

# Gregory R Grant

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2461382/publications.pdf>

Version: 2024-02-01

71  
papers

6,527  
citations

94433

37  
h-index

88630

70  
g-index

75  
all docs

75  
docs citations

75  
times ranked

12121  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nitecap: An Exploratory Circadian Analysis Web Application. <i>Journal of Biological Rhythms</i> , 2022, 37, 43-52.	2.6	18
2	Time-specific associations of wearable sensor-based cardiovascular and behavioral readouts with disease phenotypes in the outpatient setting of the Chronic Renal Insufficiency Cohort. <i>Digital Health</i> , 2022, 8, 205520762211079.	1.8	4
3	Accounting for Time: Circadian Rhythms in the Time of COVID-19. <i>Journal of Biological Rhythms</i> , 2021, 36, 4-8.	2.6	16
4	Comparative evaluation of full-length isoform quantification from RNA-Seq. <i>BMC Bioinformatics</i> , 2021, 22, 266.	2.6	15
5	MOCCASIN: a method for correcting for known and unknown confounders in RNA splicing analysis. <i>Nature Communications</i> , 2021, 12, 3353.	12.8	12
6	Sex-dependent compensatory mechanisms preserve blood pressure homeostasis in prostacyclin receptor-deficient mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	1
7	CAMPAREE: a robust and configurable RNA expression simulator. <i>BMC Genomics</i> , 2021, 22, 692.	2.8	2
8	Considerations for the Safe Operation of Schools During the Coronavirus Pandemic. <i>Frontiers in Public Health</i> , 2021, 9, 751451.	2.7	9
9	RNA-seq analysis of galaninergic neurons from ventrolateral preoptic nucleus identifies expression changes between sleep and wake. <i>BMC Genomics</i> , 2020, 21, 633.	2.8	2
10	Age attenuates the transcriptional changes that occur with sleep in the medial prefrontal cortex. <i>Aging Cell</i> , 2019, 18, e13021.	6.7	18
11	Circadian control of lung inflammation in influenza infection. <i>Nature Communications</i> , 2019, 10, 4107.	12.8	106
12	Comparative evaluation of RNA-Seq library preparation methods for strand-specificity and low input. <i>Scientific Reports</i> , 2019, 9, 13477.	3.3	22
13	A specific sequence in the genome of respiratory syncytial virus regulates the generation of copy-back defective viral genomes. <i>PLoS Pathogens</i> , 2019, 15, e1007707.	4.7	33
14	Variability in the Analgesic Response to Ibuprofen Is Associated With Cyclooxygenase Activation in Inflammatory Pain. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 632-641.	4.7	21
15	Distinct vascular genomic response of proton and gamma radiation—a pilot investigation. <i>PLoS ONE</i> , 2019, 14, e0207503.	2.5	4
16	Complete Transcriptome Profiling of Normal and Age-Related Macular Degeneration Eye Tissues Reveals Dysregulation of Anti-Sense Transcription. <i>Scientific Reports</i> , 2018, 8, 3040.	3.3	46
17	Outlier detection for improved differential splicing quantification from RNA-Seq experiments with replicates. <i>Bioinformatics</i> , 2018, 34, 1488-1497.	4.1	35
18	Overlap in signaling between Smoothed and the $\beta$ subunit of the heterotrimeric G protein G13. <i>PLoS ONE</i> , 2018, 13, e0197442.	2.5	3

#	ARTICLE	IF	CITATIONS
19	Lipocalin-Like Prostaglandin D Synthase but Not Hemopoietic Prostaglandin D Synthase Deletion Causes Hypertension and Accelerates Thrombogenesis in Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2018, 367, 425-432.	2.5	26
20	SAP97 regulates behavior and expression of schizophrenia risk enriched gene sets in mouse hippocampus. <i>PLoS ONE</i> , 2018, 13, e0200477.	2.5	15
21	Spliceosome factors target timeless (tim) mRNA to control clock protein accumulation and circadian behavior in <i>Drosophila</i> . <i>ELife</i> , 2018, 7, .	6.0	30
22	Characterizing the "POAGome": A bioinformatics-driven approach to primary open-angle glaucoma. <i>Progress in Retinal and Eye Research</i> , 2017, 58, 89-114.	15.5	57
23	Transcriptional and Cell Cycle Alterations Mark Aging of Primary Human Adipose-Derived Stem Cells. <i>Stem Cells</i> , 2017, 35, 1392-1401.	3.2	16
24	Simulation-based comprehensive benchmarking of RNA-seq aligners. <i>Nature Methods</i> , 2017, 14, 135-139.	19.0	229
25	Mitotic transcription and waves of gene reactivation during mitotic exit. <i>Science</i> , 2017, 358, 119-122.	12.6	201
26	Sleep restriction induced energy, methylation and lipogenesis metabolic switches in rat liver. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 93, 129-135.	2.8	25
27	A Pilot Characterization of the Human Chronobiome. <i>Scientific Reports</i> , 2017, 7, 17141.	3.3	70
28	A comparison of Illumina and Ion Torrent sequencing platforms in the context of differential gene expression. <i>BMC Genomics</i> , 2017, 18, 602.	2.8	57
29	Histone posttranslational modifications predict specific alternative exon subtypes in mammalian brain. <i>PLoS Computational Biology</i> , 2017, 13, e1005602.	3.2	23
30	Cardiovascular Consequences of Prostanoid I Receptor Deletion in Microsomal Prostaglandin E Synthase-1 Deficient Hyperlipidemic Mice. <i>Circulation</i> , 2016, 134, 328-338.	1.6	19
31	Investigation of the functional role of human Interleukin-8 gene haplotypes by CRISPR/Cas9 mediated genome editing. <i>Scientific Reports</i> , 2016, 6, 31180.	3.3	35
32	Timing of expression of the core clock gene <i>Bmal1</i> influences its effects on aging and survival. <i>Science Translational Medicine</i> , 2016, 8, 324ra16.	12.4	249
33	A broad-spectrum lipidomics screen of antiinflammatory drug combinations in human blood. <i>JCI Insight</i> , 2016, 1, .	5.0	33
34	Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. <i>Bioinformatics</i> , 2015, 31, 3938-3945.	4.1	90
35	Considerations for RNA-seq Analysis of Circadian Rhythms. <i>Methods in Enzymology</i> , 2015, 551, 349-367.	1.0	68
36	Detection Theory in Identification of RNA-DNA Sequence Differences Using RNA-Sequencing. <i>PLoS ONE</i> , 2014, 9, e112040.	2.5	7

#	ARTICLE	IF	CITATIONS
37	Myeloid Cell COX-2 deletion reduces mammary tumor growth through enhanced cytotoxic T-lymphocyte function. <i>Carcinogenesis</i> , 2014, 35, 1788-1797.	2.8	41
38	Erythropoietin Upregulation in Pulmonary Arterial Hypertension. <i>Pulmonary Circulation</i> , 2014, 4, 269-279.	1.7	18
39	IVT-seq reveals extreme bias in RNA sequencing. <i>Genome Biology</i> , 2014, 15, R86.	9.6	134
40	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	19.0	467
41	Cell Selective Cardiovascular Biology of Microsomal Prostaglandin E Synthase-1. <i>Circulation</i> , 2013, 127, 233-243.	1.6	42
42	Drug Resistance and Pseudoresistance. <i>Circulation</i> , 2013, 127, 377-385.	1.6	187
43	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. <i>BMC Genomics</i> , 2013, 14, 486.	2.8	151
44	Response to Letters Regarding Article, "Drug Resistance and Pseudoresistance: An Unintended Consequence of Enteric Coating Aspirin". <i>Circulation</i> , 2013, 128, e191.	1.6	0
45	Transcriptional Pausing Controls a Rapid Antiviral Innate Immune Response in <i>Drosophila</i> . <i>Cell Host and Microbe</i> , 2012, 12, 531-543.	11.0	78
46	Obesity in mice with adipocyte-specific deletion of clock component Arntl. <i>Nature Medicine</i> , 2012, 18, 1768-1777.	30.7	370
47	Deep sequencing the circadian and diurnal transcriptome of <i>Drosophila</i> brain. <i>Genome Research</i> , 2012, 22, 1266-1281.	5.5	155
48	Vascular COX-2 Modulates Blood Pressure and Thrombosis in Mice. <i>Science Translational Medicine</i> , 2012, 4, 132ra54.	12.4	194
49	Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). <i>Bioinformatics</i> , 2011, 27, 2518-2528.	4.1	298
50	Discovery Approaches to UPR in Athero-Susceptible Endothelium In Vivo. <i>Methods in Enzymology</i> , 2011, 489, 109-126.	1.0	3
51	Microsomal Prostaglandin E Synthase-1 Modulates the Response to Vascular Injury. <i>Circulation</i> , 2011, 123, 631-639.	1.6	86
52	Hypercholesterolemia Induces Side-Specific Phenotypic Changes and Peroxisome Proliferator-Activated Receptor- $\beta$ Pathway Activation in Swine Aortic Valve Endothelium. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 225-231.	2.4	39
53	Cell-Specific Determinants of Peroxisome Proliferator-Activated Receptor $\beta$ Function in Adipocytes and Macrophages. <i>Molecular and Cellular Biology</i> , 2010, 30, 2078-2089.	2.3	189
54	Propagation of adipogenic signals through an epigenomic transition state. <i>Genes and Development</i> , 2010, 24, 1035-1044.	5.9	215

#	ARTICLE	IF	CITATIONS
55	Prelesional arterial endothelial phenotypes in hypercholesterolemia: universal ABCA1 upregulation contrasts with region-specific gene expression in vivo. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2010, 298, H163-H170.	3.2	14
56	A flexible two-stage procedure for identifying gene sets that are differentially expressed. <i>Bioinformatics</i> , 2009, 25, 1019-1025.	4.1	41
57	MOLECULAR KARYOTYPE OF SPORADIC UNILATERAL RETINOBLASTOMA TUMORS. <i>Retina</i> , 2009, 29, 1002-1012.	1.7	16
58	Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. <i>PLoS Genetics</i> , 2007, 3, e143.	3.5	41
59	Human microRNA-155 on Chromosome 21 Differentially Interacts with Its Polymorphic Target in the AGTR1 3' UTR: A Mechanism for Functional Single-Nucleotide Polymorphisms Related to Phenotypes. <i>American Journal of Human Genetics</i> , 2007, 81, 405-413.	6.2	335
60	Analysis and Management of Microarray Gene Expression Data. <i>Current Protocols in Molecular Biology</i> , 2007, 77, Unit 19.6.	2.9	34
61	STAC: A method for testing the significance of DNA copy number aberrations across multiple array-CGH experiments. <i>Genome Research</i> , 2006, 16, 1149-1158.	5.5	152
62	Integrative Genomics Identifies Distinct Molecular Classes of Neuroblastoma and Shows That Multiple Genes Are Targeted by Regional Alterations in DNA Copy Number. <i>Cancer Research</i> , 2006, 66, 6050-6062.	0.9	178
63	A practical false discovery rate approach to identifying patterns of differential expression in microarray data. <i>Bioinformatics</i> , 2005, 21, 2684-2690.	4.1	91
64	Spatial Heterogeneity of Endothelial Phenotypes Correlates With Side-Specific Vulnerability to Calcification in Normal Porcine Aortic Valves. <i>Circulation Research</i> , 2005, 96, 792-799.	4.5	238
65	Regional determinants of arterial endothelial phenotype dominate the impact of gender or short-term exposure to a high-fat diet. <i>Biochemical and Biophysical Research Communications</i> , 2005, 332, 142-148.	2.1	14
66	Coexisting proinflammatory and antioxidative endothelial transcription profiles in a disturbed flow region of the adult porcine aorta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2482-2487.	7.1	322
67	PlasmoDB: the Plasmodium genome resource. A database integrating experimental and computational data. <i>Nucleic Acids Research</i> , 2003, 31, 212-215.	14.5	329
68	Fidelity and enhanced sensitivity of differential transcription profiles following linear amplification of nanogram amounts of endothelial mRNA. <i>Physiological Genomics</i> , 2003, 13, 147-156.	2.3	103
69	Comparison of different labeling methods for two-channel high-density microarray experiments. <i>Physiological Genomics</i> , 2002, 10, 169-179.	2.3	57
70	PlasmoDB: the Plasmodium genome resource. An integrated database providing tools for accessing, analyzing and mapping expression and sequence data (both finished and unfinished). <i>Nucleic Acids Research</i> , 2002, 30, 87-90.	14.5	110
71	The Plasmodium genome database. <i>Nature</i> , 2002, 419, 490-492.	27.8	156