James Lyons-Weiler

List of Publications by Year
in descending order

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	Acute exposure and chronic retention of aluminum in three vaccine schedules and effects of genetic and environmental variation. Journal of Trace Elements in Medicine and Biology, 2020, 58, 126444.	3.0	22
2	Relative Incidence of Office Visits and Cumulative Rates of Billed Diagnoses Along the Axis of Vaccination. International Journal of Environmental Research and Public Health, 2020, 17, 8674.	2.6	7
3	Impact of catch-up vaccination on aluminum exposure due to new laws and post social distancing. Journal of Trace Elements in Medicine and Biology, 2020, 62, 126649.	3.0	1
4	Pathogenic priming likely contributes to serious and critical illness and mortality in COVID-19 via autoimmunity. Journal of Translational Autoimmunity, 2020, 3, 100051.	4.0	121
5	Prediction of severity and subtype of fibrosing disease using model informed by inflammation and extracellular matrix gene index. PLoS ONE, 2020, 15, e0240986.	2.5	0
6	Reconsideration of the immunotherapeutic pediatric safe dose levels of aluminum. Journal of Trace Elements in Medicine and Biology, 2018, 48, 67-73.	3.0	24
7	Interleukin-17 limits hypoxia-inducible factor 1α and development of hypoxic granulomas during tuberculosis. JCI Insight, 2017, 2, .	5.0	45
8	DNA methylation in the pathophysiology of hyperphenylalaninemia in the PAH enu2 mouse model of phenylketonuria. Molecular Genetics and Metabolism, 2016, 119, 1-7.	1.1	17
9	Altered DNA methylation in PAH deficient phenylketonuria. Molecular Genetics and Metabolism, 2015, 115, 72-77.	1.1	20
10	Direct Regulation of Diurnal Drd3 Expression and Cocaine Reward by NPAS2. Biological Psychiatry, 2015, 77, 425-433.	1.3	79
11	Expression of three topologically distinct membrane proteins elicits unique stress response pathways in the yeast<i>Saccharomyces cerevisiae</i>. Physiological Genomics, 2015, 47, 198-214.	2.3	10
12	Differential hippocampal gene expression and pathway analysis in an etiology‐based mouse model of major depressive disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 457-466.	1.7	21
13	Methylome repatterning in a mouse model of Maternal PKU Syndrome. Molecular Genetics and Metabolism, 2014, 113, 194-199.	1.1	6
14	The Effect of Environmental Enrichment on Substantia Nigra Gene Expression after Traumatic Brain Injury in Rats. Journal of Neurotrauma, 2013, 30, 259-270.	3.4	22
15	Su1999 Dietary Modulation of the Colonic Gene Expression in High Colon Cancer Risk African Americans. Gastroenterology, 2013, 144, S-528.	1.3	0
16	Variations in Discovery‐Based Preeclampsia Candidate Genes. Clinical and Translational Science, 2012, 5, 333-339.	3.1	9
17	Mechanism of transfer of functional microRNAs between mouse dendritic cells via exosomes. Blood, 2012, 119, 756-766.	1.4	1,164
18	Profiling molecular changes induced by hydrogen treatment of lung allografts prior to procurement. Biochemical and Biophysical Research Communications, 2012, 425, 873-879.	2.1	23

#	ARTICLE	IF	CITATIONS
19	Lung tissues in patients with systemic sclerosis have gene expression patterns unique to pulmonary fibrosis and pulmonary hypertension. Arthritis and Rheumatism, 2011, 63, 783-794.	6.7	208
20	Molecular Profiling Of Lung Tissues And Primary Fibroblasts From Patients With Systemic Sclerosis. , 2010, , .		0
21	Cellular factors associated with latency and spontaneous Epstein–Barr virus reactivation in B-lymphoblastoid cell lines. Virology, 2010, 400, 53-67.	2.4	36
22	Determining the statistical significance of survivorship prediction models. Journal of Evaluation in Clinical Practice, 2010, 16, 155-165.	1.8	11
23	Evaluation of the Consensus of Four Peptide Identification Algorithms for Tandem Mass Spectrometry Based Proteomics. Journal of Proteomics and Bioinformatics, 2010, 03, 039-047.	0.4	34
24	Abstract 4624: Differentiation of female donors classified as "normal" with benign disease and with breast cancer based on blood RNA signature. , 2010, , .		0
25	Altered Global Gene Expression in First Trimester Placentas of Women Destined to Develop Preeclampsia. Placenta, 2009, 30, 15-24.	1.5	226
26	Optimization of the Use of Consensus Methods for the Detection and Putative Identification of Peptides via Mass-spectrometry Using Protein Standard Mixtures. Journal of Proteomics and Bioinformatics, 2009, 02, 262-273.	0.4	17
27	Efficiency Analysis of Competing Tests for Finding Differentially Expressed Genes in Lung Adenocarcinoma. Cancer Informatics, 2008, 6, CIN.S791.	1.9	26
28	Intersession reproducibility of mass spectrometry profiles and its effect on accuracy of multivariate classification models. Bioinformatics, 2007, 23, 3065-3072.	4.1	15
29	Heritability of Oral Microbial Species in Caries-Active and Caries-Free Twins. Twin Research and Human Genetics, 2007, 10, 821-828.	0.6	60
30	Clinical decision modeling system. BMC Medical Informatics and Decision Making, 2007, 7, 23.	3.0	11
31	Feature Selection and Dimensionality Reduction in Genomics and Proteomics. , 2007, , 149-172.		14
32	Progression-Associated Genes in Astrocytoma Identified by Novel Microarray Gene Expression Data Reanalysis. Methods in Molecular Biology, 2007, 377, 203-221.	0.9	27
33	Hepatic Gene Expression Response to Acute Indomethacin Exposure. Molecular Diagnosis and Therapy, 2006, 10, 187-196.	3.8	6
34	Molecular overlap of fly circadian rhythms and human pancreatic cancer. Cancer Letters, 2006, 243, 55-57.	7.2	51
35	Gene expression patterns in isolated keloid fibroblasts. Wound Repair and Regeneration, 2006, 14, 463-470.	3.0	59
36	Assessment of protein stability in cerebrospinal fluid using surface-enhanced laser desorption/ionization time-of-flight mass spectrometry protein profiling. Clinical Proteomics, 2006, 2, 91-101.	2.1	15

#	Article	IF	Citations
37	Proteomic Analysis of Urine in Kidney Transplant Patients with BK Virus Nephropathy. Journal of the American Society of Nephrology: JASN, 2006, 17, 3248-3256.	6.1	52
38	Identification of ATF-3, caveolin-1, DLC-1, and NM23-H2 as putative antitumorigenic, progesterone-regulated genes for ovarian cancer cells by gene profiling. Oncogene, 2005, 24, 1774-1787.	5.9	104
39	Standards of Excellence and Open Questions in Cancer Biomarker Research: An Informatics Perspective. Cancer Informatics, 2005, 1, 117693510500100.	1.9	5
40	Serum Proteomic Profiling and Analysis. , 2005, , 649-659.		0
41	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. Cancer Informatics, 2005, 1, 117693510500100.	1.9	7
42	Prediction of Lymph Node Metastasis by Analysis of Gene Expression Profiles in Primary Lung Adenocarcinomas. Clinical Cancer Research, 2005, 11, 4128-4135.	7.0	57
43	Microbial Risk Indicators of Early Childhood Caries. Journal of Clinical Microbiology, 2005, 43, 5753-5759.	3.9	178
44	Feature Selection for Classification of SELDI-TOF-MS Proteomic Profiles. Applied Bioinformatics, 2005, 4, 227-246.	1.6	28
45	Standards of excellence and open questions in cancer biomarker research: an informatics perspective. Cancer Informatics, 2005, 1, 1-7.	1.9	15
46	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. Cancer Informatics, 2005, 1, 53-77.	1.9	18
47	Tests for finding complex patterns of differential expression in cancers: towards individualized medicine. BMC Bioinformatics, 2004, 5, 110.	2.6	38
48	Challenges and Opportunities for Biological Language Modelling in Biomedical High-Throughput Genomic and Proteomic Informatics. Applied Bioinformatics, 2004, 3, 77-80.	1.6	0
49	caGEDA. Applied Bioinformatics, 2004, 3, 49-62.	1.6	76
50	A Classification-Based Machine Learning Approach for the Analysis of Genome-Wide Expression Data. Genome Research, 2003, 13, 503-512.	5.5	40
51	Overcoming confounded controls in the analysis of gene expression data from microarray experiments. Applied Bioinformatics, 2003, 2, 197-208.	1.6	14
52	Intron sliding in conserved gene families. Trends in Genetics, 2000, 16, 430-432.	6.7	104
53	Independent and combined analyses of sequences from all three genomic compartments converge on the root of flowering plant phylogeny. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13166-13171.	7.1	188
54	Branch Length Heterogeneity Leads to Nonindependent Branch Length Estimates and Can Decrease the Efficiency of Methods of Phylogenetic Inference. Journal of Molecular Evolution, 1999, 49, 392-405.	1.8	14

#	Article	IF	Citations
55	Null Model Selection, Compositional Bias, Character State Bias, and the Limits of Phylogenetic Information. Molecular Biology and Evolution, 1999, 16, 1400-1405.	8.9	17
56	Optimal outgroup analysis. Biological Journal of the Linnean Society, 1998, 64, 493-511.	1.6	74
57	Finding Optimal Ingroup Topologies and Convexities When the Choice of Outgroups Is Not Obvious. Molecular Phylogenetics and Evolution, 1998, 9, 348-357.	2.7	41
58	Optimal outgroup analysis. Biological Journal of the Linnean Society, 1998, 64, 493-511.	1.6	7
59	A Phylogenetic Approach to the Problem of Differential Lineage Sorting. Molecular Biology and Evolution, 1997, 14, 968-975.	8.9	23
60	Escaping from the Felsenstein Zone by Detecting Long Branches in Phylogenetic Data. Molecular Phylogenetics and Evolution, 1997, 8, 375-384.	2.7	83
61	Relative apparent synapomorphy analysis (RASA). I: The statistical measurement of phylogenetic signal. Molecular Biology and Evolution, 1996, 13, 749-757.	8.9	135
62	Who are We, and Who (or What) Do We Want to Become? An Evolutionary Perspective on Biotransformative Technologies. Biological Theory, 0, , 1.	1.5	0
63	Progression-Associated Genes in Astrocytoma Identified by Novel Microarray Gene Expression Data Reanalysis. , 0, , 203-222.		0