Runsheng Chen

List of Publications by Year
in descending order

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205 papers	17,618 citations	26567 56 h-index	14702 127 g-index
209 all docs	209 docs citations	209 times ranked	23307 citing authors

#	Article	IF	Citations
1	A Draft Sequence of the Rice Genome (Oryza sativa L. ssp. indica). Science, 2002, 296, 79-92.	6.0	3,146
2	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. Nucleic Acids Research, 2013, 41, e166-e166.	6.5	1,658
3	Topological structure analysis of the protein-protein interaction network in budding yeast. Nucleic Acids Research, 2003, 31, 2443-2450.	6.5	614
4	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. Nucleic Acids Research, 2016, 44, D203-D208.	6.5	574
5	The Long Noncoding RNA lncTCF7 Promotes Self-Renewal of Human Liver Cancer Stem Cells through Activation of Wnt Signaling. Cell Stem Cell, 2015, 16, 413-425.	5.2	529
6	Global Epigenetic and Transcriptional Trends among Two Rice Subspecies and Their Reciprocal Hybrids. Plant Cell, 2010, 22, 17-33.	3.1	514
7	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. Nucleic Acids Research, 2018, 46, D308-D314.	6.5	434
8	Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157. Nucleic Acids Research, 2002, 30, 4432-4441.	6.5	431
9	NONCODEv4: exploring the world of long non-coding RNA genes. Nucleic Acids Research, 2014, 42, D98-D103.	6.5	398
10	LncRNA profile study reveals a three-lncRNA signature associated with the survival of patients with oesophageal squamous cell carcinoma. Gut, 2014, 63, 1700-1710.	6.1	385
11	NONCODE v3.0: integrative annotation of long noncoding RNAs. Nucleic Acids Research, 2012, 40, D210-D215.	6.5	383
12	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. Molecular Cell, 2007, 26, 539-551.	4.5	347
13	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. Nature Genetics, 2012, 44, 890-894.	9.4	295
14	NONCODE: an integrated knowledge database of non-coding RNAs. Nucleic Acids Research, 2004, 33, D112-D115.	6.5	270
15	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. Cell Research, 2015, 25, 193-207.	5.7	266
16	A Complete Sequence of the T. tengcongensis Genome. Genome Research, 2002, 12, 689-700.	2.4	209
17	Mesenchymal Stem Cells Promote Hepatocarcinogenesis via lncRNAâ€"MUF Interaction with ANXA2 and miR-34a. Cancer Research, 2017, 77, 6704-6716.	0.4	193
18	Myostatin Induces Cyclin D1 Degradation to Cause Cell Cycle Arrest through a Phosphatidylinositol 3-Kinase/AKT/GSK-3Î² Pathway and Is Antagonized by Insulin-like Growth Factor 1. Journal of Biological Chemistry, 2007, 282, 3799-3808.	1.6	186

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19	Long non-coding RNAs function annotation: a global prediction method based on bi-colored networks. Nucleic Acids Research, 2013, 41, e35-e35.	6.5	174
20	Long noncoding RNA lncKdm2b is required for ILC3 maintenance by initiation of Zfp292 expression. Nature Immunology, 2017, 18, 499-508.	7.0	174
21	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	6.5	174
22	piRBase: a comprehensive database of piRNA sequences. Nucleic Acids Research, 2019, 47, D175-D180.	6.5	169
23	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	6.5	168
24	Transcriptional inhibiton of Hoxd4 expression by miRNA-10a in human breast cancer cells. BMC Molecular Biology, 2009, 10, 12.	3.0	167
25	NONCODEV6: an updated database dedicated to long non-coding RNA annotation in both animals and plants. Nucleic Acids Research, 2021, 49, D165-D171.	6.5	166
26	Long Noncoding RNA ADINR Regulates Adipogenesis by Transcriptionally Activating C/EBPÎ±. Stem Cell Reports, 2015, 5, 856-865.	2.3	154
27	A long noncoding RNA critically regulates Bcr-Abl-mediated cellular transformation by acting as a competitive endogenous RNA. Oncogene, 2015, 34, 1768-1779.	2.6	149
28	Antibody responses to individual proteins of SARS coronavirus and their neutralization activities. Microbes and Infection, 2005, 7, 882-889.	1.0	146
29	NPInter v2.0: an updated database of ncRNA interactions. Nucleic Acids Research, 2014, 42, D104-D108.	6.5	141
30	piRBase: a web resource assisting piRNA functional study. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau110.	1.4	132
31	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw057.	1.4	130
32	ncFANs: a web server for functional annotation of long non-coding RNAs. Nucleic Acids Research, 2011, 39, W118-W124.	6.5	123
33	BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. Bioinformatics, 2016, 32, 1740-1742.	1.8	119
34	LncRNA HAND2â€AS1 promotes liver cancer stem cell selfâ€renewal via BMP signaling. EMBO Journal, 2019, 38, e101110.	3.5	117
35	NONCODE v2.0: decoding the non-coding. Nucleic Acids Research, 2007, 36, D170-D172.	6.5	115
36	The human microbiome: A hot spot of microbial horizontal gene transfer. Genomics, 2012, 100, 265-270.	1.3	109

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37	NPInter v4.0: an integrated database of ncRNA interactions. Nucleic Acids Research, 2020, 48, D160-D165.	6.5	106
38	Organization of the Caenorhabditis elegans small non-coding transcriptome: Genomic features, biogenesis, and expression. Genome Research, 2005, 16, 20-29.	2.4	104
39	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	6.5	103
40	De novo prediction of RNAâ€“protein interactions from sequence information. Molecular BioSystems, 2013, 9, 133-142.	2.9	102
41	A novel antisense long noncoding <scp>RNA</scp>,<i><scp>TWISTED LEAF</scp></i>, maintains leaf blade flattening by regulating its associated sense R2R3â€<scp>MYB</scp> gene in rice. New Phytologist, 2018, 218, 774-788.	3.5	96
42	Model-based analysis of two-color arrays (MA2C). Genome Biology, 2007, 8, R178.	13.9	95
43	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. Nucleic Acids Research, 2006, 34, D150-D152.	6.5	93
44	Association Study With 33 Single-Nucleotide Polymorphisms in 11 Candidate Genes for Hypertension in Chinese. Hypertension, 2006, 47, 1147-1154.	1.3	90
45	SmProt: a database of small proteins encoded by annotated coding and non-coding RNA loci. Briefings in Bioinformatics, 2018, 19, bbx005.	3.2	85
46	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. PLoS ONE, 2007, 2, e294.	1.1	82
47	Genomic Features and Regulatory Roles of Intermediate-Sized Non-Coding RNAs in Arabidopsis. Molecular Plant, 2014, 7, 514-527.	3.9	77
48	<i>LncKdm2b</i> controls selfâ€renewal of embryonic stem cells via activating expression of transcription factor <i>Zbtb3</i>. EMBO Journal, 2018, 37, .	3.5	75
49	ER-residential Nogo-B accelerates NAFLD-associated HCC mediated by metabolic reprogramming of oxLDL lipophagy. Nature Communications, 2019, 10, 3391.	5.8	75
50	Evolution and migration history of the Chinese population inferred from Chinese Y-chromosome evidence. Journal of Human Genetics, 2004, 49, 339-348.	1.1	74
51	The long noncoding RNA SNHG1 promotes tumor growth through regulating transcription of both local and distal genes. Oncogene, 2017, 36, 6774-6783.	2.6	74
52	Systematic identification of genes involved in divergent skeletal muscle growth rates of broiler and layer chickens. BMC Genomics, 2009, 10, 87.	1.2	71
53	Genomic and transcriptomic analysis of the Asian honeybee Apis cerana provides novel insights into honeybee biology. Scientific Reports, 2018, 8, 822.	1.6	68
54	A Global Identification and Analysis of Small Nucleolar RNAs and Possible Intermediate-Sized Non-Coding RNAs in Oryza sativa. Molecular Plant, 2013, 6, 830-846.	3.9	66

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55	MicroRNA-encoding long non-coding RNAs. BMC Genomics, 2008, 9, 236.	1.2	60
56	Recipe for a Busy Bee: MicroRNAs in Honey Bee Caste Determination. PLoS ONE, 2013, 8, e81661.	1.1	60
57	LncRNA MT1JP functions as a tumor suppressor by interacting with TIAR to modulate the p53 pathway. Oncotarget, 2016, 7, 15787-15800.	0.8	59
58	The DNA sequence, annotation and analysis of human chromosome 3. Nature, 2006, 440, 1194-1198.	13.7	53
59	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. Genome Research, 2007, 17, 1471-1477.	2.4	53
60	The novel long non-coding RNA CRG regulates Drosophila locomotor behavior. Nucleic Acids Research, 2012, 40, 11714-11727.	6.5	53
61	Long noncoding RNA LINC01186, regulated by TGF-Î²/SMAD3, inhibits migration and invasion through Epithelial-Mesenchymal-Transition in lung cancer. Gene, 2017, 608, 1-12.	1.0	50
62	Transcriptional profiling analysis and functional prediction of long noncoding RNAs in cancer. Oncotarget, 2016, 7, 8131-8142.	0.8	49
63	The interactome as a tree--an attempt to visualize the protein-protein interaction network in yeast. Nucleic Acids Research, 2004, 32, 4804-4811.	6.5	43
64	GenomeComp: a visualization tool for microbial genome comparison. Journal of Microbiological Methods, 2003, 54, 423-426.	0.7	42
65	Haplotype analysis of the matrix metalloproteinase 3 gene and myocardial infarction in a Chinese Han population. Thrombosis and Haemostasis, 2004, 92, 867-873.	1.8	41
66	Prediction of structured non-coding RNAs in the genomes of the nematodesCaenorhabditis elegans andCaenorhabditis briggsae. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2006, 306B, 379-392.	0.6	39
67	Transcriptome profiling of esophageal squamous cell carcinoma reveals a long noncoding RNA acting as a tumor suppressor. Oncotarget, 2015, 6, 17065-17080.	0.8	39
68	SpatialDB: a database for spatially resolved transcriptomes. Nucleic Acids Research, 2020, 48, D233-D237.	6.5	37
69	MicroRNA regulation of messenger-like noncoding RNAs: a network of mutual microRNA control. Trends in Genetics, 2008, 24, 323-327.	2.9	36
70	FlexStem: improving predictions of RNA secondary structures with pseudoknots by reducing the search space. Bioinformatics, 2008, 24, 1994-2001.	1.8	36
71	A draft sequence of the rice (Oryza sativa ssp.indica) genome. Science Bulletin, 2001, 46, 1937-1942.	1.7	35
72	Transcriptome-wide analysis of TDP-43 binding small RNAs identifies miR-NID1 (miR-8485), a novel miRNA that represses NRXN1 expression. Genomics, 2014, 103, 76-82.	1.3	35

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73	TDP-43 regulates cancer-associated microRNAs. Protein and Cell, 2018, 9, 848-866.	4.8	35
74	Identification of gene expression modifications in myostatin-stimulated myoblasts. Biochemical and Biophysical Research Communications, 2005, 326, 660-666.	1.0	34
75	Conservation analysis of small RNA genes in Escherichia coli. Bioinformatics, 2004, 20, 599-603.	1.8	33
76	Integrated analysis of multiple data sources reveals modular structure of biological networks. Biochemical and Biophysical Research Communications, 2006, 345, 302-309.	1.0	33
77	LncVar: a database of genetic variation associated with long non-coding genes. Bioinformatics, 2017, 33, 112-118.	1.8	33
78	Long noncoding RNA lncHand2 promotes liver repopulation via c-Met signaling. Journal of Hepatology, 2018, 69, 861-872.	1.8	32
79	Noncoding RNA: from dark matter to bright star. Science China Life Sciences, 2020, 63, 463-468.	2.3	32
80	Phylogeny Based on Whole Genome as inferred from Complete Information Set Analysis. Journal of Biological Physics, 2002, 28, 439-447.	0.7	30
81	Profiling Caenorhabditis elegans non-coding RNA expression with a combined microarray. Nucleic Acids Research, 2006, 34, 2976-2983.	6.5	30
82	NMPP: a user-customized NimbleGen microarray data processing pipeline. Bioinformatics, 2006, 22, 2955-2957.	1.8	29
83	Plasminogen Activator Inhibitor-1 Gene. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 948-954.	1.1	29
84	Integrated Sequence-Structure Motifs Suffice to Identify microRNA Precursors. PLoS ONE, 2012, 7, e32797.	1.1	29
85	Functional Characterization of Long Noncoding RNA Lnc_bc060912 in Human Lung Carcinoma Cells. Biochemistry, 2015, 54, 2895-2902.	1.2	29
86	LincK contributes to breast tumorigenesis by promoting proliferation and epithelial-to-mesenchymal transition. Journal of Hematology and Oncology, 2019, 12, 19.	6.9	29
87	Conserved distances between vertebrate highly conserved elements. Human Molecular Genetics, 2006, 15, 2911-2922.	1.4	28
88	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. Methods in Molecular Biology, 2016, 1402, 243-254.	0.4	28
89	LncRNA16 is a potential biomarker for diagnosis of early-stage lung cancer that promotes cell proliferation by regulating the cell cycle. Oncotarget, 2017, 8, 7867-7877.	0.8	28
90	Long noncoding RNA AVAN promotes antiviral innate immunity by interacting with TRIM25 and enhancing the transcription of FOXO3a. Cell Death and Differentiation, 2021, 28, 2900-2915.	5.0	28

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91	SmProt: A Reliable Repository with Comprehensive Annotation of Small Proteins Identified from Ribosome Profiling. Genomics, Proteomics and Bioinformatics, 2021, 19, 602-610.	3.0	28
92	Phylophenetic properties of metabolic pathway topologies as revealed by global analysis. BMC Bioinformatics, 2006, 7, 252.	1.2	27
93	The Properties and Functions of Virus Encoded microRNA, siRNA, and Other Small Noncoding RNAs. Critical Reviews in Microbiology, 2008, 34, 175-188.	2.7	27
94	Profiling the long noncoding RNA interaction network in the regulatory elements of target genes by chromatin in situ reverse transcription sequencing. Genome Research, 2019, 29, 1521-1532.	2.4	27
95	BCL9 provides multi-cellular communication properties in colorectal cancer by interacting with paraspeckle proteins. Nature Communications, 2020, 11, 19.	5.8	27
96	Association of Î±1A adrenergic receptor gene variants on chromosome 8p21 with human stage 2 hypertension. Journal of Hypertension, 2006, 24, 1049-1056.	0.3	26
97	Predicting Housekeeping Genes Based on Fourier Analysis. PLoS ONE, 2011, 6, e21012.	1.1	26
98	Modeling and docking of the three-dimensional structure of the human melanocortin 4 receptor. The Protein Journal, 2003, 22, 335-344.	1.1	25
99	Differential expression profiling between the relative normal and dystrophic muscle tissues from the same LGMD patient. Journal of Translational Medicine, 2006, 4, 53.	1.8	25
100	Systematic identification and characterization of chicken (Gallus gallus) ncRNAs. Nucleic Acids Research, 2009, 37, 6562-6574.	6.5	25
101	antiCODE: a natural sense-antisense transcripts database. BMC Bioinformatics, 2007, 8, 319.	1.2	24
102	Deeply Mining a Universe of Peptides Encoded by Long Noncoding RNAs. Molecular and Cellular Proteomics, 2021, 20, 100109.	2.5	24
103	G Protein Î²3 Subunit Gene Variants and Essential Hypertension in the Northern Chinese Han Population. Annals of Human Genetics, 2005, 69, 468-473.	0.3	23
104	Toward Automated Identification of Glycan Branching Patterns Using Multistage Mass Spectrometry with Intelligent Precursor Selection. Analytical Chemistry, 2018, 90, 14412-14422.	3.2	23
105	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. International Journal of Cell Biology, 2012, 2012, 1-9.	1.0	22
106	GADD45A inhibits autophagy by regulating the interaction between BECN1 and PIK3C3. Autophagy, 2015, 11, 2247-2258.	4.3	22
107	Computational identification of piRNA targets on mouse mRNAs. Bioinformatics, 2016, 32, 1170-1177.	1.8	22
108	LRIK interacts with the Ku70â€“Ku80 heterodimer enhancing the efficiency of NHEJ repair. Cell Death and Differentiation, 2020, 27, 3337-3353.	5.0	22

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109	Association of the Polymorphism rs13259960 in <i><scp>SLEAR</scp></i> With Predisposition to Systemic Lupus Erythematosus. Arthritis and Rheumatology, 2020, 72, 985-996.	2.9	22
110	Date of origin of the SARS coronavirus strains. BMC Infectious Diseases, 2004, 4, 3.	1.3	20
111	Predicting Molecular Formulas of Fragment Ions with Isotope Patterns in Tandem Mass Spectra. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 217-230.	1.9	20
112	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. FEBS Letters, 2006, 580, 1891-1896.	1.3	20
113	Fractal dimension of exon and intron sequences. Journal of Theoretical Biology, 1995, 175, 23-26.	0.8	19
114	Construction and structural modeling of a single-chain Fv-asparaginase fusion protein resistant to proteolysis. Biotechnology and Bioengineering, 2000, 70, 456-463.	1.7	19
115	Experimental RNomics and genomic comparative analysis reveal a large group of species-specific small non-message RNAs in the silkworm Bombyx mori. Nucleic Acids Research, 2011, 39, 3792-3805.	6.5	19
116	Systematic identification and evolutionary features of rhesus monkey small nucleolar RNAs. BMC Genomics, 2010, 11, 61.	1.2	18
117	DRME: Count-based differential RNA methylation analysis at small sample size scenario. Analytical Biochemistry, 2016, 499, 15-23.	1.1	18
118	Differential expression of miRNAs related to caste differentiation in the honey bee, Apis mellifera. Apidologie, 2016, 47, 495-508.	0.9	18
119	Identification and characterization of simple sequence repeats in the genomes of Shigella species. Gene, 2003, 322, 85-92.	1.0	16
120	Reversibly switchable DNA nanocompartment on surfaces. Nucleic Acids Research, 2004, 32, e144-e144.	6.5	16
121	Angiotensin II type I receptor gene and myocardial infarction. Pharmacogenetics and Genomics, 2004, 14, 673-681.	5.7	16
122	Microarray analysis of ncRNA expression patterns in Caenorhabditis elegans after RNAi against snoRNA associated proteins. BMC Genomics, 2008, 9, 278.	1.2	16
123	Lateralization of gene expression in the honeybee brain during olfactory learning. Scientific Reports, 2016, 6, 34727.	1.6	16
124	In vivo analysis of Caenorhabditis elegans noncoding RNA promoter motifs. BMC Molecular Biology, 2008, 9, 71.	3.0	15
125	A functional intronic variant in the tyrosine hydroxylase (TH) gene confers risk of essential hypertension in the Northern Chinese Han population. Clinical Science, 2008, 115, 151-158.	1.8	15
126	The long noncoding RNA ASNR regulates degradation of Bcl-2 mRNA through its interaction with AUF1. Scientific Reports, 2016, 6, 32189.	1.6	15

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127	Expression in Escherichia coli, Purification and Characterization of Thermoanaerobacter tengcongensis Ribosome Recycling Factor. Journal of Biochemistry, 2005, 138, 89-94.	0.9	14
128	Dynamic Changes in Subgraph Preference Profiles of Crucial Transcription Factors. PLoS Computational Biology, 2006, 2, e47.	1.5	14
129	Deep Profiling of the Novel Intermediate-Size Noncoding RNAs in Intraerythrocytic Plasmodium falciparum. PLoS ONE, 2014, 9, e92946.	1.1	14
130	Lipoprotein Lipase Gene Polymorphisms and Blood Pressure Levels in the Northern Chinese Han Population. Hypertension Research, 2004, 27, 373-378.	1.5	14
131	Identifying Hfq-binding small RNA targets in Escherichia coli. Biochemical and Biophysical Research Communications, 2006, 343, 950-955.	1.0	13
132	Genome-scale identification of Caenorhabditis elegans regulatory elements by tiling-array mapping of DNase I hypersensitive sites. BMC Genomics, 2009, 10, 92.	1.2	13
133	Identification and Analysis of Intermediate Size Noncoding RNAs in the Human Fetal Brain. PLoS ONE, 2011, 6, e21652.	1.1	13
134	Systematic identification of non-coding RNA 2,2,7-trimethylguanosine cap structures in Caenorhabditis elegans. BMC Molecular Biology, 2007, 8, 86.	3.0	12
135	The Caenorhabditis elegans intermediate-size transcriptome shows high degree of stage-specific expression. Nucleic Acids Research, 2011, 39, 5203-5214.	6.5	12
136	The Landscape of Viral Expression Reveals Clinically Relevant Viruses with Potential Capability of Promoting Malignancy in Lower-Grade Glioma. Clinical Cancer Research, 2017, 23, 2177-2185.	3.2	12
137	LncRNA HRCEG, regulated by HDAC1, inhibits cells proliferation and epithelial-mesenchymal-transition in gastric cancer. Cancer Genetics, 2020, 241, 25-33.	0.2	12
138	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. Genome Biology, 2021, 22, 233.	3.8	12
139	A novel scoring schema for peptide identification by searching protein sequence databases using tandem mass spectrometry data. BMC Bioinformatics, 2006, 7, 222.	1.2	11
140	A differential sequencing-based analysis of the <i>C. elegans</i> noncoding transcriptome. Rna, 2012, 18, 626-639.	1.6	11
141	Regulatory elements of Caenorhabditis elegans ribosomal protein genes. BMC Genomics, 2012, 13, 433.	1.2	11
142	Computational Methods to Predict Long Noncoding RNA Functions Based on Co-expression Network. Methods in Molecular Biology, 2014, 1182, 209-218.	0.4	11
143	Identification and functional characterization of intermediate-size non-coding RNAs in maize. BMC Genomics, 2018, 19, 730.	1.2	11
144	Long noncoding RNA<i>SMRG</i>regulates<i>Drosophila</i>macrochaetes by antagonizing<i>scute</i>through E(spl)mÎ². RNA Biology, 2019, 16, 42-53.	1.5	11

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145	Identification and characterization of long non-coding RNA Carip in modulating spatial learning and memory. Cell Reports, 2022, 38, 110398.	2.9	11
146	Î²-Catenin safeguards the ground state of mousepluripotency by strengthening the robustness of the transcriptional apparatus. Science Advances, 2020, 6, eaba1593.	4.7	10
147	Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division. Genome Research, 2020, 30, 1570-1582.	2.4	9
148	Systematic study of novel lncRNAs in different gastrointestinal cancer cells. Discovery Medicine, 2016, 21, 159-71.	0.5	9
149	A new method of preparing fiber-optic DNA biosensor and its array for gene detection. Science in China Series C: Life Sciences, 2001, 44, 33-39.	1.3	8
150	Gene's Functional Arrangement as a Measure of thePhylogenetic Relationships of Microorganisms. Journal of Biological Physics, 2002, 28, 55-62.	0.7	8
151	Phylogeny of SARS-CoV as inferred from complete genome comparison. Science Bulletin, 2003, 48, 1175-1178.	1.7	8
152	A binary matrix factorization algorithm for protein complex prediction. Proteome Science, 2011, 9, S18.	0.7	8
153	Identification of Intermediate-Size Non-Coding RNAs Involved in the UV-Induced DNA Damage Response in C. elegans. PLoS ONE, 2012, 7, e48066.	1.1	8
154	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. Protein and Cell, 2012, 3, 148-152.	4.8	8
155	Large-scale study of long non-coding RNA functions based on structure and expression features. Science China Life Sciences, 2013, 56, 953-959.	2.3	8
156	The influences of PRG-1 on the expression of small RNAs and mRNAs. BMC Genomics, 2014, 15, 321.	1.2	8
157	Discovery of Plasma Membrane-Associated RNAs through APEX-seq. Cell Biochemistry and Biophysics, 2021, 79, 905-917.	0.9	8
158	De Novo Approach to Classify Protein-Coding and Noncoding Transcripts Based on Sequence Composition. Methods in Molecular Biology, 2014, 1182, 203-207.	0.4	8
159	Expression profiling and functional prediction of long noncoding RNAs in nasopharyngeal nonkeratinizing carcinoma. Discovery Medicine, 2016, 21, 239-50.	0.5	8
160	Characterization of -Asparaginase Fused with a Protective ScFv and the Protection Mechanism. Biochemical and Biophysical Research Communications, 2000, 276, 197-203.	1.0	7
161	Proteome-wide analysis of protein function composition reveals the clustering and phylogenetic properties of organisms. Molecular Phylogenetics and Evolution, 2002, 25, 101-111.	1.2	7
162	One Novel Long Noncoding RNA lnc10 in Drosophila. Journal of Genetics and Genomics, 2014, 41, 79-82.	1.7	7

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163	NG-Circos: next-generation Circos for data visualization and interpretation. NAR Genomics and Bioinformatics, 2020, 2, lqaa069.	1.5	7
164	Coincident indices of exons and introns. Computers in Biology and Medicine, 1993, 23, 333-343.	3.9	6
165	Fractal Geometry Study of DNA Binding Proteins. Journal of Theoretical Biology, 1994, 171, 239-249.	0.8	6
166	Identification of selenocysteine insertion sequence (SECIS) element in eukaryotic selenoproteins by RNA Draw program. Science Bulletin, 2001, 46, 1159-1161.	1.7	6
167	AN ITERATIVE ALGORITHM TO QUANTIFY FACTORS INFLUENCING PEPTIDE FRAGMENTATION DURING TANDEM MASS SPECTROMETRY. Journal of Bioinformatics and Computational Biology, 2007, 05, 297-311.	0.3	6
168	Light-induced protein translocation by genetically encoded unnatural amino acid in Caenorhabditis elegans. Protein and Cell, 2013, 4, 883-886.	4.8	5
169	Analysis of the p53/CEP-1 regulated non-coding transcriptome in C. elegans by an NSR-seq strategy. Protein and Cell, 2014, 5, 770-782.	4.8	5
170	Genome-wide analysis of mammalian DNA segment fusion/fission. Journal of Theoretical Biology, 2006, 240, 200-208.	0.8	4
171	Analyzing and modeling the inhibitory effect of phosphatidic acid on the GTPâ€Î³â€S binding activity of GoÎ±. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1732-1743.	1.5	4
172	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. Genomics, 2010, 96, 308-315.	1.3	4
173	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. BMC Bioinformatics, 2011, 12, 53.	1.2	4
174	On Bioinformatic Resources. Genomics, Proteomics and Bioinformatics, 2015, 13, 1-3.	3.0	4
175	Comparison between phylogeny of introns and exons in primate. Science Bulletin, 1999, 44, 1940-1946.	1.7	3
176	Conservation of ribosomal protein gene ordering in 16 complete genomes. Science in China Series C: Life Sciences, 2000, 43, 120-128.	1.3	3
177	Small RNA in rice genome. Science in China Series C: Life Sciences, 2002, 45, 497.	1.3	3
178	Comparison of properties of tumor necrosis factor-Î± converting enzyme (TACE) and some matrix metalloproteases (MMPs) in catalytic domains. Journal of Huazhong University of Science and Technology [Medical Sciences], 2006, 26, 637-639.	1.0	3
179	A binary matrix factorization algorithm for protein complex prediction. , 2010, , .		3
180	Genome-wide identification of cancer-related polyadenylated and non-polyadenylated RNAs in human breast and lung cell lines. Science China Life Sciences, 2013, 56, 503-512.	2.3	3

#	ARTICLE	IF	CITATIONS
181	Association of echocardiographic left ventricular structure and â^'344C/T aldosterone synthase gene variant: A meta-analysis. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2015, 16, 858-871.	1.0	3
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200	Gold nanoparticle-assisted primer walking for closing the human chromosomal gap. Analytical Methods, 2013, 5, 4746.	1.3	0
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