

Zhaohui Steve Qin

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.

141
papers

19,337
citations

44
h-index

139
g-index

164
ext. papers

21,907
ext. citations

9.8
avg, IF

6.99
L-index

#	Paper	IF	Citations
141	ATAD3A mediates activation of RAS-independent mitochondrial ERK1/2 signaling, favoring head and neck cancer development.. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022 , 41, 43	12.8	2
140	Single-cell chromatin accessibility landscape in kidney identifies additional cell-of-origin in heterogenous papillary renal cell carcinoma.. <i>Nature Communications</i> , 2022 , 13, 31	17.4	3
139	UALCAN: An update to the integrated cancer data analysis platform.. <i>Neoplasia</i> , 2022 , 25, 18-27	6.4	44
138	Extensive Chromatin Structure-Function Associations Revealed by Accurate 3D Compartmentalization Characterization.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 845118	5.7	0
137	A neutralizing antibody target in early HIV-1 infection was recapitulated in rhesus macaques immunized with the transmitted/founder envelope sequence.. <i>PLoS Pathogens</i> , 2022 , 18, e1010488	7.6	
136	Multiomics Analysis of Structural Magnetic Resonance Imaging of the Brain and Cerebrospinal Fluid Metabolomics in Cognitively Normal and Impaired Adults.. <i>Frontiers in Aging Neuroscience</i> , 2021 , 13, 796067	5.3	0
135	Systematic Exploration in Tissue-Pathway Associations of Complex Traits Using Comprehensive eQTLs Catalog. <i>Frontiers in Big Data</i> , 2021 , 4, 719737	2.8	0
134	Super-Enhancer-Associated Transcription Factors Maintain Transcriptional Regulation in Mature Podocytes. <i>Journal of the American Society of Nephrology: JASN</i> , 2021 , 32, 1323-1337	12.7	1
133	Identification of Genetic Variants for Prioritized miRNA-targeted Genes Associated with Complex Traits. <i>Advances in Science, Technology and Engineering Systems</i> , 2021 , 6, 418-423	0.3	
132	Glucocorticoid receptor wields chromatin interactions to tune transcription for cytoskeleton stabilization in podocytes. <i>Communications Biology</i> , 2021 , 4, 675	6.7	1
131	A machine learning approach to brain epigenetic analysis reveals kinases associated with Alzheimer's disease. <i>Nature Communications</i> , 2021 , 12, 4472	17.4	9
130	Adolescent stress sensitizes the adult neuroimmune transcriptome and leads to sex-specific microglial and behavioral phenotypes. <i>Neuropsychopharmacology</i> , 2021 , 46, 949-958	8.7	10
129	Chromatin architecture reveals cell type-specific target genes for kidney disease risk variants. <i>BMC Biology</i> , 2021 , 19, 38	7.3	2
128	Pan-cancer analysis of pathway-based gene expression pattern at the individual level reveals biomarkers of clinical prognosis. <i>Cell Reports Methods</i> , 2021 , 1, 100050-100050		3
127	Plasma Metabolic Phenotypes of HPV-Associated versus Smoking-Associated Head and Neck Cancer and Patient Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 1858-1866	4	
126	Systematic Evaluation of DNA Sequence Variations on Transcription Factor Binding Affinity. <i>Frontiers in Genetics</i> , 2021 , 12, 667866	4.5	1
125	DeconPeaker, a Deconvolution Model to Identify Cell Types Based on Chromatin Accessibility in ATAC-Seq Data of Mixture Samples. <i>Frontiers in Genetics</i> , 2020 , 11, 392	4.5	5

124	Lack of RAN-mediated toxicity in Huntington's disease knock-in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 4411-4417	11.5	13
123	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 647-656	3	1
122	Signatures of somatic mutations and gene expression from p16INK4A positive head and neck squamous cell carcinomas (HNSCC). <i>PLoS ONE</i> , 2020 , 15, e0238497	3.7	2
121	Truncation of mutant huntingtin in knock-in mice demonstrates exon1 huntingtin is a key pathogenic form. <i>Nature Communications</i> , 2020 , 11, 2582	17.4	15
120	Application of topic models to a compendium of ChIP-Seq datasets uncovers recurrent transcriptional regulatory modules. <i>Bioinformatics</i> , 2020 , 36, 2352-2358	7.2	0
119	An empirical bayesian approach for testing gene expression fold change and its application in detecting global dosage effects. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa072	3.7	
118	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. <i>Bioinformatics</i> , 2020 , 36, 690-697	7.2	4
117	RT States: systematic annotation of the human genome using cell type-specific replication timing programs. <i>Bioinformatics</i> , 2019 , 35, 2167-2176	7.2	4
116	Rapid Irreversible Transcriptional Reprogramming in Human Stem Cells Accompanied by Discordance between Replication Timing and Chromatin Compartment. <i>Stem Cell Reports</i> , 2019 , 13, 193-206	8	16
115	Integrative characterization of G-Quadruplexes in the three-dimensional chromatin structure. <i>Epigenetics</i> , 2019 , 14, 894-911	5.7	28
114	An Integrated System Biology Approach Yields Drug Repositioning Candidates for the Treatment of Heart Failure. <i>Frontiers in Genetics</i> , 2019 , 10, 916	4.5	1
113	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019 , 10, 880	17.4	36
112	EWS/ETS-Driven Ewing Sarcoma Requires BET Bromodomain Proteins. <i>Cancer Research</i> , 2018 , 78, 4760-4773	17.3	32
111	A comprehensive review of computational prediction of genome-wide features. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	8
110	Probabilistic and machine learning-based retrieval approaches for biomedical dataset retrieval. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	4
109	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. <i>GigaScience</i> , 2018 , 7,	7.6	1
108	Computationally Tractable Multivariate HMM in Genome-Wide Mapping Studies. <i>Methods in Molecular Biology</i> , 2017 , 1552, 135-148	1.4	1
107	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. <i>Scientific Reports</i> , 2017 , 7, 46398	4.9	17

106	Using DIVAN to assess disease/trait-associated single nucleotide variants in genome-wide scale. <i>BMC Research Notes</i> , 2017 , 10, 530	2.3	4
105	CRISPR/Cas9-mediated gene editing ameliorates neurotoxicity in mouse model of Huntington's disease. <i>Journal of Clinical Investigation</i> , 2017 , 127, 2719-2724	15.9	197
104	Omicseq: a web-based search engine for exploring omics datasets. <i>Nucleic Acids Research</i> , 2017 , 45, W445-W450	5.0	145
103	Improving Hierarchical Models Using Historical Data with Applications in High-Throughput Genomics Data Analysis. <i>Statistics in Biosciences</i> , 2017 , 9, 73-90	1.5	1
102	An approach of identifying differential nucleosome regions in multiple samples. <i>BMC Genomics</i> , 2017 , 18, 135	4.5	6
101	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , 2017 , 8, 15903	17.4	65
100	Genome-Wide STAT3 Binding Analysis after Histone Deacetylase Inhibition Reveals Novel Target Genes in Dendritic Cells. <i>Journal of Innate Immunity</i> , 2017 , 9, 126-144	6.9	8
99	Special collection of bioinformatics in the era of precision medicine. <i>Quantitative Biology</i> , 2017 , 5, 277-279	3.9	3
98	High Performance Merging of Massive Data from Genome-Wide Association Studies. <i>Lecture Notes in Computer Science</i> , 2017 , 36-40	0.9	
97	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. <i>Nucleic Acids Research</i> , 2016 , 44, 8610-8620	20.1	119
96	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016 , 7, 12522	17.4	90
95	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. <i>Nature Communications</i> , 2016 , 7, 12521	17.4	45
94	MLL1 and MLL1 fusion proteins have distinct functions in regulating leukemic transcription program. <i>Cell Discovery</i> , 2016 , 2, 16008	22.3	24
93	DIVAN: accurate identification of non-coding disease-specific risk variants using multi-omics profiles. <i>Genome Biology</i> , 2016 , 17, 252	18.3	38
92	Gene integrated set profile analysis: a context-based approach for inferring biological endpoints. <i>Nucleic Acids Research</i> , 2016 , 44, e69	20.1	9
91	Statistical challenges in analyzing methylation and long-range chromosomal interaction data. <i>Statistics in Biosciences</i> , 2016 , 8, 284-309	1.5	7
90	traseR: an R package for performing trait-associated SNP enrichment analysis in genomic intervals. <i>Bioinformatics</i> , 2016 , 32, 1214-6	7.2	11
89	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. <i>Bioinformatics</i> , 2016 , 32, 650-6	7.2	32

88	Bayesian inference with historical data-based informative priors improves detection of differentially expressed genes. <i>Bioinformatics</i> , 2016 , 32, 682-9	7.2	7
87	The single-species metagenome: subtyping core genome sequences from shotgun metagenomic data. <i>PeerJ</i> , 2016 , 4, e2571	3.1	6
86	Heat Shock Protein Beta-1 Modifies Anterior to Posterior Purkinje Cell Vulnerability in a Mouse Model of Niemann-Pick Type C Disease. <i>PLoS Genetics</i> , 2016 , 12, e1006042	6	15
85	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , 2015 , 31, 1889-96	7.2	32
84	Widespread rearrangement of 3D chromatin organization underlies polycomb-mediated stress-induced silencing. <i>Molecular Cell</i> , 2015 , 58, 216-31	17.6	219
83	Cell-Cycle Control of Bivalent Epigenetic Domains Regulates the Exit from Pluripotency. <i>Stem Cell Reports</i> , 2015 , 5, 323-36	8	62
82	Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. <i>Nucleic Acids Research</i> , 2015 , 43, e141	20.1	144
81	Combined Loss of Tet1 and Tet2 Promotes B Cell, but Not Myeloid Malignancies, in Mice. <i>Cell Reports</i> , 2015 , 13, 1692-704	10.6	65
80	PDEGEM: Modeling non-uniform read distribution in RNA-Seq data. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 2, S14	3.7	0
79	One Size Doesn't Fit All - RefEditor: Building Personalized Diploid Reference Genome to Improve Read Mapping and Genotype Calling in Next Generation Sequencing Studies. <i>PLoS Computational Biology</i> , 2015 , 11, e1004448	5	6
78	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. <i>Nucleic Acids Research</i> , 2015 , 43, 2757-66	20.1	33
77	Genome-Wide Binding Studies of Acetyl-STAT3 Demonstrates a Novel Regulatory Pathway in Dendritic Cells. <i>Blood</i> , 2015 , 126, 647-647	2.2	
76	The central role of EED in the orchestration of polycomb group complexes. <i>Nature Communications</i> , 2014 , 5, 3127	17.4	91
75	Reciprocal occupancy of BCL6 and STAT5 on Growth Hormone target genes: contrasting transcriptional outcomes and promoter-specific roles of p300 and HDAC3. <i>Molecular and Cellular Endocrinology</i> , 2014 , 395, 19-31	4.4	11
74	Therapeutic targeting of BET bromodomain proteins in castration-resistant prostate cancer. <i>Nature</i> , 2014 , 510, 278-82	50.4	650
73	Targeting MLL1 H3K4 methyltransferase activity in mixed-lineage leukemia. <i>Molecular Cell</i> , 2014 , 53, 247-61	17.6	203
72	EgoNet: identification of human disease ego-network modules. <i>BMC Genomics</i> , 2014 , 15, 314	4.5	19
71	Integrated analysis of whole-genome paired-end and mate-pair sequencing data for identifying genomic structural variations in multiple myeloma. <i>Cancer Informatics</i> , 2014 , 13, 49-53	2.4	16

70	Insulator function and topological domain border strength scale with architectural protein occupancy. <i>Genome Biology</i> , 2014 , 15, R82	18.3	195
69	H2B ubiquitylation promotes RNA Pol II processivity via PAF1 and pTEFb. <i>Molecular Cell</i> , 2014 , 54, 920-931	17.6	63
68	Direct amplification, sequencing and profiling of Chlamydia trachomatis strains in single and mixed infection clinical samples. <i>PLoS ONE</i> , 2014 , 9, e99290	3.7	20
67	PM-Seq: Using Finite Poisson Mixture Models for RNA-Seq Data Analysis and Transcript Expression Level Quantification. <i>Statistics in Biosciences</i> , 2013 , 5, 71-87	1.5	2
66	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013 , 1, 156-174	3.9	22
65	A genome-wide MeSH-based literature mining system predicts implicit gene-to-gene relationships and networks. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 3, S9	3.5	27
64	Characterization of the EZH2-MMSET histone methyltransferase regulatory axis in cancer. <i>Molecular Cell</i> , 2013 , 49, 80-93	17.6	110
63	Sparsely correlated hidden Markov models with application to genome-wide location studies. <i>Bioinformatics</i> , 2013 , 29, 533-41	7.2	14
62	Exploring the cooccurrence patterns of multiple sets of genomic intervals. <i>BioMed Research International</i> , 2013 , 2013, 617545	3	1
61	Impaired replication elongation in Tetrahymena mutants deficient in histone H3 Lys 27 monomethylation. <i>Genes and Development</i> , 2013 , 27, 1662-79	12.6	51
60	Allogeneic T cell responses are regulated by a specific miRNA-mRNA network. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4739-54	15.9	28
59	Bayesian inference of spatial organizations of chromosomes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002893	14.0	140
58	MotifOrganizer: a scalable model-based motif clustering tool for mammalian genomes. <i>Frontiers in Bioscience - Elite</i> , 2013 , 5, 785-97	1.6	1
57	The histone acetyltransferase MOF is a key regulator of the embryonic stem cell core transcriptional network. <i>Cell Stem Cell</i> , 2012 , 11, 163-78	18	143
56	HiCNorm: removing biases in Hi-C data via Poisson regression. <i>Bioinformatics</i> , 2012 , 28, 3131-3	7.2	176
55	Gene density, transcription, and insulators contribute to the partition of the Drosophila genome into physical domains. <i>Molecular Cell</i> , 2012 , 48, 471-84	17.6	374
54	GPUmotif: an ultra-fast and energy-efficient motif analysis program using graphics processing units. <i>PLoS ONE</i> , 2012 , 7, e36865	3.7	6
53	Cooperation between Polycomb and androgen receptor during oncogenic transformation. <i>Genome Research</i> , 2012 , 22, 322-31	9.7	97

52	Read-mapping using personalized diploid reference genome for RNA sequencing data reduced bias for detecting allele-specific expression 2012 , 2012, 718-724		11
51	Using Poisson mixed-effects model to quantify transcript-level gene expression in RNA-Seq. <i>Bioinformatics</i> , 2012 , 28, 63-8	7.2	25
50	FOXP3 orchestrates H4K16 acetylation and H3K4 trimethylation for activation of multiple genes by recruiting MOF and causing displacement of PLU-1. <i>Molecular Cell</i> , 2011 , 44, 770-84	17.6	55
49	SAINT: probabilistic scoring of affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2011 , 8, 70-3	21.6	480
48	Coordinated regulation of polycomb group complexes through microRNAs in cancer. <i>Cancer Cell</i> , 2011 , 20, 187-99	24.3	176
47	C/EBP β mediates growth hormone-regulated expression of multiple target genes. <i>Molecular Endocrinology</i> , 2011 , 25, 681-93		24
46	Deep sequencing reveals distinct patterns of DNA methylation in prostate cancer. <i>Genome Research</i> , 2011 , 21, 1028-41	9.7	144
45	On the detection and refinement of transcription factor binding sites using CHIP-Seq data. <i>Nucleic Acids Research</i> , 2010 , 38, 2154-67	20.1	82
44	A double-layered mixture model for the joint analysis of DNA copy number and gene expression data. <i>Journal of Computational Biology</i> , 2010 , 17, 121-37	1.7	15
43	Statistical Issues in the Analysis of CHIP-Seq and RNA-Seq Data. <i>Genes</i> , 2010 , 1, 317-34	4.2	11
42	A global protein kinase and phosphatase interaction network in yeast. <i>Science</i> , 2010 , 328, 1043-6	33.3	523
41	HPeak: an HMM-based algorithm for defining read-enriched regions in CHIP-Seq data. <i>BMC Bioinformatics</i> , 2010 , 11, 369	3.6	87
40	An integrated network of androgen receptor, polycomb, and TMPRSS2-ERG gene fusions in prostate cancer progression. <i>Cancer Cell</i> , 2010 , 17, 443-54	24.3	640
39	Computational and functional analysis of growth hormone (GH)-regulated genes identifies the transcriptional repressor B-cell lymphoma 6 (Bcl6) as a participant in GH-regulated transcription. <i>Endocrinology</i> , 2009 , 150, 3645-54	4.8	26
38	Drug-drug interaction prediction assessment. <i>Journal of Biopharmaceutical Statistics</i> , 2009 , 19, 641-57	1.3	2
37	Hierarchical hidden Markov model with application to joint analysis of CHIP-chip and CHIP-seq data. <i>Bioinformatics</i> , 2009 , 25, 1715-21	7.2	29
36	A new probabilistic rule for drug-dug interaction prediction. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2009 , 36, 1-18	2.7	3
35	Global gene expression analysis reveals evidence for decreased lipid biosynthesis and increased innate immunity in uninvolved psoriatic skin. <i>Journal of Investigative Dermatology</i> , 2009 , 129, 2795-804	4.3	123

34	Progress toward personalized medicine for glaucoma. <i>Expert Review of Ophthalmology</i> , 2009 , 4, 145-161	1.5	9
33	Query large scale microarray compendium datasets using a model-based bayesian approach with variable selection. <i>PLoS ONE</i> , 2009 , 4, e4495	3.7	3
32	Comparison of laboratory-based and phylogenetic methods to distinguish between <i>Haemophilus influenzae</i> and <i>H. haemolyticus</i> . <i>Journal of Microbiological Methods</i> , 2008 , 75, 369-71	2.8	37
31	Family-based SNP association study on 8q24 in bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 612-8	3.5	19
30	Different normalization strategies for microarray gene expression traits affect the heritability estimation. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S154	2.3	5
29	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
28	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
27	p53-mediated activation of miRNA34 candidate tumor-suppressor genes. <i>Current Biology</i> , 2007 , 17, 1298-307	3.07	951
26	Operon prediction for sequenced bacterial genomes without experimental information. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 846-54	4.8	32
25	CRCView: a web server for analyzing and visualizing microarray gene expression data using model-based clustering. <i>Bioinformatics</i> , 2007 , 23, 1843-5	7.2	10
24	Energy, quiescence and the cellular basis of animal life spans. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2006 , 143, 12-23	2.6	32
23	Clustering microarray gene expression data using weighted Chinese restaurant process. <i>Bioinformatics</i> , 2006 , 22, 1988-97	7.2	97
22	An efficient comprehensive search algorithm for tagSNP selection using linkage disequilibrium criteria. <i>Bioinformatics</i> , 2006 , 22, 220-5	7.2	61
21	Improved classification of mass spectrometry database search results using newer machine learning approaches. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 497-509	7.6	48
20	A comparison of phasing algorithms for trios and unrelated individuals. <i>American Journal of Human Genetics</i> , 2006 , 78, 437-50	11	267
19	TAGSNP SELECTION BASED ON PAIRWISE LD CRITERIA AND POWER ANALYSIS IN ASSOCIATION STUDIES 2005 ,		2
18	A haplotype map of the human genome. <i>Nature</i> , 2005 , 437, 1299-320	50.4	4818
17	Fine mapping of the psoriasis susceptibility gene PSORS1: a reassessment of risk associated with a putative risk haplotype lacking HLA-Cw6. <i>Journal of Investigative Dermatology</i> , 2005 , 124, 921-30	4.3	17

16	Protein tyrosine phosphatase gene PTPN22 polymorphism in psoriasis: lack of evidence for association. <i>Journal of Investigative Dermatology</i> , 2005 , 125, 395-6	4.3	18
15	Structural comparison of metabolic networks in selected single cell organisms. <i>BMC Bioinformatics</i> , 2005 , 6, 8	3.6	62
14	HapBlock: haplotype block partitioning and tag SNP selection software using a set of dynamic programming algorithms. <i>Bioinformatics</i> , 2005 , 21, 131-4	7.2	95
13	High throughput screening of co-expressed gene pairs with controlled false discovery rate (FDR) and minimum acceptable strength (MAS). <i>Journal of Computational Biology</i> , 2005 , 12, 1029-45	1.7	38
12	Statistical resynchronization and Bayesian detection of periodically expressed genes. <i>Nucleic Acids Research</i> , 2004 , 32, 447-55	20.1	44
11	Haplotype block partitioning and tag SNP selection using genotype data and their applications to association studies. <i>Genome Research</i> , 2004 , 14, 908-16	9.7	119
10	Incorporating genotyping uncertainty in haplotype inference for single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , 2004 , 74, 495-510	11	34
9	Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data. <i>Lecture Notes in Computer Science</i> , 2004 , 96-112	0.9	
8	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. <i>Lecture Notes in Computer Science</i> , 2004 , 48-61	0.9	2
7	Scale Mixture Models with Applications to Bayesian Inference. <i>AIP Conference Proceedings</i> , 2003 ,	0	2
6	Identification of co-regulated genes through Bayesian clustering of predicted regulatory binding sites. <i>Nature Biotechnology</i> , 2003 , 21, 435-9	44.5	83
5	Bayesian haplotype inference for multiple linked single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , 2002 , 70, 157-69	11	531
4	Partition-ligation-expectation-maximization algorithm for haplotype inference with single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , 2002 , 71, 1242-7	11	425
3	Multipoint Metropolis Method with Application to Hybrid Monte Carlo. <i>Journal of Computational Physics</i> , 2001 , 172, 827-840	4.1	18
2	Model-Based Methods for Transcript Expression-Level Quantification in RNA-Seq	105-125	
1	The single-species metagenome: subtyping <i>Staphylococcus aureus</i> core genome sequences from shotgun metagenomic data		1