

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.

271 papers	7,657 citations	46 h-index	75 g-index
296 ext. papers	10,238 ext. citations	7.4 avg, IF	5.82 L-index

#	Paper	IF	Citations
271	Identifying individualized risk subpathways reveals pan-cancer molecular classification based on multi-omics data.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 838-849	6.8	0
270	Comprehensive characterization of human-virus protein-protein interactions reveals disease comorbidities and potential antiviral drugs.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 1244-1253	6.8	1
269	Applicability of Anticancer Drugs for the Triple-Negative Breast Cancer Based on Homologous Recombination Repair Deficiency.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 845950	5.7	0
268	Identifying metabolic reprogramming phenotypes with glycolysis-lipid metabolism discoordination and intercellular communication for lung adenocarcinoma metastasis.. <i>Communications Biology</i> , 2022 , 5, 198	6.7	0
267	Single-Cell Transcriptomic Analysis Reveals a Tumor-Reactive T Cell Signature Associated With Clinical Outcome and Immunotherapy Response In Melanoma. <i>Frontiers in Immunology</i> , 2021 , 12, 758288	8.4	3
266	Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes.. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 768981	5.7	1
265	ImmReg: the regulon atlas of immune-related pathways across cancer types. <i>Nucleic Acids Research</i> , 2021 , 49, 12106-12118	20.1	1
264	Same total normal forms sperm counts of males from Lhasa and Shanghai, China. <i>Environmental Science and Pollution Research</i> , 2021 , 1	5.1	
263	Dynamic regulatory networks of T cell trajectory dissect transcriptional control of T cell state transition. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 26, 1115-1129	10.7	1
262	Dietary Intake of Calcium and Magnesium in Relation to Severe Headache or Migraine. <i>Frontiers in Nutrition</i> , 2021 , 8, 653765	6.2	2
261	Nomograms for Predicting Axillary Lymph Node Status Reconciled With Preoperative Breast Ultrasound Images. <i>Frontiers in Oncology</i> , 2021 , 11, 567648	5.3	0
260	Multilevel prioritization of gene regulators associated with consensus molecular subtypes of colorectal cancer. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
259	A urine-based DNA methylation assay to facilitate early detection and risk stratification of bladder cancer. <i>Clinical Epigenetics</i> , 2021 , 13, 91	7.7	11
258	Case Report: Anti-N-Methyl-D-Aspartate Receptor Encephalitis in an Elderly Patient With Primary Sjögren's Syndrome. <i>Frontiers in Neurology</i> , 2021 , 12, 656024	4.1	0
257	MeImmS: Predict Clinical Benefit of Anti-PD-1/PD-L1 Treatments Based on DNA Methylation in Non-small Cell Lung Cancer. <i>Frontiers in Genetics</i> , 2021 , 12, 676449	4.5	3
256	Alternative splicing perturbation landscape identifies RNA binding proteins as potential therapeutic targets in cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 24, 792-806	10.7	2
255	Individualized lncRNA differential expression profile reveals heterogeneity of breast cancer. <i>Oncogene</i> , 2021 , 40, 4604-4614	9.2	4

254	CeRNASeek: an R package for identification and analysis of ceRNA regulation. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
253	SurvivalMeth: a web server to investigate the effect of DNA methylation-related functional elements on prognosis. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	19
252	GABC: A comprehensive resource and Genome Atlas for Breast Cancer. <i>International Journal of Cancer</i> , 2021 , 148, 988-994	7.5	1
251	Lnc2Cancer 3.0: an updated resource for experimentally supported lncRNA/circRNA cancer associations and web tools based on RNA-seq and scRNA-seq data. <i>Nucleic Acids Research</i> , 2021 , 49, D1251-D1258	20.1	44
250	LnCeCell: a comprehensive database of predicted lncRNA-associated ceRNA networks at single-cell resolution. <i>Nucleic Acids Research</i> , 2021 , 49, D125-D133	20.1	17
249	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> , 2021 , 49, D1244-D1250	20.1	12
248	IDH clonal heterogeneity segregates a subgroup of non-1p/19q codeleted gliomas with unfavourable clinical outcome. <i>Neuropathology and Applied Neurobiology</i> , 2021 , 47, 394-405	5.2	1
247	Systematic analysis of enhancer regulatory circuit perturbation driven by copy number variations in malignant glioma. <i>Theranostics</i> , 2021 , 11, 3060-3073	12.1	1
246	Association Between Dietary Iron Intake and Serum Ferritin and Severe Headache or Migraine. <i>Frontiers in Nutrition</i> , 2021 , 8, 685564	6.2	0
245	Dissecting immune cell stat regulation network reveals biomarkers to predict ICB therapy responders in melanoma. <i>Journal of Translational Medicine</i> , 2021 , 19, 296	8.5	2
244	Substrate Stiffness Modulates the Growth, Phenotype, and Chemoresistance of Ovarian Cancer Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 718834	5.7	5
243	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> , 2021 ,	13.4	1
242	Combined homologous recombination repair deficiency and immune activation analysis for predicting intensified responses of anthracycline, cyclophosphamide and taxane chemotherapy in triple-negative breast cancer. <i>BMC Medicine</i> , 2021 , 19, 190	11.4	3
241	Discovering a qualitative transcriptional signature of homologous recombination defectiveness for prostate cancer. <i>IScience</i> , 2021 , 24, 103135	6.1	1
240	Models for Predicting Sentinel and Non-sentinel Lymph Nodes Based on Pre-operative Ultrasonic Breast Imaging to Optimize Axillary Strategies. <i>Ultrasound in Medicine and Biology</i> , 2021 , 47, 3101-3110	3.5	1
239	Identifying and characterizing lincRNA genomic clusters reveals its cooperative functions in human cancer.. <i>Journal of Translational Medicine</i> , 2021 , 19, 509	8.5	0
238	ncDRMarker: a computational method for identifying non-coding RNA signatures of drug resistance based on heterogeneous network. <i>Annals of Translational Medicine</i> , 2020 , 8, 1395	3.2	1
237	Clonal tumor mutations in homologous recombination genes predict favorable clinical outcome in ovarian cancer treated with platinum-based chemotherapy. <i>Gynecologic Oncology</i> , 2020 , 158, 66-76	4.9	2

236	LncSpA: LncRNA Spatial Atlas of Expression across Normal and Cancer Tissues. <i>Cancer Research</i> , 2020 , 80, 2067-2071	10.1	14
235	Pan-cancer characterization of immune-related lncRNAs identifies potential oncogenic biomarkers. <i>Nature Communications</i> , 2020 , 11, 1000	17.4	142
234	Berberine prevents primary peritoneal adhesion and adhesion reformation by directly inhibiting TIMP-1. <i>Acta Pharmaceutica Sinica B</i> , 2020 , 10, 812-824	15.5	7
233	Prioritizing Gene Cascading Paths to Model Colorectal Cancer Through Engineered Organoids. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 12	5.8	1
232	Combination of multiple tumor-infiltrating immune cells predicts clinical outcome in colon cancer. <i>Clinical Immunology</i> , 2020 , 215, 108412	9	9
231	LnCeVar: a comprehensive database of genomic variations that disturb ceRNA network regulation. <i>Nucleic Acids Research</i> , 2020 , 48, D111-D117	20.1	36
230	LncTarD: a manually-curated database of experimentally-supported functional lncRNA-target regulations in human diseases. <i>Nucleic Acids Research</i> , 2020 , 48, D118-D126	20.1	42
229	Transcriptome analysis reveals a reprogramming energy metabolism-related signature to improve prognosis in colon cancer. <i>PeerJ</i> , 2020 , 8, e9458	3.1	1
228	Complex impact of DNA methylation on transcriptional dysregulation across 22 human cancer types. <i>Nucleic Acids Research</i> , 2020 , 48, 2287-2302	20.1	13
227	RNAactDrug: a comprehensive database of RNAs associated with drug sensitivity from multi-omics data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2167-2174	13.4	9
226	Identification and comprehensive characterization of lncRNAs with copy number variations and their driving transcriptional perturbed subpathways reveal functional significance for cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2153-2166	13.4	2
225	ZEB2-AS1 Accelerates Epithelial/Mesenchymal Transition Through miR-1205/CRKL Pathway in Colorectal Cancer. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2020 , 35, 153-162	3.9	8
224	GDF11 inhibits cardiomyocyte pyroptosis and exerts cardioprotection in acute myocardial infarction mice by upregulation of transcription factor HOXA3. <i>Cell Death and Disease</i> , 2020 , 11, 917	9.8	13
223	Identifying bifurcated paths with differential function impact in glioblastomas evolution. <i>International Journal of Cancer</i> , 2020 , 147, 3139-3151	7.5	
222	Myasthenia Gravis Coexisting With Primary Sjögren's Syndrome: Report of Three Cases and Literature Review. <i>Frontiers in Neurology</i> , 2020 , 11, 939	4.1	1
221	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 957-969	13.4	10
220	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. <i>Oncogene</i> , 2020 , 39, 677-689	9.2	5
219	E. coli diversity: low in colorectal cancer. <i>BMC Medical Genomics</i> , 2020 , 13, 59	3.7	3

218	Dynamic Expression of mA Regulators During Multiple Human Tissue Development and Cancers. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 629030	5.7	1
217	Comprehensive analysis of long noncoding RNA (lncRNA)-chromatin interactions reveals lncRNA functions dependent on binding diverse regulatory elements. <i>Journal of Biological Chemistry</i> , 2019 , 294, 15613-15622	5.4	18
216	Comprehensive Characterization of Somatic Mutations Impacting lncRNA Expression for Pan-Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 66-79	10.7	12
215	Landscape of Enhancer-Enhancer Cooperative Regulation during Human Cardiac Commitment. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 17, 840-851	10.7	6
214	Downregulated MCOLN1 Attenuates The Progression Of Non-Small-Cell Lung Cancer By Inhibiting Lysosome-Autophagy. <i>Cancer Management and Research</i> , 2019 , 11, 8607-8617	3.6	8
213	Gain-of-Function Mutations: An Emerging Advantage for Cancer Biology. <i>Trends in Biochemical Sciences</i> , 2019 , 44, 659-674	10.3	24
212	Support Vector Machine for Analyzing Contributions of Brain Regions During Task-State fMRI. <i>Frontiers in Neuroinformatics</i> , 2019 , 13, 10	3.9	13
211	Revealing clonality and subclonality of driver genes for clinical survival benefits in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019 , 175, 91-104	4.4	6
210	Survey of miRNA-miRNA cooperative regulation principles across cancer types. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1621-1638	13.4	17
209	Landscape of the long non-coding RNA transcriptome in human heart. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1812-1825	13.4	11
208	Identifying subpathway signatures for individualized anticancer drug response by integrating multi-omics data. <i>Journal of Translational Medicine</i> , 2019 , 17, 255	8.5	8
207	Identifying Cancer Driver lncRNAs Bridged by Functional Effectors through Integrating Multi-omics Data in Human Cancers. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 17, 362-373	10.7	20
206	Computational Epigenetics for Breast Cancer 2019 , 233-246		
205	Discovering Rare Genes Contributing to Cancer Stemness and Invasive Potential by GBM Single-Cell Transcriptional Analysis. <i>Cancers</i> , 2019 , 11,	6.6	3
204	MERIT: Systematic Analysis and Characterization of Mutational Effect on RNA Interactome Topology. <i>Hepatology</i> , 2019 , 70, 532-546	11.2	16
203	Systematic identification of lincRNA-based prognostic biomarkers by integrating lincRNA expression and copy number variation in lung adenocarcinoma. <i>International Journal of Cancer</i> , 2019 , 144, 1723-1734	7.5	43
202	Breast cancer prognosis signature: linking risk stratification to disease subtypes. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2130-2140	13.4	26
201	LncACTdb 2.0: an updated database of experimentally supported ceRNA interactions curated from low- and high-throughput experiments. <i>Nucleic Acids Research</i> , 2019 , 47, D121-D127	20.1	70

200	Lnc2Cancer v2.0: updated database of experimentally supported long non-coding RNAs in human cancers. <i>Nucleic Acids Research</i> , 2019 , 47, D1028-D1033	20.1	114
199	CancerSEA: a cancer single-cell state atlas. <i>Nucleic Acids Research</i> , 2019 , 47, D900-D908	20.1	127
198	Sex difference of mutation clonality in diffuse glioma evolution. <i>Neuro-Oncology</i> , 2019 , 21, 201-213	1	16
197	CellMarker: a manually curated resource of cell markers in human and mouse. <i>Nucleic Acids Research</i> , 2019 , 47, D721-D728	20.1	305
196	Systematic review regulatory principles of non-coding RNAs in cardiovascular diseases. <i>Briefings in Bioinformatics</i> , 2019 , 20, 66-76	13.4	12
195	Identifying mutual exclusivity across cancer genomes: computational approaches to discover genetic interaction and reveal tumor vulnerability. <i>Briefings in Bioinformatics</i> , 2019 , 20, 254-266	13.4	19
194	Inferences of individual drug responses across diverse cancer types using a novel competing endogenous RNA network. <i>Molecular Oncology</i> , 2018 , 12, 1429-1446	7.9	18
193	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. <i>Nucleic Acids Research</i> , 2018 , 46, 1113-1123	20.1	59
192	Lnc2Meth: a manually curated database of regulatory relationships between long non-coding RNAs and DNA methylation associated with human disease. <i>Nucleic Acids Research</i> , 2018 , 46, D133-D138	20.1	35
191	MSDD: a manually curated database of experimentally supported associations among miRNAs, SNPs and human diseases. <i>Nucleic Acids Research</i> , 2018 , 46, D181-D185	20.1	29
190	DiseaseEnhancer: a resource of human disease-associated enhancer catalog. <i>Nucleic Acids Research</i> , 2018 , 46, D78-D84	20.1	43
189	SEECancer: a resource for somatic events in evolution of cancer genome. <i>Nucleic Acids Research</i> , 2018 , 46, D1018-D1026	20.1	8
188	Combinatorial epigenetic regulation of non-coding RNAs has profound effects on oncogenic pathways in breast cancer subtypes. <i>Briefings in Bioinformatics</i> , 2018 , 19, 52-64	13.4	12
187	LnChrom: a resource of experimentally validated lncRNA-chromatin interactions in human and mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	24
186	FACER: comprehensive molecular and functional characterization of epigenetic chromatin regulators. <i>Nucleic Acids Research</i> , 2018 , 46, 10019-10033	20.1	8
185	Transcriptome analysis reveals a long non-coding RNA signature to improve biochemical recurrence prediction in prostate cancer. <i>Oncotarget</i> , 2018 , 9, 24936-24949	3.3	7
184	A pan-cancer atlas of cancer hallmark-associated candidate driver lncRNAs. <i>Molecular Oncology</i> , 2018 , 12, 1980-2005	7.9	13
183	Capturing functional long non-coding RNAs through integrating large-scale causal relations from gene perturbation experiments. <i>EBioMedicine</i> , 2018 , 35, 369-380	8.8	14

182	Genomic-Scale Prioritization of Disease-Related Non-coding RNAs. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1094, 29-37	3.6	
181	Computational Inferring of Risk Subpathways Mediated by Dysfunctional Non-coding RNAs. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1094, 87-95	3.6	
180	Non-coding RNA Resources. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1094, 1-7	3.6	9
179	TIP: A Web Server for Resolving Tumor Immunophenotype Profiling. <i>Cancer Research</i> , 2018 , 78, 6575-6580.	4.1	109
178	Apoptosis-inducing effects and growth inhibitory of a novel chalcone, in human hepatic cancer cells and lung cancer cells. <i>Biomedicine and Pharmacotherapy</i> , 2018 , 105, 195-203	7.5	11
177	Insight into HOTAIR structural features and functions as landing pads for transcription regulation proteins. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 485, 679-685	3.4	14
176	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , 2017 , 7, 46566	4.9	13
175	Cooperative genomic alteration network reveals molecular classification across 12 major cancer types. <i>Nucleic Acids Research</i> , 2017 , 45, 567-582	20.1	17
174	GFI1 downregulation promotes inflammation-linked metastasis of colorectal cancer. <i>Cell Death and Differentiation</i> , 2017 , 24, 929-943	12.7	10
173	RNA Function Prediction. <i>Methods in Molecular Biology</i> , 2017 , 1654, 17-28	1.4	9
172	Validation study of the safety attitudes questionnaire (SAQ) in public hospitals of Heilongjiang province, China. <i>PLoS ONE</i> , 2017 , 12, e0179486	3.7	11
171	miRNA-miRNA crosstalk: from genomics to phenomics. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1002-1011	13.4	16
170	A comprehensive overview of lncRNA annotation resources. <i>Briefings in Bioinformatics</i> , 2017 , 18, 236-249	13.4	85
169	The LncRNA Connectivity Map: Using LncRNA Signatures to Connect Small Molecules, LncRNAs, and Diseases. <i>Scientific Reports</i> , 2017 , 7, 6655	4.9	19
168	BioM2MetDisease: a manually curated database for associations between microRNAs, metabolites, small molecules and metabolic diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	2
167	sPAGM: inferring subpathway activity by integrating gene and miRNA expression-robust functional signature identification for melanoma prognoses. <i>Scientific Reports</i> , 2017 , 7, 15322	4.9	5
166	Acute exposure to fine particulate matter and cardiovascular hospital emergency room visits in Beijing, China. <i>Environmental Pollution</i> , 2017 , 220, 317-327	9.3	53
165	Characterization of soluble N-ethylmaleimide-sensitive factor attachment protein receptor gene STX18 variations for possible roles in congenital heart diseases. <i>Gene</i> , 2017 , 598, 79-83	3.8	5

164	LincSNP 2.0: an updated database for linking disease-associated SNPs to human long non-coding RNAs and their TFBSs. <i>Nucleic Acids Research</i> , 2017 , 45, D74-D78	20.1	64
163	Improved method for prioritization of disease associated lncRNAs based on ceRNA theory and functional genomics data. <i>Oncotarget</i> , 2017 , 8, 4642-4655	3.3	20
162	Competing endogenous RNA network analysis identifies critical genes among the different breast cancer subtypes. <i>Oncotarget</i> , 2017 , 8, 10171-10184	3.3	21
161	Systemically identifying and prioritizing risk lncRNAs through integration of pan-cancer phenotype associations. <i>Oncotarget</i> , 2017 , 8, 12041-12051	3.3	10
160	LncSubpathway: a novel approach for identifying dysfunctional subpathways associated with risk lncRNAs by integrating lncRNA and mRNA expression profiles and pathway topologies. <i>Oncotarget</i> , 2017 , 8, 15453-15469	3.3	8
159	Cancer killers in the human gut microbiota: diverse phylogeny and broad spectra. <i>Oncotarget</i> , 2017 , 8, 49574-49591	3.3	22
158	Multiple gene-specific DNA methylation in blood leukocytes and colorectal cancer risk: a case-control study in China. <i>Oncotarget</i> , 2017 , 8, 61239-61252	3.3	9
157	Lnc2Cancer: a manually curated database of experimentally supported lncRNAs associated with various human cancers. <i>Nucleic Acids Research</i> , 2016 , 44, D980-5	20.1	243
156	Crosstalk of dynamic functional modules in lung development of rhesus macaques. <i>Molecular BioSystems</i> , 2016 , 12, 1342-9		7
155	Identifying the crosstalk of dysfunctional pathways mediated by lncRNAs in breast cancer subtypes. <i>Molecular BioSystems</i> , 2016 , 12, 711-20		23
154	Fine Particulate Air Pollution and Hospital Emergency Room Visits for Respiratory Disease in Urban Areas in Beijing, China, in 2013. <i>PLoS ONE</i> , 2016 , 11, e0153099	3.7	103
153	Dysregulated long intergenic non-coding RNA modules contribute to heart failure. <i>Oncotarget</i> , 2016 , 7, 59676-59690	3.3	15
152	MIRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , 2016 , 7, 55012-55025	3.3	9
151	Systematically characterizing dysfunctional long intergenic non-coding RNAs in multiple brain regions of major psychosis. <i>Oncotarget</i> , 2016 , 7, 71087-71098	3.3	30
150	EGFRvIII/integrin β interaction in hypoxic and vitronectinenriching microenvironment promote GBM progression and metastasis. <i>Oncotarget</i> , 2016 , 7, 4680-94	3.3	42
149	Dissecting dysfunctional crosstalk pathways regulated by miRNAs during glioma progression. <i>Oncotarget</i> , 2016 , 7, 25769-82	3.3	6
148	Construction of a lncRNA-mediated feed-forward loop network reveals global topological features and prognostic motifs in human cancers. <i>Oncotarget</i> , 2016 , 7, 45937-45947	3.3	15
147	Identifying and functionally characterizing tissue-specific and ubiquitously expressed human lncRNAs. <i>Oncotarget</i> , 2016 , 7, 7120-33	3.3	57

146	Comprehensive characterization of lncRNA-mRNA related ceRNA network across 12 major cancers. <i>Oncotarget</i> , 2016 , 7, 64148-64167	3.3	133
145	Longitudinal Associations between Triglycerides and Metabolic Syndrome Components in a Beijing Adult Population, 2007-2012. <i>International Journal of Medical Sciences</i> , 2016 , 13, 445-50	3.7	9
144	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , 2016 , 7, 69837-69846	3.3	16
143	Spatiotemporal Cluster Patterns of Hand, Foot, and Mouth Disease at the County Level in Mainland China, 2008-2012. <i>PLoS ONE</i> , 2016 , 11, e0147532	3.7	16
142	Identification and characterization of lncRNA mediated transcriptional dysregulation dictates lncRNA roles in glioblastoma. <i>Oncotarget</i> , 2016 , 7, 45027-45041	3.3	27
141	Extensive ceRNA-ceRNA interaction networks mediated by miRNAs regulate development in multiple rhesus tissues. <i>Nucleic Acids Research</i> , 2016 , 44, 9438-9451	20.1	38
140	Copy number variation of E3 ubiquitin ligase genes in peripheral blood leukocyte and colorectal cancer. <i>Scientific Reports</i> , 2016 , 6, 29869	4.9	8
139	'Traffic light rules': Chromatin states direct miRNA-mediated network motifs running by integrating epigenome and regulatome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016 , 1860, 1475-88	4	9
138	Identification of a lncRNA involved functional module for esophageal cancer subtypes. <i>Molecular BioSystems</i> , 2016 , 12, 3312-3323		9
137	Identification of prognostic biomarkers in glioblastoma using a long non-coding RNA-mediated, competitive endogenous RNA network. <i>Oncotarget</i> , 2016 , 7, 41737-41747	3.3	33
136	CLIC1 a novel biomarker of intraperitoneal metastasis in serous epithelial ovarian cancer. <i>Tumor Biology</i> , 2015 , 36, 4175-9	2.9	22
135	A novel dysregulated pathway-identification analysis based on global influence of within-pathway effects and crosstalk between pathways. <i>Journal of the Royal Society Interface</i> , 2015 , 12, 20140937	4.1	11
134	Integrative analysis of lung development-cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015 , 11, 1271-84		7
133	Gene Perturbation Atlas (GPA): a single-gene perturbation repository for characterizing functional mechanisms of coding and non-coding genes. <i>Scientific Reports</i> , 2015 , 5, 10889	4.9	14
132	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , 2015 , 31, 3638-44	7.2	45
131	Identification of lncRNA-associated competing triplets reveals global patterns and prognostic markers for cancer. <i>Nucleic Acids Research</i> , 2015 , 43, 3478-89	20.1	172
130	ncRDeathDB: A comprehensive bioinformatics resource for deciphering network organization of the ncRNA-mediated cell death system. <i>Autophagy</i> , 2015 , 11, 1917-26	10.2	50
129	Chinese herbal therapy and Western drug use, belief and adherence for hypertension management in the rural areas of Heilongjiang province, China. <i>PLoS ONE</i> , 2015 , 10, e0123508	3.7	3

128	Spatiotemporal-specific lncRNAs in the brain, colon, liver and lung of macaque during development. <i>Molecular BioSystems</i> , 2015 , 11, 3253-63		26
127	The mRNA related ceRNA-ceRNA landscape and significance across 20 major cancer types. <i>Nucleic Acids Research</i> , 2015 , 43, 8169-82	20.1	138
126	Identification of module biomarkers from the dysregulated ceRNA-ceRNA interaction network in lung adenocarcinoma. <i>Molecular BioSystems</i> , 2015 , 11, 3048-58		41
125	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , 2015 , 11, 656-63		19
124	Identification of cancer-related lncRNAs through integrating genome, regulome and transcriptome features. <i>Molecular BioSystems</i> , 2015 , 11, 126-36		68
123	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , 2015 , 5, 11566	4.9	31
122	MeSiC: A Model-Based Method for Estimating 5 mC Levels at Single-CpG Resolution from MeDIP-seq. <i>Scientific Reports</i> , 2015 , 5, 14699	4.9	8
121	Construction and analysis of dynamic transcription factor regulatory networks in the progression of glioma. <i>Scientific Reports</i> , 2015 , 5, 15953	4.9	11
120	Co-lncRNA: investigating the lncRNA combinatorial effects in GO annotations and KEGG pathways based on human RNA-Seq data. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	91
119	Chromatin states modify network motifs contributing to cell-specific functions. <i>Scientific Reports</i> , 2015 , 5, 11938	4.9	9
118	Identifying ultrasound and clinical features of breast cancer molecular subtypes by ensemble decision. <i>Scientific Reports</i> , 2015 , 5, 11085	4.9	41
117	Systematically Prioritizing Functional Differentially Methylated Regions (fDMRs) by Integrating Multi-omics Data in Colorectal Cancer. <i>Scientific Reports</i> , 2015 , 5, 12789	4.9	4
116	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015 , 5, 13044	4.9	23
115	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015 , 5, 17201	4.9	29
114	Genome-wide DNA methylome reveals the dysfunction of intronic microRNAs in major psychosis. <i>BMC Medical Genomics</i> , 2015 , 8, 62	3.7	23
113	miRSponge: a manually curated database for experimentally supported miRNA sponges and ceRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	76
112	Risk Factors of Myopic Shift among Primary School Children in Beijing, China: A Prospective Study. <i>International Journal of Medical Sciences</i> , 2015 , 12, 633-8	3.7	32
111	Construction and analysis of lncRNA-lncRNA synergistic networks to reveal clinically relevant lncRNAs in cancer. <i>Oncotarget</i> , 2015 , 6, 25003-16	3.3	33

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