

Rajanikanth Vadigepalli

List of Publications by Citations

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109
papers

1,366
citations

21
h-index

32
g-index

138
ext. papers

1,797
ext. citations

3.5
avg, IF

4.43
L-index

#	Paper	IF	Citations
109	PAINT: a promoter analysis and interaction network generation tool for gene regulatory network identification. <i>OMICS A Journal of Integrative Biology</i> , 2003 , 7, 235-52	3.8	112
108	Decorin protein core affects the global gene expression profile of the tumor microenvironment in a triple-negative orthotopic breast carcinoma xenograft model. <i>PLoS ONE</i> , 2012 , 7, e45559	3.7	70
107	A distributed state estimation and control algorithm for plantwide processes. <i>IEEE Transactions on Control Systems Technology</i> , 2003 , 11, 119-127	4.8	61
106	Chronic ethanol feeding alters miRNA expression dynamics during liver regeneration. <i>Alcoholism: Clinical and Experimental Research</i> , 2013 , 37 Suppl 1, E59-69	3.7	53
105	MicroRNA profiling in lung cancer reveals new molecular markers for diagnosis. <i>Acta Cytologica</i> , 2012 , 56, 645-54	3	48
104	Robust Control of a Multivariable Experimental Four-Tank System. <i>Industrial & Engineering Chemistry Research</i> , 2001 , 40, 1916-1927	3.9	47
103	Temporal changes in innate immune signals in a rat model of alcohol withdrawal in emotional and cardiorespiratory homeostatic nuclei. <i>Journal of Neuroinflammation</i> , 2012 , 9, 97	10.1	41
102	Erythroid-induced commitment of K562 cells results in clusters of differentially expressed genes enriched for specific transcription regulatory elements. <i>Physiological Genomics</i> , 2004 , 19, 117-30	3.6	40
101	Chronic ethanol feeding enhances miR-21 induction during liver regeneration while inhibiting proliferation in rats. <i>American Journal of Physiology - Renal Physiology</i> , 2012 , 303, G733-43	5.1	39
100	Single-Cell Transcriptional Analysis Reveals Novel Neuronal Phenotypes and Interaction Networks Involved in the Central Circadian Clock. <i>Frontiers in Neuroscience</i> , 2016 , 10, 481	5.1	34
99	Effects of developmental lead exposure on the hippocampal transcriptome: influences of sex, developmental period, and lead exposure level. <i>Toxicological Sciences</i> , 2012 , 129, 108-25	4.4	33
98	HuR Contributes to TRAIL Resistance by Restricting Death Receptor 4 Expression in Pancreatic Cancer Cells. <i>Molecular Cancer Research</i> , 2016 , 14, 599-611	6.6	32
97	Inputs drive cell phenotype variability. <i>Genome Research</i> , 2014 , 24, 930-41	9.7	28
96	Ethanol diverts early neuronal differentiation trajectory of embryonic stem cells by disrupting the balance of lineage specifiers. <i>PLoS ONE</i> , 2013 , 8, e63794	3.7	28
95	Structural analysis of large-scale systems for distributed state estimation and control applications. <i>Control Engineering Practice</i> , 2003 , 11, 895-905	3.9	27
94	Ethanol alters the balance of Sox2, Oct4, and Nanog expression in distinct subpopulations during differentiation of embryonic stem cells. <i>Stem Cells and Development</i> , 2013 , 22, 2196-210	4.4	25
93	Sex-based differences in gene expression in hippocampus following postnatal lead exposure. <i>Toxicology and Applied Pharmacology</i> , 2011 , 256, 179-90	4.6	25

92	Chronic alcohol exposure alters transcription broadly in a key integrative brain nucleus for homeostasis: the nucleus tractus solitarius. <i>Physiological Genomics</i> , 2005 , 24, 45-58	3.6	24
91	Temporal and functional profile of the transcriptional regulatory network in the early regenerative response to partial hepatectomy in the rat. <i>BMC Genomics</i> , 2008 , 9, 527	4.5	23
90	Credible practice of modeling and simulation in healthcare: ten rules from a multidisciplinary perspective. <i>Journal of Translational Medicine</i> , 2020 , 18, 369	8.5	22
89	Inhibition of miR-21 rescues liver regeneration after partial hepatectomy in ethanol-fed rats. <i>American Journal of Physiology - Renal Physiology</i> , 2016 , 311, G794-G806	5.1	22
88	Credibility, Replicability, and Reproducibility in Simulation for Biomedicine and Clinical Applications in Neuroscience. <i>Frontiers in Neuroinformatics</i> , 2018 , 12, 18	3.9	21
87	Transcriptional regulatory network analysis during epithelial-mesenchymal transformation of retinal pigment epithelium. <i>Molecular Vision</i> , 2008 , 14, 1414-28	2.3	21
86	Single-Cell Glia and Neuron Gene Expression in the Central Amygdala in Opioid Withdrawal Suggests Inflammation With Correlated Gut Dysbiosis. <i>Frontiers in Neuroscience</i> , 2019 , 13, 665	5.1	19
85	A Comprehensive Integrated Anatomical and Molecular Atlas of Rat Intrinsic Cardiac Nervous System. <i>IScience</i> , 2020 , 23, 101140	6.1	19
84	From promoter analysis to transcriptional regulatory network prediction using PAINT. <i>Methods in Molecular Biology</i> , 2007 , 408, 49-68	1.4	19
83	Innervation and Neuronal Control of the Mammalian Sinoatrial Node a Comprehensive Atlas. <i>Circulation Research</i> , 2021 , 128, 1279-1296	15.7	19
82	MicroRNA network changes in the brain stem underlie the development of hypertension. <i>Physiological Genomics</i> , 2015 , 47, 388-99	3.6	18
81	Integrated live imaging and molecular profiling of embryoid bodies reveals a synchronized progression of early differentiation. <i>Scientific Reports</i> , 2016 , 6, 31623	4.9	17
80	Systems analysis of non-parenchymal cell modulation of liver repair across multiple regeneration modes. <i>BMC Systems Biology</i> , 2015 , 9, 71	3.5	17
79	The inflammatory and normal transcriptome of mouse bladder detrusor and mucosa. <i>BMC Physiology</i> , 2006 , 6, 1	0	17
78	Bladder inflammatory transcriptome in response to tachykinins: neurokinin 1 receptor-dependent genes and transcription regulatory elements. <i>BMC Urology</i> , 2007 , 7, 7	2.2	15
77	Inflammation-associated suppression of metabolic gene networks in acute and chronic liver disease. <i>Archives of Toxicology</i> , 2020 , 94, 205-217	5.8	15
76	Adiponectin fine-tuning of liver regeneration dynamics revealed through cellular network modelling. <i>Journal of Physiology</i> , 2015 , 593, 365-83	3.9	14
75	Computational modeling of cytokine signaling in microglia. <i>Molecular BioSystems</i> , 2015 , 11, 3332-46		14

74	Systemic leukotriene B receptor antagonism lowers arterial blood pressure and improves autonomic function in the spontaneously hypertensive rat. <i>Journal of Physiology</i> , 2016 , 594, 5975-5989	3.9	14
73	Coordinated dynamic gene expression changes in the central nucleus of the amygdala during alcohol withdrawal. <i>Alcoholism: Clinical and Experimental Research</i> , 2013 , 37 Suppl 1, E88-100	3.7	14
72	Robust dynamic balance of AP-1 transcription factors in a neuronal gene regulatory network. <i>BMC Systems Biology</i> , 2010 , 4, 171	3.5	14
71	Integrative gene regulatory network analysis reveals light-induced regional gene expression phase shift programs in the mouse suprachiasmatic nucleus. <i>PLoS ONE</i> , 2012 , 7, e37833	3.7	14
70	Continuous-time identification of gene expression models. <i>OMICS A Journal of Integrative Biology</i> , 2003 , 7, 373-86	3.8	13
69	Novel Influences of IL-10 on CNS Inflammation Revealed by Integrated Analyses of Cytokine Networks and Microglial Morphology. <i>Frontiers in Cellular Neuroscience</i> , 2017 , 11, 233	6.1	12
68	Identifying functional gene regulatory network phenotypes underlying single cell transcriptional variability. <i>Progress in Biophysics and Molecular Biology</i> , 2015 , 117, 87-98	4.7	11
67	A novel comparative pattern analysis approach identifies chronic alcohol mediated dysregulation of transcriptomic dynamics during liver regeneration. <i>BMC Genomics</i> , 2016 , 17, 260	4.5	11
66	Molecular modeling of ErbB4/HER4 kinase in the context of the HER4 signaling network helps rationalize the effects of clinically identified HER4 somatic mutations on the cell phenotype. <i>Biotechnology Journal</i> , 2013 , 8, 1452-64	5.6	11
65	Unconventional systems analysis problems in molecular biology: a case study in gene regulatory network modeling. <i>Computers and Chemical Engineering</i> , 2005 , 29, 547-563	4	11
64	Intracellular Information Processing through Encoding and Decoding of Dynamic Signaling Features. <i>PLoS Computational Biology</i> , 2015 , 11, e1004563	5	10
63	Rapid temporal changes in the expression of a set of neuromodulatory genes during alcohol withdrawal in the dorsal vagal complex: molecular evidence of homeostatic disturbance. <i>Alcoholism: Clinical and Experimental Research</i> , 2012 , 36, 1688-700	3.7	10
62	Dynamic transcriptomic response to acute hypertension in the nucleus tractus solitarius. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2008 , 295, R15-27	3.2	10
61	Systems analysis of circadian time-dependent neuronal epidermal growth factor receptor signaling. <i>Genome Biology</i> , 2006 , 7, R48	18.3	10
60	Introduction to the Virtual Issue Alcohol and Epigenetic Regulation: Do the Products of Alcohol Metabolism Drive Epigenetic Control of Gene Expression in Alcohol-Related Disorders?. <i>Alcoholism: Clinical and Experimental Research</i> , 2018 , 42, 845-848	3.7	8
59	Epidermal growth factor receptor-induced circadian-time-dependent gene regulation in suprachiasmatic nucleus. <i>NeuroReport</i> , 2006 , 17, 1437-41	1.7	8
58	A novel, dynamic pattern-based analysis of NF- κ B binding during the priming phase of liver regeneration reveals switch-like functional regulation of target genes. <i>Frontiers in Physiology</i> , 2015 , 6, 189	4.6	6
57	Structural properties of gene regulatory networks: definitions and connections. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009 , 6, 158-70	3	6

56	Modeling cytokine regulatory network dynamics driving neuroinflammation in central nervous system disorders. <i>Drug Discovery Today: Disease Models</i> , 2016 , 19, 59-67	1.3	6
55	Single-Cell Gene Expression Analysis Identifies Chronic Alcohol-Mediated Shift in Hepatocyte Molecular States After Partial Hepatectomy. <i>Gene Expression</i> , 2019 , 19, 97-119	3.4	5
54	In Vivo Zonal Variation and Liver Cell-Type Specific NF- κ B Localization after Chronic Adaptation to Ethanol and following Partial Hepatectomy. <i>PLoS ONE</i> , 2015 , 10, e0140236	3.7	5
53	Integrated Computational Model of Intracellular Signaling and microRNA Regulation Predicts the Network Balances and Timing Constraints Critical to the Hepatic Stellate Cell Activation Process. <i>Processes</i> , 2014 , 2, 773-794	2.9	5
52	Hepatic lipocalin 2 promotes liver fibrosis and portal hypertension. <i>Scientific Reports</i> , 2020 , 10, 15558	4.9	5
51	Computational Modeling of Spatiotemporal Ca(2+) Signal Propagation Along Hepatocyte Cords. <i>IEEE Transactions on Biomedical Engineering</i> , 2016 , 63, 2047-55	5	5
50	Integrated Multiomics Reveals Glucose Use Reprogramming and Identifies a Novel Hexokinase in Alcoholic Hepatitis. <i>Gastroenterology</i> , 2021 , 160, 1725-1740.e2	13.3	5
49	Cellular network modeling and single cell gene expression analysis reveals novel hepatic stellate cell phenotypes controlling liver regeneration dynamics. <i>BMC Systems Biology</i> , 2018 , 12, 86	3.5	5
48	Combining Laser Capture Microdissection and Microfluidic qPCR to Analyze Transcriptional Profiles of Single Cells: A Systems Biology Approach to Opioid Dependence. <i>Journal of Visualized Experiments</i> , 2020 ,	1.6	4
47	Molecular variability elicits a tunable switch with discrete neuromodulatory response phenotypes. <i>Journal of Computational Neuroscience</i> , 2016 , 40, 65-82	1.4	4
46	Multiscale model of dynamic neuromodulation integrating neuropeptide-induced signaling pathway activity with membrane electrophysiology. <i>Biophysical Journal</i> , 2015 , 108, 211-23	2.9	4
45	A single cell transcriptomics map of paracrine networks in the intrinsic cardiac nervous system. <i>iScience</i> , 2021 , 24, 102713	6.1	4
44	Pattern analysis uncovers a chronic ethanol-induced disruption of the switch-like dynamics of C/EBP- β and C/EBP- δ genome-wide binding during liver regeneration. <i>Physiological Genomics</i> , 2017 , 49, 11-26	3.6	3
43	Investigating the Effects of Brainstem Neuronal Adaptation on Cardiovascular Homeostasis. <i>Frontiers in Neuroscience</i> , 2020 , 14, 470	5.1	3
42	SPSNet: subpopulation-sensitive network-based analysis of heterogeneous gene expression data. <i>BMC Systems Biology</i> , 2018 , 12, 28	3.5	3
41	A novel comparative pattern count analysis reveals a chronic ethanol-induced dynamic shift in immediate early NF- κ B genome-wide promoter binding during liver regeneration. <i>Molecular BioSystems</i> , 2016 , 12, 1037-56		3
40	Analysis and neuronal modeling of the nonlinear characteristics of a local cardiac reflex in the rat. <i>Neural Computation</i> , 2001 , 13, 2239-71	2.9	3
39	A data-driven modeling approach to identify disease-specific multi-organ networks driving physiological dysregulation. <i>PLoS Computational Biology</i> , 2017 , 13, e1005627	5	3

38	Modeling the Dynamics of Human Liver Failure Post Liver Resection. <i>Processes</i> , 2018 , 6,	2.9	3
37	Causality Analysis and Cell Network Modeling of Spatial Calcium Signaling Patterns in Liver Lobules. <i>Frontiers in Physiology</i> , 2018 , 9, 1377	4.6	3
36	Adaptive transcriptional dynamics of A2 neurons and central cardiovascular control pathways. <i>Experimental Physiology</i> , 2012 , 97, 462-8	2.4	2
35	3D single cell scale anatomical map of sex-dependent variability of the rat intrinsic cardiac nervous system		2
34	Diurnal Patterns of Gene Expression in the Dorsal Vagal Complex and the Central Nucleus of the Amygdala - Non-rhythm-generating Brain Regions. <i>Frontiers in Neuroscience</i> , 2020 , 14, 375	5.1	1
33	Computational Modeling as an Approach to Study the Cellular and Molecular Regulatory Networks Driving Liver Regeneration 2015 , 185-198		1
32	Optimizing In Vivo Gene Delivery to Liver Cells Using Polyethylenimine Based Nanoparticles. <i>Journal of Pharmaceutical Sciences and Pharmacology</i> , 2014 , 1, 154-159		1
31	Retinoic Acid Fluctuation Activates an Uneven, Direction-Dependent Network-Wide Robustness Response in Early Embryogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 747969	5.7	1
30	A spatially-tracked single cell transcriptomics map of neuronal networks in the intrinsic cardiac nervous system		1
29	Innervation and Neuronal Control of the Mammalian Sinoatrial Node: A Comprehensive Atlas		1
28	A Novel Mouse Model of Acute-on-Chronic Cholestatic Alcoholic Liver Disease: A Systems Biology Comparison With Human Alcoholic Hepatitis. <i>Alcoholism: Clinical and Experimental Research</i> , 2020 , 44, 87-101	3.7	1
27	3D single cell scale anatomical map of sex-dependent variability of the rat intrinsic cardiac nervous system. <i>IScience</i> , 2021 , 24, 102795	6.1	1
26	Model-based virtual patient analysis of human liver regeneration predicts critical perioperative factors controlling the dynamic mode of response to resection. <i>BMC Systems Biology</i> , 2019 , 13, 9	3.5	0
25	Input-output signal processing plasticity of vagal motor neurons in response to cardiac ischemic injury. <i>IScience</i> , 2021 , 24, 102143	6.1	0
24	Optimization of Gene Delivery to Liver Cells Using a Biodegradable Polymer Based Nanoparticles. <i>Journal of Pharmaceutical Sciences and Pharmacology</i> , 2014 , 1, 141-145		
23	Dynamic Transcriptomics: Transcriptomic Discovery of a Biological Multiple-Input Multiple-Output Heart Control Mechanism. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2013 , 46, 1-5		
22	Single Cell Scale Neuronal and Glial Gene Expression and Putative Cell Phenotypes and Networks in the Nucleus Tractus Solitarius in an Alcohol Withdrawal Time Series. <i>Frontiers in Systems Neuroscience</i> , 2021 , 15, 739790	3.5	
21	A Spatial Model of Hepatic Calcium Signaling and Glucose Metabolism Under Autonomic Control Reveals Functional Consequences of Varying Liver Innervation Patterns Across Species.. <i>Frontiers in Physiology</i> , 2021 , 12, 748962	4.6	

20	Transcriptome Analysis of Human Hematopoietic Progenitor Cells during In Vitro Erythroid Differentiation.. <i>Blood</i> , 2005 , 106, 1750-1750	2.2
19	Integrated signaling and electrophysiological model of angiotensin II induced neuronal adaptation in the brain. <i>FASEB Journal</i> , 2007 , 21, A1352	0.9
18	Analysis of transcriptional regulation underlying central neural control mechanisms in acute hypertension. <i>FASEB Journal</i> , 2007 , 21, A465	0.9
17	Multi-scale modeling of neuronal adaptation mediated by angiotensin II in the central regulation of blood pressure. <i>FASEB Journal</i> , 2008 , 22, 756.2	0.9
16	Single Cell Gene Expression Analysis and 3-D Mapping of Cardiac Ganglia. <i>FASEB Journal</i> , 2018 , 32, 863.6o.9	
15	Putative MicroRNA Regulatory Networks in Hepatic Stellate Cells Underlying Chronic Ethanol-Mediated Impairment of Liver Regeneration after Partial Hepatectomy. <i>FASEB Journal</i> , 2018 , 32, 546.5	0.9
14	Investigating Single-cell Transcriptome Dynamics of the Dorsal Motor Nucleus of the Vagus (DMV) in a Rat Model of Remote Ischemic-Reperfusion Cardioprotection (RIPC). <i>FASEB Journal</i> , 2019 , 33, 742.3	0.9
13	Intrinsic Cardiac Ganglionic Neurons Projecting to the SA node in the Rat and Pig Hearts: Retrograde Labeling and Neurolucida 3-D Reconstruction. <i>FASEB Journal</i> , 2019 , 33, 773.2	0.9
12	High-Resolution Chronology of Murine Biological Responses to 70% Partial Hepatectomy. <i>FASEB Journal</i> , 2019 , 33, 496.44	0.9
11	Dynamic Regulation of microRNA Networks in the Brainstem Characterize Hypertension Development. <i>FASEB Journal</i> , 2015 , 29, 984.12	0.9
10	Time series analysis of transcriptional regulation of NF-kB targeted genes in vivo during the onset of liver regeneration. <i>FASEB Journal</i> , 2010 , 24, 749.6	0.9
9	Ethanol effects on cell cycle related genes in regenerating rat liver. <i>FASEB Journal</i> , 2011 , 25, 115.3	0.9
8	Chronic alcohol effects on NF-B genome-wide binding dynamics during early onset of liver regeneration. <i>FASEB Journal</i> , 2011 , 25, 998.8	0.9
7	Ethanol Interferes with Gene Regulatory Networks of Embryonic Stem Cells. <i>FASEB Journal</i> , 2011 , 25, 1002.4	0.9
6	Adaptive Single Neuron Hypertensive Gene Expression Programs in the Nucleus Tractus Solitarius. <i>FASEB Journal</i> , 2012 , 26, 1035.19	0.9
5	Genome-wide combinatorial transcriptional regulatory dynamics during early onset of liver regeneration and chronic alcohol intake. <i>FASEB Journal</i> , 2012 , 26, 274.5	0.9
4	Profiling candidate housekeeping genes for data normalization in chronic ethanol treated rat liver regeneration model. <i>FASEB Journal</i> , 2012 , 26, 145.7	0.9
3	Adaptation to chronic alcohol intake alters STAT3 genome-wide binding dynamics during liver regeneration. <i>FASEB Journal</i> , 2013 , 27, 872.4	0.9

- 2 Genome-wide combinatorial transcriptional regulatory dynamics during early onset of liver regeneration and chronic alcohol intake. *FASEB Journal*, **2013**, 27, 1161.5 0.9
- 1 Neuroinflammation, Glia, and Cytokines: Networks of Networks **2022**, 2281-2287