Brian D Gregory

List of Publications by Year
in descending order

114 papers	10,215 citations	47006 47 h-index	37204 96 g-index
117 all docs	117 docs citations	117 times ranked	15205 citing authors

#	ARTICLE	IF	CITATIONS
1	KMT2A–MAML2 rearrangement emerged and regressed during neuroblastoma therapy without leukemia after 12.8‑year follow‑up. Pediatric Blood and Cancer, 2022, 69, e29344.	1.5	1
2	Data-Independent Acquisition for the Detection of Mononucleoside RNA Modifications by Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2022, 33, 885-893.	2.8	7
3	A Conserved Long Intergenic Non-coding RNA Containing snoRNA Sequences, lncCOBRA1, Affects Arabidopsis Germination and Development. Frontiers in Plant Science, 2022, 13, .	3.6	7
4	mRNA N^6‑methyladenosine is critical for cold tolerance in Arabidopsis. Plant Journal, 2022, 111, 1052-1068.	5.7	23
5	The impact of epitranscriptomic marks on post-transcriptional regulation in plants. Briefings in Functional Genomics, 2021, 20, 113-124.	2.7	16
6	Messenger RNA 5′ NAD+ Capping Is a Dynamic Regulatory Epitranscriptome Mark That Is Required for Proper Response to Abscisic Acid in Arabidopsis. Developmental Cell, 2021, 56, 125-140.e6.	7.0	40
7	Global Analysis of RNA-Dependent RNA Polymerase-Dependent Small RNAs Reveals New Substrates and Functions for These Proteins and SGS3 in Arabidopsis. Non-coding RNA, 2021, 7, 28.	2.6	10
8	The Epigenome and Beyond: How Does Non-genetic Inheritance Change Our View of Evolution?. Integrative and Comparative Biology, 2021, , .	2.0	5
9	Dynamic changes in RNA–protein interactions and RNA secondary structure in mammalian erythropoiesis. Life Science Alliance, 2021, 4, e202000659.	2.8	3
10	NAD-seq for profiling the NAD+ capped transcriptome of Arabidopsis thaliana. STAR Protocols, 2021, 2, 100901.	1.2	2
11	Elucidation of DNA methylation on N6-adenine with deep learning. Nature Machine Intelligence, 2020, 2, 466-475.	16.0	7
12	mRNA adenosine methylase (MTA) deposits m^{6}A on pri-miRNAs to modulate miRNA biogenesis in *Arabidopsis thaliana*. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21785-21795.	7.1	83
13	N^6‑methyladenosine and RNA secondary structure affect transcript stability and protein abundance during systemic salt stress in Arabidopsis. Plant Direct, 2020, 4, e00239.	1.9	41
14	HiPR: High-throughput probabilistic RNA structure inference. Computational and Structural Biotechnology Journal, 2020, 18, 1539-1547.	4.1	0
15	Electronic cigarette exposure disrupts blood-brain barrier integrity and promotes neuroinflammation. Brain, Behavior, and Immunity, 2020, 88, 363-380.	4.1	32
16	HIPPIE2: a method for fine-scale identification of physically interacting chromatin regions. NAR Genomics and Bioinformatics, 2020, 2, lqaa022.	3.2	2
17	Using RNA Affinity Purification Followed by Mass Spectrometry to Identify RNA-Binding Proteins (RBPs). Methods in Molecular Biology, 2020, 2166, 241-253.	0.9	4
18	Impact of poly(A)-tail G-content on Arabidopsis PAB binding and their role in enhancing translational efficiency. Genome Biology, 2019, 20, 189.	8.8	49

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19	Transcription Is Just the Beginning of Gene Expression Regulation: The Functional Significance of RNA-Binding Proteins to Post-transcriptional Processes in Plants. Plant and Cell Physiology, 2019, 60, 1939-1952.	3.1	24
20	Using Protein Interaction Profile Sequencing (PIP-seq) to Identify RNA Secondary Structure and RNAâ€"Protein Interaction Sites of Long Noncoding RNAs in Plants. Methods in Molecular Biology, 2019, 1933, 343-361.	0.9	6
21	Computationally Characterizing Protein-Bound Long Noncoding RNAs and Their Secondary Structure Using Protein Interaction Profile Sequencing (PIP-Seq) in Plants. Methods in Molecular Biology, 2019, 1933, 363-380.	0.9	4
22	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct, 2019, 3, e00109.	1.9	14
23	HAMR: High-Throughput Annotation of Modified Ribonucleotides. Methods in Molecular Biology, 2019, 1870, 51-67.	0.9	18
24	Read Mapping and Transcript Assembly: A Scalable and High-Throughput Workflow for the Processing and Analysis of Ribonucleic Acid Sequencing Data. Frontiers in Genetics, 2019, 10, 1361.	2.3	20
25	EPIC-CoGe: managing and analyzing genomic data. Bioinformatics, 2018, 34, 2651-2653.	4.1	33
26	Dysregulation of the epigenetic landscape of normal aging in Alzheimerâ€™s disease. Nature Neuroscience, 2018, 21, 497-505.	14.8	236
27	Differential Regulation of <i>LET-7</i> by LIN28B Isoformâ€"Specific Functions. Molecular Cancer Research, 2018, 16, 403-416.	3.4	13
28	N6-Methyladenosine Inhibits Local Ribonucleolytic Cleavage to Stabilize mRNAs in Arabidopsis. Cell Reports, 2018, 25, 1146-1157.e3.	6.4	175
29	IRE1B degrades RNAs encoding proteins that interfere with the induction of autophagy by ER stress in <i>Arabidopsis thaliana</i>. Autophagy, 2018, 14, 1562-1573.	9.1	66
30	Shedding some blue light on alternative promoter usage in plants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7654-7656.	7.1	7
31	Does RNA secondary structure drive translation or vice versa?. Nature Structural and Molecular Biology, 2018, 25, 641-643.	8.2	13
32	The LIN28Bâ€"IMP1 post-transcriptional regulon has opposing effects on oncogenic signaling in the intestine. Genes and Development, 2018, 32, 1020-1034.	5.9	20
33	New insights into the plant epitranscriptome. Journal of Experimental Botany, 2018, 69, 4659-4665.	4.8	30
34	Plant 24-nt reproductive phasiRNAs from intramolecular duplex mRNAs in diverse monocots. Genome Research, 2018, 28, 1333-1344.	5.5	49
35	PNPase knockout results in mtDNA loss and an altered metabolic gene expression program. PLoS ONE, 2018, 13, e0200925.	2.5	13
36	The nucleotides they are a-changinâ€™: function of RNA binding proteins in post-transcriptional messenger RNA editing and modification in Arabidopsis. Current Opinion in Plant Biology, 2018, 45, 88-95.	7.1	20

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37	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of <i>linc-ADAL</i> in adipocyte metabolism. Science Translational Medicine, 2018, 10, .	12.4	42
38	Nuclear m6A reader YTHDC1 regulates alternative polyadenylation and splicing during mouse oocyte development. PLoS Genetics, 2018, 14, e1007412.	3.5	386
39	The Macronuclear Genome of Stentor coeruleus Reveals Tiny Introns in a Giant Cell. Current Biology, 2017, 27, 569-575.	3.9	105
40	A Global View of RNA-Protein Interactions Identifies Post-transcriptional Regulators of Root Hair Cell Fate. Developmental Cell, 2017, 41, 204-220.e5.	7.0	53
41	Genome-wide TOP2A DNA cleavage is biased toward translocated and highly transcribed loci. Genome Research, 2017, 27, 1238-1249.	5.5	49
42	In Silico Identification of RNA Modifications from High-Throughput Sequencing Data Using HAMR. Methods in Molecular Biology, 2017, 1562, 211-229.	0.9	12
43	Global analysis of ribosome-associated noncoding RNAs unveils new modes of translational regulation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10018-E10027.	7.1	168
44	<scp>RNA</scp> structure, binding, and coordination in <i>Arabidopsis</i>. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1426.	6.4	14
45	Reading the Epitranscriptome. The Enzymes, 2017, 41, 269-298.	1.7	19
46	Chromatin dynamics during the differentiation of long-term hematopoietic stem cells to multipotent progenitors. Blood Advances, 2017, 1, 887-898.	5.2	17
47	Changes in the Transcriptome of Human Astrocytes Accompanying Oxidative Stress-Induced Senescence. Frontiers in Aging Neuroscience, 2016, 8, 208.	3.4	72
48	A comprehensive database of high-throughput sequencing-based RNA secondary structure probing data (Structure Surfer). BMC Bioinformatics, 2016, 17, 215.	2.6	17
49	Protein Interaction Profile Sequencing (PIPâ€seq). Current Protocols in Molecular Biology, 2016, 116, 27.5.1-27.5.15.	2.9	16
50	Genome-Wide Mapping of Uncapped and Cleaved Transcripts Reveals a Role for the Nuclear mRNA Cap-Binding Complex in Cotranslational RNA Decay in Arabidopsis. Plant Cell, 2016, 28, 2385-2397.	6.6	79
51	Loss of NAD Homeostasis Leads to Progressive and Reversible Degeneration of Skeletal Muscle. Cell Metabolism, 2016, 24, 269-282.	16.2	273
52	Protein Interaction Profile Sequencing (PIPâ€seq) in Plants. Current Protocols in Plant Biology, 2016, 1, 163-183.	2.8	3
53	Genome-Wide Approaches for RNA Structure Probing. Advances in Experimental Medicine and Biology, 2016, 907, 29-59.	1.6	16
54	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic Toxoplasma gondii genomes. Nature Communications, 2016, 7, 10147.	12.8	243

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55	Global Transcriptional Profiling of Diapause and Climatic Adaptation in <i>Drosophila melanogaster</i>. Molecular Biology and Evolution, 2016, 33, 707-720.	8.9	59
56	Cytoplasmic poly(A) binding protein-1 binds to genomically encoded sequences within mammalian mRNAs. Rna, 2016, 22, 61-74.	3.5	44
57	DASHR: database of small human noncoding RNAs. Nucleic Acids Research, 2016, 44, D216-D222.	14.5	74
58	Terpene metabolic engineering <i>via</i> nuclear or chloroplast genomes profoundly and globally impacts offâ€target pathways through metabolite signalling. Plant Biotechnology Journal, 2016, 14, 1862-1875.	8.3	29
59	The Conservation and Function of RNA Secondary Structure in Plants. Annual Review of Plant Biology, 2016, 67, 463-488.	18.7	74
60	The Msi Family of RNA-Binding Proteins Function Redundantly as Intestinal Oncoproteins. Cell Reports, 2015, 13, 2440-2455.	6.4	88
61	Chemical Modifications Mark Alternatively Spliced and Uncapped Messenger RNAs in Arabidopsis. Plant Cell, 2015, 27, 3024-3037.	6.6	42
62	Global Analysis of the RNA-Protein Interaction and RNA Secondary Structure Landscapes of the Arabidopsis Nucleus. Molecular Cell, 2015, 57, 376-388.	9.7	105
63	Transcriptome-wide ribonuclease-mediated protein footprinting to identify RNAâ€"protein interaction sites. Methods, 2015, 72, 76-85.	3.8	12
64	Transcriptome-wide measurement of plant RNA secondary structure. Current Opinion in Plant Biology, 2015, 27, 36-43.	7.1	14
65	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. Genes and Development, 2015, 29, 1362-1376.	5.9	196
66	Essential Role for Endogenous siRNAs during Meiosis in Mouse Oocytes. PLoS Genetics, 2015, 11, e1005013.	3.5	97
67	Functional Analysis and Transcriptomic Profiling of iPSC-Derived Macrophages and Their Application in Modeling Mendelian Disease. Circulation Research, 2015, 117, 17-28.	4.5	120
68	Transformation of the intestinal epithelium by the MSI2 RNA-binding protein. Nature Communications, 2015, 6, 6517.	12.8	110
69	The long noncoding RNA landscape in hypoxic and inflammatory renal epithelial injury. American Journal of Physiology - Renal Physiology, 2015, 309, F901-F913.	2.7	70
70	Detection of Pol IV/RDR2-dependent transcripts at the genomic scale in <i>Arabidopsis</i> reveals features and regulation of siRNA biogenesis. Genome Research, 2015, 25, 235-245.	5.5	143
71	HIPPIE: a high-throughput identification pipeline for promoter interacting enhancer elements. Bioinformatics, 2015, 31, 1290-1292.	4.1	52
72	Transcriptomic Changes Due to Cytoplasmic TDP-43 Expression Reveal Dysregulation of Histone Transcripts and Nuclear Chromatin. PLoS ONE, 2015, 10, e0141836.	2.5	40

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73	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose LincRNA Signatures of Cardiometabolic Diseases. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 902-912.	2.4	75
74	Paternal Poly (ADP-ribose) Metabolism Modulates Retention of Inheritable Sperm Histones and Early Embryonic Gene Expression. PLoS Genetics, 2014, 10, e1004317.	3.5	72
75	RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome. Genome Biology, 2014, 15, R3.	9.6	76
76	Using machine learning and high-throughput RNA sequencing to classify the precursors of small non-coding RNAs. Methods, 2014, 67, 28-35.	3.8	12
77	Improved genome-wide mapping of uncapped and cleaved transcripts in eukaryotesâ€"GMUCT 2.0. Methods, 2014, 67, 64-73.	3.8	48
78	Inactivation of Yeast Isw2 Chromatin Remodeling Enzyme Mimics Longevity Effect of Calorie Restriction via Induction of Genotoxic Stress Response. Cell Metabolism, 2014, 19, 952-966.	16.2	69
79	A MicroRNA Precursor Surveillance System in Quality Control of MicroRNA Synthesis. Molecular Cell, 2014, 55, 868-879.	9.7	74
80	Genomic approaches for studying transcriptional and post-transcriptional processes. Methods, 2014, 67, 1-2.	3.8	0
81	<scp>RNA</scp> polymerase <scp>V</scp> targets transcriptional silencing components to promoters of proteinâ€coding genes. Plant Journal, 2013, 73, 179-189.	5.7	61
82	Genomic era analyses of RNA secondary structure and RNA-binding proteins reveal their significance to post-transcriptional regulation in plants. Plant Science, 2013, 205-206, 55-62.	3.6	45
83	CoRAL: predicting non-coding RNAs from small RNA-sequencing data. Nucleic Acids Research, 2013, 41, e137-e137.	14.5	26
84	HAMR: high-throughput annotation of modified ribonucleotides. Rna, 2013, 19, 1684-1692.	3.5	125
85	Lamin B1 depletion in senescent cells triggers large-scale changes in gene expression and the chromatin landscape. Genes and Development, 2013, 27, 1787-1799.	5.9	440
86	High-throughput identification of long-range regulatory elements and their target promoters in the human genome. Nucleic Acids Research, 2013, 41, 4835-4846.	14.5	26
87	ArabidopsismRNA secondary structure correlates with protein function and domains. Plant Signaling and Behavior, 2013, 8, e24301.	2.4	18
88	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. PLoS ONE, 2013, 8, e66883.	2.5	60
89	Analysis of the Host Transcriptome from Demyelinating Spinal Cord of Murine Coronavirus-Infected Mice. PLoS ONE, 2013, 8, e75346.	2.5	34
90	Dicer-2 Processes Diverse Viral RNA Species. PLoS ONE, 2013, 8, e55458.	2.5	101

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91	Regulatory Impact of RNA Secondary Structure across the *Arabidopsis* Transcriptome. Plant Cell, 2012, 24, 4346-4359.	6.6	124
92	SAVoR: a server for sequencing annotation and visualization of RNA structures. Nucleic Acids Research, 2012, 40, W59-W64.	14.5	14
93	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the *Arabidopsis* epigenome. Genes and Development, 2012, 26, 1825-1836.	5.9	137
94	Global Analysis of RNA Secondary Structure in Two Metazoans. Cell Reports, 2012, 1, 69-82.	6.4	126
95	Mili and Miwi target RNA repertoire reveals piRNA biogenesis and function of Miwi in spermiogenesis. Nature Structural and Molecular Biology, 2012, 19, 773-781.	8.2	221
96	Invited: Multiclass RNA function classification using next-generation sequencing. , 2011, , .		0
97	The Functions of RNA-Dependent RNA Polymerases in Arabidopsis. The Arabidopsis Book, 2011, 9, e0146.	0.5	122
98	A High-Throughput Sequencing-Based Methodology to Identify All Uncapped and Cleaved RNA Molecules in Eukaryotic Genomes. Methods in Molecular Biology, 2011, 732, 209-223.	0.9	8
99	Two Plant Viral Suppressors of Silencing Require the Ethylene-Inducible Host Transcription Factor RAV2 to Block RNA Silencing. PLoS Pathogens, 2010, 6, e1000729.	4.7	124
100	Genome-Wide Double-Stranded RNA Sequencing Reveals the Functional Significance of Base-Paired RNAs in Arabidopsis. PLoS Genetics, 2010, 6, e1001141.	3.5	127
101	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. Current Opinion in Plant Biology, 2009, 12, 107-118.	7.1	261
102	Whole-Genome Microarrays: Applications and Technical Issues. Methods in Molecular Biology, 2009, 553, 39-56.	0.9	9
103	Utilizing tiling microarrays for whole€genome analysis in plants. Plant Journal, 2008, 53, 636-644.	5.7	44
104	Rsd family proteins make simultaneous interactions with regions 2 and 4 of the primary sigma factor. Molecular Microbiology, 2008, 70, 1136-1151.	2.5	36
105	Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis. Cell, 2008, 133, 523-536.	28.9	2,229
106	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. Developmental Cell, 2008, 14, 854-866.	7.0	394
107	Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the Arabidopsis Transcriptome. Cell, 2007, 131, 1340-1353.	28.9	298
108	Mapping the genome landscape using tiling array technology. Current Opinion in Plant Biology, 2007, 10, 534-542.	7.1	61

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109	ETHYLENE-INSENSITIVE5 encodes a 5'->3' exoribonuclease required for regulation of the EIN3-targeting F-box proteins EBF1/2. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13286-13293.	7.1	163
110	An altered-specificity DNA-binding mutant of Escherichia coliÏƒ70 facilitates the analysis of Ïƒ70 function in vivo. Molecular Microbiology, 2005, 56, 1208-1219.	2.5	22
111	An Artificial Activator that Contacts a Normally Occluded Surface of the RNA Polymerase Holoenzyme. Journal of Molecular Biology, 2005, 353, 497-506.	4.2	6
112	A Family of Anti-Ïƒ70 Proteins in T4-type Phages and Bacteria that are Similar to AsiA, a Transcription Inhibitor and Co-activator of Bacteriophage T4. Journal of Molecular Biology, 2004, 344, 1183-1197.	4.2	33
113	The Arabidopsis dwarf1 Mutant Is Defective in the Conversion of 24-Methylenecholesterol to Campesterol in Brassinosteroid Biosynthesis1. Plant Physiology, 1999, 119, 897-908.	4.8	227
114	Messenger RNA 5â€™ NAD+ Capping is a Dynamic Regulatory Epitranscriptome Mark that is Required for Proper Response to Abscisic Acid in Arabidopsis. SSRN Electronic Journal, 0, , .	0.4	1