

Jennifer L Clarke

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

3,909
citations

201674

27
h-index

123424

61
g-index

85
all docs

85
docs citations

85
times ranked

7382
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression predictors of breast cancer outcomes. <i>Lancet, The</i> , 2003, 361, 1590-1596.	13.7	581
2	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 445-458.	6.2	290
3	The effects of child abuse and neglect on cognitive functioning in adulthood. <i>Journal of Psychiatric Research</i> , 2012, 46, 500-506.	3.1	272
4	Gene expression phenotypic models that predict the activity of oncogenic pathways. <i>Nature Genetics</i> , 2003, 34, 226-230.	21.4	247
5	An Integrated Genomic-Based Approach to Individualized Treatment of Patients With Advanced-Stage Ovarian Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 517-525.	1.6	247
6	Patterns of Gene Expression That Characterize Long-term Survival in Advanced Stage Serous Ovarian Cancers. <i>Clinical Cancer Research</i> , 2005, 11, 3686-3696.	7.0	246
7	Probiotic Bifidobacterium strains and galactooligosaccharides improve intestinal barrier function in obese adults but show no synergism when used together as synbiotics. <i>Microbiome</i> , 2018, 6, 121.	11.1	202
8	Integrated modeling of clinical and gene expression information for personalized prediction of disease outcomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8431-8436.	7.1	200
9	Gene Expression Phenotypes of Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 1922-1927.	2.4	131
10	Label-Free Quantitative LC-MS Proteomics of Alzheimer's Disease and Normally Aged Human Brains. <i>Journal of Proteome Research</i> , 2012, 11, 3053-3067.	3.7	131
11	A New Mouse Model for the Study of Human Breast Cancer Metastasis. <i>PLoS ONE</i> , 2012, 7, e47995.	2.5	126
12	Osteosarcoma: improvement in survival limited to high-grade patients only. <i>Journal of Cancer Research and Clinical Oncology</i> , 2011, 137, 597-607.	2.5	102
13	High insulin-like growth factor-2 (IGF-2) gene expression is an independent predictor of poor survival for patients with advanced stage serous epithelial ovarian cancer. <i>Gynecologic Oncology</i> , 2005, 96, 355-361.	1.4	84
14	Microarray Analysis of Early Stage Serous Ovarian Cancers Shows Profiles Predictive of Favorable Outcome. <i>Clinical Cancer Research</i> , 2009, 15, 2448-2455.	7.0	67
15	The Role of SATB1 in Breast Cancer Pathogenesis. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1284-1296.	6.3	67
16	Role of whole grains versus fruits and vegetables in reducing subclinical inflammation and promoting gastrointestinal health in individuals affected by overweight and obesity: a randomized controlled trial. <i>Nutrition Journal</i> , 2018, 17, 72.	3.4	67
17	Statistical expression deconvolution from mixed tissue samples. <i>Bioinformatics</i> , 2010, 26, 1043-1049.	4.1	59
18	Epigenetic pathways and glioblastoma treatment. <i>Epigenetics</i> , 2013, 8, 785-795.	2.7	54

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19	Prognostic index score and clinical prediction model of local regional recurrence after mastectomy in breast cancer patients. <i>International Journal of Radiation Oncology Biology Physics</i> , 2006, 64, 1401-1409.	0.8	52
20	Effects of processing moisture on the physical properties and in vitro digestibility of starch and protein in extruded brown rice and pinto bean composite flours. <i>Food Chemistry</i> , 2016, 211, 726-733.	8.2	42
21	A gut pathobiont synergizes with the microbiota to instigate inflammatory disease marked by immunoreactivity against other symbionts but not itself. <i>Scientific Reports</i> , 2017, 7, 17707.	3.3	41
22	Infiltrating S100A8+ myeloid cells promote metastatic spread of human breast cancer and predict poor clinical outcome. <i>Breast Cancer Research and Treatment</i> , 2014, 148, 41-59.	2.5	40
23	Predicting antibiotic resistance gene abundance in activated sludge using shotgun metagenomics and machine learning. <i>Water Research</i> , 2021, 202, 117384.	11.3	40
24	A Novel MAPK ϵ microRNA Signature Is Predictive of Hormone-Therapy Resistance and Poor Outcome in ER-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 373-385.	7.0	39
25	Cranberries and Cancer: An Update of Preclinical Studies Evaluating the Cancer Inhibitory Potential of Cranberry and Cranberry Derived Constituents. <i>Antioxidants</i> , 2016, 5, 27.	5.1	38
26	Impact of dietary pattern of the fecal donor on in vitro fermentation properties of whole grains and brans. <i>Journal of Functional Foods</i> , 2017, 29, 281-289.	3.4	33
27	Time series modeling of cell cycle exit identifies Brd4 dependent regulation of cerebellar neurogenesis. <i>Nature Communications</i> , 2019, 10, 3028.	12.8	33
28	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer's disease target. <i>Brain</i> , 2018, 141, 2721-2739.	7.6	31
29	Association between baseline abundance of <i>Peptoniphilus</i> , a Gram-positive anaerobic coccus, and wound healing outcomes of DFUs. <i>PLoS ONE</i> , 2020, 15, e0227006.	2.5	24
30	MicroRNA alterations in Barrett's esophagus, esophageal adenocarcinoma, and esophageal adenocarcinoma cell lines following cranberry extract treatment: Insights for chemoprevention. <i>Journal of Carcinogenesis</i> , 2011, 10, 34.	2.5	24
31	Epigenetic Pathways and Glioblastoma Treatment: Insights From Signaling Cascades. <i>Journal of Cellular Biochemistry</i> , 2015, 116, 351-363.	2.6	22
32	Existing and Potential Statistical and Computational Approaches for the Analysis of 3D CT Images of Plant Roots. <i>Agronomy</i> , 2018, 8, 71.	3.0	21
33	In silico and Ex vivo approaches identify a role for toll-like receptor 4 in colorectal cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2014, 33, 45.	8.6	20
34	Body composition, pre-diabetes and cardiovascular disease risk in early schizophrenia. <i>Microbial Biotechnology</i> , 2017, 11, 229-236.	1.7	16
35	Identifying Glioblastoma Gene Networks Based on Hypergeometric Test Analysis. <i>PLoS ONE</i> , 2014, 9, e115842.	2.5	15
36	Short term dynamics of the sputum microbiome among COPD patients. <i>PLoS ONE</i> , 2018, 13, e0191499.	2.5	15

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37	Regional and Temporal Differences in Gene Expression of LH _{BETA} T _{AG} Retinoblastoma Tumors. , 2011, 52, 5359.		14
38	Simultaneous analysis of tumor and stromal gene expression profiles from xenograft models. Breast Cancer Research and Treatment, 2012, 131, 321-324.	2.5	13
39	A systematic review and meta-analysis of the efficacy of processing stages and interventions for controlling <i>Campylobacter</i> contamination during broiler chicken processing. Comprehensive Reviews in Food Science and Food Safety, 2022, 21, 227-271.	11.7	13
40	Clustering Categorical Data via Ensembling Dissimilarity Matrices. Journal of Computational and Graphical Statistics, 2018, 27, 195-208.	1.7	12
41	Bayesian Weibull tree models for survival analysis of clinico-genomic data. Statistical Methodology, 2008, 5, 238-262.	0.5	10
42	Development of Advanced Imaging Criteria for the Endoscopic Identification of Inflammatory Polyps. Clinical and Translational Gastroenterology, 2015, 6, e128.	2.5	10
43	Development of a Multiplex Real-Time PCR Assay for Predicting Macrolide and Tetracycline Resistance Associated with Bacterial Pathogens of Bovine Respiratory Disease. Pathogens, 2021, 10, 64.	2.8	9
44	The application of the skin virome for human identification. Forensic Science International: Genetics, 2022, 57, 102662.	3.1	8
45	Post-ER Stress Biogenesis of Golgi Is Governed by Giantin. Cells, 2019, 8, 1631.	4.1	7
46	Cranberry Polyphenols in Esophageal Cancer Inhibition: New Insights. Nutrients, 2022, 14, 969.	4.1	6
47	Statistical Problem Classes and Their Links to Information Theory. Econometric Reviews, 2014, 33, 337-371.	1.1	5
48	Reclassifying Pseudopolyps in Inflammatory Bowel Disease: Histologic and Endoscopic Description in the New Era of Mucosal Healing. Crohn's & Colitis 360, 2019, 1, otz033.	1.1	5
49	A General Hybrid Clustering Technique. Journal of Computational and Graphical Statistics, 2019, 28, 540-551.	1.7	5
50	Prequential analysis of complex data with adaptive model reselection. Statistical Analysis and Data Mining, 2009, 2, 274-290.	2.8	4
51	Retinoblastoma treatment: impact of the glycolytic inhibitor 2-deoxy-d-glucose on molecular genomics expression in LHBETATAG retinal tumors. Clinical Ophthalmology, 2012, 6, 817.	1.8	4
52	Characteristics of cross-hybridization and cross-alignment of expression in pseudo-xenograft samples by RNA-Seq and microarrays. Journal of Clinical Bioinformatics, 2013, 3, 8.	1.2	4
53	NAPPN: Who We Are, Where We Are Going, and Why You Should Join Us!. The Plant Phenome Journal, 2019, 2, 1-4.	2.0	4
54	Student-led workshops: Filling skills gaps in computational research for life scientists. Journal of Natural Resources and Life Sciences Education, 2021, 50, e20052.	1.5	4

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55	Prediction in several conventional contexts. <i>Statistics Surveys</i> , 2012, 6, .	11.3	3
56	EnsCat: clustering of categorical data via ensembling. <i>BMC Bioinformatics</i> , 2016, 17, 380.	2.6	3
57	Analysis of genetic and nongenetic factors influencing triglycerides-lowering drug effects based on paired observations. <i>BMC Proceedings</i> , 2018, 12, 46.	1.6	3
58	Assessment of the Doseâ€“Response Relationship Between Folate Exposure and Cognitive Impairment: Synthesizing Data from Documented Studies. <i>Risk Analysis</i> , 2020, 40, 276-293.	2.7	3
59	Gluten Cross-Contact in Restaurant-Scale Pasta Cooking. <i>Journal of Food Protection</i> , 2021, 84, 2159-2162.	1.7	3
60	A Bayes testing approach to metagenomic profiling in bacteria. <i>Statistics and Its Interface</i> , 2015, 8, 173-185.	0.3	3
61	Proanthocyanidins mitigate bile acidâ€“induced changes in GSTT2 levels in a panel of racially diverse patientâ€“derived primary esophageal cell cultures. <i>Molecular Carcinogenesis</i> , 2022, 61, 281-287.	2.7	3
62	Estimating the proportions in a mixed sample using transcriptomics. <i>Stat</i> , 2014, 3, 313-325.	0.4	2
63	Modeling association in microbial communities with clique loglinear models. <i>Annals of Applied Statistics</i> , 2019, 13, .	1.1	2
64	Alignment behaviors of short peptides provide a roadmap for functional profiling of metagenomic data. <i>BMC Genomics</i> , 2015, 16, 1080.	2.8	1
65	O2â€“06â€“01: The Human Brainome: Human Brain Genome, Transcriptome, and Proteome Integration. <i>Alzheimer's and Dementia</i> , 2016, 12, P237.	0.8	1
66	Detecting bacterial genomes in a metagenomic sample using NGS reads. <i>Statistics and Its Interface</i> , 2015, 8, 477-494.	0.3	1
67	Ten simple rules to ruin a collaborative environment. <i>PLoS Computational Biology</i> , 2022, 18, e1009957.	3.2	1
68	An ensemble approach to improved prediction from multitype data. , 2008, , 302-317.		0
69	Abstract 4597: MAPK-mediated gene expression in ER-negative breast cancer: Role of miRNAs and Ago2. , 2010, , .		0
70	Abstract 3946: Investigation of a hyperactive MAPK microRNA expression profile reveals potential role for microRNAs in the generation and maintenance of ER- phenotype in breast cancer. , 2011, , .		0
71	Abstract 4196: Identification and investigation of ethnic specific gene expression differences in non-cancerous breast tissue. , 2012, , .		0
72	Abstract 3171: Hyperactive MAPK dysregulation of microRNAs contributes to the ER-negative phenotype in breast cancer. , 2012, , .		0

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73	Abstract 2994: Characteristics of cross-hybridization/cross-alignment of expression in xenograft samples by RNAseq and microarrays. , 2012, , .		0
74	Abstract PR03: Investigation of transcriptome differences in breast cancer tissues from African American and East African patients with triple-negative breast cancer.. , 2012, , .		0
75	Abstract B35: Cumulative results from an investigation of transcriptome differences in breast cancer samples from African American and East African triple-negative breast cancer patients. , 2014, , .		0
76	Abstract P4-07-07: A MAPK microRNA signature significantly associated with poor outcome and predictive of response to tamoxifen therapy in ER+ breast cancer. , 2015, , .		0
77	Abstract 65: An integrated bioinformatics approach for identifying patient-specific gene networks and novel therapeutic targets in glioblastoma. , 2015, , .		0
78	Metabolic Syndrome, Gut Microbiome and Dietary Bioactive Peptides, an Unexplored Triad. Diabetes, 2018, 4, 1.	0.1	0
79	Quantitative modeling of the survival of <i>Listeria monocytogenes</i> in soy sauce-based acidified food products. International Journal of Food Microbiology, 2022, 370, 109635.	4.7	0
80	Genome Sequence of Feline Papillomavirus Strain P20 Assembled from Metagenomic Data from the Skin of a House Cat Owner. Microbiology Resource Announcements, 0, , .	0.6	0