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List of Publications by Year
in descending order

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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	Bronchial gene expression signature associated with rate of subsequent FEV₁ decline in individuals with and at risk of COPD. Thorax, 2022, 77, 31-39.	5.6	8
2	The molecular and cellular mechanisms associated with the destruction of terminal bronchioles in COPD. European Respiratory Journal, 2022, 59, 2101411.	6.7	17
3	Temporal and Quantitative Transcriptomic Differences Define Sexual Dimorphism in Murine Postnatal Bone Aging. JBMR Plus, 2022, 6, e10579.	2.7	4
4	Murine Gut Microbiome Meta-analysis Reveals Alterations in Carbohydrate Metabolism in Response to Aging. MSystems, 2022, 7, e0124821.	3.8	5
5	Distinguishing Smoking-Related Lung Disease Phenotypes Via Imaging and Molecular Features. Chest, 2021, 159, 549-563.	0.8	6
6	The transition from normal lung anatomy to minimal and established fibrosis in idiopathic pulmonary fibrosis (IPF). EBioMedicine, 2021, 66, 103325.	6.1	16
7	Abstract 856: Proteomic analysis of serum in workers exposed to diesel engine exhaust. , 2021, , .		0
8	Abstract 2434: Transcriptional crosstalk between YAP, TEAD and TP63 is associated with early lung carcinogenesis. , 2021, , .		0
9	Yap/Taz inhibit goblet cell fate to maintain lung epithelial homeostasis. Cell Reports, 2021, 36, 109347.	6.4	24
10	Abstract 171: Cloud-based bulk and single-cell RNAseq pipelines in the Terra platform for the Lung PCA. , 2021, , .		0
11	Elevated T cell repertoire diversity is associated with progression of lung squamous cell premalignant lesions. , 2021, 9, e002647.		1
12	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
13	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
14	Identifying a nasal gene expression signature associated with hyperinflation and treatment response in severe COPD. Scientific Reports, 2020, 10, 17415.	3.3	2
15	Gene Expression Alterations in the Bronchial Epithelium of e-Cigarette Users. Chest, 2019, 156, 764-773.	0.8	15
16	Tobacco-Related Alterations in Airway Gene Expression are Rapidly Reversed Within Weeks Following Smoking-Cessation. Scientific Reports, 2019, 9, 6978.	3.3	16
17	Molecular subtyping reveals immune alterations associated with progression of bronchial premalignant lesions. Nature Communications, 2019, 10, 1856.	12.8	70
18	Effect of long-term corticosteroid treatment on microRNA and gene-expression profiles in COPD. European Respiratory Journal, 2019, 53, 1801202.	6.7	29

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19	Characterizing smoking-induced transcriptional heterogeneity in the human bronchial epithelium at single-cell resolution. Science Advances, 2019, 5, eaaw3413.	10.3	64
20	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
21	The Airway Transcriptome as a Biomarker for Early Lung Cancer Detection. Clinical Cancer Research, 2018, 24, 2984-2992.	7.0	30
22	Nondestructive cryomicro-CT imaging enables structural and molecular analysis of human lung tissue. Journal of Applied Physiology, 2017, 122, 161-169.	2.5	39
23	Detecting the Presence and Progression of Premalignant Lung Lesions via Airway Gene Expression. Clinical Cancer Research, 2017, 23, 5091-5100.	7.0	37
24	Alterations in Bronchial Airway miRNA Expression for Lung Cancer Detection. Cancer Prevention Research, 2017, 10, 651-659.	1.5	31
25	The cellular and molecular determinants of emphysematous destruction in COPD. Scientific Reports, 2017, 7, 9562.	3.3	53
26	Molecular Impact of Electronic Cigarette Aerosol Exposure in Human Bronchial Epithelium. Toxicological Sciences, 2017, 155, 248-257.	3.1	56
27	Shared Gene Expression Alterations in Nasal and Bronchial Epithelium for Lung Cancer Detection. Journal of the National Cancer Institute, 2017, 109, .	6.3	44
28	Nasal gene expression differentiates COPD from controls and overlaps bronchial gene expression. Respiratory Research, 2017, 18, 213.	3.6	33
29	Identification of transforming growth factor-beta-regulated microRNAs and the microRNA-targetomes in primary lung fibroblasts. PLoS ONE, 2017, 12, e0183815.	2.5	34
30	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
31	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
32	A Randomized Phase IIb Trial of myo-Inositol in Smokers with Bronchial Dysplasia. Cancer Prevention Research, 2016, 9, 906-914.	1.5	29
33	Clinical Utility of a Bronchial Genomic Classifier in Patients With Suspected Lung Cancer. Chest, 2016, 150, 210-218.	0.8	34
34	Asthmaâ€“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
35	The Achillesâ€™ heel of senescent cells: from transcriptome to senolytic drugs. Aging Cell, 2015, 14, 644-658.	6.7	1,534
36	A Bronchial Genomic Classifier for the Diagnostic Evaluation of Lung Cancer. New England Journal of Medicine, 2015, 373, 243-251.	27.0	230

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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	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
39	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
40	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. Rna, 2015, 21, 164-171.	3.5	31
41	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
42	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
43	Gene Co-Expression Modules as Clinically Relevant Hallmarks of Breast Cancer Diversity. PLoS ONE, 2014, 9, e88309.	2.5	94
44	Genetic regulation of gene expression in the lung identifiesCST3andCD22as potential causal genes for airflow obstruction. Thorax, 2014, 69, 997-1004.	5.6	30
45	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
46	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
47	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
48	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
49	miR-638 regulates gene expression networks associated with emphysematous lung destruction. Genome Medicine, 2013, 5, 114.	8.2	62
50	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
51	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
52	SIRT1 Pathway Dysregulation in the Smoke-Exposed Airway Epithelium and Lung Tumor Tissue. Cancer Research, 2012, 72, 5702-5711.	0.9	18
53	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
54	A single-sample microarray normalization method to facilitate personalized-medicine workflows. Genomics, 2012, 100, 337-344.	2.9	212

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55	A gene expression signature of emphysema-related lung destruction and its reversal by the tripeptide GHK. Genome Medicine, 2012, 4, 67.	8.2	94
56	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
57	FAM83A confers EGFR-TKI resistance in breast cancer cells and in mice. Journal of Clinical Investigation, 2012, 122, 3211-3220.	8.2	126
58	A gene expression signature of emphysematous lung destruction and its reversal by the tripeptide GHK. Genome Medicine, 2012, 4, 67.	8.2	37
59	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
60	A chronic obstructive pulmonary disease related signature in squamous cell lung cancer. Lung Cancer, 2011, 72, 177-183.	2.0	26
61	Applying gene expression microarrays to pulmonary disease. Respirology, 2011, 16, 407-418.	2.3	9
62	Discovering biological connections between experimental conditions based on common patterns of differential gene expression. BMC Bioinformatics, 2011, 12, 381.	2.6	21
63	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
64	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
65	Similarities and differences between smoking-related gene expression in nasal and bronchial epithelium. Physiological Genomics, 2010, 41, 1-8.	2.3	107
66	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
67	Transcriptional profiling and biochemical analysis of mechanically induced cartilaginous tissues in a rat model. Arthritis and Rheumatism, 2010, 62, 1108-1118.	6.7	16
68	Airway PI3K Pathway Activation Is an Early and Reversible Event in Lung Cancer Development. Science Translational Medicine, 2010, 2, 26ra25.	12.4	215
69	Presence of a Putative Tumor-Initiating Progenitor Cell Population Predicts Poor Prognosis in Smokers with Nonâ€“Small Cell Lung Cancer. Cancer Research, 2010, 70, 6639-6648.	0.9	53
70	Smad Signaling Is Required to Maintain Epigenetic Silencing during Breast Cancer Progression. Cancer Research, 2010, 70, 968-978.	0.9	162
71	Aging, Depot Origin, and Preadipocyte Gene Expression. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2010, 65A, 242-251.	3.6	76
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	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
74	Comparison of Proteomic and Transcriptomic Profiles in the Bronchial Airway Epithelium of Current and Never Smokers. PLoS ONE, 2009, 4, e5043.	2.5	66
75	Replication licensing promotes cyclin D1 expression and G₁progression in untransformed human cells. Cell Cycle, 2009, 8, 125-136.	2.6	59
76	Airway Gene Expression in Chronic Obstructive Pulmonary Disease. Proceedings of the American Thoracic Society, 2009, 6, 697-700.	3.5	30
77	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
78	The UCSC Cancer Genomics Browser. Nature Methods, 2009, 6, 239-240.	19.0	167
79	Clinical Impact of High-Throughput Gene Expression Studies in Lung Cancer. Journal of Thoracic Oncology, 2009, 4, 109-118.	1.1	22
80	Gene expression abnormalities in histologically normal breast epithelium of breast cancer patients. International Journal of Cancer, 2008, 122, 1557-1566.	5.1	105
81	Smoking-induced gene expression changes in the bronchial airway are reflected in nasal and buccal epithelium. BMC Genomics, 2008, 9, 259.	2.8	194
82	Characterization of the mid-foregut transcriptome identifies genes regulated during lung bud induction. Gene Expression Patterns, 2008, 8, 124-139.	0.8	22
83	Dicer, Drosha, and Outcomes in Patients with Ovarian Cancer. New England Journal of Medicine, 2008, 359, 2641-2650.	27.0	633
84	A Prediction Model for Lung Cancer Diagnosis that Integrates Genomic and Clinical Features. Cancer Prevention Research, 2008, 1, 56-64.	1.5	89
85	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
86	Tumor-specific and Proliferation-specific Gene Expression Typifies Murine Transgenic B Cell Lymphomagenesis. Journal of Biological Chemistry, 2007, 282, 4803-4811.	3.4	30
87	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
88	Reversible and permanent effects of tobacco smoke exposure on airway epithelial gene expression. Genome Biology, 2007, 8, R201.	9.6	217
89	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
90	Airway epithelial gene expression in the diagnostic evaluation of smokers with suspect lung cancer. Nature Medicine, 2007, 13, 361-366.	30.7	507

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91	COMPARISON OF SMOKING-INDUCED GENE EXPRESSION ON AFFYMETRIX EXON AND 3'-BASED EXPRESSION ARRAYS. , 2007, , .		2
92	Comparison of smoking-induced gene expression on Affymetrix Exon and 3'-based expression arrays. Genome Informatics, 2007, 18, 247-57.	0.4	12
93	A Common Genetic Variant Is Associated with Adult and Childhood Obesity. Science, 2006, 312, 279-283.	12.6	652
94	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
95	Differential gene expression in pulmonary artery endothelial cells exposed to sickle cell plasma. Physiological Genomics, 2005, 21, 293-298.	2.3	19
96	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
97	Pharmacogenomic Identification of Targets for Adjuvant Therapy with the Topoisomerase Poison Camptothecin. Cancer Research, 2004, 64, 2096-2104.	0.9	38
98	Previously unidentified changes in renal cell carcinoma gene expression identified by parametric analysis of microarray data. BMC Cancer, 2003, 3, 31.	2.6	228
99	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
100	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