

Suyan Tian

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5239794/publications.pdf>

Version: 2024-02-01

49
papers

1,539
citations

566801

15
h-index

315357

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. <i>Journal of Investigative Dermatology</i> , 2011, 131, 677-687.	0.3	526
2	Meta-Analysis Derived (MAD) Transcriptome of Psoriasis Defines the "Core" Pathogenesis of Disease. <i>PLoS ONE</i> , 2012, 7, e44274.	1.1	149
3	Meta-analysis derived atopic dermatitis (MADAD) transcriptome defines a robust AD signature highlighting the involvement of atherosclerosis and lipid metabolism pathways. <i>BMC Medical Genomics</i> , 2015, 8, 60.	0.7	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. <i>Nutrition and Diabetes</i> , 2020, 10, 38.	1.5	96
5	Increased expression of interleukin-17 pathway genes in nonlesional skin of moderate-to-severe psoriasis vulgaris. <i>British Journal of Dermatology</i> , 2016, 174, 136-145.	1.4	83
6	Multiple Interferon Stimulated Genes Synergize with the Zinc Finger Antiviral Protein to Mediate Anti-Alphavirus Activity. <i>PLoS ONE</i> , 2012, 7, e37398.	1.1	62
7	Shrinking the Psoriasis Assessment Gap: Early Gene-Expression Profiling Accurately Predicts Response to Long-Term Treatment. <i>Journal of Investigative Dermatology</i> , 2017, 137, 305-312.	0.3	57
8	Cellular Immune Suppression in Paraneoplastic Neurologic Syndromes Targeting Intracellular Antigens. <i>Archives of Neurology</i> , 2012, 69, 1132-40.	4.9	49
9	A ferroptosis-related gene signature predicts overall survival in patients with lung adenocarcinoma. <i>Future Oncology</i> , 2021, 17, 1533-1544.	1.1	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. <i>Biology Direct</i> , 2015, 10, 15.	1.9	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. <i>PLoS ONE</i> , 2012, 7, e45698.	1.1	24
12	Dendritic cells loaded with FK506 kill T cells in an antigen-specific manner and prevent autoimmunity in vivo. <i>ELife</i> , 2013, 2, e00105.	2.8	22
13	Ideal glycated hemoglobin cutoff points for screening diabetes and prediabetes in a Chinese population. <i>Journal of Diabetes Investigation</i> , 2016, 7, 695-702.	1.1	19
14	Classification and survival prediction for early-stage lung adenocarcinoma and squamous cell carcinoma patients. <i>Oncology Letters</i> , 2017, 14, 5464-5470.	0.8	19
15	Identification of Subtype-Specific Prognostic Genes for Early-Stage Lung Adenocarcinoma and Squamous Cell Carcinoma Patients Using an Embedded Feature Selection Algorithm. <i>PLoS ONE</i> , 2015, 10, e0134630.	1.1	16
16	Identification of monotonically differentially expressed genes for non-small cell lung cancer. <i>BMC Bioinformatics</i> , 2019, 20, 177.	1.2	16
17	Evaluation of different obesity indices as predictors of type 2 diabetes mellitus in a Chinese population. <i>Journal of Diabetes</i> , 2015, 15, 15.	0.8	15
18	Harnessing Naturally Occurring Tumor Immunity: A Clinical Vaccine Trial in Prostate Cancer. <i>PLoS ONE</i> , 2010, 5, e12367.	1.1	14

#	ARTICLE	IF	CITATIONS
19	Classification of Non-Small Cell Lung Cancer Using Significance Analysis of Microarray-Gene Set Reduction Algorithm. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	14
20	Weighted-SAMGSR: combining significance analysis of microarray-gene set reduction algorithm with pathway topology-based weights to select relevant genes. <i>Biology Direct</i> , 2016, 11, 50.	1.9	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. <i>International Journal of Endocrinology</i> , 2022, 2022, 1-9.	0.6	14
22	Multi-TGDR: A Regularization Method for Multi-Class Classification in Microarray Experiments. <i>PLoS ONE</i> , 2013, 8, e78302.	1.1	13
23	Visualization-Aided Classification Ensembles Discriminate Lung Adenocarcinoma and Squamous Cell Carcinoma Samples Using Their Gene Expression Profiles. <i>PLoS ONE</i> , 2014, 9, e110052.	1.1	13
24	Association of polymorphism of PTPN 11 encoding SHP-2 with gastric atrophy but not gastric cancer in <i>Helicobacter pylori</i> seropositive Chinese population. <i>BMC Gastroenterology</i> , 2012, 12, 89.	0.8	12
25	Identification of differentially-expressed genes between early-stage adenocarcinoma and squamous cell carcinoma lung cancer using meta-analysis methods. <i>Oncology Letters</i> , 2017, 13, 3314-3322.	0.8	12
26	Incorporating Pathway Information into Feature Selection towards Better Performed Gene Signatures. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	12
27	Neutrophil-Lymphocyte Ratio as a Prognostic Parameter in NSCLC Patients Receiving EGFR-TKIs: A Systematic Review and Meta-Analysis. <i>Journal of Oncology</i> , 2021, 2021, 1-7.	0.6	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. <i>BMC Bioinformatics</i> , 2014, 15, 97.	1.2	10
29	Identification of prognostic genes and gene sets for early-stage non-small cell lung cancer using bi-level selection methods. <i>Scientific Reports</i> , 2017, 7, 46164.	1.6	9
30	Hierarchical-TGDR. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 278-287.	0.7	7
31	Weighted gene expression profiles identify diagnostic and prognostic genes for lung adenocarcinoma and squamous cell carcinoma. <i>Journal of International Medical Research</i> , 2020, 48, 030006051989383.	0.4	7
32	A longitudinal feature selection method identifies relevant genes to distinguish complicated injury and uncomplicated injury over time. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 115.	1.5	5
33	Feature selection based on differentially correlated gene pairs reveals the mechanism of IFN- β therapy for multiple sclerosis. <i>PeerJ</i> , 2020, 8, e8812.	0.9	5
34	Identification of Genes Discriminating Multiple Sclerosis Patients from Controls by Adapting a Pathway Analysis Method. <i>PLoS ONE</i> , 2016, 11, e0165543.	1.1	4
35	Identification of subtype-specific prognostic signatures using Cox models with redundant gene elimination. <i>Oncology Letters</i> , 2018, 15, 8545-8555.	0.8	4
36	Fundamental asymmetry of insertions and deletions in genomes size evolution. <i>Journal of Theoretical Biology</i> , 2019, 482, 109983.	0.8	4

#	ARTICLE	IF	CITATIONS
37	The cox-filter method identifies respective subtype-specific lncRNA prognostic signatures for two human cancers. BMC Medical Genomics, 2020, 13, 18.	0.7	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.	0.6	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.	0.9	3
40	Identification of Monotonically Differentially Expressed Genes for IFN- γ -Treated Multiple Sclerosis Patients. BioMed Research International, 2019, 2019, 1-6.	0.9	3
41	To select relevant features for longitudinal gene expression data by extending a pathway analysis method. F1000Research, 2018, 7, 1166.	0.8	3
42	An ensemble of the iCluster method to analyze longitudinal lncRNA expression data for psoriasis patients. Human Genomics, 2021, 15, 23.	1.4	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.	0.7	1
44	Identification of Monotonically Differentially Expressed Genes across Pathologic Stages for Cancers. Journal of Oncology, 2020, 2020, 1-9.	0.6	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.	0.7	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.	0.9	1
47	Identification of long non-coding RNA signatures for squamous cell carcinomas and adenocarcinomas. Aging, 2021, 13, 2459-2479.	1.4	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.	0.8	0
49	Exploring exosome data to identify prognostic gene signatures for lung adenocarcinoma. Future Oncology, 2021, 17, 4745-4756.	1.1	0