Runsheng Chen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

12,964 50 203 111 h-index g-index citations papers 8.6 15,638 5.8 209 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
203	Identification and characterization of long non-coding RNA Carip in modulating spatial learning and memory <i>Cell Reports</i> , 2022 , 38, 110398	10.6	O
202	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
201	Discovery of Plasma Membrane-Associated RNAs through APEX-seq. <i>Cell Biochemistry and Biophysics</i> , 2021 , 79, 905-917	3.2	1
200	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
199	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D18-D28	20.1	84
198	Deeply Mining a Universe of Peptides Encoded by Long Noncoding RNAs. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100109	7.6	5
197	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021 , 22, 233	18.3	2
196	SmProt: A Reliable Repository with Comprehensive Annotation of Small Proteins Identified from Ribosome Profiling. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	1
195	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
194	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
193	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020 , 48, D160-D10	5520.1	50
192	SpatialDB: a database for spatially resolved transcriptomes. <i>Nucleic Acids Research</i> , 2020 , 48, D233-D23	3 7 20.1	16
191	Genetic variations associated with long noncoding RNAs. Essays in Biochemistry, 2020, 64, 867-873	7.6	O
190	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
189	BCL9 provides multi-cellular communication properties in colorectal cancer by interacting with paraspeckle proteins. <i>Nature Communications</i> , 2020 , 11, 19	17.4	13
188	NG-Circos: next-generation Circos for data visualization and interpretation. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa069	3.7	1
187	Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division. <i>Genome Research</i> , 2020 , 30, 1570-1582	9.7	4

(2018-2020)

186	Ecatenin safeguards the ground state of mousepluripotency by strengthening the robustness of the transcriptional apparatus. <i>Science Advances</i> , 2020 , 6, eaba1593	14.3	5
185	LincK 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
184	LncRNA HAND2-AS1 promotes liver cancer stem cell self-renewal via BMP signaling. <i>EMBO Journal</i> , 2019 , 38, e101110	13	71
183	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
182	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
181	piRBase: a comprehensive database of piRNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D175-D180	20.1	105
180	Long noncoding RNA SMRG regulates Drosophila macrochaetes by antagonizing scute through E(spl)m[]RNA Biology, 2019 , 16, 42-53	4.8	3
179	LncVar: Deciphering Genetic Variations Associated with Long Noncoding Genes. <i>Methods in Molecular Biology</i> , 2019 , 1870, 189-198	1.4	2
178	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
177	XPF plays an indispensable role in relieving silver nanoparticle induced DNA damage stress in human cells. <i>Toxicology Letters</i> , 2018 , 288, 44-54	4.4	3
176	Long noncoding RNA lncHand2 promotes liver repopulation via c-Met signaling. <i>Journal of Hepatology</i> , 2018 , 69, 861-872	13.4	23
175	Genomic and transcriptomic analysis of the Asian honeybee Apis cerana provides novel insights into honeybee biology. <i>Scientific Reports</i> , 2018 , 8, 822	4.9	21
174	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
173	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018 , 46, D308-D314	20.1	276
172	controls self-renewal of embryonic stem cells via activating expression of transcription factor. <i>EMBO Journal</i> , 2018 , 37,	13	59
171	TDP-43 regulates cancer-associated microRNAs. <i>Protein and Cell</i> , 2018 , 9, 848-866	7.2	19
170	Dynamic-BM: multispecies Dynamic BodyMap database from temporal RNA-seq data. <i>Briefings in Bioinformatics</i> , 2018 , 19, 1302-1309	13.4	1
169	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

168	Identification and functional characterization of intermediate-size non-coding RNAs in maize. <i>BMC Genomics</i> , 2018 , 19, 730	4.5	6
167	Long noncoding RNA LINC01186, regulated by TGF-/ISMAD3, inhibits migration and invasion through Epithelial-Mesenchymal-Transition in lung cancer. <i>Gene</i> , 2017 , 608, 1-12	3.8	46
166	Identification and analysis of intermediate-size noncoding RNAs in the rhesus macaque fetal brain. Journal of Genetics and Genomics, 2017, 44, 171-174	4	
165	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
164	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
163	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
162	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
161	LncVar: a database of genetic variation associated with long non-coding genes. <i>Bioinformatics</i> , 2017 , 33, 112-118	7.2	29
160	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017 , 45, D128-D134	20.1	119
159	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
158	Proboscis Extension Reflex in [Honeybee] with Only One Antenna. <i>Bio-protocol</i> , 2017 , 7, e2624	0.9	
157	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, 41-8	3.7	1
156	BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. <i>Bioinformatics</i> , 2016 , 32, 1740-2	7.2	64
155	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
154	Computational identification of piRNA targets on mouse mRNAs. <i>Bioinformatics</i> , 2016 , 32, 1170-7	7.2	14
153	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016 , 499, 15-23	3.1	12
152	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2016 , 1402, 243-254	1.4	25
151	Differential expression of miRNAs related to caste differentiation in the honey bee, Apis mellifera. <i>Apidologie</i> , 2016 , 47, 495-508	2.3	11

150	Transcriptional profiling analysis and functional prediction of long noncoding RNAs in cancer. <i>Oncotarget</i> , 2016 , 7, 8131-42	3.3	45
149	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
148	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
147	Lateralization of gene expression in the honeybee brain during olfactory learning. <i>Scientific Reports</i> , 2016 , 6, 34727	4.9	11
146	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
145	Systematic study of novel lncRNAs in different gastrointestinal cancer cells. <i>Discovery Medicine</i> , 2016 , 21, 159-71	2.5	9
144	Expression profiling and functional prediction of long noncoding RNAs in nasopharyngeal nonkeratinizing carcinoma. <i>Discovery Medicine</i> , 2016 , 21, 239-50	2.5	8
143	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. <i>Cell Research</i> , 2015 , 25, 193-2	2 07 4.7	185
142	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
141	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D123-9	20.1	89
140	Functional Characterization of Long Noncoding RNA Lnc_bc060912 in Human Lung Carcinoma Cells. <i>Biochemistry</i> , 2015 , 54, 2895-902	3.2	28
139	Long Noncoding RNA ADINR Regulates Adipogenesis by Transcriptionally Activating C/EBP\(\text{BStem}\) Cell Reports, 2015 , 5, 856-865	8	119
138	On bioinformatic resources. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 1-3	6.5	3
137	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
136	GADD45A inhibits autophagy by regulating the interaction between BECN1 and PIK3C3. <i>Autophagy</i> , 2015 , 11, 2247-58	10.2	17
135	Association of echocardiographic left ventricular structure and -344C/T aldosterone synthase gene variant: A meta-analysis. <i>JRAAS - Journal of the Renin-Angiotensin-Aldosterone System</i> , 2015 , 16, 858-71	3	2
134	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
133	Genomic features and regulatory roles of intermediate-sized non-coding RNAs in Arabidopsis. <i>Molecular Plant</i> , 2014 , 7, 514-27	14.4	48

132	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
131	Analysis of the p53/CEP-1 regulated non-coding transcriptome in C. elegans by an NSR-seq strategy. <i>Protein and Cell</i> , 2014 , 5, 770-82	7.2	4
130	The influences of PRG-1 on the expression of small RNAs and mRNAs. <i>BMC Genomics</i> , 2014 , 15, 321	4.5	3
129	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
128	Deep profiling of the novel intermediate-size noncoding RNAs in intraerythrocytic Plasmodium falciparum. <i>PLoS ONE</i> , 2014 , 9, e92946	3.7	8
127	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
126	NONCODEv4: exploring the world of long non-coding RNA genes. <i>Nucleic Acids Research</i> , 2014 , 42, D98	- 1:03 1	342
125	piRBase: a web resource assisting piRNA functional study. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau110	5	98
124	NPInter v2.0: an updated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2014 , 42, D104-8	20.1	101
123	One novel long noncoding RNA lnc10 in Drosophila. <i>Journal of Genetics and Genomics</i> , 2014 , 41, 79-82	4	6
122	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
121	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, 503-12	8.5	1
120	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
119	Light-induced protein translocation by genetically encoded unnatural amino acid in Caenorhabditis elegans. <i>Protein and Cell</i> , 2013 , 4, 883-6	7.2	3
118	Gold nanoparticle-assisted primer walking for closing the human chromosomal gap. <i>Analytical Methods</i> , 2013 , 5, 4746	3.2	
117	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
116	De novo prediction of RNA-protein interactions from sequence information. <i>Molecular BioSystems</i> , 2013 , 9, 133-42		74
115	Genome comparisons as a tool for antimicrobial target discovery. <i>Methods in Molecular Biology</i> , 2013 , 993, 31-8	1.4	

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114	A global identification and analysis of small nucleolar RNAs and possible intermediate-sized non-coding RNAs in Oryza sativa. <i>Molecular Plant</i> , 2013 , 6, 830-46	14.4	52
113	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. <i>Nucleic Acids Research</i> , 2013 , 41, e166	20.1	879
112	Recipe for a busy bee: microRNAs in Honey Bee caste determination. <i>PLoS ONE</i> , 2013 , 8, e81661	3.7	53
111	The human microbiome: a hot spot of microbial horizontal gene transfer. <i>Genomics</i> , 2012 , 100, 265-70	4.3	79
110	A differential sequencing-based analysis of the C. elegans noncoding transcriptome. <i>Rna</i> , 2012 , 18, 626	- 359 8	10
109	Regulatory elements of Caenorhabditis elegans ribosomal protein genes. <i>BMC Genomics</i> , 2012 , 13, 433	4.5	6
108	Integrated sequence-structure motifs suffice to identify microRNA precursors. <i>PLoS ONE</i> , 2012 , 7, e327	'93 7	26
107	Identification of intermediate-size non-coding RNAs involved in the UV-induced DNA damage response in C. elegans. <i>PLoS ONE</i> , 2012 , 7, e48066	3.7	7
106	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
105	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. <i>Protein and Cell</i> , 2012 , 3, 148-52	7.2	7
104	Distinct MicroRNA Subcellular Size and Expression Patterns in Human Cancer Cells. <i>International Journal of Cell Biology</i> , 2012 , 2012, 672462	2.6	19
103	NONCODE v3.0: integrative annotation of long noncoding RNAs. <i>Nucleic Acids Research</i> , 2012 , 40, D210)-5 0.1	313
102	The novel long non-coding RNA CRG regulates Drosophila locomotor behavior. <i>Nucleic Acids Research</i> , 2012 , 40, 11714-27	20.1	45
101	Transcription Network Analysis by A Sparse Binary Factor Analysis Algorithm. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 68-79	3.8	2
100	Transcription network analysis by a sparse binary factor analysis algorithm. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 198	3.8	
99	Estimating the quality of reprogrammed cells using ES cell differentiation expression patterns. <i>PLoS ONE</i> , 2011 , 6, e15336	3.7	1
98	Predicting housekeeping genes based on Fourier analysis. <i>PLoS ONE</i> , 2011 , 6, e21012	3.7	11
97	A binary matrix factorization algorithm for protein complex prediction. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S18	2.6	5

96	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. <i>BMC Bioinformatics</i> , 2011 , 12, 53	3.6	3
95	The Caenorhabditis elegans intermediate-size transcriptome shows high degree of stage-specific expression. <i>Nucleic Acids Research</i> , 2011 , 39, 5203-14	20.1	11
94	Experimental RNomics and genomic comparative analysis reveal a large group of species-specific small non-message RNAs in the silkworm Bombyx mori. <i>Nucleic Acids Research</i> , 2011 , 39, 3792-805	20.1	15
93	ncFANs: a web server for functional annotation of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2011 , 39, W118-24	20.1	106
92	Identification and analysis of intermediate size noncoding RNAs in the human fetal brain. <i>PLoS ONE</i> , 2011 , 6, e21652	3.7	12
91	A binary matrix factorization algorithm for protein complex prediction 2010 ,		3
90	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
89	Global epigenetic and transcriptional trends among two rice subspecies and their reciprocal hybrids. <i>Plant Cell</i> , 2010 , 22, 17-33	11.6	421
88	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		
87	Systematic identification and evolutionary features of rhesus monkey small nucleolar RNAs. <i>BMC Genomics</i> , 2010 , 11, 61	4.5	17
86	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	2.3	1
85	Systematic identification and characterization of chicken (Gallus gallus) ncRNAs. <i>Nucleic Acids Research</i> , 2009 , 37, 6562-74	20.1	23
84	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
83	Genome-scale identification of Caenorhabditis elegans regulatory elements by tiling-array mapping of DNase I hypersensitive sites. <i>BMC Genomics</i> , 2009 , 10, 92	4.5	12
82	Transcriptional inhibiton of Hoxd4 expression by miRNA-10a in human breast cancer cells. <i>BMC Molecular Biology</i> , 2009 , 10, 12	4.5	141
81	MicroRNA-encoding long non-coding RNAs. <i>BMC Genomics</i> , 2008 , 9, 236	4.5	53
8o	Microarray analysis of ncRNA expression patterns in Caenorhabditis elegans after RNAi against snoRNA associated proteins. <i>BMC Genomics</i> , 2008 , 9, 278	4.5	13
79	MicroRNA regulation of messenger-like noncoding RNAs: a network of mutual microRNA control.	8.5	

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78	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
77	Assessing TF regulatory relationships of divergently transcribed genes. <i>Genomics</i> , 2008 , 92, 316-21	4.3	2
76	FlexStem: improving predictions of RNA secondary structures with pseudoknots by reducing the search space. <i>Bioinformatics</i> , 2008 , 24, 1994-2001	7.2	27
75	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
74	In vivo analysis of Caenorhabditis elegans noncoding RNA promoter motifs. <i>BMC Molecular Biology</i> , 2008 , 9, 71	4.5	15
73	Analyzing and modeling the inhibitory effect of phosphatidic acid on the GTP-gamma-S binding activity of Goalpha. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1732-43	4.2	3
72	NONCODE v2.0: decoding the non-coding. <i>Nucleic Acids Research</i> , 2008 , 36, D170-2	20.1	108
71	Global identification and characterization of transcriptionally active regions in the rice genome. <i>PLoS ONE</i> , 2007 , 2, e294	3.7	63
70	Systematic identification of non-coding RNA 2,2,7-trimethylguanosine cap structures in Caenorhabditis elegans. <i>BMC Molecular Biology</i> , 2007 , 8, 86	4.5	8
69	antiCODE: a natural sense-antisense transcripts database. <i>BMC Bioinformatics</i> , 2007 , 8, 319	3.6	22
68	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
67	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
66	Mapping the C. elegans noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , 2007 , 17, 1471-7	9.7	49
65	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
64	Model-based analysis of two-color arrays (MA2C). <i>Genome Biology</i> , 2007 , 8, R178	18.3	91
63	Genome-wide analysis of mammalian DNA segment fusion/fission. <i>Journal of Theoretical Biology</i> , 2006 , 240, 200-8	2.3	3
62	Comparison of properties of tumor necrosis factor-alpha 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, 637-9		3
61	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

60	Phylophenetic properties of metabolic pathway topologies as revealed by global analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 252	3.6	23
59	Prediction of structured non-coding RNAs in the genomes of the nematodes Caenorhabditis elegans and Caenorhabditis briggsae. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006 , 306, 379-92	1.8	36
58	Profiling Caenorhabditis elegans non-coding RNA expression with a combined microarray. <i>Nucleic Acids Research</i> , 2006 , 34, 2976-83	20.1	29
57	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
56	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006 , 34, D150-2	20.1	63
55	Dynamic changes in subgraph preference profiles of crucial transcription factors. <i>PLoS Computational Biology</i> , 2006 , 2, e47	5	12
54	NMPP: a user-customized NimbleGen microarray data processing pipeline. <i>Bioinformatics</i> , 2006 , 22, 295	5 7 72	27
53	Conserved distances between vertebrate highly conserved elements. <i>Human Molecular Genetics</i> , 2006 , 15, 2911-22	5.6	19
52	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	3- 3:4	25
51	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
50	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
49	Identifying Hfq-binding small RNA targets in Escherichia coli. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 343, 950-5	3.4	11
48	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
47	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
46	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006 , 440, 1194-8	50.4	43
45	Organization of the Caenorhabditis elegans small non-coding transcriptome: genomic features, biogenesis, and expression. <i>Genome Research</i> , 2006 , 16, 20-9	9.7	90
44	Identification of gene expression modifications in myostatin-stimulated myoblasts. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 326, 660-6	3.4	30
43	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

(2003-2005)

42	NONCODE: an integrated knowledge database of non-coding RNAs. <i>Nucleic Acids Research</i> , 2005 , 33, D112-5	20.1	223
41	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
40	Antibody responses to individual proteins of SARS coronavirus and their neutralization activities. <i>Microbes and Infection</i> , 2005 , 7, 882-9	9.3	109
39	Expression in Escherichia coli, purification and characterization of Thermoanaerobacter tengcongensis ribosome recycling factor. <i>Journal of Biochemistry</i> , 2005 , 138, 89-94	3.1	13
38	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
37	Conservation analysis of small RNA genes in Escherichia coli. <i>Bioinformatics</i> , 2004 , 20, 599-603	7.2	25
36	The interactome as a treean attempt to visualize the protein-protein interaction network in yeast. <i>Nucleic Acids Research</i> , 2004 , 32, 4804-11	20.1	36
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