

# Rosemary I Braun

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

17,102  
citations

394421

19  
h-index

361022

35  
g-index

42  
all docs

42  
docs citations

42  
times ranked

23850  
citing authors

#	ARTICLE	IF	CITATIONS
1	Light at night in older age is associated with obesity, diabetes, and hypertension. <i>Sleep</i> , 2023, 46, .	1.1	25
2	Validation of blood-based transcriptomic circadian phenotyping in older adults. <i>Sleep</i> , 2022, 45, .	1.1	1
3	Autonomic dysregulation and sleep homeostasis in insomnia. <i>Sleep</i> , 2021, 44, .	1.1	24
4	Comment on “Circadian rhythms in the absence of the clock gene <i>Bmal1</i> ” <i>Science</i> , 2021, 372, .	12.6	15
5	TimeCycle: topology inspired method for the detection of cycling transcripts in circadian time-series data. <i>Bioinformatics</i> , 2021, 37, 4405-4413.	4.1	3
6	Rest-activity rhythm disturbance in liver cirrhosis and association with cognitive impairment. <i>Sleep</i> , 2021, 44, .	1.1	10
7	Circadian Gene Expression Rhythms During Critical Illness. <i>Critical Care Medicine</i> , 2020, 48, e1294-e1299.	0.9	27
8	NAD <sup>+</sup> Controls Circadian Reprogramming through PER2 Nuclear Translocation to Counter Aging. <i>Molecular Cell</i> , 2020, 78, 835-849.e7.	9.7	116
9	TimeTrial: An Interactive Application for Optimizing the Design and Analysis of Transcriptomic Time-Series Data in Circadian Biology Research. <i>Journal of Biological Rhythms</i> , 2020, 35, 439-451.	2.6	17
10	Mutation, drift and selection in single-driver hematologic malignancy: Example of secondary myelodysplastic syndrome following treatment of inherited neutropenia. <i>PLoS Computational Biology</i> , 2019, 15, e1006664.	3.2	7
11	GeneSurrounder: network-based identification of disease genes in expression data. <i>BMC Bioinformatics</i> , 2019, 20, 229.	2.6	6
12	Reply to Laing et al.: Accurate prediction of circadian time across platforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5206-5208.	7.1	6
13	Strengthening sleep’s autonomic interaction via acoustic enhancement of slow oscillations. <i>Sleep</i> , 2019, 42, .	1.1	50
14	Next steps for modelling the evolution of ornamental signals. <i>Animal Behaviour</i> , 2018, 138, e11-e13.	1.9	0
15	Semi-supervised network inference using simulated gene expression dynamics. <i>Bioinformatics</i> , 2018, 34, 1148-1156.	4.1	6
16	Pro-inflammatory cytokine and high doses of ionizing radiation have similar effects on the expression of NF-kappaB-dependent genes. <i>Cellular Signalling</i> , 2018, 46, 23-31.	3.6	28
17	Integrative analysis reveals disrupted pathways regulated by microRNAs in cancer. <i>Nucleic Acids Research</i> , 2018, 46, 1089-1101.	14.5	28
18	Time-lagged Ordered Lasso for network inference. <i>BMC Bioinformatics</i> , 2018, 19, 545.	2.6	11

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19	regQTLs: Single nucleotide polymorphisms that modulate microRNA regulation of gene expression in tumors. <i>PLoS Genetics</i> , 2018, 14, e1007837.	3.5	24
20	Universal method for robust detection of circadian state from gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9247-E9256.	7.1	115
21	Habitual light exposure relative to circadian timing in delayed sleep-wake phase disorder. <i>Sleep</i> , 2018, 41, .	1.1	18
22	Acoustic Enhancement of Sleep Slow Oscillations and Concomitant Memory Improvement in Older Adults. <i>Frontiers in Human Neuroscience</i> , 2017, 11, 109.	2.0	183
23	Handicap principle implies emergence of dimorphic ornaments. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161970.	2.6	11
24	Systems Analysis of High-Throughput Data. <i>Advances in Experimental Medicine and Biology</i> , 2014, 844, 153-187.	1.6	21
25	Multi-SNP Analysis of GWAS Data Identifies Pathways Associated with Nonalcoholic Fatty Liver Disease. <i>PLoS ONE</i> , 2013, 8, e65982.	2.5	19
26	Discovery Analysis of TCGA Data Reveals Association between Germline Genotype and Survival in Ovarian Cancer Patients. <i>PLoS ONE</i> , 2013, 8, e55037.	2.5	30
27	Abstract 740: Investigating the role of epigenetic mechanisms upon aberrant signaling network activation.. , 2013, , .		0
28	Partition decoupling for multi-gene analysis of gene expression profiling data. <i>BMC Bioinformatics</i> , 2011, 12, 497.	2.6	11
29	Pathways of Distinction Analysis: A New Technique for Multi-SNP Analysis of GWAS Data. <i>PLoS Genetics</i> , 2011, 7, e1002101.	3.5	56
30	Needles in the Haystack: Identifying Individuals Present in Pooled Genomic Data. <i>PLoS Genetics</i> , 2009, 5, e1000668.	3.5	48
31	MicroRNA Expression in Squamous Cell Carcinoma and Adenocarcinoma of the Esophagus: Associations with Survival. <i>Clinical Cancer Research</i> , 2009, 15, 6192-6200.	7.0	347
32	Identifying differential correlation in gene/pathway combinations. <i>BMC Bioinformatics</i> , 2008, 9, 488.	2.6	24
33	Imaging the Migration Pathways for O <sub>2</sub> , CO, NO, and Xe Inside Myoglobin. <i>Biophysical Journal</i> , 2006, 91, 1844-1857.	0.5	258
34	Scalable molecular dynamics with NAMD. <i>Journal of Computational Chemistry</i> , 2005, 26, 1781-1802.	3.3	15,208
35	Molecular Dynamics Simulations of Micelle Formation around Dimeric Glycophorin A Transmembrane Helices. <i>Biophysical Journal</i> , 2004, 87, 754-763.	0.5	79
36	Genetically engineered gold-binding polypeptides: structure prediction and molecular dynamics. <i>Journal of Biomaterials Science, Polymer Edition</i> , 2002, 13, 747-757.	3.5	143

#	ARTICLE	IF	CITATIONS
37	Reconstructing Potentials of Mean Force through Time Series Analysis of Steered Molecular Dynamics Simulations. <i>Journal of Computational Physics</i> , 1999, 151, 190-211.	3.8	115