Marc E Lenburg

List of Publications by Year
in descending order

100 papers	10,914 citations	50276 46 h-index	36028 97 g-index
108 all docs	108 docs citations	108 times ranked	17497 citing authors

#	Article	IF	Citations
1	The Achilles' heel of senescent cells: from transcriptome to senolytic drugs. Aging Cell, 2015, 14, 644-658.	6.7	1,534
2	Nef induces CD4 endocytosis: Requirement for a critical dileucine motif in the membrane-proximal CD4 cytoplasmic domain. Cell, 1994, 76, 853-864.	28.9	727
3	A Common Genetic Variant Is Associated with Adult and Childhood Obesity. Science, 2006, 312, 279-283.	12.6	652
4	Dicer, Drosha, and Outcomes in Patients with Ovarian Cancer. New England Journal of Medicine, 2008, 359, 2641-2650.	27.0	633
5	Airway epithelial gene expression in the diagnostic evaluation of smokers with suspect lung cancer. Nature Medicine, 2007, 13, 361-366.	30.7	507
6	MicroRNAs as modulators of smoking-induced gene expression changes in human airway epithelium. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2319-2324.	7.1	402
7	Identification of depot-specific human fat cell progenitors through distinct expression profiles and developmental gene patterns. American Journal of Physiology - Endocrinology and Metabolism, 2007, 292, E298-E307.	3.5	309
8	MYC pathway activation in triple-negative breast cancer is synthetic lethal with CDK inhibition. Journal of Experimental Medicine, 2012, 209, 679-696.	8.5	309
9	Chemotherapy response and recurrence-free survival in neoadjuvant breast cancer depends on biomarker profiles: results from the I-SPY 1 TRIAL (CALGB 150007/150012; ACRIN 6657). Breast Cancer Research and Treatment, 2012, 132, 1049-1062.	2.5	286
10	Asthma–COPD Overlap. Clinical Relevance of Genomic Signatures of Type 2 Inflammation in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 758-766.	5.6	257
11	Epithelial Mesenchymal Transition Traits in Human Breast Cancer Cell Lines Parallel the CD44hi/CD24lo/- Stem Cell Phenotype in Human Breast Cancer. Journal of Mammary Gland Biology and Neoplasia, 2010, 15, 235-252.	2.7	252
12	A Bronchial Genomic Classifier for the Diagnostic Evaluation of Lung Cancer. New England Journal of Medicine, 2015, 373, 243-251.	27.0	230
13	Previously unidentified changes in renal cell carcinoma gene expression identified by parametric analysis of microarray data. BMC Cancer, 2003, 3, 31.	2.6	228
14	Reversible and permanent effects of tobacco smoke exposure on airway epithelial gene expression. Genome Biology, 2007, 8, R201.	9.6	217
15	Airway PI3K Pathway Activation Is an Early and Reversible Event in Lung Cancer Development. Science Translational Medicine, 2010, 2, 26ra25.	12.4	215
16	A single-sample microarray normalization method to facilitate personalized-medicine workflows. Genomics, 2012, 100, 337-344.	2.9	212
17	Host Response to the Lung Microbiome in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 438-445.	5.6	195
18	Smoking-induced gene expression changes in the bronchial airway are reflected in nasal and buccal epithelium. BMC Genomics, 2008, 9, 259.	2.8	194

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19	The UCSC Cancer Genomics Browser. Nature Methods, 2009, 6, 239-240.	19.0	167
20	Smad Signaling Is Required to Maintain Epigenetic Silencing during Breast Cancer Progression. Cancer Research, 2010, 70, 968-978.	0.9	162
21	Characterizing the Impact of Smoking and Lung Cancer on the Airway Transcriptome Using RNA-Seq. Cancer Prevention Research, 2011, 4, 803-817.	1.5	144
22	A Dynamic Bronchial Airway Gene Expression Signature of Chronic Obstructive Pulmonary Disease and Lung Function Impairment. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 933-942.	5.6	142
23	FAM83A confers EGFR-TKI resistance in breast cancer cells and in mice. Journal of Clinical Investigation, 2012, 122, 3211-3220.	8.2	126
24	DNA Methylation Is Globally Disrupted and Associated with Expression Changes in Chronic Obstructive Pulmonary Disease Small Airways. American Journal of Respiratory Cell and Molecular Biology, 2014, 50, 912-922.	2.9	122
25	The expression level of HJURP has an independent prognostic impact and predicts the sensitivity to radiotherapy in breast cancer. Breast Cancer Research, 2010, 12, R18.	5.0	115
26	Integrated Genomics Reveals Convergent Transcriptomic Networks Underlying Chronic Obstructive Pulmonary Disease and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 948-960.	5.6	110
27	Similarities and differences between smoking-related gene expression in nasal and bronchial epithelium. Physiological Genomics, 2010, 41, 1-8.	2.3	107
28	Gene expression abnormalities in histologically normal breast epithelium of breast cancer patients. International Journal of Cancer, 2008, 122, 1557-1566.	5.1	105
29	A gene expression signature of emphysema-related lung destruction and its reversal by the tripeptide GHK. Genome Medicine, 2012, 4, 67.	8.2	94
30	Gene Co-Expression Modules as Clinically Relevant Hallmarks of Breast Cancer Diversity. PLoS ONE, 2014, 9, e88309.	2.5	94
31	A Prediction Model for Lung Cancer Diagnosis that Integrates Genomic and Clinical Features. Cancer Prevention Research, 2008, 1, 56-64.	1.5	89
32	Aging, Depot Origin, and Preadipocyte Gene Expression. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2010, 65A, 242-251.	3.6	76
33	Molecular Profiling of Premalignant Lesions in Lung Squamous Cell Carcinomas Identifies Mechanisms Involved in Stepwise Carcinogenesis. Cancer Prevention Research, 2014, 7, 487-495.	1.5	74
34	Molecular subtyping reveals immune alterations associated with progression of bronchial premalignant lesions. Nature Communications, 2019, 10, 1856.	12.8	70
35	Comparison of Proteomic and Transcriptomic Profiles in the Bronchial Airway Epithelium of Current and Never Smokers. PLoS ONE, 2009, 4, e5043.	2.5	66
36	Airway gene expression in COPD is dynamic with inhaled corticosteroid treatment and reflects biological pathways associated with disease activity. Thorax, 2014, 69, 14-23.	5.6	65

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37	Derivation of a bronchial genomic classifier for lung cancer in a prospective study of patients undergoing diagnostic bronchoscopy. BMC Medical Genomics, 2015, 8, 18.	1.5	64
38	Characterizing smoking-induced transcriptional heterogeneity in the human bronchial epithelium at single-cell resolution. Science Advances, 2019, 5, eaaw3413.	10.3	64
39	miR-638 regulates gene expression networks associated with emphysematous lung destruction. Genome Medicine, 2013, 5, 114.	8.2	62
40	Replication licensing promotes cyclin D1 expression and G_1 progression in untransformed human cells. Cell Cycle, 2009, 8, 125-136.	2.6	59
41	MicroRNA 4423 is a primate-specific regulator of airway epithelial cell differentiation and lung carcinogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18946-18951.	7.1	57
42	Molecular Impact of Electronic Cigarette Aerosol Exposure in Human Bronchial Epithelium. Toxicological Sciences, 2017, 155, 248-257.	3.1	56
43	Presence of a Putative Tumor-Initiating Progenitor Cell Population Predicts Poor Prognosis in Smokers with Non–Small Cell Lung Cancer. Cancer Research, 2010, 70, 6639-6648.	0.9	53
44	The cellular and molecular determinants of emphysematous destruction in COPD. Scientific Reports, 2017, 7, 9562.	3.3	53
45	Cholinergic Receptor and Cyclic Stretch-Mediated Inflammatory Gene Expression in Intact ASM. American Journal of Respiratory Cell and Molecular Biology, 2006, 34, 417-425.	2.9	49
46	Reliability and Reproducibility of Gene Expression Measurements Using Amplified RNA from Laser-Microdissected Primary Breast Tissue with Oligonucleotide Arrays. Journal of Molecular Diagnostics, 2005, 7, 57-64.	2.8	47
47	Transcriptomic Studies of the Airway Field of Injury Associated with Smoking-Related Lung Disease. Proceedings of the American Thoracic Society, 2011, 8, 173-179.	3.5	47
48	Shared Gene Expression Alterations in Nasal and Bronchial Epithelium for Lung Cancer Detection. Journal of the National Cancer Institute, 2017, 109, .	6.3	44
49	Nondestructive cryomicro-CT imaging enables structural and molecular analysis of human lung tissue. Journal of Applied Physiology, 2017, 122, 161-169.	2.5	39
50	Pharmacogenomic Identification of Targets for Adjuvant Therapy with the Topoisomerase Poison Camptothecin. Cancer Research, 2004, 64, 2096-2104.	0.9	38
51	PGE2-Driven Expression of c-Myc and OncomiR-17-92 Contributes to Apoptosis Resistance in NSCLC. Molecular Cancer Research, 2014, 12, 765-774.	3.4	37
52	Detecting the Presence and Progression of Premalignant Lung Lesions via Airway Gene Expression. Clinical Cancer Research, 2017, 23, 5091-5100.	7.0	37
53	A gene expression signature of emphysematous lung destruction and its reversal by the tripeptide GHK. Genome Medicine, 2012, 4, 67.	8.2	37
54	Translating the COPD Transcriptome: Insights into Pathogenesis and Tools for Clinical Management. Proceedings of the American Thoracic Society, 2008, 5, 834-841.	3.5	36

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55	Clinical Utility of a Bronchial Genomic Classifier in Patients With Suspected Lung Cancer. Chest, 2016, 150, 210-218.	0.8	34
56	Identification of transforming growth factor-beta-regulated microRNAs and the microRNA-targetomes in primary lung fibroblasts. PLoS ONE, 2017, 12, e0183815.	2.5	34
57	Nasal gene expression differentiates COPD from controls and overlaps bronchial gene expression. Respiratory Research, 2017, 18, 213.	3.6	33
58	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. Rna, 2015, 21, 164-171.	3.5	31
59	Alterations in Bronchial Airway miRNA Expression for Lung Cancer Detection. Cancer Prevention Research, 2017, 10, 651-659.	1.5	31
60	Tumor-specific and Proliferation-specific Gene Expression Typifies Murine Transgenic B Cell Lymphomagenesis. Journal of Biological Chemistry, 2007, 282, 4803-4811.	3.4	30
61	Airway Gene Expression in Chronic Obstructive Pulmonary Disease. Proceedings of the American Thoracic Society, 2009, 6, 697-700.	3.5	30
62	Genetic regulation of gene expression in the lung identifies *CST3* and *CD22* as potential causal genes for airflow obstruction. Thorax, 2014, 69, 997-1004.	5.6	30
63	The Airway Transcriptome as a Biomarker for Early Lung Cancer Detection. Clinical Cancer Research, 2018, 24, 2984-2992.	7.0	30
64	A Randomized Phase IIb Trial of *myo*-Inositol in Smokers with Bronchial Dysplasia. Cancer Prevention Research, 2016, 9, 906-914.	1.5	29
65	Effect of long-term corticosteroid treatment on microRNA and gene-expression profiles in COPD. European Respiratory Journal, 2019, 53, 1801202.	6.7	29
66	A chronic obstructive pulmonary disease related signature in squamous cell lung cancer. Lung Cancer, 2011, 72, 177-183.	2.0	26
67	Yap/Taz inhibit goblet cell fate to maintain lung epithelial homeostasis. Cell Reports, 2021, 36, 109347.	6.4	24
68	Characterization of the mid-foregut transcriptome identifies genes regulated during lung bud induction. Gene Expression Patterns, 2008, 8, 124-139.	0.8	22
69	Clinical Impact of High-Throughput Gene Expression Studies in Lung Cancer. Journal of Thoracic Oncology, 2009, 4, 109-118.	1.1	22
70	Discovering biological connections between experimental conditions based on common patterns of differential gene expression. BMC Bioinformatics, 2011, 12, 381.	2.6	21
71	Differential gene expression in pulmonary artery endothelial cells exposed to sickle cell plasma. Physiological Genomics, 2005, 21, 293-298.	2.3	19
72	Protein Kinase CK1Î±LS Promotes Vascular Cell Proliferation and Intimal Hyperplasia. American Journal of Pathology, 2010, 177, 1562-1572.	3.8	18

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73	SIRT1 Pathway Dysregulation in the Smoke-Exposed Airway Epithelium and Lung Tumor Tissue. Cancer Research, 2012, 72, 5702-5711.	0.9	18
74	Gene-expression profiling of buccal epithelium among non-smoking women exposed to household air pollution from smoky coal. Carcinogenesis, 2015, 36, bgv150.	2.8	17
75	The molecular and cellular mechanisms associated with the destruction of terminal bronchioles in COPD. European Respiratory Journal, 2022, 59, 2101411.	6.7	17
76	Transcriptional profiling and biochemical analysis of mechanically induced cartilaginous tissues in a rat model. Arthritis and Rheumatism, 2010, 62, 1108-1118.	6.7	16
77	Tobacco-Related Alterations in Airway Gene Expression are Rapidly Reversed Within Weeks Following Smoking-Cessation. Scientific Reports, 2019, 9, 6978.	3.3	16
78	The transition from normal lung anatomy to minimal and established fibrosis in idiopathic pulmonary fibrosis (IPF). EBioMedicine, 2021, 66, 103325.	6.1	16
79	Gene Expression Alterations in the Bronchial Epithelium of e-Cigarette Users. Chest, 2019, 156, 764-773.	0.8	15
80	Improving lung cancer risk stratification leveraging whole transcriptome RNA sequencing and machine learning across multiple cohorts. BMC Medical Genomics, 2020, 13, 151.	1.5	13
81	Comparison of smoking-induced gene expression on Affymetrix Exon and 3'-based expression arrays. Genome Informatics, 2007, 18, 247-57.	0.4	12
82	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. Breast Cancer Research, 2016, 18, 70.	5.0	11
83	Applying gene expression microarrays to pulmonary disease. Respirology, 2011, 16, 407-418.	2.3	9
84	Open-access database of candidate associations from a genome-wide SNP scan of the Framingham Heart Study. Nature Genetics, 2007, 39, 135-136.	21.4	8
85	Bronchial gene expression signature associated with rate of subsequent FEV_1 decline in individuals with and at risk of COPD. Thorax, 2022, 77, 31-39.	5.6	8
86	Distinguishing Smoking-Related Lung Disease Phenotypes Via Imaging and Molecular Features. Chest, 2021, 159, 549-563.	0.8	6
87	Personalized Management of Chronic Obstructive Pulmonary Disease via Transcriptomic Profiling of the Airway and Lung. Annals of the American Thoracic Society, 2013, 10, S190-S196.	3.2	5
88	Murine Gut Microbiome Meta-analysis Reveals Alterations in Carbohydrate Metabolism in Response to Aging. MSystems, 2022, 7, e0124821.	3.8	5
89	Disruption of the cytoskeleton-extracellular matrix linkage promotes the accumulation of plasminogen activators in F9 derived parietal endoderm. Differentiation, 1992, 50, 153-162.	1.9	4
90	Temporal and Quantitative Transcriptomic Differences Define Sexual Dimorphism in Murine Postnatal Bone Aging. JBMR Plus, 2022, 6, e10579.	2.7	4

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91	Comparison of Nasal Epithelial Smoking-Induced Gene Expression on Affymetrix Exon 1.0 and Gene 1.0 ST Arrays. Scientific World Journal, The, 2013, 2013, 1-7.	2.1	3
92	Identifying a nasal gene expression signature associated with hyperinflation and treatment response in severe COPD. Scientific Reports, 2020, 10, 17415.	3.3	2
93	COMPARISON OF SMOKING-INDUCED GENE EXPRESSION ON AFFYMETRIX EXON AND 3'-BASED EXPRESSION ARRAYS. , 2007, , .		2
94	Elevated T cell repertoire diversity is associated with progression of lung squamous cell premalignant lesions. , 2021, 9, e002647.		1
95	MYC pathway activation in triple-negative breast cancer is synthetic lethal with CDK inhibition. Journal of Cell Biology, 2012, 197, i1-i1.	5.2	1
96	Pathologic and gene expression comparison of CT- screen detected and routinely detected stage I/0 lung adenocarcinoma in NCCN risk-matched cohorts.. Cancer Treatment and Research Communications, 2021, 29, 100486.	1.7	1
97	Abstract 856: Proteomic analysis of serum in workers exposed to diesel engine exhaust. , 2021, , .		0
98	Abstract 2434: Transcriptional crosstalk between YAP, TEAD and TP63 is associated with early lung carcinogenesis. , 2021, , .		0
99	Abstract 171: Cloud-based bulk and single-cell RNAseq pipelines in the Terra platform for the Lung PCA. , 2021, , .		0
100	Characterizing the T cell repertoire in lung squamous cell premalignancy and its association with lesion outcome.. Journal of Clinical Oncology, 2019, 37, 102-102.	1.6	0