

Ren Zhang

List of Publications by Year in descending order

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63
papers

5,234
citations

147801

31
h-index

123424

61
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all docs

63
docs citations

63
times ranked

5831
citing authors

#	ARTICLE	IF	CITATIONS
1	An updated ANGPTL3-4-8 model as a mechanism of triglyceride partitioning between fat and oxidative tissues. <i>Progress in Lipid Research</i> , 2022, 85, 101140.	11.6	41
2	DEG 15, an update of the Database of Essential Genes that includes built-in analysis tools. <i>Nucleic Acids Research</i> , 2021, 49, D677-D686.	14.5	119
3	Regulation of hepatic circadian metabolism by the E3 ubiquitin ligase HRD1-controlled CREBH/PPAR α transcriptional program. <i>Molecular Metabolism</i> , 2021, 49, 101192.	6.5	14
4	The Potential of ANGPTL8 Antagonism to Simultaneously Reduce Triglyceride and Increase HDL-Cholesterol Plasma Levels. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 795370.	2.4	7
5	Regulation of hepatic autophagy by stress-sensing transcription factor CREBH. <i>FASEB Journal</i> , 2019, 33, 7896-7914.	0.5	18
6	Deficiency of the Mitochondrial NAD Kinase Causes Stress-Induced Hepatic Steatosis in Mice. <i>Gastroenterology</i> , 2018, 154, 224-237.	1.3	35
7	ANGPTL8 promotes the ability of ANGPTL3 to bind and inhibit lipoprotein lipase. <i>Molecular Metabolism</i> , 2017, 6, 1137-1149.	6.5	142
8	A lipasin/Angptl8 monoclonal antibody lowers mouse serum triglycerides involving increased postprandial activity of the cardiac lipoprotein lipase. <i>Scientific Reports</i> , 2016, 5, 18502.	3.3	72
9	The ANGPTL3-4-8 model, a molecular mechanism for triglyceride trafficking. <i>Open Biology</i> , 2016, 6, 150272.	3.6	179
10	Differential response in levels of high-density lipoprotein cholesterol to one-year metformin treatment in prediabetic patients by race/ethnicity. <i>Cardiovascular Diabetology</i> , 2015, 14, 79.	6.8	22
11	mypub.org, a customizable URL shortener for the NCBI My Bibliography. <i>BioEssays</i> , 2015, 37, 835-835.	2.5	0
12	MNADK, a Long-Awaited Human Mitochondrion-Localized NAD Kinase. <i>Journal of Cellular Physiology</i> , 2015, 230, 1697-1701.	4.1	37
13	Gene Essentiality Analysis Based on DEG 10, an Updated Database of Essential Genes. <i>Methods in Molecular Biology</i> , 2015, 1279, 219-233.	0.9	40
14	A Brief Review: The Z-curve Theory and its Application in Genome Analysis. <i>Current Genomics</i> , 2014, 15, 78-94.	1.6	34
15	A dual role of lipasin (betatrophin) in lipid metabolism and glucose homeostasis: consensus and controversy. <i>Cardiovascular Diabetology</i> , 2014, 13, 133.	6.8	90
16	Liver-Enriched Transcription Factor CREBH Interacts With Peroxisome Proliferator-Activated Receptor α to Regulate Metabolic Hormone FGF21. <i>Endocrinology</i> , 2014, 155, 769-782.	2.8	105
17	DEG 10, an update of the database of essential genes that includes both protein-coding genes and noncoding genomic elements: Table 1.. <i>Nucleic Acids Research</i> , 2014, 42, D574-D580.	14.5	504
18	An explanation for recent discrepancies in levels of human circulating betatrophin. <i>Diabetologia</i> , 2014, 57, 2232-2234.	6.3	95

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19	Elevated circulating lipasin/betatrophin in human type 2 diabetes and obesity. <i>Scientific Reports</i> , 2014, 4, 5013.	3.3	204
20	Identification of Horizontally-transferred Genomic Islands and Genome Segmentation Points by Using the GC Profile Method. <i>Current Genomics</i> , 2014, 15, 113-121.	1.6	26
21	Lipasin, thermoregulated in brown fat, is a novel but atypical member of the angiotensin-like protein family. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 1126-1131.	2.1	118
22	Emerging roles of Lipasin as a critical lipid regulator. <i>Biochemical and Biophysical Research Communications</i> , 2013, 432, 401-405.	2.1	118
23	MNADK, a novel liver-enriched mitochondrion-localized NAD kinase. <i>Biology Open</i> , 2013, 2, 432-438.	1.2	34
24	Hkat, a novel nutritionally regulated transmembrane protein in adipose tissues. <i>Scientific Reports</i> , 2012, 2, 825.	3.3	2
25	Lipasin, a novel nutritionally-regulated liver-enriched factor that regulates serum triglyceride levels. <i>Biochemical and Biophysical Research Communications</i> , 2012, 424, 786-792.	2.1	311
26	Nrac, a Novel Nutritionally-Regulated Adipose and Cardiac-Enriched Gene. <i>PLoS ONE</i> , 2012, 7, e46254.	2.5	6
27	A rebuttal to the comments on the genome order index and the Z-curve. <i>Biology Direct</i> , 2011, 6, 10.	4.6	2
28	DEG 5.0, a database of essential genes in both prokaryotes and eukaryotes. <i>Nucleic Acids Research</i> , 2009, 37, D455-D458.	14.5	449
29	Accurate Localization of the Integration Sites of Two Genomic Islands at Single-Nucleotide Resolution in the Genome of <i>Bacillus cereus</i> ATCC 10987. <i>Comparative and Functional Genomics</i> , 2008, 2008, 1-6.	2.0	7
30	The impact of comparative genomics on infectious disease research. <i>Microbes and Infection</i> , 2006, 8, 1613-1622.	1.9	23
31	Interactions between PIAS Proteins and SOX9 Result in an Increase in the Cellular Concentrations of SOX9. <i>Journal of Biological Chemistry</i> , 2006, 281, 14417-14428.	3.4	65
32	Constitutive activation of MKK6 in chondrocytes of transgenic mice inhibits proliferation and delays endochondral bone formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 365-370.	7.1	96
33	Identification of replication origins in archaeal genomes based on the Z-curve method. <i>Archaea</i> , 2005, 1, 335-346.	2.3	85
34	Segmentation algorithm for DNA sequences. <i>Physical Review E</i> , 2005, 72, 041917.	2.1	33
35	Genomic Islands in the <i>Corynebacterium efficiens</i> Genome. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3126-3130.	3.1	22
36	A systematic method to identify genomic islands and its applications in analyzing the genomes of <i>Corynebacterium glutamicum</i> and <i>Vibrio vulnificus</i> CMCP6 chromosome I. <i>Bioinformatics</i> , 2004, 20, 612-622.	4.1	81

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37	Interactions between Sox9 and β -catenin control chondrocyte differentiation. <i>Genes and Development</i> , 2004, 18, 1072-1087.	5.9	670
38	DEG: a database of essential genes. <i>Nucleic Acids Research</i> , 2004, 32, 271D-272.	14.5	416
39	Genomic islands in <i>Rhodospseudomonas palustris</i> . <i>Nature Biotechnology</i> , 2004, 22, 1078-1079.	17.5	15
40	Identification of replication origins in the genome of the methanogenic archaeon, <i>Methanocaldococcus jannaschii</i> . <i>Extremophiles</i> , 2004, 8, 253-258.	2.3	22
41	Isochore Structures in the Genome of the Plant <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2004, 59, 227-238.	1.8	24
42	A nucleotide composition constraint of genome sequences. <i>Computational Biology and Chemistry</i> , 2004, 28, 149-153.	2.3	17
43	Isochore structures in the mouse genome. <i>Genomics</i> , 2004, 83, 384-394.	2.9	20
44	Multiple replication origins of the archaeon <i>Halobacterium</i> species NRC-1. <i>Biochemical and Biophysical Research Communications</i> , 2003, 302, 728-734.	2.1	77
45	ZCURVE_CoV: a new system to recognize protein coding genes in coronavirus genomes, and its applications in analyzing SARS-CoV genomes. <i>Biochemical and Biophysical Research Communications</i> , 2003, 307, 382-388.	2.1	34
46	An isochore map of the human genome based on the Z curve method. <i>Gene</i> , 2003, 317, 127-135.	2.2	34
47	Q9, a content-balancing accuracy index to evaluate algorithms of protein secondary structure prediction. <i>International Journal of Biochemistry and Cell Biology</i> , 2003, 35, 1256-1262.	2.8	8
48	Identification of genomic islands in the genome of <i>Bacillus cereus</i> by comparative analysis with <i>Bacillus anthracis</i> . <i>Physiological Genomics</i> , 2003, 16, 19-23.	2.3	27
49	The Z curve database: a graphic representation of genome sequences. <i>Bioinformatics</i> , 2003, 19, 593-599.	4.1	123
50	Evaluation of Gene-Finding Algorithms by a Content- Balancing Accuracy Index. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002, 19, 1045-1052.	3.5	19
51	Single replication origin of the archaeon <i>Methanosarcina mazei</i> revealed by the Z curve method. <i>Biochemical and Biophysical Research Communications</i> , 2002, 297, 396-400.	2.1	31
52	Using a Euclid distance discriminant method to find protein coding genes in the yeast genome. <i>Computers & Chemistry</i> , 2002, 26, 195-206.	1.2	14
53	A Novel Method to Calculate the G+C Content of Genomic DNA Sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 19, 333-341.	3.5	47
54	A refined accuracy index to evaluate algorithms of protein secondary structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 520-522.	2.6	10

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55	A Graphic Approach to Evaluate Algorithms of Secondary Structure Prediction. Journal of Biomolecular Structure and Dynamics, 2000, 17, 829-842.	3.5	7
56	Skewed distribution of protein secondary structure contents over the conformational triangle. Protein Engineering, Design and Selection, 1999, 12, 807-810.	2.1	7
57	A Quadratic Discriminant Analysis of Protein Structure Classification Based on the Helix/Strand Content. Journal of Theoretical Biology, 1999, 201, 189-199.	1.7	2
58	A new quantitative criterion to distinguish between $\hat{\alpha}/\hat{\beta}^2$ and $\hat{\alpha}+\hat{\beta}^2$ proteins (domains). FEBS Letters, 1998, 440, 153-157.	2.8	4
59	Distribution of mapping points of 20 amino acids in the tetrahedral space. Amino Acids, 1997, 12, 167-177.	2.7	2
60	Z Curves, An Intutive Tool for Visualizing and Analyzing the DNA Sequences. Journal of Biomolecular Structure and Dynamics, 1994, 11, 767-782.	3.5	235
61	Diagrammatic representation of the distribution of DNA bases and its applications. International Journal of Biological Macromolecules, 1991, 13, 45-49.	7.5	7
62	Analysis of distribution of bases in the coding sequences by a digrammatic technique. Nucleic Acids Research, 1991, 19, 6313-6317.	14.5	125
63	Extraction of koumine from Gelsemium Elegans Benth. and its therapeutic effect on collagen-induced arthritis in mice. Food Science and Technology, 0, , .	1.7	1