

Zhifu Sun

List of Publications by Year in descending order

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Version: 2024-02-01

135
papers

8,329
citations

46984

47
h-index

53190

85
g-index

138
all docs

138
docs citations

138
times ranked

17454
citing authors

#	ARTICLE	IF	CITATIONS
1	Estrogen receptor beta repurposes EZH2 to suppress oncogenic NF κ B/p65 signaling in triple negative breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 20.	2.3	9
2	DNA methylation profile of liver tissue in end-stage cholestatic liver disease. <i>Epigenomics</i> , 2022, 14, 481-497.	1.0	2
3	Novel lincRNA Discovery and Tissue-Specific Gene Expression across 30 Normal Human Tissues. <i>Genes</i> , 2021, 12, 614.	1.0	4
4	Evaluation of circulating cell-free DNA in cholestatic liver disease using liver-specific methylation markers. <i>BMC Gastroenterology</i> , 2021, 21, 149.	0.8	3
5	A novel ferroptosis phenotype-related clinical-molecular prognostic signature for hepatocellular carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 6618-6633.	1.6	24
6	RNF20 and RNF40 regulate vitamin D receptor-dependent signaling in inflammatory bowel disease. <i>Cell Death and Differentiation</i> , 2021, 28, 3161-3175.	5.0	10
7	BMI1 maintains the Treg epigenomic landscape to prevent inflammatory bowel disease. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	10
8	Deregulation of Long Intergenic Non-coding RNAs in CD4+ T Cells of Lamina Propria in Crohn's Disease Through Transcriptome Profiling. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 96-109.	0.6	18
9	MCAM abnormal expression and clinical outcome associations are highly cancer dependent as revealed through pan-cancer analysis. <i>Briefings in Bioinformatics</i> , 2020, 21, 709-718.	3.2	4
10	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	13.5	217
11	Protein expression shift and potential diagnostic markers through proteomics profiling of tuberculous pleurisy biopsy tissues. <i>International Journal of Infectious Diseases</i> , 2020, 99, 245-252.	1.5	5
12	Transcriptome Profiling of Acquired Gefitinib Resistant Lung Cancer Cells Reveals Dramatically Changed Transcription Programs and New Treatment Targets. <i>Frontiers in Oncology</i> , 2020, 10, 1424.	1.3	10
13	Spectrum of EGFR aberrations and potential clinical implications: insights from integrative pan-cancer analysis. <i>Cancer Communications</i> , 2020, 40, 43-59.	3.7	45
14	Marked Up-Regulation of ACE2 in Hearts of Patients With Obstructive Hypertrophic Cardiomyopathy: Implications for SARS-CoV-2-Mediated COVID-19. <i>Mayo Clinic Proceedings</i> , 2020, 95, 1354-1368.	1.4	49
15	Apatinib Reverses Paclitaxel-resistant Lung Cancer Cells (A549) Through Blocking the Function of ABCB1 Transporter. <i>Anticancer Research</i> , 2019, 39, 5461-5471.	0.5	14
16	DNA methylation patterns in human iPSC-derived sensory neuronal differentiation. <i>Epigenetics</i> , 2019, 14, 927-937.	1.3	9
17	Predict drug sensitivity of cancer cells with pathway activity inference. <i>BMC Medical Genomics</i> , 2019, 12, 15.	0.7	36
18	Use of FFPE-derived DNA in next generation sequencing: DNA extraction methods. <i>PLoS ONE</i> , 2019, 14, e0211400.	1.1	62

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19	Association between ALS and retroviruses: evidence from bioinformatics analysis. <i>BMC Bioinformatics</i> , 2019, 20, 680.	1.2	7
20	Discovery, Validation, and Application of Novel Methylated DNA Markers for Detection of Esophageal Cancer in Plasma. <i>Clinical Cancer Research</i> , 2019, 25, 7396-7404.	3.2	33
21	Androgen Mediation and Antiandrogens Mitigation of the Epidermal Growth Factor Receptor (EGFR) Inhibitor-Induced Rash: Results From a Pilot Randomized Trial and Small Translational Case Series. <i>American Journal of Hospice and Palliative Medicine</i> , 2019, 36, 519-525.	0.8	4
22	Contraction of T cell richness in lung cancer brain metastases. <i>Scientific Reports</i> , 2018, 8, 2171.	1.6	74
23	Pathways Impacted by Genomic Alterations in Pulmonary Carcinoid Tumors. <i>Clinical Cancer Research</i> , 2018, 24, 1691-1704.	3.2	53
24	Nomogram prediction of overall survival for patients with non-small-cell lung cancer incorporating pretreatment peripheral blood markers. <i>European Journal of Cardio-thoracic Surgery</i> , 2018, 53, 1214-1222.	0.6	23
25	Molecular profiling reveals immunogenic cues in anaplastic large cell lymphomas with DUSP22 rearrangements. <i>Blood</i> , 2018, 132, 1386-1398.	0.6	97
26	Indel sensitive and comprehensive variant/mutation detection from RNA sequencing data for precision medicine. <i>BMC Medical Genomics</i> , 2018, 11, 67.	0.7	5
27	Distinct epigenetic landscapes underlie the pathobiology of pancreatic cancer subtypes. <i>Nature Communications</i> , 2018, 9, 1978.	5.8	177
28	Indel detection from RNA-seq data: tool evaluation and strategies for accurate detection of actionable mutations. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw069.	3.2	44
29	The Role of the Histone Methyltransferase Enhancer of Zeste Homolog 2 (EZH2) in the Pathobiological Mechanisms Underlying Inflammatory Bowel Disease (IBD). <i>Journal of Biological Chemistry</i> , 2017, 292, 706-722.	1.6	59
30	UCLncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. <i>Scientific Reports</i> , 2017, 7, 14196.	1.6	29
31	Adipose tissue DNA methylome changes in development of new-onset diabetes after kidney transplantation. <i>Epigenomics</i> , 2017, 9, 1423-1435.	1.0	8
32	Genetic predisposition to lung cancer: comprehensive literature integration, meta-analysis, and multiple evidence assessment of candidate-gene association studies. <i>Scientific Reports</i> , 2017, 7, 8371.	1.6	87
33	Comprehensive Profiling of lincRNAs in Lung Adenocarcinoma of Never Smokers Reveals Their Roles in Cancer Development and Prognosis. <i>Genes</i> , 2017, 8, 321.	1.0	8
34	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. <i>Rare Tumors</i> , 2017, 9, 50-53.	0.3	8
35	Neutrophil Elastase. , 2017, , 3088-3091.		0
36	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. <i>American Journal of Epidemiology</i> , 2016, 183, kwv187.	1.6	23

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37	Multiple-level validation identifies <i>PARK2</i> in the development of lung cancer and chronic obstructive pulmonary disease. <i>Oncotarget</i> , 2016, 7, 44211-44223.	0.8	42
38	Statistical method evaluation for differentially methylated CpGs in base resolution next-generation DNA sequencing data. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw133.	3.2	21
39	X chromosome abnormal inactivation: a unique factor for women's diseases?. <i>Epigenomics</i> , 2016, 8, 447-450.	1.0	5
40	Preeclampsia/Eclampsia candidate genes show altered methylation in maternal leukocytes of preeclamptic women at the time of delivery. <i>Hypertension in Pregnancy</i> , 2016, 35, 394-404.	0.5	22
41	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. <i>Acta Neuropathologica</i> , 2016, 132, 197-211.	3.9	49
42	Long noncoding and circular RNAs in lung cancer: advances and perspectives. <i>Epigenomics</i> , 2016, 8, 1275-1287.	1.0	59
43	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISH and IHC in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016, 11, 1891-1900.	0.5	37
44	A genetic cell context-dependent role for ZEB1 in lung cancer. <i>Nature Communications</i> , 2016, 7, 12231.	5.8	54
45	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. <i>Bioinformatics</i> , 2016, 32, 469-471.	1.8	27
46	ChIP-seq in studying epigenetic mechanisms of disease and promoting precision medicine: progresses and future directions. <i>Epigenomics</i> , 2016, 8, 1239-1258.	1.0	22
47	Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing data. <i>BMC Genomics</i> , 2016, 17, 149.	1.2	3
48	Epstein-Barr Virus EBNA-2 Polymorphic Patterns in Nasopharyngeal Carcinoma in Southern China. <i>Intervirology</i> , 2015, 58, 386-392.	1.2	1
49	Sequence analysis of EBV immune evasion gene BNLF2a in EBV associated tumors and healthy individuals from nasopharyngeal carcinoma endemic and non-endemic regions of China. <i>Journal of Medical Virology</i> , 2015, 87, 1946-1952.	2.5	7
50	New DNA Methylation Markers for Pancreatic Cancer: Discovery, Tissue Validation, and Pilot Testing in Pancreatic Juice. <i>Clinical Cancer Research</i> , 2015, 21, 4473-4481.	3.2	108
51	Common Oncogene Mutations and Novel SND1-BRAF Transcript Fusion in Lung Adenocarcinoma from Never Smokers. <i>Scientific Reports</i> , 2015, 5, 9755.	1.6	43
52	DNA methylation and RNA expression profiles in lung adenocarcinomas of never-smokers. <i>Cancer Genetics</i> , 2015, 208, 253-260.	0.2	14
53	The Cistrome and Gene Signature of Androgen Receptor Splice Variants in Castration Resistant Prostate Cancer Cells. <i>Journal of Urology</i> , 2015, 193, 690-698.	0.2	57
54	Sequence variation of Epstein-Barr virus (EBV) BCRF1 in lymphomas in non-endemic areas of nasopharyngeal carcinoma. <i>Archives of Virology</i> , 2015, 160, 441-445.	0.9	5

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55	DNA methylation profiling: comparison of genome-wide sequencing methods and the Infinium Human Methylation 450 Bead Chip. <i>Epigenomics</i> , 2015, 7, 1287-1302.	1.0	66
56	Chromosome X genomic and epigenomic aberrations and clinical implications in breast cancer by base resolution profiling. <i>Epigenomics</i> , 2015, 7, 1099-1110.	1.0	12
57	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. <i>Epigenomics</i> , 2015, 7, 813-828.	1.0	97
58	High-throughput long noncoding RNA profiling for diagnostic and prognostic markers in cancer: opportunities and challenges. <i>Epigenomics</i> , 2015, 7, 1075-1078.	1.0	7
59	Exosomal miR-1290 and miR-375 as Prognostic Markers in Castration-resistant Prostate Cancer. <i>European Urology</i> , 2015, 67, 33-41.	0.9	533
60	Folate Receptor-1 (FOLR1) Expression and Function in Triple Negative Tumors. <i>PLoS ONE</i> , 2015, 10, e0122209.	1.1	103
61	Sequence Variation Analysis of Epstein-Barr Virus Nuclear Antigen 1 Gene in the Virus Associated Lymphomas of Northern China. <i>PLoS ONE</i> , 2015, 10, e0140529.	1.1	8
62	LncRNA <i>MALAT1</i> enhances oncogenic activities of EZH2 in castration-resistant prostate cancer. <i>Oncotarget</i> , 2015, 6, 41045-41055.	0.8	154
63	Aberrant signature methylome by DNMT1 hot spot mutation in hereditary sensory and autonomic neuropathy 1E. <i>Epigenetics</i> , 2014, 9, 1184-1193.	1.3	55
64	MACE: model based analysis of ChIP-exo. <i>Nucleic Acids Research</i> , 2014, 42, e156-e156.	6.5	84
65	Sequence analysis of EBV immediate-early gene BZLF1 and BRLF1 in lymphomas. <i>Journal of Medical Virology</i> , 2014, 86, 1788-1795.	2.5	5
66	CrossMap: a versatile tool for coordinate conversion between genome assemblies. <i>Bioinformatics</i> , 2014, 30, 1006-1007.	1.8	553
67	HiChIP: a high-throughput pipeline for integrative analysis of ChIP-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 280.	1.2	55
68	Conserved recurrent gene mutations correlate with pathway deregulation and clinical outcomes of lung adenocarcinoma in never-smokers. <i>BMC Medical Genomics</i> , 2014, 7, 32.	0.7	49
69	Clinical biomarkers of pulmonary carcinoid tumors in never smokers via profiling miRNA and target mRNA. <i>Cell and Bioscience</i> , 2014, 4, 35.	2.1	15
70	CAP-miRSeq: a comprehensive analysis pipeline for microRNA sequencing data. <i>BMC Genomics</i> , 2014, 15, 423.	1.2	138
71	Neutrophil Elastase. , 2014, , 1-5.		0
72	Characterization of human plasma-derived exosomal RNAs by deep sequencing. <i>BMC Genomics</i> , 2013, 14, 319.	1.2	860

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73	Increased BCAR1 Predicts Poor Outcomes of Non-small Cell Lung Cancer in Multiple-Center Patients. <i>Annals of Surgical Oncology</i> , 2013, 20, 701-708.	0.7	15
74	Gene variations of Epstein-Barr virus nuclear antigen 3A in nasopharyngeal carcinomas, gastric carcinomas and healthy carriers in northern China. <i>Archives of Virology</i> , 2013, 158, 2041-2048.	0.9	2
75	Pharmacologic reversion of epigenetic silencing of the PRKD1 promoter blocks breast tumor cell invasion and metastasis. <i>Breast Cancer Research</i> , 2013, 15, R66.	2.2	74
76	Epigenetic silencing of WNT5A in Epstein-Barr virus-associated gastric carcinoma. <i>Archives of Virology</i> , 2013, 158, 123-132.	0.9	23
77	769 Novel Methylated DNA Markers Predict Site of Gastrointestinal Cancer. <i>Gastroenterology</i> , 2013, 144, S-84.	0.6	4
78	Network-based approach identified cell cycle genes as predictor of overall survival in lung adenocarcinoma patients. <i>Lung Cancer</i> , 2013, 80, 91-98.	0.9	36
79	Genome-wide methylation profiling demonstrates hypermethylation in maternal leukocyte DNA in preeclamptic compared to normotensive pregnancies. <i>Hypertension in Pregnancy</i> , 2013, 32, 257-269.	0.5	31
80	Endoxifen's Molecular Mechanisms of Action Are Concentration Dependent and Different than That of Other Anti-Estrogens. <i>PLoS ONE</i> , 2013, 8, e54613.	1.1	38
81	An Integrated Model of the Transcriptome of HER2-Positive Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e79298.	1.1	18
82	Impact of Library Preparation on Downstream Analysis and Interpretation of RNA-Seq Data: Comparison between Illumina PolyA and NuGEN Ovation Protocol. <i>PLoS ONE</i> , 2013, 8, e71745.	1.1	19
83	Gene Expression, Single Nucleotide Variant and Fusion Transcript Discovery in Archival Material from Breast Tumors. <i>PLoS ONE</i> , 2013, 8, e81925.	1.1	49
84	Global Methylation Profiling for Risk Prediction of Prostate Cancer. <i>Clinical Cancer Research</i> , 2012, 18, 2882-2895.	3.2	118
85	TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. <i>Bioinformatics</i> , 2012, 28, 277-278.	1.8	59
86	Genetic Variants Associated with the Risk of Chronic Obstructive Pulmonary Disease with and without Lung Cancer. <i>Cancer Prevention Research</i> , 2012, 5, 365-373.	0.7	26
87	Normal early pregnancy. <i>Epigenetics</i> , 2012, 7, 729-734.	1.3	22
88	Increased miR-708 Expression in NSCLC and Its Association with Poor Survival in Lung Adenocarcinoma from Never Smokers. <i>Clinical Cancer Research</i> , 2012, 18, 3658-3667.	3.2	105
89	SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , 2012, 28, 2180-2181.	1.8	49
90	Gemcitabine metabolic pathway genetic polymorphisms and response in patients with non-small cell lung cancer. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 105-116.	0.7	33

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91	Chronic Caloric Restriction Preserves Mitochondrial Function in Senescence without Increasing Mitochondrial Biogenesis. <i>Cell Metabolism</i> , 2012, 16, 777-788.	7.2	183
92	Concordance of Changes in Metabolic Pathways Based on Plasma Metabolomics and Skeletal Muscle Transcriptomics in Type 1 Diabetes. <i>Diabetes</i> , 2012, 61, 1004-1016.	0.3	55
93	Genetic association with overall survival of taxane-treated lung cancer patients - a genome-wide association study in human lymphoblastoid cell lines followed by a clinical association study. <i>BMC Cancer</i> , 2012, 12, 422.	1.1	40
94	Germline Copy Number Variation and Ovarian Cancer Survival. <i>Frontiers in Genetics</i> , 2012, 3, 142.	1.1	11
95	Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. <i>Frontiers in Oncology</i> , 2012, 2, 12.	1.3	46
96	Sequence analysis of Epstein-Barr virus EBNA-2 gene coding amino acid 148-487 in nasopharyngeal and gastric carcinomas. <i>Virology Journal</i> , 2012, 9, 49.	1.4	11
97	Characterization of Epstein-Barr virus gp350/220 gene variants in virus isolates from gastric carcinoma and nasopharyngeal carcinoma. <i>Archives of Virology</i> , 2012, 157, 207-216.	0.9	8
98	A novel bioinformatics pipeline for identification and characterization of fusion transcripts in breast cancer and normal cell lines. <i>Nucleic Acids Research</i> , 2011, 39, e100-e100.	6.5	94
99	Model based user interface design for predicting lung cancer treatment outcomes. , 2011, 2011, 75-8.		3
100	Estrogen receptor-beta sensitizes breast cancer cells to the anti-estrogenic actions of endoxifen. <i>Breast Cancer Research</i> , 2011, 13, R27.	2.2	58
101	Genes Associated with Recurrence of Hepatocellular Carcinoma: Integrated Analysis by Gene Expression and Methylation Profiling. <i>Journal of Korean Medical Science</i> , 2011, 26, 1428.	1.1	37
102	Systematic Evaluation of Genetic Variants in Three Biological Pathways on Patient Survival in Low-Stage Non-small Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2011, 6, 1488-1495.	0.5	18
103	Changes in cardiac gene expression after pig-to-primate orthotopic xenotransplantation. <i>Xenotransplantation</i> , 2011, 18, 14-27.	1.6	50
104	Batch effect correction for genome-wide methylation data with Illumina Infinium platform. <i>BMC Medical Genomics</i> , 2011, 4, 84.	0.7	108
105	Sulfatase 1 and sulfatase 2 in hepatocellular carcinoma: Associated signaling pathways, tumor phenotypes, and survival. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 122-135.	1.5	55
106	Genetic Variation Predicting Cisplatin Cytotoxicity Associated with Overall Survival in Lung Cancer Patients Receiving Platinum-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2011, 17, 5801-5811.	3.2	87
107	Genetic Variations in Multiple Drug Action Pathways and Survival in Advanced Stage Non-Small Cell Lung Cancer Treated with Chemotherapy. <i>Clinical Cancer Research</i> , 2011, 17, 3830-3840.	3.2	25
108	Identification of a Clinically Relevant Androgen-Dependent Gene Signature in Prostate Cancer. <i>Cancer Research</i> , 2011, 71, 1978-1988.	0.4	38

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109	Integrated Analysis of Gene Expression, CpG Island Methylation, and Gene Copy Number in Breast Cancer Cells by Deep Sequencing. PLoS ONE, 2011, 6, e17490.	1.1	128
110	Neutrophil Elastase. , 2011, , 2509-2512.		0
111	MicroRNA expression in ACTH-producing pituitary tumors: up-regulation of microRNA-122 and -493 in pituitary carcinomas. Endocrine, 2010, 38, 67-75.	1.1	83
112	Glutathione Pathway Genetic Polymorphisms and Lung Cancer Survival After Platinum-Based Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 811-821.	1.1	42
113	Prognostic factors for limited-stage small cell lung cancer: A study of 284 patients. Lung Cancer, 2010, 67, 221-226.	0.9	80
114	Cystic fibrosis transmembrane conductance regulator gene mutation and lung cancer risk. Lung Cancer, 2010, 70, 14-21.	0.9	42
115	Sequence analysis of the Epstein-Barr virus (EBV) BRLF1 gene in nasopharyngeal and gastric carcinomas. Virology Journal, 2010, 7, 341.	1.4	14
116	Genetic variants and risk of lung cancer in never smokers: a genome-wide association study. Lancet Oncology, The, 2010, 11, 321-330.	5.1	218
117	Fine Mapping of Chromosome 6q23-25 Region in Familial Lung Cancer Families Reveals <i>RGS17</i> as a Likely Candidate Gene. Clinical Cancer Research, 2009, 15, 2666-2674.	3.2	80
118	Cell Proliferation and Epidermal Growth Factor Signaling in Non-small Cell Lung Adenocarcinoma Cell Lines Are Dependent on Rin1. Journal of Biological Chemistry, 2009, 284, 26331-26339.	1.6	31
119	Effects of the 5 alpha-reductase inhibitor dutasteride on gene expression in prostate cancer xenografts. Prostate, 2009, 69, 1730-1743.	1.2	17
120	Impact of sample acquisition and linear amplification on gene expression profiling of lung adenocarcinoma: laser capture micro-dissection cell-sampling versus bulk tissue-sampling. BMC Medical Genomics, 2009, 2, 13.	0.7	29
121	The Role of Desmoglein-3 in the Diagnosis of Squamous Cell Carcinoma of the Lung. American Journal of Pathology, 2009, 174, 1629-1637.	1.9	76
122	Evaluation of Glutathione Metabolic Genes on Outcomes in Advanced Non-small Cell Lung Cancer Patients after Initial Treatment with Platinum-Based Chemotherapy: An NCCTG-97-24-51 Based Study. Journal of Thoracic Oncology, 2009, 4, 479-485.	0.5	20
123	Non-Overlapping and Non-Cell-Type-Specific Gene Expression Signatures Predict Lung Cancer Survival. Journal of Clinical Oncology, 2008, 26, 877-883.	0.8	92
124	Alpha1-Antitrypsin Deficiency Carriers, Tobacco Smoke, Chronic Obstructive Pulmonary Disease, and Lung Cancer Risk. Archives of Internal Medicine, 2008, 168, 1097.	4.3	139
125	Refining Prognosis in Non-Small-Cell Lung Cancer. New England Journal of Medicine, 2007, 356, 189-191.	13.9	6
126	Gene-expression profiling in lung cancer: still early days. Pharmacogenomics, 2007, 8, 129-132.	0.6	3

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127	Inactivation of LLC1 gene in nonsmall cell lung cancer. <i>International Journal of Cancer</i> , 2007, 120, 2353-2358.	2.3	10
128	Role of the Glutathione Metabolic Pathway in Lung Cancer Treatment and Prognosis: A Review. <i>Journal of Clinical Oncology</i> , 2006, 24, 1761-1769.	0.8	119
129	Histologic grade is an independent prognostic factor for survival in non-small cell lung cancer: An analysis of 5018 hospital- and 712 population-based cases. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2006, 131, 1014-1020.	0.4	128
130	A Gene Expression Signature Predicts Survival of Patients with Stage I Non-Small Cell Lung Cancer. <i>PLoS Medicine</i> , 2006, 3, e467.	3.9	272
131	Gene Expression Profiling on Lung Cancer Outcome Prediction: Present Clinical Value and Future Premise. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 2063-2068.	1.1	41
132	α 1-Antitrypsin and Neutrophil Elastase Imbalance and Lung Cancer Risk. <i>Chest</i> , 2005, 128, 445-452.	0.4	77
133	Can gene expression profiling predict survival for patients with squamous cell carcinoma of the lung?. <i>Molecular Cancer</i> , 2004, 3, 35.	7.9	31
134	Role of imbalance between neutrophil elastase and α 1-antitrypsin in cancer development and progression. <i>Lancet Oncology</i> , 2004, 5, 182-190.	5.1	227
135	Genome-wide methylation profiling reveals differentially methylated genes in blood DNA of small-cell lung cancer patients. <i>Precision Clinical Medicine</i> , 0, , .	1.3	3