

Runsheng Chen

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203
papers

12,964
citations

50
h-index

111
g-index

209
ext. papers

15,638
ext. citations

8.6
avg, IF

5.8
L-index

#	Paper	IF	Citations
203	A draft sequence of the rice genome (<i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , 2002 , 296, 79-92	33.3	2356
202	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. <i>Nucleic Acids Research</i> , 2013 , 41, e166	20.1	879
201	Topological structure analysis of the protein-protein interaction network in budding yeast. <i>Nucleic Acids Research</i> , 2003 , 31, 2443-50	20.1	489
200	The long noncoding RNA lncTCF7 promotes self-renewal of human liver cancer stem cells through activation of Wnt signaling. <i>Cell Stem Cell</i> , 2015 , 16, 413-25	18	437
199	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2016 , 44, D203-8	20.1	429
198	Global epigenetic and transcriptional trends among two rice subspecies and their reciprocal hybrids. <i>Plant Cell</i> , 2010 , 22, 17-33	11.6	421
197	Genome sequence of <i>Shigella flexneri</i> 2a: insights into pathogenicity through comparison with genomes of <i>Escherichia coli</i> K12 and O157. <i>Nucleic Acids Research</i> , 2002 , 30, 4432-41	20.1	361
196	NONCODEv4: exploring the world of long non-coding RNA genes. <i>Nucleic Acids Research</i> , 2014 , 42, D98-103	20.1	342
195	NONCODE v3.0: integrative annotation of long noncoding RNAs. <i>Nucleic Acids Research</i> , 2012 , 40, D210-5	20.1	313
194	LncRNA profile study reveals a three-lncRNA signature associated with the survival of patients with oesophageal squamous cell carcinoma. <i>Gut</i> , 2014 , 63, 1700-10	19.2	296
193	Evolutionarily conserved multisubunit RBL2/p130 and E2F4 protein complex represses human cell cycle-dependent genes in quiescence. <i>Molecular Cell</i> , 2007 , 26, 539-51	17.6	286
192	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018 , 46, D308-D314	20.1	276
191	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , 2012 , 44, 890-4	36.3	243
190	NONCODE: an integrated knowledge database of non-coding RNAs. <i>Nucleic Acids Research</i> , 2005 , 33, D112-5	20.1	223
189	A complete sequence of the <i>T. tengcongensis</i> genome. <i>Genome Research</i> , 2002 , 12, 689-700	9.7	189
188	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. <i>Cell Research</i> , 2015 , 25, 193-207	14.7	185
187	Long noncoding RNA lncKdm2b is required for ILC3 maintenance by initiation of Zfp292 expression. <i>Nature Immunology</i> , 2017 , 18, 499-508	19.1	154

186	Myostatin induces cyclin D1 degradation to cause cell cycle arrest through a phosphatidylinositol 3-kinase/AKT/GSK-3 beta pathway and is antagonized by insulin-like growth factor 1. <i>Journal of Biological Chemistry</i> , 2007 , 282, 3799-808	5.4	151
185	Mesenchymal Stem Cells Promote Hepatocarcinogenesis via lncRNA-MUF Interaction with ANXA2 and miR-34a. <i>Cancer Research</i> , 2017 , 77, 6704-6716	10.1	148
184	Long non-coding RNAs function annotation: a global prediction method based on bi-colored networks. <i>Nucleic Acids Research</i> , 2013 , 41, e35	20.1	144
183	Transcriptional inhibition of Hoxd4 expression by miRNA-10a in human breast cancer cells. <i>BMC Molecular Biology</i> , 2009 , 10, 12	4.5	141
182	A long noncoding RNA critically regulates Bcr-Abl-mediated cellular transformation by acting as a competitive endogenous RNA. <i>Oncogene</i> , 2015 , 34, 1768-79	9.2	127
181	Long Noncoding RNA ADINR Regulates Adipogenesis by Transcriptionally Activating C/EBP β Stem. <i>Cell Reports</i> , 2015 , 5, 856-865	8	119
180	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017 , 45, D128-D134	20.1	119
179	Antibody responses to individual proteins of SARS coronavirus and their neutralization activities. <i>Microbes and Infection</i> , 2005 , 7, 882-9	9.3	109
178	NONCODE v2.0: decoding the non-coding. <i>Nucleic Acids Research</i> , 2008 , 36, D170-2	20.1	108
177	ncFANs: a web server for functional annotation of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2011 , 39, W118-24	20.1	106
176	piRBase: a comprehensive database of piRNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D175-D180	20.1	105
175	NPInter v2.0: an updated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2014 , 42, D104-8	20.1	101
174	piRBase: a web resource assisting piRNA functional study. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau110	5	98
173	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	95
172	Model-based analysis of two-color arrays (MA2C). <i>Genome Biology</i> , 2007 , 8, R178	18.3	91
171	Organization of the <i>Caenorhabditis elegans</i> small non-coding transcriptome: genomic features, biogenesis, and expression. <i>Genome Research</i> , 2006 , 16, 20-9	9.7	90
170	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D123-9	20.1	89
169	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D18-D28	20.1	84

168	Association study with 33 single-nucleotide polymorphisms in 11 candidate genes for hypertension in Chinese. <i>Hypertension</i> , 2006 , 47, 1147-54	8.5	80
167	The human microbiome: a hot spot of microbial horizontal gene transfer. <i>Genomics</i> , 2012 , 100, 265-70	4.3	79
166	De novo prediction of RNA-protein interactions from sequence information. <i>Molecular BioSystems</i> , 2013 , 9, 133-42		74
165	LncRNA HAND2-AS1 promotes liver cancer stem cell self-renewal via BMP signaling. <i>EMBO Journal</i> , 2019 , 38, e101110	13	71
164	BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. <i>Bioinformatics</i> , 2016 , 32, 1740-2	7.2	64
163	Global identification and characterization of transcriptionally active regions in the rice genome. <i>PLoS ONE</i> , 2007 , 2, e294	3.7	63
162	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006 , 34, D150-2	20.1	63
161	SmProt: a database of small proteins encoded by annotated coding and non-coding RNA loci. <i>Briefings in Bioinformatics</i> , 2018 , 19, 636-643	13.4	60
160	The long noncoding RNA SNHG1 promotes tumor growth through regulating transcription of both local and distal genes. <i>Oncogene</i> , 2017 , 36, 6774-6783	9.2	60
159	controls self-renewal of embryonic stem cells via activating expression of transcription factor. <i>EMBO Journal</i> , 2018 , 37,	13	59
158	Systematic identification of genes involved in divergent skeletal muscle growth rates of broiler and layer chickens. <i>BMC Genomics</i> , 2009 , 10, 87	4.5	56
157	MicroRNA-encoding long non-coding RNAs. <i>BMC Genomics</i> , 2008 , 9, 236	4.5	53
156	Recipe for a busy bee: microRNAs in Honey Bee caste determination. <i>PLoS ONE</i> , 2013 , 8, e81661	3.7	53
155	A global identification and analysis of small nucleolar RNAs and possible intermediate-sized non-coding RNAs in <i>Oryza sativa</i> . <i>Molecular Plant</i> , 2013 , 6, 830-46	14.4	52
154	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020 , 48, D160-D165	20.1	50
153	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , 2007 , 17, 1471-7	9.7	49
152	Genomic features and regulatory roles of intermediate-sized non-coding RNAs in Arabidopsis. <i>Molecular Plant</i> , 2014 , 7, 514-27	14.4	48
151	Long noncoding RNA LINC01186, regulated by TGF- β /SMAD3, inhibits migration and invasion through Epithelial-Mesenchymal-Transition in lung cancer. <i>Gene</i> , 2017 , 608, 1-12	3.8	46

150	The novel long non-coding RNA CRG regulates <i>Drosophila</i> locomotor behavior. <i>Nucleic Acids Research</i> , 2012 , 40, 11714-27	20.1	45
149	Transcriptional profiling analysis and functional prediction of long noncoding RNAs in cancer. <i>Oncotarget</i> , 2016 , 7, 8131-42	3.3	45
148	LncRNA MT1JP functions as a tumor suppressor by interacting with TIAR to modulate the p53 pathway. <i>Oncotarget</i> , 2016 , 7, 15787-800	3.3	45
147	NONCODEV6: an updated database dedicated to long non-coding RNA annotation in both animals and plants. <i>Nucleic Acids Research</i> , 2021 , 49, D165-D171	20.1	45
146	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006 , 440, 1194-8	50.4	43
145	Evolution and migration history of the Chinese population inferred from Chinese Y-chromosome evidence. <i>Journal of Human Genetics</i> , 2004 , 49, 339-348	4.3	43
144	GenomeComp: a visualization tool for microbial genome comparison. <i>Journal of Microbiological Methods</i> , 2003 , 54, 423-6	2.8	39
143	Transcriptome profiling of esophageal squamous cell carcinoma reveals a long noncoding RNA acting as a tumor suppressor. <i>Oncotarget</i> , 2015 , 6, 17065-80	3.3	37
142	Prediction of structured non-coding RNAs in the genomes of the nematodes <i>Caenorhabditis elegans</i> and <i>Caenorhabditis briggsae</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006 , 306, 379-92	1.8	36
141	Haplotype analysis of the matrix metalloproteinase 3 gene and myocardial infarction in a Chinese Han population. The Beijing atherosclerosis study. <i>Thrombosis and Haemostasis</i> , 2004 , 92, 867-73	7	36
140	The interactome as a tree--an attempt to visualize the protein-protein interaction network in yeast. <i>Nucleic Acids Research</i> , 2004 , 32, 4804-11	20.1	36
139	MicroRNA regulation of messenger-like noncoding RNAs: a network of mutual microRNA control. <i>Trends in Genetics</i> , 2008 , 24, 323-7	8.5	35
138	A novel antisense long noncoding RNA, TWISTED LEAF, maintains leaf blade flattening by regulating its associated sense R2R3-MYB gene in rice. <i>New Phytologist</i> , 2018 , 218, 774-788	9.8	34
137	ER-residential Nogo-B accelerates NAFLD-associated HCC mediated by metabolic reprogramming of oxLDL lipophagy. <i>Nature Communications</i> , 2019 , 10, 3391	17.4	32
136	Identification of gene expression modifications in myostatin-stimulated myoblasts. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 326, 660-6	3.4	30
135	LncVar: a database of genetic variation associated with long non-coding genes. <i>Bioinformatics</i> , 2017 , 33, 112-118	7.2	29
134	Profiling <i>Caenorhabditis elegans</i> non-coding RNA expression with a combined microarray. <i>Nucleic Acids Research</i> , 2006 , 34, 2976-83	20.1	29
133	Functional Characterization of Long Noncoding RNA Lnc_bc060912 in Human Lung Carcinoma Cells. <i>Biochemistry</i> , 2015 , 54, 2895-902	3.2	28

132	Transcriptome-wide analysis of TDP-43 binding small RNAs identifies miR-NID1 (miR-8485), a novel miRNA that represses NRXN1 expression. <i>Genomics</i> , 2014 , 103, 76-82	4.3	28
131	FlexStem: improving predictions of RNA secondary structures with pseudoknots by reducing the search space. <i>Bioinformatics</i> , 2008 , 24, 1994-2001	7.2	27
130	NMPP: a user-customized NimbleGen microarray data processing pipeline. <i>Bioinformatics</i> , 2006 , 22, 2955-7	7.2	27
129	Integrated sequence-structure motifs suffice to identify microRNA precursors. <i>PLoS ONE</i> , 2012 , 7, e32797	3.7	26
128	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2016 , 1402, 243-254	1.4	25
127	Plasminogen activator inhibitor-1 gene: selection of tagging single nucleotide polymorphisms and association with coronary heart disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2006 , 26, 948-54	9.4	25
126	Integrated analysis of multiple data sources reveals modular structure of biological networks. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 345, 302-9	3.4	25
125	Conservation analysis of small RNA genes in Escherichia coli. <i>Bioinformatics</i> , 2004 , 20, 599-603	7.2	25
124	A draft sequence of the rice (<i>Oryza sativa</i> ssp.indica) genome. <i>Science Bulletin</i> , 2001 , 46, 1937-1942		24
123	Long noncoding RNA lncHand2 promotes liver repopulation via c-Met signaling. <i>Journal of Hepatology</i> , 2018 , 69, 861-872	13.4	23
122	LncRNA16 is a potential biomarker for diagnosis of early-stage lung cancer that promotes cell proliferation by regulating the cell cycle. <i>Oncotarget</i> , 2017 , 8, 7867-7877	3.3	23
121	Systematic identification and characterization of chicken (<i>Gallus gallus</i>) ncRNAs. <i>Nucleic Acids Research</i> , 2009 , 37, 6562-74	20.1	23
120	The properties and functions of virus encoded microRNA, siRNA, and other small noncoding RNAs. <i>Critical Reviews in Microbiology</i> , 2008 , 34, 175-88	7.8	23
119	Phylogenetic properties of metabolic pathway topologies as revealed by global analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 252	3.6	23
118	Modeling and docking of the three-dimensional structure of the human melanocortin 4 receptor. <i>The Protein Journal</i> , 2003 , 22, 335-44		23
117	antiCODE: a natural sense-antisense transcripts database. <i>BMC Bioinformatics</i> , 2007 , 8, 319	3.6	22
116	Association of alpha1A adrenergic receptor gene variants on chromosome 8p21 with human stage 2 hypertension. <i>Journal of Hypertension</i> , 2006 , 24, 1049-56	1.9	22
115	Genomic and transcriptomic analysis of the Asian honeybee <i>Apis cerana</i> provides novel insights into honeybee biology. <i>Scientific Reports</i> , 2018 , 8, 822	4.9	21

114	G protein beta 3 subunit gene variants and essential hypertension in the northern Chinese Han population. <i>Annals of Human Genetics</i> , 2005 , 69, 468-73	2.2	21
113	Predicting molecular formulas of fragment ions with isotope patterns in tandem mass spectra. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 217-30	3	20
112	Differential expression profiling between the relative normal and dystrophic muscle tissues from the same LGMD patient. <i>Journal of Translational Medicine</i> , 2006 , 4, 53	8.5	20
111	LinK contributes to breast tumorigenesis by promoting proliferation and epithelial-to-mesenchymal transition. <i>Journal of Hematology and Oncology</i> , 2019 , 12, 19	22.4	19
110	TDP-43 regulates cancer-associated microRNAs. <i>Protein and Cell</i> , 2018 , 9, 848-866	7.2	19
109	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. <i>International Journal of Cell Biology</i> , 2012 , 2012, 672462	2.6	19
108	Conserved distances between vertebrate highly conserved elements. <i>Human Molecular Genetics</i> , 2006 , 15, 2911-22	5.6	19
107	Fractal dimension of exon and intron sequences. <i>Journal of Theoretical Biology</i> , 1995 , 175, 23-6	2.3	19
106	Date of origin of the SARS coronavirus strains. <i>BMC Infectious Diseases</i> , 2004 , 4, 3	4	18
105	Profiling the long noncoding RNA interaction network in the regulatory elements of target genes by chromatin in situ reverse transcription sequencing. <i>Genome Research</i> , 2019 , 29, 1521-1532	9.7	17
104	GADD45A inhibits autophagy by regulating the interaction between BECN1 and PIK3C3. <i>Autophagy</i> , 2015 , 11, 2247-58	10.2	17
103	Systematic identification and evolutionary features of rhesus monkey small nucleolar RNAs. <i>BMC Genomics</i> , 2010 , 11, 61	4.5	17
102	Phylogeny Based on Whole Genome as inferred from Complete Information Set Analysis. <i>Journal of Biological Physics</i> , 2002 , 28, 439-47	1.6	17
101	SpatialDB: a database for spatially resolved transcriptomes. <i>Nucleic Acids Research</i> , 2020 , 48, D233-D237 _{20.1}		16
100	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. <i>FEBS Letters</i> , 2006 , 580, 1891-6	3.8	16
99	Reversibly switchable DNA nanocompartment on surfaces. <i>Nucleic Acids Research</i> , 2004 , 32, e144	20.1	16
98	Identification and characterization of simple sequence repeats in the genomes of Shigella species. <i>Gene</i> , 2003 , 322, 85-92	3.8	16
97	Construction and structural modeling of a single-chain Fv α sparaginase fusion protein resistant to proteolysis. <i>Biotechnology and Bioengineering</i> , 2000 , 70, 456-463	4.9	16

96	Association of the Polymorphism rs13259960 in SLEAR With Predisposition to Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2020 , 72, 985-996	9.5	15
95	Experimental RNomics and genomic comparative analysis reveal a large group of species-specific small non-message RNAs in the silkworm <i>Bombyx mori</i> . <i>Nucleic Acids Research</i> , 2011 , 39, 3792-805	20.1	15
94	In vivo analysis of <i>Caenorhabditis elegans</i> noncoding RNA promoter motifs. <i>BMC Molecular Biology</i> , 2008 , 9, 71	4.5	15
93	Computational identification of piRNA targets on mouse mRNAs. <i>Bioinformatics</i> , 2016 , 32, 1170-7	7.2	14
92	A functional intronic variant in the tyrosine hydroxylase (TH) gene confers risk of essential hypertension in the Northern Chinese Han population. <i>Clinical Science</i> , 2008 , 115, 151-8	6.5	14
91	Angiotensin II type I receptor gene and myocardial infarction: tagging SNPs and haplotype based association study. The Beijing atherosclerosis study. <i>Pharmacogenetics and Genomics</i> , 2004 , 14, 673-81		14
90	Toward Automated Identification of Glycan Branching Patterns Using Multistage Mass Spectrometry with Intelligent Precursor Selection. <i>Analytical Chemistry</i> , 2018 , 90, 14412-14422	7.8	14
89	Microarray analysis of ncRNA expression patterns in <i>Caenorhabditis elegans</i> after RNAi against snoRNA associated proteins. <i>BMC Genomics</i> , 2008 , 9, 278	4.5	13
88	Expression in <i>Escherichia coli</i> , purification and characterization of <i>Thermoanaerobacter tengcongensis</i> ribosome recycling factor. <i>Journal of Biochemistry</i> , 2005 , 138, 89-94	3.1	13
87	BCL9 provides multi-cellular communication properties in colorectal cancer by interacting with paraspeckle proteins. <i>Nature Communications</i> , 2020 , 11, 19	17.4	13
86	The long noncoding RNA ASNR regulates degradation of Bcl-2 mRNA through its interaction with AUF1. <i>Scientific Reports</i> , 2016 , 6, 32189	4.9	13
85	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016 , 499, 15-23	3.1	12
84	Genome-scale identification of <i>Caenorhabditis elegans</i> regulatory elements by tiling-array mapping of DNase I hypersensitive sites. <i>BMC Genomics</i> , 2009 , 10, 92	4.5	12
83	Dynamic changes in subgraph preference profiles of crucial transcription factors. <i>PLoS Computational Biology</i> , 2006 , 2, e47	5	12
82	Lipoprotein lipase gene polymorphisms and blood pressure levels in the Northern Chinese Han population. <i>Hypertension Research</i> , 2004 , 27, 373-8	4.7	12
81	Identification and analysis of intermediate size noncoding RNAs in the human fetal brain. <i>PLoS ONE</i> , 2011 , 6, e21652	3.7	12
80	Differential expression of miRNAs related to caste differentiation in the honey bee, <i>Apis mellifera</i> . <i>Apidologie</i> , 2016 , 47, 495-508	2.3	11
79	Predicting housekeeping genes based on Fourier analysis. <i>PLoS ONE</i> , 2011 , 6, e21012	3.7	11

78	The <i>Caenorhabditis elegans</i> intermediate-size transcriptome shows high degree of stage-specific expression. <i>Nucleic Acids Research</i> , 2011 , 39, 5203-14	20.1	11
77	A novel scoring schema for peptide identification by searching protein sequence databases using tandem mass spectrometry data. <i>BMC Bioinformatics</i> , 2006 , 7, 222	3.6	11
76	Identifying Hfq-binding small RNA targets in <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2006 , 343, 950-5	3.4	11
75	Lateralization of gene expression in the honeybee brain during olfactory learning. <i>Scientific Reports</i> , 2016 , 6, 34727	4.9	11
74	Computational methods to predict long noncoding RNA functions based on co-expression network. <i>Methods in Molecular Biology</i> , 2014 , 1182, 209-18	1.4	10
73	A differential sequencing-based analysis of the <i>C. elegans</i> noncoding transcriptome. <i>Rna</i> , 2012 , 18, 626-398	3.9	10
72	LRiK interacts with the Ku70-Ku80 heterodimer enhancing the efficiency of NHEJ repair. <i>Cell Death and Differentiation</i> , 2020 , 27, 3337-3353	12.7	9
71	Systematic study of novel lncRNAs in different gastrointestinal cancer cells. <i>Discovery Medicine</i> , 2016 , 21, 159-71	2.5	9
70	Large-scale study of long non-coding RNA functions based on structure and expression features. <i>Science China Life Sciences</i> , 2013 , 56, 953-9	8.5	8
69	The Landscape of Viral Expression Reveals Clinically Relevant Viruses with Potential Capability of Promoting Malignancy in Lower-Grade Glioma. <i>Clinical Cancer Research</i> , 2017 , 23, 2177-2185	12.9	8
68	Deep profiling of the novel intermediate-size noncoding RNAs in intraerythrocytic <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2014 , 9, e92946	3.7	8
67	Systematic identification of non-coding RNA 2,2,7-trimethylguanosine cap structures in <i>Caenorhabditis elegans</i> . <i>BMC Molecular Biology</i> , 2007 , 8, 86	4.5	8
66	Expression profiling and functional prediction of long noncoding RNAs in nasopharyngeal nonkeratinizing carcinoma. <i>Discovery Medicine</i> , 2016 , 21, 239-50	2.5	8
65	Identification of intermediate-size non-coding RNAs involved in the UV-induced DNA damage response in <i>C. elegans</i> . <i>PLoS ONE</i> , 2012 , 7, e48066	3.7	7
64	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. <i>Protein and Cell</i> , 2012 , 3, 148-52	7.2	7
63	Gene Functional Arrangement as a Measure of the Phylogenetic Relationships of Microorganisms. <i>Journal of Biological Physics</i> , 2002 , 28, 55-62	1.6	7
62	A new method of preparing fiber-optic DNA biosensor and its array for gene detection. <i>Science in China Series C: Life Sciences</i> , 2001 , 44, 33-9		7
61	lncRNA HRCEG, regulated by HDAC1, inhibits cells proliferation and epithelial-mesenchymal-transition in gastric cancer. <i>Cancer Genetics</i> , 2020 , 241, 25-33	2.3	7

60	One novel long noncoding RNA lnc10 in <i>Drosophila</i> . <i>Journal of Genetics and Genomics</i> , 2014 , 41, 79-82	4	6
59	Regulatory elements of <i>Caenorhabditis elegans</i> ribosomal protein genes. <i>BMC Genomics</i> , 2012 , 13, 433	4.5	6
58	Proteome-wide analysis of protein function composition reveals the clustering and phylogenetic properties of organisms. <i>Molecular Phylogenetics and Evolution</i> , 2002 , 25, 101-11	4.1	6
57	Phylogeny of SARS-CoV as inferred from complete genome comparison. <i>Science Bulletin</i> , 2003 , 48, 1175-1178		6
56	Identification and functional characterization of intermediate-size non-coding RNAs in maize. <i>BMC Genomics</i> , 2018 , 19, 730	4.5	6
55	A binary matrix factorization algorithm for protein complex prediction. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S18	2.6	5
54	An iterative algorithm to quantify factors influencing peptide fragmentation during tandem mass spectrometry. <i>Journal of Bioinformatics and Computational Biology</i> , 2007 , 5, 297-311	1	5
53	Identification of selenocysteine insertion sequence (SECIS) element in eukaryotic selenoproteins by RNA Draw program. <i>Science Bulletin</i> , 2001 , 46, 1159-1161		5
52	Fractal geometry study of DNA binding proteins. <i>Journal of Theoretical Biology</i> , 1994 , 171, 239-49	2.3	5
51	Long noncoding RNA AVAN promotes antiviral innate immunity by interacting with TRIM25 and enhancing the transcription of FOXO3a		5
50	β-Catenin safeguards the ground state of mouse pluripotency by strengthening the robustness of the transcriptional apparatus. <i>Science Advances</i> , 2020 , 6, eaba1593	14.3	5
49	Long noncoding RNA AVAN promotes antiviral innate immunity by interacting with TRIM25 and enhancing the transcription of FOXO3a. <i>Cell Death and Differentiation</i> , 2021 , 28, 2900-2915	12.7	5
48	Deeply Mining a Universe of Peptides Encoded by Long Noncoding RNAs. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100109	7.6	5
47	Analysis of the p53/CEP-1 regulated non-coding transcriptome in <i>C. elegans</i> by an NSR-seq strategy. <i>Protein and Cell</i> , 2014 , 5, 770-82	7.2	4
46	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010 , 96, 308-15	4.3	4
45	Characterization of l-asparaginase fused with a protective ScFv and the protection mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 276, 197-203	3.4	4
44	Coincident indices of exons and introns. <i>Computers in Biology and Medicine</i> , 1993 , 23, 333-43	7	4
43	De novo approach to classify protein-coding and noncoding transcripts based on sequence composition. <i>Methods in Molecular Biology</i> , 2014 , 1182, 203-7	1.4	4

42	Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division. <i>Genome Research</i> , 2020 , 30, 1570-1582	9.7	4
41	On bioinformatic resources. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 1-3	6.5	3
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