

Chao Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,611
citations

471509

17
h-index

315739

38
g-index

51
all docs

51
docs citations

51
times ranked

3328
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting skeletal endothelium to ameliorate bone loss. <i>Nature Medicine</i> , 2018, 24, 823-833.	30.7	218
2	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	9.6	214
3	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018, 5, 180061.	5.3	152
4	The p53 Family Coordinates Wnt and Nodal Inputs in Mesendodermal Differentiation of Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 70-86.	11.1	121
5	miR-17-92 Cluster Regulates Adult Hippocampal Neurogenesis, Anxiety, and Depression. <i>Cell Reports</i> , 2016, 16, 1653-1663.	6.4	102
6	Lipid Deprivation Induces a Stable, Naive-to-Primed Intermediate State of Pluripotency in Human PSCs. <i>Cell Stem Cell</i> , 2019, 25, 120-136.e10.	11.1	98
7	Identification of low abundance microbiome in clinical samples using whole genome sequencing. <i>Genome Biology</i> , 2015, 16, 265.	8.8	90
8	Growth of the Developing Cerebral Cortex Is Controlled by MicroRNA-7 through the p53 Pathway. <i>Cell Reports</i> , 2014, 7, 1184-1196.	6.4	85
9	Dynamic evolution of clonal epialleles revealed by methylome. <i>Genome Biology</i> , 2014, 15, 472.	8.8	67
10	Role of plant MicroRNA in cross-species regulatory networks of humans. <i>BMC Systems Biology</i> , 2016, 10, 60.	3.0	53
11	c-Jun N-Terminal Kinases (JNKs) Are Critical Mediators of Osteoblast Activity In Vivo. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1811-1815.	2.8	37
12	The Gastric Microbiome and Its Influence on Gastric Carcinogenesis. <i>Hematology/Oncology Clinics of North America</i> , 2017, 31, 389-408.	2.2	27
13	Effector prediction in host-pathogen interaction based on a Markov model of a ubiquitous EPIYA motif. <i>BMC Genomics</i> , 2010, 11, S1.	2.8	26
14	Mosaic: making biological sense of complex networks. <i>Bioinformatics</i> , 2012, 28, 1943-1944.	4.1	26
15	Encoding of Contextual Fear Memory Requires De Novo Proteins in the Prelimbic Cortex. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2017, 2, 158-169.	1.5	25
16	NOA: a cytoscape plugin for network ontology analysis. <i>Bioinformatics</i> , 2013, 29, 2066-2067.	4.1	24
17	Osteoclasts are not a source of SLIT3. <i>Bone Research</i> , 2020, 8, 11.	11.4	23
18	CryoPause: A New Method to Immediately Initiate Experiments after Cryopreservation of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 355-365.	4.8	21

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19	IRTKS is correlated with progression and survival time of patients with gastric cancer. <i>Gut</i> , 2018, 67, 1400-1409.	12.1	20
20	Polytomy identification in microbial phylogenetic reconstruction. <i>BMC Systems Biology</i> , 2011, 5, S2.	3.0	15
21	INFLUENCE OF mRNA FEATURES ON siRNA INTERFERENCE EFFICACY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1341004.	0.8	15
22	Genome-wide comparison of allele-specific gene expression between African and European populations. <i>Human Molecular Genetics</i> , 2018, 27, 1067-1077.	2.9	15
23	Using an intervening sequence of <i>Faecalibacterium</i> 16S rDNA to identify poultry feces. <i>Water Research</i> , 2013, 47, 6415-6422.	11.3	14
24	Risk Assessment of Gastric Cancer Caused by <i>Helicobacter pylori</i> Using CagA Sequence Markers. <i>PLoS ONE</i> , 2012, 7, e36844.	2.5	14
25	Transmembrane Protein Alignment and Fold Recognition Based on Predicted Topology. <i>PLoS ONE</i> , 2013, 8, e69744.	2.5	13
26	Increased genetic diversity of ADME genes in African Americans compared with their putative ancestral source populations and implications for Pharmacogenomics. <i>BMC Genetics</i> , 2014, 15, 52.	2.7	13
27	BridgeDb app: unifying identifier mapping services for Cytoscape. <i>F1000Research</i> , 2014, 3, 148.	1.6	11
28	MUFOLD-DB: a processed protein structure database for protein structure prediction and analysis. <i>BMC Genomics</i> , 2014, 15, S2.	2.8	10
29	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. <i>Journal of Computer Science and Technology</i> , 2012, 27, 225-239.	1.5	9
30	A Comparison of Homogenization vs. Enzymatic Lysis for Microbiome Profiling in Clinical Endoscopic Biopsy Tissue Samples. <i>Frontiers in Microbiology</i> , 2019, 9, 3246.	3.5	9
31	Improving transmembrane protein consensus topology prediction using inter-helical interaction. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 2679-2686.	2.6	7
32	Multicenter Phase II Study of Cabazitaxel in Advanced Gastroesophageal Cancer: Association of HER2 Expression and M2-Like Tumor-Associated Macrophages with Patient Outcome. <i>Clinical Cancer Research</i> , 2020, 26, 4756-4766.	7.0	7
33	epihet for intra-tumoral epigenetic heterogeneity analysis and visualization. <i>Scientific Reports</i> , 2021, 11, 376.	3.3	6
34	An association analysis between psychophysical characteristics and genome-wide gene expression changes in human adaptation to the extreme climate at the Antarctic Dome Argus. <i>Molecular Psychiatry</i> , 2015, 20, 536-544.	7.9	5
35	An integrated probabilistic approach for gene function prediction using multiple sources of high-throughput data. <i>International Journal of Computational Biology and Drug Design</i> , 2008, 1, 254.	0.3	4
36	Clinical data analysis reveals three subtypes of gastric cancer. , 2012, , .		3

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37	Characterization of the weak calcium binding of trimeric globular adiponectin. <i>Cell Biochemistry and Function</i> , 2013, 31, 338-343.	2.9	3
38	Design and Implementation of Probability-Based Scoring Function for Peptide Mass Fingerprinting Protein Identification. , 2006, 2006, 4556-9.		2
39	RNA-protein distance patterns in ribosomes reveal the mechanism of translational attenuation. <i>Science China Life Sciences</i> , 2014, 57, 1131-1139.	4.9	2
40	Abstract 4938: Molecular mechanisms of intrinsic resistance to taxanes in gastric cancer. , 2016, , .		2
41	Detection and application of CagA sequence markers for assessing risk factor of gastric cancer caused by <i>Helicobacter pylori</i> . , 2010, , .		1
42	Network stratification analysis for identifying function-specific network layers. <i>Molecular BioSystems</i> , 2016, 12, 1232-1240.	2.9	1
43	GeneFAS: GeneFAS: A Tool for the Prediction of Gene function Using Multiple Sources of Data. <i>Methods in Molecular Biology</i> , 2008, 439, 369-386.	0.9	1
44	Bioinformatics Applications in Clinical Microbiology. <i>Translational Medicine Research</i> , 2017, , 353-367.	0.0	0
45	Big Health Data Mining. <i>Health Information Science</i> , 2017, , 169-184.	0.4	0
46	Whole-genome sequencing (WGS) to identify <i>H. pylori</i> and its impact on the gastric microbiome.. <i>Journal of Clinical Oncology</i> , 2014, 32, 11070-11070.	1.6	0
47	Abstract 897: Elucidating the molecular basis of intrinsic taxane resistance in gastric cancer. , 2014, , .		0
48	Identification of the gastric microbiome from endoscopic biopsy samples using whole genome sequencing.. <i>Journal of Clinical Oncology</i> , 2015, 33, 8-8.	1.6	0
49	Abstract 3600: Impaired taxane binding to MTs in intrinsically taxane resistant gastric cancer cells without β -tubulin mutation. , 2015, , .		0
50	Abstract 2932: Impaired taxane binding to MT pore sites mediates intrinsic drug resistance in diffuse gastric cancer. , 2016, , .		0
51	Abstract 3295: Microbiome profiling and immunological characterization on gastrointestinal tract tumors. , 2016, , .		0