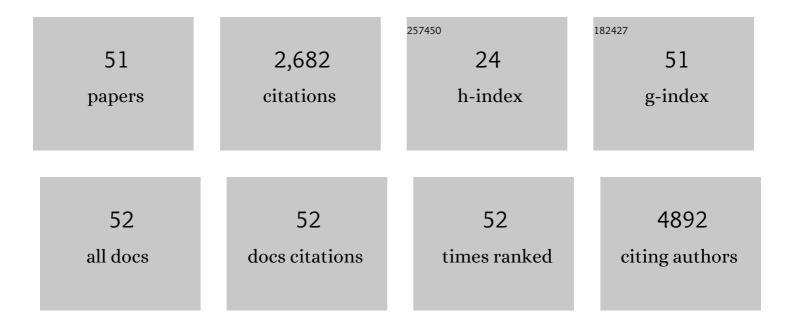
John R Stevens

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Plant–soil feedbacks: a metaâ€analytical review. Ecology Letters, 2008, 11, 980-992.	6.4	802
2	A Metaâ€Analytic Review of Corridor Effectiveness. Conservation Biology, 2010, 24, 660-668.	4.7	407
3	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
4	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
5	The PI3K/AKT signaling pathway: Associations of miRNAs with dysregulated gene expression in colorectal cancer. Molecular Carcinogenesis, 2018, 57, 243-261.	2.7	83
6	Expression Profiles of miRNA Subsets Distinguish Human Colorectal Carcinoma and Normal Colonic Mucosa. Clinical and Translational Gastroenterology, 2016, 7, e152.	2.5	82
7	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
8	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
9	Hierarchical Dependence in Meta-Analysis. Journal of Educational and Behavioral Statistics, 2009, 34, 46-73.	1.7	68
10	[23] Random Forests for Microarrays. Methods in Enzymology, 2006, 411, 422-432.	1.0	65
11	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
12	A comparison of multiple testing adjustment methods with block-correlation positively-dependent tests. PLoS ONE, 2017, 12, e0176124.	2.5	57
13	MicroRNAâ€ŧranscription 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
14	Colorectal tumor molecular phenotype and miRNA: expression profiles and prognosis. Modern Pathology, 2016, 29, 915-927.	5.5	41
15	Site-specific associations between miRNA expression and survival in colorectal cancer cases. Oncotarget, 2016, 7, 60193-60205.	1.8	41
16	Increased Susceptibility to Atrial Fibrillation Secondary to Atrial Fibrosis in Transgenic Goats Expressing Transforming Growth Factorâ€Î²1. Journal of Cardiovascular Electrophysiology, 2016, 27, 1220-1229.	1.7	40
17	Association of cigarette smoking and microRNA expression in rectal cancer: Insight into tumor phenotype. Cancer Epidemiology, 2016, 45, 98-107.	1.9	36
18	Disruption of epidermal specific gene expression and delayed skin development in AP-2Î ³ mutant mice. Developmental Biology, 2008, 317, 187-195.	2.0	34

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19	Poor maternal nutrition during gestation in sheep alters prenatal muscle growth and development in offspring. Journal of Animal Science, 2020, 98, .	0.5	32
20	miRNA involvement in cell cycle regulation in colorectal cancer cases. Genes and Cancer, 2018, 9, 53-65.	1.9	29
21	Diet and lifestyle factors associated with miRNA expression in colorectal tissue. Pharmacogenomics and Personalized Medicine, 2017, Volume10, 1-16.	0.7	28
22	Infrequently expressed miRNAs influence survival after diagnosis with colorectal cancer. Oncotarget, 2017, 8, 83845-83859.	1.8	28
23	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
24	Most soil trophic guilds increase plant growth: a metaâ€analytical review. Oikos, 2014, 123, 1409-1419.	2.7	26
25	Power in pairs: assessing the statistical value of paired samples in tests for differential expression. BMC Genomics, 2018, 19, 953.	2.8	26
26	Genetic variants in the TGFβ-signaling pathway influence expression of miRNAs in colon and rectal normal mucosa and tumor tissue. Oncotarget, 2017, 8, 16765-16783.	1.8	25
27	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
28	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
29	Infrequently expressed miRNAs in colorectal cancer tissue and tumor molecular phenotype. Modern Pathology, 2017, 30, 1152-1169.	5.5	17
30	Expression of Wnt-signaling pathway genes and their associations with miRNAs in colorectal cancer. Oncotarget, 2018, 9, 6075-6085.	1.8	17
31	Meta-Analysis Combines Affymetrix Microarray Results Across Laboratories. Comparative and Functional Genomics, 2005, 6, 116-122.	2.0	16
32	<i>metahdep</i> : meta-analysis of hierarchically dependent gene expression studies. Bioinformatics, 2009, 25, 2619-2620.	4.1	15
33	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
34	Transcription factorâ€microRNA associations and their impact on colorectal cancer survival. Molecular Carcinogenesis, 2017, 56, 2512-2526.	2.7	13
35	Incorporation of subject-level covariates in quantile normalization of miRNA data. BMC Genomics, 2015, 16, 1045.	2.8	11
36	Accounting for Missing Data in Clinical Research. JAMA - Journal of the American Medical Association, 2016, 315, 517.	7.4	11

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37	An Assessment of Database-Validated microRNA Target Genes in Normal Colonic Mucosa: Implications for Pathway Analysis. Cancer Informatics, 2017, 16, 117693511771640.	1.9	9
38	A comparison of probe-level and probeset models for small-sample gene expression data. BMC Bioinformatics, 2010, 11, 281.	2.6	8
39	The miRNA landscape of colorectal polyps. Genes Chromosomes and Cancer, 2017, 56, 347-353.	2.8	8
40	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
41	Alterations in microRNA expression associated with alcohol consumption in rectal cancer subjects. Cancer Causes and Control, 2017, 28, 545-555.	1.8	7
42	MicroRNA-messenger RNA interactions involving JAK-STAT signaling genes in colorectal cancer. Genes and Cancer, 2018, 9, 232-246.	1.9	6
43	Service-Learning for Graduate Students through a Student-Run Consulting Program. Journal of Statistics Education, 2007, 15, .	1.4	5
44	A shortcut for multiple testing on the directed acyclic graph of gene ontology. BMC Bioinformatics, 2014, 15, 349.	2.6	5
45	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
46	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
47	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
48	A Graphical Weighted Power Improving Multiplicity Correction Approach for SNP Selections. Current Genomics, 2014, 15, 380-389.	1.6	3
49	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
50	Assessing Numerical Dependence in Gene Expression Summaries with the Jackknife Expression Difference. PLoS ONE, 2012, 7, e39570.	2.5	2
51	A Bivariate Hypothesis Testing Approach for Mapping the Trait-Influential Gene. Scientific Reports, 2017, 7, 12798.	3.3	1