

Runsheng Chen

List of Publications by Year in descending order

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205
papers

17,618
citations

30551

56
h-index

16791

127
g-index

209
all docs

209
docs citations

209
times ranked

25832
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and characterization of long non-coding RNA Carip in modulating spatial learning and memory. <i>Cell Reports</i> , 2022, 38, 110398.	2.9	11
2	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.	6.5	166
3	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
4	Deeply Mining a Universe of Peptides Encoded by Long Noncoding RNAs. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100109.	2.5	24
5	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.	5.0	28
6	Discovery of Plasma Membrane-Associated RNAs through APEX-seq. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 905-917.	0.9	8
7	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021, 22, 233.	3.8	12
8	SmProt: A Reliable Repository with Comprehensive Annotation of Small Proteins Identified from Ribosome Profiling. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 602-610.	3.0	28
9	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020, 48, D160-D165.	6.5	106
10	SpatialDB: a database for spatially resolved transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, D233-D237.	6.5	37
11	lncRNA HRCEG, regulated by HDAC1, inhibits cells proliferation and epithelial-mesenchymal-transition in gastric cancer. <i>Cancer Genetics</i> , 2020, 241, 25-33.	0.2	12
12	BCL9 provides multi-cellular communication properties in colorectal cancer by interacting with paraspeckle proteins. <i>Nature Communications</i> , 2020, 11, 19.	5.8	27
13	NG-Circos: next-generation Circos for data visualization and interpretation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa069.	1.5	7
14	Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division. <i>Genome Research</i> , 2020, 30, 1570-1582.	2.4	9
15	β2-Catenin safeguards the ground state of mouse pluripotency by strengthening the robustness of the transcriptional apparatus. <i>Science Advances</i> , 2020, 6, eaba1593.	4.7	10
16	Noncoding RNA: from dark matter to bright star. <i>Science China Life Sciences</i> , 2020, 63, 463-468.	2.3	32
17	LRiK interacts with the Ku70-Ku80 heterodimer enhancing the efficiency of NHEJ repair. <i>Cell Death and Differentiation</i> , 2020, 27, 3337-3353.	5.0	22
18	Association of the Polymorphism rs13259960 in <i>SLEAR</i> With Predisposition to Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2020, 72, 985-996.	2.9	22

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19	Genetic variations associated with long noncoding RNAs. <i>Essays in Biochemistry</i> , 2020, 64, 867-873.	2.1	3
20	LncRNA HAND2-AS1 promotes liver cancer stem cell self-renewal via BMP signaling. <i>EMBO Journal</i> , 2019, 38, e101110.	3.5	117
21	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.	2.4	27
22	ER-residential Nogo-B accelerates NAFLD-associated HCC mediated by metabolic reprogramming of oxLDL lipophagy. <i>Nature Communications</i> , 2019, 10, 3391.	5.8	75
23	LincK contributes to breast tumorigenesis by promoting proliferation and epithelial-to-mesenchymal transition. <i>Journal of Hematology and Oncology</i> , 2019, 12, 19.	6.9	29
24	piRBase: a comprehensive database of piRNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D175-D180.	6.5	169
25	Long noncoding RNA <i>SMRG</i> regulates <i>Drosophila</i> macrochaetes by antagonizing <i>scute</i> through E(spl)m ¹² . <i>RNA Biology</i> , 2019, 16, 42-53.	1.5	11
26	LncVar: Deciphering Genetic Variations Associated with Long Noncoding Genes. <i>Methods in Molecular Biology</i> , 2019, 1870, 189-198.	0.4	3
27	SmProt: a database of small proteins encoded by annotated coding and non-coding RNA loci. <i>Briefings in Bioinformatics</i> , 2018, 19, bbx005.	3.2	85
28	XPF plays an indispensable role in relieving silver nanoparticle induced DNA damage stress in human cells. <i>Toxicology Letters</i> , 2018, 288, 44-54.	0.4	3
29	Long noncoding RNA lncHand2 promotes liver repopulation via c-Met signaling. <i>Journal of Hepatology</i> , 2018, 69, 861-872.	1.8	32
30	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.	1.6	68
31	A novel antisense long noncoding <i>RNA</i> , <i>TWISTED LEAF</i> , maintains leaf blade flattening by regulating its associated sense <i>R2R3MYB</i> gene in rice. <i>New Phytologist</i> , 2018, 218, 774-788.	3.5	96
32	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018, 46, D308-D314.	6.5	434
33	<i>LncKdm2b</i> controls self-renewal of embryonic stem cells via activating expression of transcription factor <i>Zbtb3</i> . <i>EMBO Journal</i> , 2018, 37, .	3.5	75
34	TDP-43 regulates cancer-associated microRNAs. <i>Protein and Cell</i> , 2018, 9, 848-866.	4.8	35
35	Toward Automated Identification of Glycan Branching Patterns Using Multistage Mass Spectrometry with Intelligent Precursor Selection. <i>Analytical Chemistry</i> , 2018, 90, 14412-14422.	3.2	23
36	Identification and functional characterization of intermediate-size non-coding RNAs in maize. <i>BMC Genomics</i> , 2018, 19, 730.	1.2	11

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37	Dynamic-BM: multispecies Dynamic BodyMap database from temporal RNA-seq data. <i>Briefings in Bioinformatics</i> , 2018, 19, 1302-1309.	3.2	1
38	Long noncoding RNA LINC01186, regulated by TGF- β 2/SMAD3, inhibits migration and invasion through Epithelial-Mesenchymal-Transition in lung cancer. <i>Gene</i> , 2017, 608, 1-12.	1.0	50
39	Identification and analysis of intermediate-size noncoding RNAs in the rhesus macaque fetal brain. <i>Journal of Genetics and Genomics</i> , 2017, 44, 171-174.	1.7	0
40	Long noncoding RNA lncKdm2b is required for ILC3 maintenance by initiation of Zfp292 expression. <i>Nature Immunology</i> , 2017, 18, 499-508.	7.0	174
41	Mesenchymal Stem Cells Promote Hepatocarcinogenesis via lncRNA- μ MUF Interaction with ANXA2 and miR-34a. <i>Cancer Research</i> , 2017, 77, 6704-6716.	0.4	193
42	The long noncoding RNA SNHG1 promotes tumor growth through regulating transcription of both local and distal genes. <i>Oncogene</i> , 2017, 36, 6774-6783.	2.6	74
43	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.	3.2	12
44	LncVar: a database of genetic variation associated with long non-coding genes. <i>Bioinformatics</i> , 2017, 33, 112-118.	1.8	33
45	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
46	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.	0.8	28
47	Proboscis Extension Reflex in <i>Apis mellifera</i> [Honeybee] with Only One Antenna. <i>Bio-protocol</i> , 2017, 7, e2624.	0.2	0
48	LncRNA MT1JP functions as a tumor suppressor by interacting with TIAR to modulate the p53 pathway. <i>Oncotarget</i> , 2016, 7, 15787-15800.	0.8	59
49	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw057.	1.4	130
50	Lateralization of gene expression in the honeybee brain during olfactory learning. <i>Scientific Reports</i> , 2016, 6, 34727.	1.6	16
51	The long noncoding RNA ASNR regulates degradation of Bcl-2 mRNA through its interaction with AUF1. <i>Scientific Reports</i> , 2016, 6, 32189.	1.6	15
52	Generating a long DNA fragment of the target ncRNA for quantitative polymerase chain reaction by combining ncRNA-oligos hybridization and oligos ligation. <i>Journal of Biotechnology</i> , 2016, 217, 41-48.	1.9	1
53	BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. <i>Bioinformatics</i> , 2016, 32, 1740-1742.	1.8	119
54	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D203-D208.	6.5	574

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55	Computational identification of piRNA targets on mouse mRNAs. <i>Bioinformatics</i> , 2016, 32, 1170-1177.	1.8	22
56	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016, 499, 15-23.	1.1	18
57	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2016, 1402, 243-254.	0.4	28
58	Differential expression of miRNAs related to caste differentiation in the honey bee, <i>Apis mellifera</i> . <i>Apidologie</i> , 2016, 47, 495-508.	0.9	18
59	Transcriptional profiling analysis and functional prediction of long noncoding RNAs in cancer. <i>Oncotarget</i> , 2016, 7, 8131-8142.	0.8	49
60	Systematic study of novel lncRNAs in different gastrointestinal cancer cells. <i>Discovery Medicine</i> , 2016, 21, 159-71.	0.5	9
61	Expression profiling and functional prediction of long noncoding RNAs in nasopharyngeal nonkeratinizing carcinoma. <i>Discovery Medicine</i> , 2016, 21, 239-50.	0.5	8
62	GADD45A inhibits autophagy by regulating the interaction between BECN1 and PIK3C3. <i>Autophagy</i> , 2015, 11, 2247-2258.	4.3	22
63	Association of echocardiographic left ventricular structure and α^*344C/T aldosterone synthase gene variant: A meta-analysis. <i>JRAAS - Journal of the Renin-Angiotensin-Aldosterone System</i> , 2015, 16, 858-871.	1.0	3
64	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. <i>Cell Research</i> , 2015, 25, 193-207.	5.7	266
65	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, 413-425.	5.2	529
66	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
67	Functional Characterization of Long Noncoding RNA lnc_bc060912 in Human Lung Carcinoma Cells. <i>Biochemistry</i> , 2015, 54, 2895-2902.	1.2	29
68	Long Noncoding RNA ADINR Regulates Adipogenesis by Transcriptionally Activating C/EBP β . <i>Stem Cell Reports</i> , 2015, 5, 856-865.	2.3	154
69	On Bioinformatic Resources. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 1-3.	3.0	4
70	A long noncoding RNA critically regulates Bcr-Abl-mediated cellular transformation by acting as a competitive endogenous RNA. <i>Oncogene</i> , 2015, 34, 1768-1779.	2.6	149
71	Transcriptome profiling of esophageal squamous cell carcinoma reveals a long noncoding RNA acting as a tumor suppressor. <i>Oncotarget</i> , 2015, 6, 17065-17080.	0.8	39
72	Deep Profiling of the Novel Intermediate-Size Noncoding RNAs in Intraerythrocytic Plasmodium falciparum. <i>PLoS ONE</i> , 2014, 9, e92946.	1.1	14

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73	LncRNA profile study reveals a three-lncRNA signature associated with the survival of patients with oesophageal squamous cell carcinoma. <i>Gut</i> , 2014, 63, 1700-1710.	6.1	385
74	NONCODEv4: exploring the world of long non-coding RNA genes. <i>Nucleic Acids Research</i> , 2014, 42, D98-D103.	6.5	398
75	piRBase: a web resource assisting piRNA functional study. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau110.	1.4	132
76	NPInter v2.0: an updated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2014, 42, D104-D108.	6.5	141
77	One Novel Long Noncoding RNA lnc10 in <i>Drosophila</i> . <i>Journal of Genetics and Genomics</i> , 2014, 41, 79-82.	1.7	7
78	Genomic Features and Regulatory Roles of Intermediate-Sized Non-Coding RNAs in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2014, 7, 514-527.	3.9	77
79	Computational Methods to Predict Long Noncoding RNA Functions Based on Co-expression Network. <i>Methods in Molecular Biology</i> , 2014, 1182, 209-218.	0.4	11
80	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, 770-782.	4.8	5
81	The influences of PRG-1 on the expression of small RNAs and mRNAs. <i>BMC Genomics</i> , 2014, 15, 321.	1.2	8
82	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.	1.3	35
83	De Novo Approach to Classify Protein-Coding and Noncoding Transcripts Based on Sequence Composition. <i>Methods in Molecular Biology</i> , 2014, 1182, 203-207.	0.4	8
84	Genome-wide identification of cancer-related polyadenylated and non-polyadenylated RNAs in human breast and lung cell lines. <i>Science China Life Sciences</i> , 2013, 56, 503-512.	2.3	3
85	Large-scale study of long non-coding RNA functions based on structure and expression features. <i>Science China Life Sciences</i> , 2013, 56, 953-959.	2.3	8
86	Light-induced protein translocation by genetically encoded unnatural amino acid in <i>Caenorhabditis elegans</i> . <i>Protein and Cell</i> , 2013, 4, 883-886.	4.8	5
87	Gold nanoparticle-assisted primer walking for closing the human chromosomal gap. <i>Analytical Methods</i> , 2013, 5, 4746.	1.3	0
88	Long non-coding RNAs function annotation: a global prediction method based on bi-colored networks. <i>Nucleic Acids Research</i> , 2013, 41, e35-e35.	6.5	174
89	De novo prediction of RNA-protein interactions from sequence information. <i>Molecular BioSystems</i> , 2013, 9, 133-142.	2.9	102
90	Genome Comparisons as a Tool for Antimicrobial Target Discovery. <i>Methods in Molecular Biology</i> , 2013, 993, 31-38.	0.4	0

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91	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, 830-846.	3.9	66
92	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. <i>Nucleic Acids Research</i> , 2013, 41, e166-e166.	6.5	1,658
93	Recipe for a Busy Bee: MicroRNAs in Honey Bee Caste Determination. <i>PLoS ONE</i> , 2013, 8, e81661.	1.1	60
94	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. <i>International Journal of Cell Biology</i> , 2012, 2012, 1-9.	1.0	22
95	NONCODE v3.0: integrative annotation of long noncoding RNAs. <i>Nucleic Acids Research</i> , 2012, 40, D210-D215.	6.5	383
96	A non-Gaussian factor analysis approach to transcription Network Component Analysis. , 2012, , .		0
97	The novel long non-coding RNA CRG regulates <i>Drosophila</i> locomotor behavior. <i>Nucleic Acids Research</i> , 2012, 40, 11714-11727.	6.5	53
98	Transcription Network Analysis by A Sparse Binary Factor Analysis Algorithm. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 68-79.	1.0	2
99	The human microbiome: A hot spot of microbial horizontal gene transfer. <i>Genomics</i> , 2012, 100, 265-270.	1.3	109
100	A differential sequencing-based analysis of the <i>C. elegans</i> noncoding transcriptome. <i>Rna</i> , 2012, 18, 626-639.	1.6	11
101	Regulatory elements of <i>Caenorhabditis elegans</i> ribosomal protein genes. <i>BMC Genomics</i> , 2012, 13, 433.	1.2	11
102	Integrated Sequence-Structure Motifs Suffice to Identify microRNA Precursors. <i>PLoS ONE</i> , 2012, 7, e32797.	1.1	29
103	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.	1.1	8
104	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , 2012, 44, 890-894.	9.4	295
105	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. <i>Protein and Cell</i> , 2012, 3, 148-152.	4.8	8
106	Transcription network analysis by a sparse binary factor analysis algorithm. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 198.	1.0	0
107	Estimating the Quality of Reprogrammed Cells Using ES Cell Differentiation Expression Patterns. <i>PLoS ONE</i> , 2011, 6, e15336.	1.1	2
108	Predicting Housekeeping Genes Based on Fourier Analysis. <i>PLoS ONE</i> , 2011, 6, e21012.	1.1	26

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109	A binary matrix factorization algorithm for protein complex prediction. <i>Proteome Science</i> , 2011, 9, S18.	0.7	8
110	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. <i>BMC Bioinformatics</i> , 2011, 12, 53.	1.2	4
111	The <i>Caenorhabditis elegans</i> intermediate-size transcriptome shows high degree of stage-specific expression. <i>Nucleic Acids Research</i> , 2011, 39, 5203-5214.	6.5	12
112	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, 3792-3805.	6.5	19
113	ncFANs: a web server for functional annotation of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, W118-W124.	6.5	123
114	Identification and Analysis of Intermediate Size Noncoding RNAs in the Human Fetal Brain. <i>PLoS ONE</i> , 2011, 6, e21652.	1.1	13
115	Bioinformatics "Mining the genome for information. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2010, 5, 391-404.	0.6	0
116	Systematic identification and evolutionary features of rhesus monkey small nucleolar RNAs. <i>BMC Genomics</i> , 2010, 11, 61.	1.2	18
117	Comparison of stationary and oscillatory dynamics described by differential equations and Boolean maps in transcriptional regulatory circuits. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2010, 374, 4749-4755.	0.9	2
118	A binary matrix factorization algorithm for protein complex prediction. , 2010, , .		3
119	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010, 96, 308-315.	1.3	4
120	Global Epigenetic and Transcriptional Trends among Two Rice Subspecies and Their Reciprocal Hybrids. <i>Plant Cell</i> , 2010, 22, 17-33.	3.1	514
121	Systematic identification and characterization of chicken (<i>Gallus gallus</i>) ncRNAs. <i>Nucleic Acids Research</i> , 2009, 37, 6562-6574.	6.5	25
122	Systematic identification of genes involved in divergent skeletal muscle growth rates of broiler and layer chickens. <i>BMC Genomics</i> , 2009, 10, 87.	1.2	71
123	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.	1.2	13
124	Transcriptional inhibition of <i>Hoxd4</i> expression by miRNA-10a in human breast cancer cells. <i>BMC Molecular Biology</i> , 2009, 10, 12.	3.0	167
125	In vivo analysis of <i>Caenorhabditis elegans</i> noncoding RNA promoter motifs. <i>BMC Molecular Biology</i> , 2008, 9, 71.	3.0	15
126	Analyzing and modeling the inhibitory effect of phosphatidic acid on the GTP-binding activity of <i>Go</i> proteins: Structure, Function and Bioinformatics, 2008, 71, 1732-1743.	1.5	4

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127	MicroRNA-encoding long non-coding RNAs. <i>BMC Genomics</i> , 2008, 9, 236.	1.2	60
128	Microarray analysis of ncRNA expression patterns in <i>Caenorhabditis elegans</i> after RNAi against snoRNA associated proteins. <i>BMC Genomics</i> , 2008, 9, 278.	1.2	16
129	MicroRNA regulation of messenger-like noncoding RNAs: a network of mutual microRNA control. <i>Trends in Genetics</i> , 2008, 24, 323-327.	2.9	36
130	The Properties and Functions of Virus Encoded microRNA, siRNA, and Other Small Noncoding RNAs. <i>Critical Reviews in Microbiology</i> , 2008, 34, 175-188.	2.7	27
131	Assessing TF regulatory relationships of divergently transcribed genes. <i>Genomics</i> , 2008, 92, 316-321.	1.3	2
132	FlexStem: improving predictions of RNA secondary structures with pseudoknots by reducing the search space. <i>Bioinformatics</i> , 2008, 24, 1994-2001.	1.8	36
133	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, 151-158.	1.8	15
134	AN ITERATIVE ALGORITHM TO QUANTIFY FACTORS INFLUENCING PEPTIDE FRAGMENTATION DURING TANDEM MASS SPECTROMETRY. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 297-311.	0.3	6
135	Myostatin Induces Cyclin D1 Degradation to Cause Cell Cycle Arrest through a Phosphatidylinositol 3-Kinase/AKT/GSK-3 β Pathway and Is Antagonized by Insulin-like Growth Factor 1. <i>Journal of Biological Chemistry</i> , 2007, 282, 3799-3808.	1.6	186
136	NONCODE v2.0: decoding the non-coding. <i>Nucleic Acids Research</i> , 2007, 36, D170-D172.	6.5	115
137	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , 2007, 17, 1471-1477.	2.4	53
138	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. <i>Molecular Cell</i> , 2007, 26, 539-551.	4.5	347
139	Model-based analysis of two-color arrays (MA2C). <i>Genome Biology</i> , 2007, 8, R178.	13.9	95
140	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. <i>PLoS ONE</i> , 2007, 2, e294.	1.1	82
141	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.	3.0	12
142	antiCODE: a natural sense-antisense transcripts database. <i>BMC Bioinformatics</i> , 2007, 8, 319.	1.2	24
143	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.	1.8	25
144	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. <i>FEBS Letters</i> , 2006, 580, 1891-1896.	1.3	20

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145	Identifying Hfq-binding small RNA targets in Escherichia coli. <i>Biochemical and Biophysical Research Communications</i> , 2006, 343, 950-955.	1.0	13
146	Integrated analysis of multiple data sources reveals modular structure of biological networks. <i>Biochemical and Biophysical Research Communications</i> , 2006, 345, 302-309.	1.0	33
147	Association of β 1A adrenergic receptor gene variants on chromosome 8p21 with human stage 2 hypertension. <i>Journal of Hypertension</i> , 2006, 24, 1049-1056.	0.3	26
148	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	13.7	53
149	Genome-wide analysis of mammalian DNA segment fusion/fission. <i>Journal of Theoretical Biology</i> , 2006, 240, 200-208.	0.8	4
150	Comparison of properties of tumor necrosis factor- α converting enzyme (TACE) and some matrix metalloproteases (MMPs) in catalytic domains. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2006, 26, 637-639.	1.0	3
151	A novel scoring schema for peptide identification by searching protein sequence databases using tandem mass spectrometry data. <i>BMC Bioinformatics</i> , 2006, 7, 222.	1.2	11
152	Phylogenetic properties of metabolic pathway topologies as revealed by global analysis. <i>BMC Bioinformatics</i> , 2006, 7, 252.	1.2	27
153	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, 306B, 379-392.	0.6	39
154	Profiling <i>Caenorhabditis elegans</i> non-coding RNA expression with a combined microarray. <i>Nucleic Acids Research</i> , 2006, 34, 2976-2983.	6.5	30
155	Association Study With 33 Single-Nucleotide Polymorphisms in 11 Candidate Genes for Hypertension in Chinese. <i>Hypertension</i> , 2006, 47, 1147-1154.	1.3	90
156	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006, 34, D150-D152.	6.5	93
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