

Brian D Gregory

List of Publications by Year in descending order

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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	Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis. <i>Cell</i> , 2008, 133, 523-536.	28.9	2,229
2	Lamin B1 depletion in senescent cells triggers large-scale changes in gene expression and the chromatin landscape. <i>Genes and Development</i> , 2013, 27, 1787-1799.	5.9	440
3	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	7.0	394
4	Nuclear m6A reader YTHDC1 regulates alternative polyadenylation and splicing during mouse oocyte development. <i>PLoS Genetics</i> , 2018, 14, e1007412.	3.5	386
5	Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the Arabidopsis Transcriptome. <i>Cell</i> , 2007, 131, 1340-1353.	28.9	298
6	Loss of NAD Homeostasis Leads to Progressive and Reversible Degeneration of Skeletal Muscle. <i>Cell Metabolism</i> , 2016, 24, 269-282.	16.2	273
7	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. <i>Current Opinion in Plant Biology</i> , 2009, 12, 107-118.	7.1	261
8	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic <i>Toxoplasma gondii</i> genomes. <i>Nature Communications</i> , 2016, 7, 10147.	12.8	243
9	Dysregulation of the epigenetic landscape of normal aging in Alzheimer's disease. <i>Nature Neuroscience</i> , 2018, 21, 497-505.	14.8	236
10	The Arabidopsis dwarf1 Mutant Is Defective in the Conversion of 24-Methylenecholesterol to Campesterol in Brassinosteroid Biosynthesis1. <i>Plant Physiology</i> , 1999, 119, 897-908.	4.8	227
11	Mili and Miwi target RNA repertoire reveals piRNA biogenesis and function of Miwi in spermiogenesis. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 773-781.	8.2	221
12	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. <i>Genes and Development</i> , 2015, 29, 1362-1376.	5.9	196
13	N6-Methyladenosine Inhibits Local Ribonucleolytic Cleavage to Stabilize mRNAs in Arabidopsis. <i>Cell Reports</i> , 2018, 25, 1146-1157.e3.	6.4	175
14	Global analysis of ribosome-associated noncoding RNAs unveils new modes of translational regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10018-E10027.	7.1	168
15	ETHYLENE-INSENSITIVE5 encodes a 5'→3' exoribonuclease required for regulation of the EIN3-targeting F-box proteins EBF1/2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13286-13293.	7.1	163
16	Detection of Pol IV/RDR2-dependent transcripts at the genomic scale in <i>Arabidopsis</i> reveals features and regulation of siRNA biogenesis. <i>Genome Research</i> , 2015, 25, 235-245.	5.5	143
17	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the <i>Arabidopsis</i> epigenome. <i>Genes and Development</i> , 2012, 26, 1825-1836.	5.9	137
18	Genome-Wide Double-Stranded RNA Sequencing Reveals the Functional Significance of Base-Paired RNAs in Arabidopsis. <i>PLoS Genetics</i> , 2010, 6, e1001141.	3.5	127

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19	Global Analysis of RNA Secondary Structure in Two Metazoans. <i>Cell Reports</i> , 2012, 1, 69-82.	6.4	126
20	HAMR: high-throughput annotation of modified ribonucleotides. <i>Rna</i> , 2013, 19, 1684-1692.	3.5	125
21	Two Plant Viral Suppressors of Silencing Require the Ethylene-Inducible Host Transcription Factor RAV2 to Block RNA Silencing. <i>PLoS Pathogens</i> , 2010, 6, e1000729.	4.7	124
22	Regulatory Impact of RNA Secondary Structure across the <i>Arabidopsis</i> Transcriptome. <i>Plant Cell</i> , 2012, 24, 4346-4359.	6.6	124
23	The Functions of RNA-Dependent RNA Polymerases in <i>Arabidopsis</i> . <i>The Arabidopsis Book</i> , 2011, 9, e0146.	0.5	122
24	Functional Analysis and Transcriptomic Profiling of iPSC-Derived Macrophages and Their Application in Modeling Mendelian Disease. <i>Circulation Research</i> , 2015, 117, 17-28.	4.5	120
25	Transformation of the intestinal epithelium by the MSI2 RNA-binding protein. <i>Nature Communications</i> , 2015, 6, 6517.	12.8	110
26	Global Analysis of the RNA-Protein Interaction and RNA Secondary Structure Landscapes of the <i>Arabidopsis</i> Nucleus. <i>Molecular Cell</i> , 2015, 57, 376-388.	9.7	105
27	The Macronuclear Genome of <i>Stentor coeruleus</i> Reveals Tiny Introns in a Giant Cell. <i>Current Biology</i> , 2017, 27, 569-575.	3.9	105
28	Dicer-2 Processes Diverse Viral RNA Species. <i>PLoS ONE</i> , 2013, 8, e55458.	2.5	101
29	Essential Role for Endogenous siRNAs during Meiosis in Mouse Oocytes. <i>PLoS Genetics</i> , 2015, 11, e1005013.	3.5	97
30	The Msi Family of RNA-Binding Proteins Function Redundantly as Intestinal Oncoproteins. <i>Cell Reports</i> , 2015, 13, 2440-2455.	6.4	88
31	mRNA adenosine methylase (MTA) deposits m ⁶ A on pri-miRNAs to modulate miRNA biogenesis in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21785-21795.	7.1	83
32	Genome-Wide Mapping of Uncapped and Cleaved Transcripts Reveals a Role for the Nuclear mRNA Cap-Binding Complex in Cotranslational RNA Decay in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2016, 28, 2385-2397.	6.6	79
33	RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome. <i>Genome Biology</i> , 2014, 15, R3.	9.6	76
34	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose lincRNA Signatures of Cardiometabolic Diseases. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 902-912.	2.4	75
35	A MicroRNA Precursor Surveillance System in Quality Control of MicroRNA Synthesis. <i>Molecular Cell</i> , 2014, 55, 868-879.	9.7	74
36	DASHR: database of small human noncoding RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D216-D222.	14.5	74

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37	The Conservation and Function of RNA Secondary Structure in Plants. <i>Annual Review of Plant Biology</i> , 2016, 67, 463-488.	18.7	74
38	Paternal Poly (ADP-ribose) Metabolism Modulates Retention of Inheritable Sperm Histones and Early Embryonic Gene Expression. <i>PLoS Genetics</i> , 2014, 10, e1004317.	3.5	72
39	Changes in the Transcriptome of Human Astrocytes Accompanying Oxidative Stress-Induced Senescence. <i>Frontiers in Aging Neuroscience</i> , 2016, 8, 208.	3.4	72
40	The long noncoding RNA landscape in hypoxic and inflammatory renal epithelial injury. <i>American Journal of Physiology - Renal Physiology</i> , 2015, 309, F901-F913.	2.7	70
41	Inactivation of Yeast Isw2 Chromatin Remodeling Enzyme Mimics Longevity Effect of Calorie Restriction via Induction of Genotoxic Stress Response. <i>Cell Metabolism</i> , 2014, 19, 952-966.	16.2	69
42	IRE1B degrades RNAs encoding proteins that interfere with the induction of autophagy by ER stress in <i>Arabidopsis thaliana</i> . <i>Autophagy</i> , 2018, 14, 1562-1573.	9.1	66
43	Mapping the genome landscape using tiling array technology. <i>Current Opinion in Plant Biology</i> , 2007, 10, 534-542.	7.1	61
44	RNA polymerase V targets transcriptional silencing components to promoters of protein-coding genes. <i>Plant Journal</i> , 2013, 73, 179-189.	5.7	61
45	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. <i>PLoS ONE</i> , 2013, 8, e66883.	2.5	60
46	Global Transcriptional Profiling of Diapause and Climatic Adaptation in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 707-720.	8.9	59
47	A Global View of RNA-Protein Interactions Identifies Post-transcriptional Regulators of Root Hair Cell Fate. <i>Developmental Cell</i> , 2017, 41, 204-220.e5.	7.0	53
48	HIPPIE: a high-throughput identification pipeline for promoter interacting enhancer elements. <i>Bioinformatics</i> , 2015, 31, 1290-1292.	4.1	52
49	Genome-wide TOP2A DNA cleavage is biased toward translocated and highly transcribed loci. <i>Genome Research</i> , 2017, 27, 1238-1249.	5.5	49
50	Plant 24-nt reproductive phasiRNAs from intramolecular duplex mRNAs in diverse monocots. <i>Genome Research</i> , 2018, 28, 1333-1344.	5.5	49
51	Impact of poly(A)-tail G-content on Arabidopsis PAB binding and their role in enhancing translational efficiency. <i>Genome Biology</i> , 2019, 20, 189.	8.8	49
52	Improved genome-wide mapping of uncapped and cleaved transcripts in eukaryotes—GMUCT 2.0. <i>Methods</i> , 2014, 67, 64-73.	3.8	48
53	Genomic era analyses of RNA secondary structure and RNA-binding proteins reveal their significance to post-transcriptional regulation in plants. <i>Plant Science</i> , 2013, 205-206, 55-62.	3.6	45
54	Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , 2008, 53, 636-644.	5.7	44

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55	Cytoplasmic poly(A) binding protein-1 binds to genomically encoded sequences within mammalian mRNAs. <i>Rna</i> , 2016, 22, 61-74.	3.5	44
56	Chemical Modifications Mark Alternatively Spliced and Uncapped Messenger RNAs in Arabidopsis. <i>Plant Cell</i> , 2015, 27, 3024-3037.	6.6	42
57	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of <i>linc-ADAL</i> in adipocyte metabolism. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	42
58	N ⁶ -methyladenosine and RNA secondary structure affect transcript stability and protein abundance during systemic salt stress in Arabidopsis. <i>Plant Direct</i> , 2020, 4, e00239.	1.9	41
59	Messenger RNA 5 ² NAD ⁺ Capping Is a Dynamic Regulatory Epitranscriptome Mark That Is Required for Proper Response to Abscisic Acid in Arabidopsis. <i>Developmental Cell</i> , 2021, 56, 125-140.e6.	7.0	40
60	Transcriptomic Changes Due to Cytoplasmic TDP-43 Expression Reveal Dysregulation of Histone Transcripts and Nuclear Chromatin. <i>PLoS ONE</i> , 2015, 10, e0141836.	2.5	40
61	Rsd family proteins make simultaneous interactions with regions 2 and 4 of the primary sigma factor. <i>Molecular Microbiology</i> , 2008, 70, 1136-1151.	2.5	36
62	Analysis of the Host Transcriptome from Demyelinating Spinal Cord of Murine Coronavirus-Infected Mice. <i>PLoS ONE</i> , 2013, 8, e75346.	2.5	34
63	A Family of Anti- σ 70 Proteins in T4-type Phages and Bacteria that are Similar to AsiA, a Transcription Inhibitor and Co-activator of Bacteriophage T4. <i>Journal of Molecular Biology</i> , 2004, 344, 1183-1197.	4.2	33
64	EPIC-CoGe: managing and analyzing genomic data. <i>Bioinformatics</i> , 2018, 34, 2651-2653.	4.1	33
65	Electronic cigarette exposure disrupts blood-brain barrier integrity and promotes neuroinflammation. <i>Brain, Behavior, and Immunity</i> , 2020, 88, 363-380.	4.1	32
66	New insights into the plant epitranscriptome. <i>Journal of Experimental Botany</i> , 2018, 69, 4659-4665.	4.8	30
67	Terpene metabolic engineering <i>via</i> nuclear or chloroplast genomes profoundly and globally impacts off-target pathways through metabolite signalling. <i>Plant Biotechnology Journal</i> , 2016, 14, 1862-1875.	8.3	29
68	CoRAL: predicting non-coding RNAs from small RNA-sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e137-e137.	14.5	26
69	High-throughput identification of long-range regulatory elements and their target promoters in the human genome. <i>Nucleic Acids Research</i> , 2013, 41, 4835-4846.	14.5	26
70	Transcription Is Just the Beginning of Gene Expression Regulation: The Functional Significance of RNA-Binding Proteins to Post-transcriptional Processes in Plants. <i>Plant and Cell Physiology</i> , 2019, 60, 1939-1952.	3.1	24
71	<i>scp</i> mRNA N ⁶ -methyladenosine is critical for cold tolerance in Arabidopsis. <i>Plant Journal</i> , 2022, 111, 1052-1068.	5.7	23
72	An altered-specificity DNA-binding mutant of <i>Escherichia coli</i> σ 70 facilitates the analysis of σ 70 function <i>in vivo</i> . <i>Molecular Microbiology</i> , 2005, 56, 1208-1219.	2.5	22

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73	The LIN28Bâ€“IMP1 post-transcriptional regulon has opposing effects on oncogenic signaling in the intestine. <i>Genes and Development</i> , 2018, 32, 1020-1034.	5.9	20
74	The nucleotides they are a-changinâ€™™: function of RNA binding proteins in post-transcriptional messenger RNA editing and modification in Arabidopsis. <i>Current Opinion in Plant Biology</i> , 2018, 45, 88-95.	7.1	20
75	Read Mapping and Transcript Assembly: A Scalable and High-Throughput Workflow for the Processing and Analysis of Ribonucleic Acid Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 1361.	2.3	20
76	Reading the Epitranscriptome. <i>The Enzymes</i> , 2017, 41, 269-298.	1.7	19
77	Arabidopsis mRNA secondary structure correlates with protein function and domains. <i>Plant Signaling and Behavior</i> , 2013, 8, e24301.	2.4	18
78	HAMR: High-Throughput Annotation of Modified Ribonucleotides. <i>Methods in Molecular Biology</i> , 2019, 1870, 51-67.	0.9	18
79	A comprehensive database of high-throughput sequencing-based RNA secondary structure probing data (Structure Surfer). <i>BMC Bioinformatics</i> , 2016, 17, 215.	2.6	17
80	Chromatin dynamics during the differentiation of long-term hematopoietic stem cells to multipotent progenitors. <i>Blood Advances</i> , 2017, 1, 887-898.	5.2	17
81	Protein Interaction Profile Sequencing (PIPâ€™seq). <i>Current Protocols in Molecular Biology</i> , 2016, 116, 27.5.1-27.5.15.	2.9	16
82	Genome-Wide Approaches for RNA Structure Probing. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 29-59.	1.6	16
83	The impact of epitranscriptomic marks on post-transcriptional regulation in plants. <i>Briefings in Functional Genomics</i> , 2021, 20, 113-124.	2.7	16
84	SAVoR: a server for sequencing annotation and visualization of RNA structures. <i>Nucleic Acids Research</i> , 2012, 40, W59-W64.	14.5	14
85	Transcriptome-wide measurement of plant RNA secondary structure. <i>Current Opinion in Plant Biology</i> , 2015, 27, 36-43.	7.1	14
86	<scp>RNA</scp> structure, binding, and coordination in <i>Arabidopsis</i>. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1426.	6.4	14
87	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	1.9	14
88	Differential Regulation of <i>LET-7</i> by LIN28B Isoformâ€™™-Specific Functions. <i>Molecular Cancer Research</i> , 2018, 16, 403-416.	3.4	13
89	Does RNA secondary structure drive translation or vice versa?. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 641-643.	8.2	13
90	PNPase knockout results in mtDNA loss and an altered metabolic gene expression program. <i>PLoS ONE</i> , 2018, 13, e0200925.	2.5	13

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91	Using machine learning and high-throughput RNA sequencing to classify the precursors of small non-coding RNAs. <i>Methods</i> , 2014, 67, 28-35.	3.8	12
92	Transcriptome-wide ribonuclease-mediated protein footprinting to identify RNA-protein interaction sites. <i>Methods</i> , 2015, 72, 76-85.	3.8	12
93	In Silico Identification of RNA Modifications from High-Throughput Sequencing Data Using HAMR. <i>Methods in Molecular Biology</i> , 2017, 1562, 211-229.	0.9	12
94	Global Analysis of RNA-Dependent RNA Polymerase-Dependent Small RNAs Reveals New Substrates and Functions for These Proteins and SGS3 in Arabidopsis. <i>Non-coding RNA</i> , 2021, 7, 28.	2.6	10
95	Whole-Genome Microarrays: Applications and Technical Issues. <i>Methods in Molecular Biology</i> , 2009, 553, 39-56.	0.9	9
96	A High-Throughput Sequencing-Based Methodology to Identify All Uncapped and Cleaved RNA Molecules in Eukaryotic Genomes. <i>Methods in Molecular Biology</i> , 2011, 732, 209-223.	0.9	8
97	Shedding some blue light on alternative promoter usage in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7654-7656.	7.1	7
98	Elucidation of DNA methylation on N6-adenine with deep learning. <i>Nature Machine Intelligence</i> , 2020, 2, 466-475.	16.0	7
99	Data-Independent Acquisition for the Detection of Mononucleoside RNA Modifications by Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 885-893.	2.8	7
100	A Conserved Long Intergenic Non-coding RNA Containing snoRNA Sequences, IncCOBRA1, Affects Arabidopsis Germination and Development. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	7
101	An Artificial Activator that Contacts a Normally Occluded Surface of the RNA Polymerase Holoenzyme. <i>Journal of Molecular Biology</i> , 2005, 353, 497-506.	4.2	6
102	Using Protein Interaction Profile Sequencing (PIP-seq) to Identify RNA Secondary Structure and RNA-Protein Interaction Sites of Long Noncoding RNAs in Plants. <i>Methods in Molecular Biology</i> , 2019, 1933, 343-361.	0.9	6
103	The Epigenome and Beyond: How Does Non-genetic Inheritance Change Our View of Evolution?. <i>Integrative and Comparative Biology</i> , 2021, , .	2.0	5
104	Computationally Characterizing Protein-Bound Long Noncoding RNAs and Their Secondary Structure Using Protein Interaction Profile Sequencing (PIP-Seq) in Plants. <i>Methods in Molecular Biology</i> , 2019, 1933, 363-380.	0.9	4
105	Using RNA Affinity Purification Followed by Mass Spectrometry to Identify RNA-Binding Proteins (RBPs). <i>Methods in Molecular Biology</i> , 2020, 2166, 241-253.	0.9	4
106	Protein Interaction Profile Sequencing (PIP-seq) in Plants. <i>Current Protocols in Plant Biology</i> , 2016, 1, 163-183.	2.8	3
107	Dynamic changes in RNA-protein interactions and RNA secondary structure in mammalian erythropoiesis. <i>Life Science Alliance</i> , 2021, 4, e202000659.	2.8	3
108	HIPPIE2: a method for fine-scale identification of physically interacting chromatin regions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa022.	3.2	2

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109	NAD-seq for profiling the NAD ⁺ capped transcriptome of Arabidopsis thaliana. STAR Protocols, 2021, 2, 100901.	1.2	2
110	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
111	Messenger RNA 5' 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
112	Invited: Multiclass RNA function classification using next-generation sequencing. , 2011, , .		0
113	Genomic approaches for studying transcriptional and post-transcriptional processes. Methods, 2014, 67, 1-2.	3.8	0
114	HiPR: High-throughput probabilistic RNA structure inference. Computational and Structural Biotechnology Journal, 2020, 18, 1539-1547.	4.1	0