Suyan Tian

List of Publications by Year
in descending order

49 papers	1,539 citations	567281 15 h-index	315739 38 g-index
51 all docs	51 docs citations	51 times ranked	2587 citing authors

#	Article	IF	Citations
1	Integrative Responses to IL-17 and TNF-α in Human Keratinocytes Account for Key Inflammatory Pathogenic Circuits in Psoriasis. Journal of Investigative Dermatology, 2011, 131, 677-687.	0.7	526
2	Meta-Analysis Derived (MAD) Transcriptome of Psoriasis Defines the "Core" Pathogenesis of Disease. PLoS ONE, 2012, 7, e44274.	2.5	149
3	Meta-analysis derived atopic dermatitis (MADAD) transcriptome defines a robust AD signature highlighting the involvement of atherosclerosis and lipid metabolism pathways. BMC Medical Genomics, 2015, 8, 60.	1.5	123
4	Effect of the ketogenic diet on glycemic control, insulin resistance, and lipid metabolism in patients with T2DM: a systematic review and meta-analysis. Nutrition and Diabetes, 2020, 10, 38.	3.2	96
5	Increased expression of interleukin‐17 pathway genes in nonlesional skin of moderate‐to‐severe psoriasis vulgaris. British Journal of Dermatology, 2016, 174, 136-145.	1.5	83
6	Multiple Interferon Stimulated Genes Synergize with the Zinc Finger Antiviral Protein to Mediate Anti-Alphavirus Activity. PLoS ONE, 2012, 7, e37398.	2.5	62
7	Shrinking the Psoriasis Assessment Gap: Early Gene-Expression Profiling Accurately Predicts Response to Long-Term Treatment. Journal of Investigative Dermatology, 2017, 137, 305-312.	0.7	57
8	Cellular Immune Suppression in Paraneoplastic Neurologic Syndromes Targeting Intracellular Antigens. Archives of Neurology, 2012, 69, 1132-40.	4.5	49
9	A ferroptosis-related gene signature predicts overall survival in patients with lung adenocarcinoma. Future Oncology, 2021, 17, 1533-1544.	2.4	30
10	Test on existence of histology subtype-specific prognostic signatures among early stage lung adenocarcinoma and squamous cell carcinoma patients using a Cox-model based filter. Biology Direct, 2015, 10, 15.	4.6	25
11	Test of IL28B Polymorphisms in Chronic Hepatitis C Patients Treated with PegIFN and Ribavirin Depends on HCV Genotypes: Results from a Meta-Analysis. PLoS ONE, 2012, 7, e45698.	2.5	24
12	Dendritic cells loaded with FK506 kill T cells in an antigen-specific manner and prevent autoimmunity in vivo. ELife, 2013, 2, e00105.	6.0	22
13	Ideal glycated hemoglobin cut‐off points for screening diabetes and prediabetes in a Chinese population. Journal of Diabetes Investigation, 2016, 7, 695-702.	2.4	19
14	Classification and survival prediction for early‐stage lung adenocarcinoma and squamous cell carcinoma patients. Oncology Letters, 2017, 14, 5464-5470.	1.8	19
15	Identification of Subtype-Specific Prognostic Genes for Early-Stage Lung Adenocarcinoma and Squamous Cell Carcinoma Patients Using an Embedded Feature Selection Algorithm. PLoS ONE, 2015, 10, e0134630.	2.5	16
16	Identification of monotonically differentially expressed genes for non-small cell lung cancer. BMC Bioinformatics, 2019, 20, 177.	2.6	16
17	Evaluation of different obesity indices as predictors of type 2 diabetes mellitus in a <scp>C</scp>hinese population基于不同肥胖指数预测中国人群2型糖尿病患病风险的研究. Journal of Diabetes, 20	1.8	15
18	Harnessing Naturally Occurring Tumor Immunity: A Clinical Vaccine Trial in Prostate Cancer. PLoS ONE, 2010, 5, e12367.	2.5	14

#	Article	IF	Citations
19	Classification of Non-Small Cell Lung Cancer Using Significance Analysis of Microarray-Gene Set Reduction Algorithm. BioMed Research International, 2016, 2016, 1-8.	1.9	14
20	Weighted-SAMGSR: combining significance analysis of microarray-gene set reduction algorithm with pathway topology-based weights to select relevant genes. Biology Direct, 2016, 11, 50.	4.6	14
21	Effect of Intermittent Fasting Diet on Glucose and Lipid Metabolism and Insulin Resistance in Patients with Impaired Glucose and Lipid Metabolism: A Systematic Review and Meta-Analysis. International Journal of Endocrinology, 2022, 2022, 1-9.	1.5	14
22	Multi-TGDR: A Regularization Method for Multi-Class Classification in Microarray Experiments. PLoS ONE, 2013, 8, e78302.	2.5	13
23	Visualization-Aided Classification Ensembles Discriminate Lung Adenocarcinoma and Squamous Cell Carcinoma Samples Using Their Gene Expression Profiles. PLoS ONE, 2014, 9, e110052.	2.5	13
24	Association of polymorphism of PTPN 11 encoding SHP-2 with gastric atrophy but not gastric cancer in Helicobacter pylori seropositive Chinese population. BMC Gastroenterology, 2012, 12, 89.	2.0	12
25	Identification of differentially-expressed genes between early-stage adenocarcinoma and squamous cell carcinoma lung cancer using meta-analysis methods. Oncology Letters, 2017, 13, 3314-3322.	1.8	12
26	Incorporating Pathway Information into Feature Selection towards Better Performed Gene Signatures. BioMed Research International, 2019, 2019, 1-12.	1.9	12
27	Neutrophil-Lymphocyte Ratio as a Prognostic Parameter in NSCLC Patients Receiving EGFR-TKIs: A Systematic Review and Meta-Analysis. Journal of Oncology, 2021, 2021, 1-7.	1.3	11
28	Multi-TGDR, a multi-class regularization method, identifies the metabolic profiles of hepatocellular carcinoma and cirrhosis infected with hepatitis B or hepatitis C virus. BMC Bioinformatics, 2014, 15, 97.	2.6	10
29	Identification of prognostic genes and gene sets for early-stage non-small cell lung cancer using bi-level selection methods. Scientific Reports, 2017, 7, 46164.	3.3	9
30	Hierarchical-TGDR. Systems Biomedicine (Austin, Tex), 2013, 1, 278-287.	0.7	7
31	Weighted gene expression profiles identify diagnostic and prognostic genes for lung adenocarcinoma and squamous cell carcinoma. Journal of International Medical Research, 2020, 48, 030006051989383.	1.0	7
32	A longitudinal feature selection method identifies relevant genes to distinguish complicated injury and uncomplicated injury over time. BMC Medical Informatics and Decision Making, 2018, 18, 115.	3.0	5
33	Feature selection based on differentially correlated gene pairs reveals the mechanism of IFN-β therapy for multiple sclerosis. PeerJ, 2020, 8, e8812.	2.0	5
34	Identification of Genes Discriminating Multiple Sclerosis Patients from Controls by Adapting a Pathway Analysis Method. PLoS ONE, 2016, 11, e0165543.	2.5	4
35	Identification of subtype‐specific prognostic signatures using Cox models with redundant gene elimination. Oncology Letters, 2018, 15, 8545-8555.	1.8	4
36	Fundamental asymmetry of insertions and deletions in genomes size evolution. Journal of Theoretical Biology, 2019, 482, 109983.	1.7	4

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37	The cox-filter method identifies respective subtype-specific lncRNA prognostic signatures for two human cancers. BMC Medical Genomics, 2020, 13, 18.	1.5	4
38	Classification of early‐stage non‐small cell lung cancer by weighing gene expression profiles with connectivity information. Biometrical Journal, 2018, 60, 537-546.	1.0	4
39	Feature Selection for Longitudinal Data by Using Sign Averages to Summarize Gene Expression Values over Time. BioMed Research International, 2019, 2019, 1-12.	1.9	3
40	Identification of Monotonically Differentially Expressed Genes for IFN-β-Treated Multiple Sclerosis Patients. BioMed Research International, 2019, 2019, 1-6.	1.9	3
41	To select relevant features for longitudinal gene expression data by extending a pathway analysis method. F1000Research, 2018, 7, 1166.	1.6	3
42	An ensemble of the iCluster method to analyze longitudinal lncRNA expression data for psoriasis patients. Human Genomics, 2021, 15, 23.	2.9	2
43	A Bioequivalence Test by the Direct Comparison of Concentration-versus-Time Curves Using Local Polynomial Smoothers. Computational and Mathematical Methods in Medicine, 2016, 2016, 1-6.	1.3	1
44	Identification of Monotonically Differentially Expressed Genes across Pathologic Stages for Cancers. Journal of Oncology, 2020, 2020, 1-9.	1.3	1
45	An edge-based statistical analysis of long non-coding RNA expression profiles reveals a negative association between Parkinson's disease and colon cancer. BMC Medical Genomics, 2021, 14, 36.	1.5	1
46	GEE-TGDR: A Longitudinal Feature Selection Algorithm and Its Application to lncRNA Expression Profiles for Psoriasis Patients Treated with Immune Therapies. BioMed Research International, 2021, 2021, 1-9.	1.9	1
47	Identification of long non-coding RNA signatures for squamous cell carcinomas and adenocarcinomas. Aging, 2021, 13, 2459-2479.	3.1	1
48	Construction of subtype‐specific prognostic gene signatures for early‐stage non‐small cell lung cancer using meta feature selection methods. Oncology Letters, 2019, 18, 2366-2375.	1.8	0
49	Exploring exosome data to identify prognostic gene signatures for lung adenocarcinoma. Future Oncology, 2021, 17, 4745-4756.	2.4	0