John R Stevens

List of Publications by Year in descending order

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Version: 2024-02-01

257450 182427 2,682 51 24 51 h-index citations g-index papers 52 52 52 4892 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The implementation of random survival forests in conflict management data: An examination of power sharing and third party mediation in post-conflict countries. PLoS ONE, 2021, 16, e0250963.	2.5	2
2	Poor maternal nutrition during gestation in sheep alters prenatal muscle growth and development in offspring. Journal of Animal Science, 2020, 98, .	0.5	32
3	The PI3K/AKT signaling pathway: Associations of miRNAs with dysregulated gene expression in colorectal cancer. Molecular Carcinogenesis, 2018, 57, 243-261.	2.7	83
4	The NF-κB signalling pathway in colorectal cancer: associations between dysregulated gene and miRNA expression. Journal of Cancer Research and Clinical Oncology, 2018, 144, 269-283.	2.5	71
5	MicroRNAâ€transcription factor interactions and their combined effect on target gene expression in colon cancer cases. Genes Chromosomes and Cancer, 2018, 57, 192-202.	2.8	42
6	Power in pairs: assessing the statistical value of paired samples in tests for differential expression. BMC Genomics, 2018, 19, 953.	2.8	26
7	miRNA involvement in cell cycle regulation in colorectal cancer cases. Genes and Cancer, 2018, 9, 53-65.	1.9	29
8	MicroRNA-messenger RNA interactions involving JAK-STAT signaling genes in colorectal cancer. Genes and Cancer, 2018, 9, 232-246.	1.9	6
9	Expression of Wnt-signaling pathway genes and their associations with miRNAs in colorectal cancer. Oncotarget, 2018, 9, 6075-6085.	1.8	17
10	Diet and lifestyle factors associated with miRNA expression in colorectal tissue. Pharmacogenomics and Personalized Medicine, 2017, Volume10, 1-16.	0.7	28
11	Infrequently expressed miRNAs in colorectal cancer tissue and tumor molecular phenotype. Modern Pathology, 2017, 30, 1152-1169.	5.5	17
12	Alterations in microRNA expression associated with alcohol consumption in rectal cancer subjects. Cancer Causes and Control, 2017, 28, 545-555.	1.8	7
13	The miRNA landscape of colorectal polyps. Genes Chromosomes and Cancer, 2017, 56, 347-353.	2.8	8
14	A Bivariate Hypothesis Testing Approach for Mapping the Trait-Influential Gene. Scientific Reports, 2017, 7, 12798.	3.3	1
15	Transcription factorâ€microRNA associations and their impact on colorectal cancer survival. Molecular Carcinogenesis, 2017, 56, 2512-2526.	2.7	13
16	SigTree: A Microbial Community Analysis Tool to Identify and Visualize Significantly Responsive Branches in a Phylogenetic Tree. Computational and Structural Biotechnology Journal, 2017, 15, 372-378.	4.1	5
17	An Assessment of Database-Validated microRNA Target Genes in Normal Colonic Mucosa: Implications for Pathway Analysis. Cancer Informatics, 2017, 16, 117693511771640.	1.9	9
18	Genetic variants in the $TGF\hat{l}^2$ -signaling pathway influence expression of miRNAs in colon and rectal normal mucosa and tumor tissue. Oncotarget, 2017, 8, 16765-16783.	1.8	25

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19	Identifying factors associated with the direction and significance of microRNA tumor-normal expression differences in colorectal cancer. BMC Cancer, 2017, 17, 707.	2.6	5
20	A comparison of multiple testing adjustment methods with block-correlation positively-dependent tests. PLoS ONE, 2017, 12, e0176124.	2.5	57
21	Infrequently expressed miRNAs influence survival after diagnosis with colorectal cancer. Oncotarget, 2017, 8, 83845-83859.	1.8	28
22	Colorectal tumor molecular phenotype and miRNA: expression profiles and prognosis. Modern Pathology, 2016, 29, 915-927.	5.5	41
23	Expression Profiles of miRNA Subsets Distinguish Human Colorectal Carcinoma and Normal Colonic Mucosa. Clinical and Translational Gastroenterology, 2016, 7, e152.	2.5	82
24	Comment on "Climate and agricultural land use change impacts on streamflow in the upper midwestern United States,―by Satish C. Gupta et al Water Resources Research, 2016, 52, 7523-7528.	4.2	15
25	Increased Susceptibility to Atrial Fibrillation Secondary to Atrial Fibrosis in Transgenic Goats Expressing Transforming Growth Factorâ $\hat{\in}\hat{i}^21$. Journal of Cardiovascular Electrophysiology, 2016, 27, 1220-1229.	1.7	40
26	Association of cigarette smoking and microRNA expression in rectal cancer: Insight into tumor phenotype. Cancer Epidemiology, 2016, 45, 98-107.	1.9	36
27	MicroRNA profiles in colorectal carcinomas, adenomas and normal colonic mucosa: variations in miRNA expression and disease progression. Carcinogenesis, 2016, 37, 245-261.	2.8	107
28	Accounting for Missing Data in Clinical Research. JAMA - Journal of the American Medical Association, 2016, 315, 517.	7.4	11
29	Site-specific associations between miRNA expression and survival in colorectal cancer cases. Oncotarget, 2016, 7, 60193-60205.	1.8	41
30	Incorporation of subject-level covariates in quantile normalization of miRNA data. BMC Genomics, 2015, 16, 1045.	2.8	11
31	An evaluation and replication of mi <scp>RNA</scp> s with disease stage and colorectal cancerâ€specific mortality. International Journal of Cancer, 2015, 137, 428-438.	5.1	119
32	Accounting for Dependence Induced by Weighted KNN Imputation in Paired Samples, Motivated by a Colorectal Cancer Study. PLoS ONE, 2015, 10, e0119876.	2.5	27
33	A shortcut for multiple testing on the directed acyclic graph of gene ontology. BMC Bioinformatics, 2014, 15, 349.	2.6	5
34	Most soil trophic guilds increase plant growth: a metaâ€analytical review. Oikos, 2014, 123, 1409-1419.	2.7	26
35	Aflatoxicosis chemoprevention by probiotic Lactobacillius and lack of effect on the major histocompatibility complex. Research in Veterinary Science, 2014, 97, 274-281.	1.9	7
36	A Graphical Weighted Power Improving Multiplicity Correction Approach for SNP Selections. Current Genomics, 2014, 15, 380-389.	1.6	3

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37	Sensing Biophysical Alterations of Human Lung Epithelial Cells (A549) in the Context of Toxicity Effects of Diesel Exhaust Particles. Cell Biochemistry and Biophysics, 2013, 67, 1147-1156.	1.8	3
38	Transcriptional profiling by RNA-Seq of peri-attachment porcine embryos generated by a variety of assisted reproductive technologies. Physiological Genomics, 2013, 45, 577-589.	2.3	19
39	Preadaptation to Cold Stress in Salmonella enterica Serovar Typhimurium Increases Survival during Subsequent Acid Stress Exposure. Applied and Environmental Microbiology, 2013, 79, 7281-7289.	3.1	59
40	Assessing Numerical Dependence in Gene Expression Summaries with the Jackknife Expression Difference. PLoS ONE, 2012, 7, e39570.	2.5	2
41	A comparison of probe-level and probeset models for small-sample gene expression data. BMC Bioinformatics, 2010, 11, 281.	2.6	8
42	A Metaâ€Analytic Review of Corridor Effectiveness. Conservation Biology, 2010, 24, 660-668.	4.7	407
43	<i>metahdep</i> : meta-analysis of hierarchically dependent gene expression studies. Bioinformatics, 2009, 25, 2619-2620.	4.1	15
44	Hierarchical Dependence in Meta-Analysis. Journal of Educational and Behavioral Statistics, 2009, 34, 46-73.	1.7	68
45	Plant–soil feedbacks: a metaâ€analytical review. Ecology Letters, 2008, 11, 980-992.	6.4	802
46	Novel functional view of the crocidolite asbestos-treated A549 human lung epithelial transcriptome reveals an intricate network of pathways with opposing functions. BMC Genomics, 2008, 9, 376.	2.8	22
47	Disruption of epidermal specific gene expression and delayed skin development in AP-2γ mutant mice. Developmental Biology, 2008, 317, 187-195.	2.0	34
48	Treatment of Late Stage Disease in a Model of Arenaviral Hemorrhagic Fever: T-705 Efficacy and Reduced Toxicity Suggests an Alternative to Ribavirin. PLoS ONE, 2008, 3, e3725.	2.5	71
49	Service-Learning for Graduate Students through a Student-Run Consulting Program. Journal of Statistics Education, 2007, 15 , .	1.4	5
50	[23] Random Forests for Microarrays. Methods in Enzymology, 2006, 411, 422-432.	1.0	65
51	Meta-Analysis Combines Affymetrix Microarray Results Across Laboratories. Comparative and Functional Genomics, 2005, 6, 116-122.	2.0	16