

List of Publications by Citations

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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	CellMarker: a manually curated resource of cell markers in human and mouse. <i>Nucleic Acids Research</i> , 2019 , 47, D721-D728	20.1	305
270	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
269	MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011 , 39, 825-36	20.1	218
268	Walking the interactome to identify human miRNA-disease associations through the functional link between miRNA targets and disease genes. <i>BMC Systems Biology</i> , 2013 , 7, 101	3.5	184
267	Prioritizing candidate disease miRNAs by topological features in the miRNA target-dysregulated network: case study of prostate cancer. <i>Molecular Cancer Therapeutics</i> , 2011 , 10, 1857-66	6.1	179
266	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
265	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009 , 37, e131	20.1	143
264	Pan-cancer characterization of immune-related lncRNAs identifies potential oncogenic biomarkers. <i>Nature Communications</i> , 2020 , 11, 1000	17.4	142
263	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
262	Prediction of potential disease-associated microRNAs based on random walk. <i>Bioinformatics</i> , 2015 , 31, 1805-15	7.2	138
261	Comprehensive characterization of lncRNA-mRNA related ceRNA network across 12 major cancers. <i>Oncotarget</i> , 2016 , 7, 64148-64167	3.3	133
260	CancerSEA: a cancer single-cell state atlas. <i>Nucleic Acids Research</i> , 2019 , 47, D900-D908	20.1	127
259	SM2miR: a database of the experimentally validated small molecules' effects on microRNA expression. <i>Bioinformatics</i> , 2013 , 29, 409-11	7.2	114
258	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
257	TIP: A Web Server for Resolving Tumor Immunophenotype Profiling. <i>Cancer Research</i> , 2018 , 78, 6575-6580	20.1	109
256	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
255	Comprehensive analysis of the functional microRNA-mRNA regulatory network identifies miRNA signatures associated with glioma malignant progression. <i>Nucleic Acids Research</i> , 2013 , 41, e203	20.1	99

254	Prevalence and associated factors of myopia in high-school students in Beijing. <i>PLoS ONE</i> , 2015 , 10, e0120764	3.7	96
253	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. <i>Genomics</i> , 2005 , 85, 16-23	4.3	95
252	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
251	The analysis of the drug-targets based on the topological properties in the human protein-protein interaction network. <i>Journal of Drug Targeting</i> , 2009 , 17, 524-32	5.4	86
250	A comprehensive overview of lncRNA annotation resources. <i>Briefings in Bioinformatics</i> , 2017 , 18, 236-249	3.4	85
249	Subpathway-GM: identification of metabolic subpathways via joint power of interesting genes and metabolites and their topologies within pathways. <i>Nucleic Acids Research</i> , 2013 , 41, e101	20.1	85
248	Augmentation of response to chemotherapy by microRNA-506 through regulation of RAD51 in serous ovarian cancers. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	80
247	Gene mining: a novel and powerful ensemble decision approach to hunting for disease genes using microarray expression profiling. <i>Nucleic Acids Research</i> , 2004 , 32, 2685-94	20.1	77
246	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
245	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
244	Identification of cancer-related lncRNAs through integrating genome, regulome and transcriptome features. <i>Molecular BioSystems</i> , 2015 , 11, 126-36		68
243	ViRBase: a resource for virus-host ncRNA-associated interactions. <i>Nucleic Acids Research</i> , 2015 , 43, D578-D581	20.1	68
242	DOSim: an R package for similarity between diseases based on Disease Ontology. <i>BMC Bioinformatics</i> , 2011 , 12, 266	3.6	65
241	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
240	The DNA methylome and transcriptome of different brain regions in schizophrenia and bipolar disorder. <i>PLoS ONE</i> , 2014 , 9, e95875	3.7	64
239	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. <i>Nucleic Acids Research</i> , 2018 , 46, 1113-1123	20.1	59
238	JAK2/STAT3 targeted therapy suppresses tumor invasion via disruption of the EGFRvIII/JAK2/STAT3 axis and associated focal adhesion in EGFRvIII-expressing glioblastoma. <i>Neuro-Oncology</i> , 2014 , 16, 1229-43	1	59
237	MLH1 promoter methylation frequency in colorectal cancer patients and related clinicopathological and molecular features. <i>PLoS ONE</i> , 2013 , 8, e59064	3.7	59

236	Identification of links between small molecules and miRNAs in human cancers based on transcriptional responses. <i>Scientific Reports</i> , 2012 , 2, 282	4.9	58
235	Prioritizing candidate disease miRNAs by integrating phenotype associations of multiple diseases with matched miRNA and mRNA expression profiles. <i>Molecular BioSystems</i> , 2014 , 10, 2800-9		57
234	Identifying and functionally characterizing tissue-specific and ubiquitously expressed human lncRNAs. <i>Oncotarget</i> , 2016 , 7, 7120-33	3.3	57
233	Identification of active transcription factor and miRNA regulatory pathways in Alzheimer's disease. <i>Bioinformatics</i> , 2013 , 29, 2596-602	7.2	54
232	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
231	Prioritizing human cancer microRNAs based on genes' functional consistency between microRNA and cancer. <i>Nucleic Acids Research</i> , 2011 , 39, e153	20.1	53
230	RAID: a comprehensive resource for human RNA-associated (RNA-RNA/RNA-protein) interaction. <i>Rna</i> , 2014 , 20, 989-93	5.8	51
229	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
228	Discovery of Time-Delayed Gene Regulatory Networks based on temporal gene expression profiling. <i>BMC Bioinformatics</i> , 2006 , 7, 26	3.6	50
227	Genome-wide DNA methylome analysis reveals epigenetically dysregulated non-coding RNAs in human breast cancer. <i>Scientific Reports</i> , 2015 , 5, 8790	4.9	48
226	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013 , 29, 2169-77	7.2	46
225	Predicting human microRNA precursors based on an optimized feature subset generated by GA-SVM. <i>Genomics</i> , 2011 , 98, 73-8	4.3	46
224	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , 2015 , 31, 3638-44	7.2	45
223	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, D1231-D1258	20.1	44
222	DiseaseEnhancer: a resource of human disease-associated enhancer catalog. <i>Nucleic Acids Research</i> , 2018 , 46, D78-D84	20.1	43
221	LincSNP: a database of linking disease-associated SNPs to human large intergenic non-coding RNAs. <i>BMC Bioinformatics</i> , 2014 , 15, 152	3.6	43
220	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
219	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

218	Health literacy in rural areas of China: hypertension knowledge survey. <i>International Journal of Environmental Research and Public Health</i> , 2013 , 10, 1125-38	4.6	42
217	In silico detection and characteristics of novel microRNA genes in the Equus caballus genome using an integrated ab initio and comparative genomic approach. <i>Genomics</i> , 2009 , 94, 125-31	4.3	42
216	EGFRvIII/integrin β interaction in hypoxic and vitronectinenriching microenvironment promote GBM progression and metastasis. <i>Oncotarget</i> , 2016 , 7, 4680-94	3.3	42
215	Identification of module biomarkers from the dysregulated ceRNA-ceRNA interaction network in lung adenocarcinoma. <i>Molecular BioSystems</i> , 2015 , 11, 3048-58		41
214	Identifying ultrasound and clinical features of breast cancer molecular subtypes by ensemble decision. <i>Scientific Reports</i> , 2015 , 5, 11085	4.9	41
213	A sub-pathway-based approach for identifying drug response principal network. <i>Bioinformatics</i> , 2011 , 27, 649-54	7.2	40
212	The implications of relationships between human diseases and metabolic subpathways. <i>PLoS ONE</i> , 2011 , 6, e21131	3.7	39
211	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
210	LnCeVar: a comprehensive database of genomic variations that disturb ceRNA network regulation. <i>Nucleic Acids Research</i> , 2020 , 48, D111-D117	20.1	36
209	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
208	A novel reannotation strategy for dissecting DNA methylation patterns of human long intergenic non-coding RNAs in cancers. <i>Nucleic Acids Research</i> , 2014 , 42, 8258-70	20.1	34
207	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
206	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
205	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
204	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
203	Topological properties of the drug targets regulated by microRNA in human protein-protein interaction network. <i>Journal of Drug Targeting</i> , 2011 , 19, 354-64	5.4	31
202	Dissection of human MiRNA regulatory influence to subpathway. <i>Briefings in Bioinformatics</i> , 2012 , 13, 175-86	13.4	30
201	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

200	LncRNA ontology: inferring lncRNA functions based on chromatin states and expression patterns. <i>Oncotarget</i> , 2015 , 6, 39793-805	3.3	30
199	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
198	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015 , 5, 17201	4.9	29
197	Prioritizing cancer-related key miRNA-target interactions by integrative genomics. <i>Nucleic Acids Research</i> , 2012 , 40, 7653-65	20.1	29
196	Discovering dysfunction of multiple microRNAs cooperation in disease by a conserved microRNA co-expression network. <i>PLoS ONE</i> , 2012 , 7, e32201	3.7	29
195	Computational identification of human long intergenic non-coding RNAs using a GA-SVM algorithm. <i>Gene</i> , 2014 , 533, 94-9	3.8	28
194	A novel method to quantify gene set functional association based on gene ontology. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 1063-72	4.1	28
193	Comparative epigenetic analyses reveal distinct patterns of oncogenic pathways activation in breast cancer subtypes. <i>Human Molecular Genetics</i> , 2014 , 23, 5378-93	5.6	27
192	Antioxidant mechanism of Rutin on hypoxia-induced pulmonary arterial cell proliferation. <i>Molecules</i> , 2014 , 19, 19036-49	4.8	27
191	Identification and characterization of lncRNA mediated transcriptional dysregulation dictates lncRNA roles in glioblastoma. <i>Oncotarget</i> , 2016 , 7, 45027-45041	3.3	27
190	Spatiotemporal-specific lncRNAs in the brain, colon, liver and lung of macaque during development. <i>Molecular BioSystems</i> , 2015 , 11, 3253-63		26
189	Identifying core gene modules in glioblastoma based on multilayer factor-mediated dysfunctional regulatory networks through integrating multi-dimensional genomic data. <i>Nucleic Acids Research</i> , 2015 , 43, 1997-2007	20.1	26
188	Characterizing the network of drugs and their affected metabolic subpathways. <i>PLoS ONE</i> , 2012 , 7, e47326	3.7	26
187	Breast cancer prognosis signature: linking risk stratification to disease subtypes. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2130-2140	13.4	26
186	Gain-of-Function Mutations: An Emerging Advantage for Cancer Biology. <i>Trends in Biochemical Sciences</i> , 2019 , 44, 659-674	10.3	24
185	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
184	Dissection of miRNA-miRNA interaction in esophageal squamous cell carcinoma. <i>PLoS ONE</i> , 2013 , 8, e73191	3.7	24
183	Identifying the crosstalk of dysfunctional pathways mediated by lncRNAs in breast cancer subtypes. <i>Molecular BioSystems</i> , 2016 , 12, 711-20		23

182	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015 , 5, 13044	4.9	23
181	Genome-wide DNA methylome reveals the dysfunction of intronic microRNAs in major psychosis. <i>BMC Medical Genomics</i> , 2015 , 8, 62	3.7	23
180	Identification of miRNA-mediated core gene module for glioma patient prediction by integrating high-throughput miRNA, mRNA expression and pathway structure. <i>PLoS ONE</i> , 2014 , 9, e96908	3.7	23
179	CLIC1 a novel biomarker of intraperitoneal metastasis in serous epithelial ovarian cancer. <i>Tumor Biology</i> , 2015 , 36, 4175-9	2.9	22
178	Identifying dysfunctional miRNA-mRNA regulatory modules by inverse activation, cofunction, and high interconnection of target genes: a case study of glioblastoma. <i>Neuro-Oncology</i> , 2013 , 15, 818-28	1	22
177	Cancer killers in the human gut microbiota: diverse phylogeny and broad spectra. <i>Oncotarget</i> , 2017 , 8, 49574-49591	3.3	22
176	Competing endogenous RNA network analysis identifies critical genes among the different breast cancer subtypes. <i>Oncotarget</i> , 2017 , 8, 10171-10184	3.3	21
175	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
174	Predicting the functions of long noncoding RNAs using RNA-seq based on Bayesian network. <i>BioMed Research International</i> , 2015 , 2015, 839590	3	20
173	Genome-wide methylome analyses reveal novel epigenetic regulation patterns in schizophrenia and bipolar disorder. <i>BioMed Research International</i> , 2015 , 2015, 201587	3	20
172	Computational identification of epigenetically regulated lncRNAs and their associated genes based on integrating genomic data. <i>FEBS Letters</i> , 2015 , 589, 521-31	3.8	20
171	CpG island methylator phenotype and prognosis of colorectal cancer in Northeast China. <i>BioMed Research International</i> , 2014 , 2014, 236361	3	20
170	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
169	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , 2015 , 11, 656-63		19
168	Dissection of the potential characteristic of miRNA-miRNA functional synergistic regulations. <i>Molecular BioSystems</i> , 2013 , 9, 217-24		19
167	The lncRNA Connectivity Map: Using lncRNA Signatures to Connect Small Molecules, lncRNAs, and Diseases. <i>Scientific Reports</i> , 2017 , 7, 6655	4.9	19
166	Comparative genomic analysis reveals evolutionary characteristics and patterns of microRNA clusters in vertebrates. <i>Gene</i> , 2013 , 512, 383-91	3.8	19
165	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

164	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
163	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
162	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
161	Integrating multi-omics for uncovering the architecture of cross-talking pathways in breast cancer. <i>PLoS ONE</i> , 2014 , 9, e104282	3.7	18
160	Strategies for genetic mapping of categorical traits. <i>Genetica</i> , 2000 , 109, 183-97	1.5	18
159	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015 , 6, 39151-64	3.3	18
158	Cooperative genomic alteration network reveals molecular classification across 12 major cancer types. <i>Nucleic Acids Research</i> , 2017 , 45, 567-582	20.1	17
157	Survey of miRNA-miRNA cooperative regulation principles across cancer types. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1621-1638	13.4	17
156	A robust approach based on Weibull distribution for clustering gene expression data. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 14	1.8	17
155	Analysis of synonymous codon usage in chloroplast genome of <i>Populus alba</i> . <i>Journal of Forestry Research</i> , 2008 , 19, 293-297	2	17
154	Risk factors for cerebrovascular disease mortality among the elderly in Beijing: a competing risk analysis. <i>PLoS ONE</i> , 2014 , 9, e87884	3.7	17
153	Prioritizing candidate disease metabolites based on global functional relationships between metabolites in the context of metabolic pathways. <i>PLoS ONE</i> , 2014 , 9, e104934	3.7	17
152	Gene expression profiling in human lung development: an abundant resource for lung adenocarcinoma prognosis. <i>PLoS ONE</i> , 2014 , 9, e105639	3.7	17
151	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
150	miRNA-miRNA crosstalk: from genomics to phenomics. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1002-1011	13.4	16
149	Identification of a core miRNA-pathway regulatory network in glioma by therapeutically targeting miR-181d, miR-21, miR-23b, E-catenin, CBP, and STAT3. <i>PLoS ONE</i> , 2014 , 9, e101903	3.7	16
148	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , 2016 , 7, 69837-69870	3.7	16
147	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

146	MERIT: Systematic Analysis and Characterization of Mutational Effect on RNA Interactome Topology. <i>Hepatology</i> , 2019 , 70, 532-546	11.2	16
145	Sex difference of mutation clonality in diffuse glioma evolution. <i>Neuro-Oncology</i> , 2019 , 21, 201-213	1	16
144	SNP@lincTFBS: an integrated database of polymorphisms in human LincRNA transcription factor binding sites. <i>PLoS ONE</i> , 2014 , 9, e103851	3.7	15
143	TMREC: A Database of Transcription Factor and MiRNA Regulatory Cascades in Human Diseases. <i>PLoS ONE</i> , 2015 , 10, e0125222	3.7	15
142	Dysregulated long intergenic non-coding RNA modules contribute to heart failure. <i>Oncotarget</i> , 2016 , 7, 59676-59690	3.3	15
141	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
140	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
139	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
138	LncSpA: LncRNA Spatial Atlas of Expression across Normal and Cancer Tissues. <i>Cancer Research</i> , 2020 , 80, 2067-2071	10.1	14
137	From phenotype to gene: detecting disease-specific gene functional modules via a text-based human disease phenotype network construction. <i>FEBS Letters</i> , 2010 , 584, 3635-43	3.8	14
136	Characterization of SMAD3 Gene Variants for Possible Roles in Ventricular Septal Defects and Other Congenital Heart Diseases. <i>PLoS ONE</i> , 2015 , 10, e0131542	3.7	14
135	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
134	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
133	Support Vector Machine for Analyzing Contributions of Brain Regions During Task-State fMRI. <i>Frontiers in Neuroinformatics</i> , 2019 , 13, 10	3.9	13
132	The trajectories and correlation between physical limitation and depression in elderly residents of Beijing, 1992-2009. <i>PLoS ONE</i> , 2012 , 7, e42999	3.7	13
131	Systematic analysis of human microRNA divergence based on evolutionary emergence. <i>FEBS Letters</i> , 2011 , 585, 240-8	3.8	13
130	Patterns of synonymous codon usage bias in chloroplast genomes of seed plants. <i>Forestry Studies in China</i> , 2008 , 10, 235-242		13
129	Phylogeography and Origin of Sheep Breeds in Northern China. <i>Conservation Genetics</i> , 2006 , 7, 117-127	2.6	13

128	mirTarPri: improved prioritization of microRNA targets through incorporation of functional genomics data. <i>PLoS ONE</i> , 2013 , 8, e53685	3.7	13
127	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
126	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
125	A pan-cancer atlas of cancer hallmark-associated candidate driver lncRNAs. <i>Molecular Oncology</i> , 2018 , 12, 1980-2005	7.9	13
124	Comprehensive Characterization of Somatic Mutations Impacting lncRNA Expression for Pan-Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 66-79	10.7	12
123	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
122	SynBioLGDB: a resource for experimentally validated logic gates in synthetic biology. <i>Scientific Reports</i> , 2015 , 5, 8090	4.9	12
121	Differential expression pattern-based prioritization of candidate genes through integrating disease-specific expression data. <i>Genomics</i> , 2011 , 98, 64-71	4.3	12
120	Systematic review regulatory principles of non-coding RNAs in cardiovascular diseases. <i>Briefings in Bioinformatics</i> , 2019 , 20, 66-76	13.4	12
119	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
118	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
117	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
116	Landscape of the long non-coding RNA transcriptome in human heart. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1812-1825	13.4	11
115	Comparison of long non-coding RNAs, microRNAs and messenger RNAs involved in initiation and progression of esophageal squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2014 , 10, 652-62	2.9	11
114	Construction and analysis of dynamic transcription factor regulatory networks in the progression of glioma. <i>Scientific Reports</i> , 2015 , 5, 15953	4.9	11
113	Effect of Qi-protecting powder (Huqi San) on expression of c-jun, c-fos and c-myc in diethylnitrosamine-mediated hepatocarcinogenesis. <i>World Journal of Gastroenterology</i> , 2007 , 13, 4192-8 ^{5.6}	5.6	11
112	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
111	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

110	GFI1 downregulation promotes inflammation-linked metastasis of colorectal cancer. <i>Cell Death and Differentiation</i> , 2017 , 24, 929-943	12.7	10
109	MPINet: metabolite pathway identification via coupling of global metabolite network structure and metabolomic profile. <i>BioMed Research International</i> , 2014 , 2014, 325697	3	10
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