

List of Publications by Year in  
Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

53 papers	2,681 citations	26 h-index	51 g-index
58 ext. papers	3,727 ext. citations	7.4 avg, IF	5.52 L-index

#	Paper	IF	Citations
53	Computational elucidation of spatial gene expression variation from spatially resolved transcriptomics data.. <i>Molecular Therapy - Nucleic Acids</i> , <b>2022</b> , 27, 404-411	10.7	2
52	Efficacy of Different Number of XELOX or SOX Chemotherapy Cycles After D2 Resection for Stage III Gastric Cancer.. <i>Journal of Gastric Cancer</i> , <b>2022</b> , 22, 107-119	3.2	0
51	Cell-free DNA 5-hydroxymethylcytosine profiles of long non-coding RNA genes enable early detection and progression monitoring of human cancers. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 197	7.7	2
50	Comparison of the Efficacy of S-1 Plus Oxaliplatin or Capecitabine Plus Oxaliplatin for Six and Eight Chemotherapy Cycles as Adjuvant Chemotherapy in Patients With Stage II-III Gastric Cancer After D2 Resection. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 684627	5.3	1
49	Pan-cancer characterization of lncRNA modifiers of immune microenvironment reveals clinically distinct de novo tumor subtypes. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 52	6.2	5
48	The pan-cancer landscape of crosstalk between epithelial-mesenchymal transition and immune evasion relevant to prognosis and immunotherapy response. <i>Npj Precision Oncology</i> , <b>2021</b> , 5, 56	9.8	7
47	Mechanistically derived patient-level framework for precision medicine identifies a personalized immune prognostic signature in high-grade serous ovarian cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	7
46	Computational recognition of lncRNA signature of tumor-infiltrating B lymphocytes with potential implications in prognosis and immunotherapy of bladder cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	60
45	Computational principles and practice for decoding immune contexture in the tumor microenvironment. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	19
44	LincSNP 3.0: an updated database for linking functional variants to human long non-coding RNAs, circular RNAs and their regulatory elements. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D1244-D1250	20.1	12
43	Parkinson-like early autonomic dysfunction induced by vagal application of DOPAL in rats. <i>CNS Neuroscience and Therapeutics</i> , <b>2021</b> , 27, 540-551	6.8	3
42	Genomic instability-derived plasma extracellular vesicle-microRNA signature as a minimally invasive predictor of risk and unfavorable prognosis in breast cancer. <i>Journal of Nanobiotechnology</i> , <b>2021</b> , 19, 22	9.4	20
41	Design, methodology, and baseline of whole city-million scale children and adolescents myopia survey (CAMS) in Wenzhou, China. <i>Eye and Vision (London, England)</i> , <b>2021</b> , 8, 31	4.9	5
40	Comprehensive characterization genetic regulation and chromatin landscape of enhancer-associated long non-coding RNAs and their implication in human cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	1
39	Self-Cross-Linked Hydrogel of Cysteamine-Grafted EPolyglutamic Acid Stabilized Tripeptide KPV for Alleviating TNBS-Induced Ulcerative Colitis in Rats. <i>ACS Biomaterials Science and Engineering</i> , <b>2021</b> , 7, 4859-4869	5.5	1
38	Contribution of Baroreflex Afferent Pathway to NPY-Mediated Regulation of Blood Pressure in Rats. <i>Neuroscience Bulletin</i> , <b>2020</b> , 36, 396-406	4.3	4
37	Hepatocellular HO-1 mediated iNOS-induced hepatoprotection against liver ischemia reperfusion injury. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 521, 1095-1100	3.4	3

36	Computational Methods and Applications for Identifying Disease-Associated lncRNAs as Potential Biomarkers and Therapeutic Targets. <i>Molecular Therapy - Nucleic Acids</i> , <b>2020</b> , 21, 156-171	10.7	18
35	Identification of tumor immune infiltration-associated lncRNAs for improving prognosis and immunotherapy response of patients with non-small cell lung cancer <b>2020</b> , 8,		116
34	Systematic Characterization of Circular RNA-Associated CeRNA Network Identified Novel circRNA Biomarkers in Alzheimer's Disease. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2019</b> , 7, 222	5.8	35
33	Large-scale integrated analysis of ovarian cancer tumors and cell lines identifies an individualized gene expression signature for predicting response to platinum-based chemotherapy. <i>Cell Death and Disease</i> , <b>2019</b> , 10, 661	9.8	11
32	Integrative analysis from multi-centre studies identifies a function-derived personalized multi-gene signature of outcome in colorectal cancer. <i>Journal of Cellular and Molecular Medicine</i> , <b>2019</b> , 23, 5270-5281	5.6	12
31	Serotonin-Mediated Cardiac Analgesia via Ah-Type Baroreceptor Activation Contributes to Silent Angina and Asymptomatic Infarction. <i>Neuroscience</i> , <b>2019</b> , 411, 150-163	3.9	5
30	Anti-Hypertensive Action of Fenofibrate via UCP2 Upregulation Mediated by PPAR Activation in Baroreflex Afferent Pathway. <i>Neuroscience Bulletin</i> , <b>2019</b> , 35, 15-24	4.3	8
29	MetSigDis: a manually curated resource for the metabolic signatures of diseases. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 203-209	13.4	82
28	Analysis of long noncoding RNAs highlights region-specific altered expression patterns and diagnostic roles in Alzheimer's disease. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 598-608	13.4	51
27	An Immune-Related Six-lncRNA Signature to Improve Prognosis Prediction of Glioblastoma Multiforme. <i>Molecular Neurobiology</i> , <b>2018</b> , 55, 3684-3697	6.2	130
26	DincRNA: a comprehensive web-based bioinformatics toolkit for exploring disease associations and ncRNA function. <i>Bioinformatics</i> , <b>2018</b> , 34, 1953-1956	7.2	168
25	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. <i>BMC Genomics</i> , <b>2018</b> , 19, 919	4.5	76
24	A novel lncRNA-focus expression signature for survival prediction in endometrial carcinoma. <i>BMC Cancer</i> , <b>2018</b> , 18, 39	4.8	44
23	Recurrence-Associated Long Non-coding RNA Signature for Determining the Risk of Recurrence in Patients with Colon Cancer. <i>Molecular Therapy - Nucleic Acids</i> , <b>2018</b> , 12, 518-529	10.7	74
22	Discovery and validation of immune-associated long non-coding RNA biomarkers associated with clinically molecular subtype and prognosis in diffuse large B cell lymphoma. <i>Molecular Cancer</i> , <b>2017</b> , 16, 16	42.1	138
21	Discovery of potential prognostic long non-coding RNA biomarkers for predicting the risk of tumor recurrence of breast cancer patients. <i>Scientific Reports</i> , <b>2016</b> , 6, 31038	4.9	70
20	A potential panel of six-long non-coding RNA signature to improve survival prediction of diffuse large-B-cell lymphoma. <i>Scientific Reports</i> , <b>2016</b> , 6, 27842	4.9	56
19	OAHG: an integrated resource for annotating human genes with multi-level ontologies. <i>Scientific Reports</i> , <b>2016</b> , 6, 34820	4.9	68

18	IntNetLncSim: an integrative network analysis method to infer human lncRNA functional similarity. <i>Oncotarget</i> , <b>2016</b> , 7, 47864-47874	3.3	42
17	Comprehensive analysis of lncRNA expression profiles reveals a novel lncRNA signature to discriminate nonequivalent outcomes in patients with ovarian cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 32433-48	3.3	110
16	Construction and analysis of dysregulated lncRNA-associated ceRNA network identified novel lncRNA biomarkers for early diagnosis of human pancreatic cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 56383-56394	3.3	109
15	Characterization of long non-coding RNA-associated ceRNA network to reveal potential prognostic lncRNA biomarkers in human ovarian cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 12598-611	3.3	190
14	Relapse-related long non-coding RNA signature to improve prognosis prediction of lung adenocarcinoma. <i>Oncotarget</i> , <b>2016</b> , 7, 29720-38	3.3	70
13	Integration of Multiple Genomic and Phenotype Data to Infer Novel miRNA-Disease Associations. <i>PLoS ONE</i> , <b>2016</b> , 11, e0148521	3.7	21
12	DisSim: an online system for exploring significant similar diseases and exhibiting potential therapeutic drugs. <i>Scientific Reports</i> , <b>2016</b> , 6, 30024	4.9	42
11	A potential signature of eight long non-coding RNAs predicts survival in patients with non-small cell lung cancer. <i>Journal of Translational Medicine</i> , <b>2015</b> , 13, 231	8.5	143
10	Prioritizing candidate disease-related long non-coding RNAs by walking on the heterogeneous lncRNA and disease network. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 760-9		140
9	A potential prognostic long non-coding RNA signature to predict metastasis-free survival of breast cancer patients. <i>Scientific Reports</i> , <b>2015</b> , 5, 16553	4.9	81
8	Identification and validation of potential prognostic lncRNA biomarkers for predicting survival in patients with multiple myeloma. <i>Journal of Experimental and Clinical Cancer Research</i> , <b>2015</b> , 34, 102	12.8	141
7	Identification of Aberrant Chromosomal Regions in Human Breast Cancer Using Gene Expression Data and Related Gene Information. <i>Medical Science Monitor</i> , <b>2015</b> , 21, 2557-66	3.2	4
6	Inferring novel lncRNA-disease associations based on a random walk model of a lncRNA functional similarity network. <i>Molecular BioSystems</i> , <b>2014</b> , 10, 2074-81		188
5	Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. <i>FEBS Letters</i> , <b>2013</b> , 587, 976-82	3.8	11
4	Comparative genomic analysis reveals evolutionary characteristics and patterns of microRNA clusters in vertebrates. <i>Gene</i> , <b>2013</b> , 512, 383-91	3.8	19
3	Inferring potential microRNA-microRNA associations based on targeting propensity and connectivity in the context of protein interaction network. <i>PLoS ONE</i> , <b>2013</b> , 8, e69719	3.7	15
2	Characterization and evolution of microRNA genes derived from repetitive elements and duplication events in plants. <i>PLoS ONE</i> , <b>2012</b> , 7, e34092	3.7	35
1	Systematic analysis of genomic organization and heterogeneities of miRNA cluster in vertebrates. <i>Molecular Biology Reports</i> , <b>2012</b> , 39, 5143-9	2.8	4

