

James Lyons-Weiler

List of Publications by Year in descending order

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63
papers

3,737
citations

218677

26
h-index

161849

54
g-index

69
all docs

69
docs citations

69
times ranked

6373
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of transfer of functional microRNAs between mouse dendritic cells via exosomes. <i>Blood</i> , 2012, 119, 756-766.	1.4	1,164
2	Altered Global Gene Expression in First Trimester Placentas of Women Destined to Develop Preeclampsia. <i>Placenta</i> , 2009, 30, 15-24.	1.5	226
3	Lung tissues in patients with systemic sclerosis have gene expression patterns unique to pulmonary fibrosis and pulmonary hypertension. <i>Arthritis and Rheumatism</i> , 2011, 63, 783-794.	6.7	208
4	Independent and combined analyses of sequences from all three genomic compartments converge on the root of flowering plant phylogeny. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13166-13171.	7.1	188
5	Microbial Risk Indicators of Early Childhood Caries. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5753-5759.	3.9	178
6	Relative apparent synapomorphy analysis (RASA). I: The statistical measurement of phylogenetic signal. <i>Molecular Biology and Evolution</i> , 1996, 13, 749-757.	8.9	135
7	Pathogenic priming likely contributes to serious and critical illness and mortality in COVID-19 via autoimmunity. <i>Journal of Translational Autoimmunity</i> , 2020, 3, 100051.	4.0	121
8	Intron sliding in conserved gene families. <i>Trends in Genetics</i> , 2000, 16, 430-432.	6.7	104
9	Identification of ATF-3, caveolin-1, DLC-1, and NM23-H2 as putative antitumorigenic, progesterone-regulated genes for ovarian cancer cells by gene profiling. <i>Oncogene</i> , 2005, 24, 1774-1787.	5.9	104
10	Escaping from the Felsenstein Zone by Detecting Long Branches in Phylogenetic Data. <i>Molecular Phylogenetics and Evolution</i> , 1997, 8, 375-384.	2.7	83
11	Direct Regulation of Diurnal <i>Drd3</i> Expression and Cocaine Reward by NPAS2. <i>Biological Psychiatry</i> , 2015, 77, 425-433.	1.3	79
12	caGEDA. <i>Applied Bioinformatics</i> , 2004, 3, 49-62.	1.6	76
13	Optimal outgroup analysis. <i>Biological Journal of the Linnean Society</i> , 1998, 64, 493-511.	1.6	74
14	Heritability of Oral Microbial Species in Caries-Active and Caries-Free Twins. <i>Twin Research and Human Genetics</i> , 2007, 10, 821-828.	0.6	60
15	Gene expression patterns in isolated keloid fibroblasts. <i>Wound Repair and Regeneration</i> , 2006, 14, 463-470.	3.0	59
16	Prediction of Lymph Node Metastasis by Analysis of Gene Expression Profiles in Primary Lung Adenocarcinomas. <i>Clinical Cancer Research</i> , 2005, 11, 4128-4135.	7.0	57
17	Proteomic Analysis of Urine in Kidney Transplant Patients with BK Virus Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2006, 17, 3248-3256.	6.1	52
18	Molecular overlap of fly circadian rhythms and human pancreatic cancer. <i>Cancer Letters</i> , 2006, 243, 55-57.	7.2	51

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19	Interleukin-17 limits hypoxia-inducible factor 1 α and development of hypoxic granulomas during tuberculosis. <i>JCI Insight</i> , 2017, 2, .	5.0	45
20	Finding Optimal Ingroup Topologies and Convexities When the Choice of Outgroups Is Not Obvious. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 348-357.	2.7	41
21	A Classification-Based Machine Learning Approach for the Analysis of Genome-Wide Expression Data. <i>Genome Research</i> , 2003, 13, 503-512.	5.5	40
22	Tests for finding complex patterns of differential expression in cancers: towards individualized medicine. <i>BMC Bioinformatics</i> , 2004, 5, 110.	2.6	38
23	Cellular factors associated with latency and spontaneous Epstein-Barr virus reactivation in B-lymphoblastoid cell lines. <i>Virology</i> , 2010, 400, 53-67.	2.4	36
24	Evaluation of the Consensus of Four Peptide Identification Algorithms for Tandem Mass Spectrometry Based Proteomics. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 039-047.	0.4	34
25	Feature Selection for Classification of SELDI-TOF-MS Proteomic Profiles. <i>Applied Bioinformatics</i> , 2005, 4, 227-246.	1.6	28
26	Progression-Associated Genes in Astrocytoma Identified by Novel Microarray Gene Expression Data Reanalysis. <i>Methods in Molecular Biology</i> , 2007, 377, 203-221.	0.9	27
27	Efficiency Analysis of Competing Tests for Finding Differentially Expressed Genes in Lung Adenocarcinoma. <i>Cancer Informatics</i> , 2008, 6, CIN.S791.	1.9	26
28	Reconsideration of the immunotherapeutic pediatric safe dose levels of aluminum. <i>Journal of Trace Elements in Medicine and Biology</i> , 2018, 48, 67-73.	3.0	24
29	A Phylogenetic Approach to the Problem of Differential Lineage Sorting. <i>Molecular Biology and Evolution</i> , 1997, 14, 968-975.	8.9	23
30	Profiling molecular changes induced by hydrogen treatment of lung allografts prior to procurement. <i>Biochemical and Biophysical Research Communications</i> , 2012, 425, 873-879.	2.1	23
31	The Effect of Environmental Enrichment on Substantia Nigra Gene Expression after Traumatic Brain Injury in Rats. <i>Journal of Neurotrauma</i> , 2013, 30, 259-270.	3.4	22
32	Acute exposure and chronic retention of aluminum in three vaccine schedules and effects of genetic and environmental variation. <i>Journal of Trace Elements in Medicine and Biology</i> , 2020, 58, 126444.	3.0	22
33	Differential hippocampal gene expression and pathway analysis in an etiology-based mouse model of major depressive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2014, 165, 457-466.	1.7	21
34	Altered DNA methylation in PAH deficient phenylketonuria. <i>Molecular Genetics and Metabolism</i> , 2015, 115, 72-77.	1.1	20
35	Assessing the statistical significance of the achieved classification error of classifiers constructed using serum peptide profiles, and a prescription for random sampling repeated studies for massive high-throughput genomic and proteomic studies. <i>Cancer Informatics</i> , 2005, 1, 53-77.	1.9	18
36	Null Model Selection, Compositional Bias, Character State Bias, and the Limits of Phylogenetic Information. <i>Molecular Biology and Evolution</i> , 1999, 16, 1400-1405.	8.9	17

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37	DNA methylation in the pathophysiology of hyperphenylalaninemia in the PAH enu2 mouse model of phenylketonuria. <i>Molecular Genetics and Metabolism</i> , 2016, 119, 1-7.	1.1	17
38	Optimization of the Use of Consensus Methods for the Detection and Putative Identification of Peptides via Mass-spectrometry Using Protein Standard Mixtures. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 262-273.	0.4	17
39	Assessment of protein stability in cerebrospinal fluid using surface-enhanced laser desorption/ionization time-of-flight mass spectrometry protein profiling. <i>Clinical Proteomics</i> , 2006, 2, 91-101.	2.1	15
40	Intersession reproducibility of mass spectrometry profiles and its effect on accuracy of multivariate classification models. <i>Bioinformatics</i> , 2007, 23, 3065-3072.	4.1	15
41	Standards of excellence and open questions in cancer biomarker research: an informatics perspective. <i>Cancer Informatics</i> , 2005, 1, 1-7.	1.9	15
42	Branch Length Heterogeneity Leads to Nonindependent Branch Length Estimates and Can Decrease the Efficiency of Methods of Phylogenetic Inference. <i>Journal of Molecular Evolution</i> , 1999, 49, 392-405.	1.8	14
43	Feature Selection and Dimensionality Reduction in Genomics and Proteomics. , 2007, , 149-172.		14
44	Overcoming confounded controls in the analysis of gene expression data from microarray experiments. <i>Applied Bioinformatics</i> , 2003, 2, 197-208.	1.6	14
45	Clinical decision modeling system. <i>BMC Medical Informatics and Decision Making</i> , 2007, 7, 23.	3.0	11
46	Determining the statistical significance of survivorship prediction models. <i>Journal of Evaluation in Clinical Practice</i> , 2010, 16, 155-165.	1.8	11
47	Expression of three topologically distinct membrane proteins elicits unique stress response pathways in the yeast <i>Saccharomyces cerevisiae</i> . <i>Physiological Genomics</i> , 2015, 47, 198-214.	2.3	10
48	Variations in Discovery-Based Preeclampsia Candidate Genes. <i>Clinical and Translational Science</i> , 2012, 5, 333-339.	3.1	9
49	Assessing the Statistical Significance of the Achieved Classification Error of Classifiers Constructed using Serum Peptide Profiles, and a Prescription for Random Sampling Repeated Studies for Massive High-Throughput Genomic and Proteomic Studies. <i>Cancer Informatics</i> , 2005, 1, 117693510500100.	1.9	7
50	Relative Incidence of Office Visits and Cumulative Rates of Billed Diagnoses Along the Axis of Vaccination. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 8674.	2.6	7
51	Optimal outgroup analysis. <i>Biological Journal of the Linnean Society</i> , 1998, 64, 493-511.	1.6	7
52	Hepatic Gene Expression Response to Acute Indomethacin Exposure. <i>Molecular Diagnosis and Therapy</i> , 2006, 10, 187-196.	3.8	6
53	Methylome repatterning in a mouse model of Maternal PKU Syndrome. <i>Molecular Genetics and Metabolism</i> , 2014, 113, 194-199.	1.1	6
54	Standards of Excellence and Open Questions in Cancer Biomarker Research: An Informatics Perspective. <i>Cancer Informatics</i> , 2005, 1, 117693510500100.	1.9	5

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55	Impact of catch-up vaccination on aluminum exposure due to new laws and post social distancing. <i>Journal of Trace Elements in Medicine and Biology</i> , 2020, 62, 126649.	3.0	1
56	Challenges and Opportunities for Biological Language Modelling in Biomedical High-Throughput Genomic and Proteomic Informatics. <i>Applied Bioinformatics</i> , 2004, 3, 77-80.	1.6	0
57	Serum Proteomic Profiling and Analysis. , 2005, , 649-659.		0
58	Molecular Profiling Of Lung Tissues And Primary Fibroblasts From Patients With Systemic Sclerosis. , 2010, , .		0
59	Su1999 Dietary Modulation of the Colonic Gene Expression in High Colon Cancer Risk African Americans. <i>Gastroenterology</i> , 2013, 144, S-528.	1.3	0
60	Who are We, and Who (or What) Do We Want to Become? An Evolutionary Perspective on Biotransformative Technologies. <i>Biological Theory</i> , 0, , 1.	1.5	0
61	Abstract 4624: Differentiation of female donors classified as "normal" with benign disease and with breast cancer based on blood RNA signature. , 2010, , .		0
62	Prediction of severity and subtype of fibrosing disease using model informed by inflammation and extracellular matrix gene index. <i>PLoS ONE</i> , 2020, 15, e0240986.	2.5	0
63	Progression-Associated Genes in Astrocytoma Identified by Novel Microarray Gene Expression Data Reanalysis. , 0, , 203-222.		0