D205-D209.	6.5	17
34	Transcriptomic profiling of the oyster pathogen <i>Vibrio splendidus</i> opens a window on the evolutionary dynamics of the small RNA repertoire in the <i>Vibrio</i> genus. <i>Rna</i> , 2012, 18, 2201-2219.	1.6	53
35	Characterization of novel genomic alterations and therapeutic approaches using acute megakaryoblastic leukemia xenograft models. <i>Journal of Experimental Medicine</i> , 2012, 209, 2017-2031.	4.2	87
36	RNAspace.org: An integrated environment for the prediction, annotation, and analysis of ncRNA. <i>Rna</i> , 2011, 17, 1947-1956.	1.6	25

#	ARTICLE	IF	CITATIONS
37	Genome-wide discovery and analysis of microRNAs and other small RNAs from rice embryogenic callus. <i>RNA Biology</i> , 2011, 8, 538-547.	1.5	125
38	Plant noncoding RNA gene discovery by "single-genome comparative genomics". <i>Rna</i> , 2011, 17, 390-400.	1.6	4
39	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
40	CsfG, a sporulation-specific, small non-coding RNA highly conserved in endospore formers. <i>RNA Biology</i> , 2011, 8, 358-364.	1.5	32
41	ARNold: A web tool for the prediction of Rho-independent transcription terminators. <i>RNA Biology</i> , 2011, 8, 11-13.	1.5	263
42	Experimental discovery of small RNAs in <i>Staphylococcus aureus</i> reveals a riboregulator of central metabolism. <i>Nucleic Acids Research</i> , 2010, 38, 6620-6636.	6.5	155
43	RsaOG, a new <i>Staphylococcal</i> family of highly transcribed non-coding RNA. <i>RNA Biology</i> , 2010, 7, 116-119.	1.5	16
44	Premature terminator analysis sheds light on a hidden world of bacterial transcriptional attenuation. <i>Genome Biology</i> , 2010, 11, R97.	13.9	29
45	Using Alu Elements as Polyadenylation Sites: A Case of Retroposon Exaptation. <i>Molecular Biology and Evolution</i> , 2009, 26, 327-334.	3.5	81
46	Single-pass classification of all noncoding sequences in a bacterial genome using phylogenetic profiles. <i>Genome Research</i> , 2009, 19, 1084-1092.	2.4	66
47	ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009, 93, 213-220.	1.3	87
48	Transcription attenuation in bacteria: theme and variations. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 482-492.	3.8	37
49	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	13.9	301
50	Entropy Measures Quantify Global Splicing Disorders in Cancer. <i>PLoS Computational Biology</i> , 2008, 4, e1000011.	1.5	53
51	Mireval: a web tool for simple microRNA prediction in genome sequences. <i>Bioinformatics</i> , 2008, 24, 1394-1396.	1.8	41
52	Metagenome Annotation Using a Distributed Grid of Undergraduate Students. <i>PLoS Biology</i> , 2008, 6, e296.	2.6	19
53	RNA stem-loops: To be or not to be cleaved by RNase III. <i>Rna</i> , 2007, 13, 457-462.	1.6	68
54	Beyond the 3' end: experimental validation of extended transcript isoforms. <i>Nucleic Acids Research</i> , 2007, 35, 1947-1957.	6.5	18

#	ARTICLE	IF	CITATIONS
55	AltTrans: transcript pattern variants annotated for both alternative splicing and alternative polyadenylation. BMC Bioinformatics, 2006, 7, 169.	1.2	30
56	Conservation of alternative polyadenylation patterns in mammalian genes. BMC Genomics, 2006, 7, 189.	1.2	47
57	Differential Repression of Alternative Transcripts: A Screen for miRNA Targets. PLoS Computational Biology, 2006, 2, e43.	1.5	58
58	The disparate nature of "intergenic" polyadenylation sites. Rna, 2006, 12, 1794-1801.	1.6	25
59	Computing expectation values for RNA motifs using discrete convolutions. BMC Bioinformatics, 2005, 6, 118.	1.2	7
60	Profile-based detection of microRNA precursors in animal genomes. Bioinformatics, 2005, 21, 841-845.	1.8	83
61	The ERPIN server: an interface to profile-based RNA motif identification. Nucleic Acids Research, 2004, 32, W160-W165.	6.5	43
62	Sequence determinants in human polyadenylation site selection. BMC Genomics, 2003, 4, 7.	1.2	122
63	Novel Selenoproteins Identified from Genomic Sequence Data. Methods in Enzymology, 2002, 347, 57-70.	0.4	12
64	A survey of metazoan selenocysteine insertion sequences. Biochimie, 2002, 84, 953-959.	1.3	19
65	RNAML: A standard syntax for exchanging RNA information. Rna, 2002, 8, 707-717.	1.6	91
66	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. Immunogenetics, 2002, 54, 469-478.	1.2	4
67	Direct RNA motif definition and identification from multiple sequence alignments using secondary structure profiles 1 Edited by J. Doudna. Journal of Molecular Biology, 2001, 313, 1003-1011.	2.0	269
68	RNAMotif, an RNA secondary structure definition and search algorithm. Nucleic Acids Research, 2001, 29, 4724-4735.	6.5	421
69	Identification of Alternate Polyadenylation Sites and Analysis of their Tissue Distribution Using EST Data. Genome Research, 2001, 11, 1520-1526.	2.4	151
70	From RNA Structure to the Identification of New Genes. The Example of Selenoproteins.. Journal of Health Science, 2000, 46, 405-408.	0.9	0
71	Patterns of Variant Polyadenylation Signal Usage in Human Genes. Genome Research, 2000, 10, 1001-1010.	2.4	603
72	Predicting U-turns in Ribosomal RNA with Comparative Sequence Analysis. Journal of Molecular Biology, 2000, 300, 791-803.	2.0	85

#	ARTICLE	IF	CITATIONS
73	Determination of the rpoB gene sequences of Bartonella henselae and Bartonella quintana for phylogenetic analysis. Research in Microbiology, 2000, 151, 831-836.	1.0	13
74	Novel Selenoproteins Identified in Silico and in Vivo by Using a Conserved RNA Structural Motif. Journal of Biological Chemistry, 1999, 274, 38147-38154.	1.6	234
75	Quantitative Analysis of the T Cell Repertoire Selected by a Single Peptide-Major Histocompatibility Complex. Journal of Experimental Medicine, 1998, 187, 1871-1883.	4.2	43
76	Gene Structure, Expression Pattern, and Biological Activity of Mouse Killer Cell Activating Receptor-associated Protein (KARAP)/DAP-12. Journal of Biological Chemistry, 1998, 273, 34115-34119.	1.6	135
77	Alternate Polyadenylation in Human mRNAs: A Large-Scale Analysis by EST-Clustering. Genome Research, 1998, 8, 524-530.	2.4	117
78	No tRNA ^{3Lys} Unwinding in a Complex with HIV NCp7. Journal of Biological Chemistry, 1997, 272, 25143-25148.	1.6	26
79	Identification of Base-triples in RNA using Comparative Sequence Analysis. Journal of Molecular Biology, 1995, 248, 27-43.	2.0	76
80	An RNA pattern matching program with enhanced performance and portability. Bioinformatics, 1994, 10, 211-212.	1.8	40
81	A major family of motifs involving G ? A mismatches in ribosomal RNA. Journal of Molecular Biology, 1994, 242, 1-8.	2.0	126
82	Fitting the structurally diverse animal mitochondrial tRNA ^{Ser} to common three-dimensional constraints. Journal of Molecular Biology, 1994, 236, 982-989.	2.0	72
83	Modeling the Three-dimensional Structure of RNA Using Discrete Nucleotide Conformational Sets. Journal of Molecular Biology, 1993, 229, 1049-1064.	2.0	85
84	Modeling the three-dimensional structure of RNA.. FASEB Journal, 1993, 7, 97-105.	0.2	28
85	Pattern searching/alignment with RNA primary and secondary structures: an effective descriptor for tRNA. Bioinformatics, 1990, 6, 325-331.	1.8	62
86	Seeking RNA Motifs in Genomic Sequences. , 0, , 577-594.		1