Yi Jiang

List of Publications by Year
in descending order

		516710	289244
49 papers	1,954 citations	16 h-index	40 g-index
54 all docs	54 docs citations	54 times ranked	4597 citing authors

#	Article	IF	Citations
1	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	12.6	805
2	Early prediction of disease progression in COVID-19 pneumonia patients with chest CT and clinical characteristics. Nature Communications, 2020, 11, 4968.	12.8	183
3	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	14.5	148
4	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. Nature Genetics, 2020, 52, 1239-1246.	21.4	134
5	The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. Science Translational Medicine, 2018, 10, .	12.4	81
6	Preoperative CT for Characterization of Aggressive Macrotrabecular-Massive Subtype and Vessels That Encapsulate Tumor Clusters Pattern in Hepatocellular Carcinoma. Radiology, 2021, 300, 219-229.	7.3	53
7	Sex-differential DNA methylation and associated regulation networks in human brain implicated in the sex-biased risks of psychiatric disorders. Molecular Psychiatry, 2021, 26, 835-848.	7.9	47
8	Clinicopathologic implications of CD8+/Foxp3+ ratio and miR-574-3p/PD-L1 axis in spinal chordoma patients. Cancer Immunology, Immunotherapy, 2018, 67, 209-224.	4.2	40
9	Expression of programmed death-1 ligand (PD-L1) in tumor-infiltrating lymphocytes is associated with favorable spinal chordoma prognosis. American Journal of Translational Research (discontinued), 2016, 8, 3274-87.	0.0	35
10	Clinical Impact of the Immune Microenvironment in Spinal Chordoma: Immunoscore as an Independent Favorable Prognostic Factor. Neurosurgery, 2019, 84, E318-E333.	1.1	33
11	NUPR1 promotes the proliferation and metastasis of oral squamous cell carcinoma cells by activating TFE3-dependent autophagy. Signal Transduction and Targeted Therapy, 2022, 7, 130.	17.1	31
12	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. American Journal of Human Genetics, 2018, 102, 1031-1047.	6.2	26
13	A four-factor immune risk score signature predicts the clinical outcome of patients with spinal chordoma. Clinical and Translational Medicine, 2020, 10, 224-237.	4.0	22
14	Genomic profiles and their associations with TMB, PD-L1 expression, and immune cell infiltration landscapes in synchronous multiple primary lung cancers. , 2021, 9, e003773.		21
15	Integrative analyses prioritize GNL3 as a risk gene for bipolar disorder. Molecular Psychiatry, 2020, 25, 2672-2684.	7.9	18
16	Sarcopenia associates with increased risk of hepatocellular carcinoma among male patients with cirrhosis. Clinical Nutrition, 2020, 39, 3132-3139.	5.0	18
17	Upregulated human telomerase reverse transcriptase (hTERT) expression is associated with spinal chordoma growth, invasion and poor prognosis. American Journal of Translational Research (discontinued), 2016, 8, 516-29.	0.0	17
18	Transcription factor POU3F2 regulates TRIM8 expression contributing to cellular functions implicated in schizophrenia. Molecular Psychiatry, 2021, 26, 3444-3460.	7.9	16

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19	Integrin β4 Is an Effective and Efficient Marker in Synchronously Highlighting Lymphatic and Blood Vascular Invasion, and Perineural Aggression in Malignancy. American Journal of Surgical Pathology, 2020, 44, 681-690.	3.7	16
20	Regulation of 25‐hydroxyvitamin D‐1‐hydroxylase and 24‐hydroxylase in keratinocytes by <scp>PTH</scp> and <scp>FGF</scp>23. Experimental Dermatology, 2018, 27, 1201-1209.	2.9	15
21	Prediction of response of collagen-induced arthritis rats to methotrexate: An 1H-NMR-based urine metabolomic analysis. Journal of Huazhong University of Science and Technology [Medical Sciences], 2012, 32, 438-443.	1.0	13
22	Clinicopathological and Prognostic Characteristics in Extra-Axial Chordomas: An Integrative Analysis of 86 Cases and Comparison With Axial Chordomas. Neurosurgery, 2019, 85, E527-E542.	1.1	13
23	Reduced expression of E-cadherin and p120-catenin and elevated expression of PLC-γ1 and PIKE are associated with aggressiveness of oral squamous cell carcinoma. International Journal of Clinical and Experimental Pathology, 2015, 8, 9042-51.	0.5	13
24	Alteration of cystic airway mesenchyme in congenital pulmonary airway malformation. Scientific Reports, 2019, 9, 5296.	3.3	11
25	Inhibition of 4NQO-Induced Oral Carcinogenesis by Dietary Oyster Shell Calcium. Integrative Cancer Therapies, 2016, 15, 96-101.	2.0	10
26	BrainEXP: a database featuring with spatiotemporal expression variations and co-expression organizations in human brains. Bioinformatics, 2019, 35, 172-174.	4.1	10
27	MiR‐199a‐3p modulates the function of dendritic cells involved in transplantation tolerance by targeting CD86. Hla, 2019, 94, 493-503.	0.6	10
28	Older Age Is Associated with Decreased Levels of VDR, CYP27B1, and CYP24A1 and Increased Levels of PTH in Human Parathyroid Glands. International Journal of Endocrinology, 2020, 2020, 1-6.	1.5	10
29	p120‐catenin suppresses proliferation and tumor growth of oral squamous cell carcinoma via inhibiting nuclear phospholipase C‐γ1 signaling. Journal of Cellular Physiology, 2020, 235, 9399-9413.	4.1	8
30	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. PLoS Computational Biology, 2020, 16, e1007522.	3.2	8
31	G-CSF: A vehicle for communication between trophoblasts and macrophages which may cause problems in recurrent spontaneous abortion. Placenta, 2022, 121, 164-172.	1.5	7
32	p120‐Catenin Is Required for Dietary Calcium Suppression of Oral Carcinogenesis in Mice. Journal of Cellular Physiology, 2017, 232, 1360-1367.	4.1	6
33	Inhibition of 4-nitroquinoline-1-oxide-induced oral carcinogenesis by dietary calcium. International Journal of Clinical and Experimental Pathology, 2015, 8, 3529-42.	0.5	6
34	Interleukin-6, tumor necrosis factor-alpha and receptor activator of nuclear factor kappa ligand are elevated in hypertrophic gastric mucosa of pachydermoperiostosis. Scientific Reports, 2017, 7, 9686.	3.3	4
35	Agonal Factors Distort Gene-Expression Patterns in Human Postmortem Brains. Frontiers in Neuroscience, 2021, 15, 614142.	2.8	4
36	Computer-aided diagnosis system of lung carcinoma using Convolutional Neural Networks. , 2020, , .		3

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37	Cross-Disorder Analysis of De Novo Mutations in Neuropsychiatric Disorders. Journal of Autism and Developmental Disorders, 2022, 52, 1299-1313.	2.7	3
38	Impact of 63-bp deletion and single-base mutation in mpt64 gene on M.tb diagnosis. International Journal of Clinical and Experimental Pathology, 2015, 8, 3210-4.	0.5	3
39	SMAP is a pipeline for sample matching in proteogenomics. Nature Communications, 2022, 13, 744.	12.8	3
40	Case Report: Primary Intraosseous Poorly Differentiated Synovial Sarcoma of the Femur. Frontiers in Oncology, 2022, 12, 754131.	2.8	3
41	Erdheim-Chester disease with asymmetric talus involvement: A case report. World Journal of Clinical Cases, 2020, 8, 614-623.	0.8	1
42	Short-term pulmonary infiltrate with eosinophilia caused by asthma: a phenotype of severe, eosinophilic asthma? Five cases and a review of the literature. Allergy, Asthma and Clinical Immunology, 2019, 15, 48.	2.0	0
43	Protein Structure Prediction and Bioinfamatic Analysis of Novel Fusion Gene IKZF1/Pfas in BPDCN. Blood, 2021, 138, 4319-4319.	1.4	0
44	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
45	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
46	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
47	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
48	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
49	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0