

Kang Ning

List of Publications by Citations

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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.

121
papers

2,907
citations

28
h-index

51
g-index

142
ext. papers

4,062
ext. citations

6.3
avg, IF

5.56
L-index

#	Paper	IF	Citations
121	Network Pharmacology Databases for Traditional Chinese Medicine: Review and Assessment. <i>Frontiers in Pharmacology</i> , 2019 , 10, 123	5.6	306
120	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012 , 6, 1-10	11.9	245
119	Choreography of Transcriptomes and Lipidomes of <i>Nannochloropsis</i> Reveals the Mechanisms of Oil Synthesis in Microalgae. <i>Plant Cell</i> , 2014 , 26, 1645-1665	11.6	243
118	<i>Nannochloropsis</i> genomes reveal evolution of microalgal oleaginous traits. <i>PLoS Genetics</i> , 2014 , 10, e1004094	10.4	173
117	Comparative analysis of different label-free mass spectrometry based protein abundance estimates and their correlation with RNA-Seq gene expression data. <i>Journal of Proteome Research</i> , 2012 , 11, 2261-71	5.6	108
116	TCM-Mesh: The database and analytical system for network pharmacology analysis for TCM preparations. <i>Scientific Reports</i> , 2017 , 7, 2821	4.9	106
115	Using indirect protein-protein interactions for protein complex prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 435-66	1	103
114	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp. <i>Plant Physiology</i> , 2015 , 169, 2444-61	6.6	89
113	Biological ingredient analysis of traditional Chinese medicine preparation based on high-throughput sequencing: the story for Liuwei Dihuang Wan. <i>Scientific Reports</i> , 2014 , 4, 5147	4.9	76
112	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. <i>Scientific Reports</i> , 2017 , 7, 40371	4.9	64
111	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae <i>Nannochloropsis</i> . <i>Scientific Reports</i> , 2014 , 4, 5454	4.9	61
110	Distribution of antibiotic resistance genes in an agriculturally disturbed lake in China: Their links with microbial communities, antibiotics, and water quality. <i>Journal of Hazardous Materials</i> , 2020 , 393, 122426	12.8	57
109	Parallel-META 2.0: enhanced metagenomic data analysis with functional annotation, high performance computing and advanced visualization. <i>PLoS ONE</i> , 2014 , 9, e89323	3.7	54
108	Examination of the relationship between essential genes in PPI network and hub proteins in reverse nearest neighbor topology. <i>BMC Bioinformatics</i> , 2010 , 11, 505	3.6	51
107	Computational analysis of unassigned high-quality MS/MS spectra in proteomic data sets. <i>Proteomics</i> , 2010 , 10, 2712-8	4.8	51
106	QC-Chain: fast and holistic quality control method for next-generation sequencing data. <i>PLoS ONE</i> , 2013 , 8, e60234	3.7	49
105	The utility of mass spectrometry-based proteomic data for validation of novel alternative splice forms reconstructed from RNA-Seq data: a preliminary assessment. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 11, S14	3.6	49

104	Nannochloropsis plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. <i>BMC Genomics</i> , 2013 , 14, 534	4.5	45
103	MCL-CAW: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. <i>BMC Bioinformatics</i> , 2010 , 11, 504	3.6	44
102	GMrepo: a database of curated and consistently annotated human gut metagenomes. <i>Nucleic Acids Research</i> , 2020 , 48, D545-D553	20.1	41
101	Stereotypes About Enterotype: the Old and New Ideas. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 4-12	6.5	40
100	Distinct roles for carbohydrate-binding modules of glycoside hydrolase 10 (GH10) and GH11 xylanases from <i>Caldicellulosiruptor</i> sp. strain F32 in thermostability and catalytic efficiency. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2006-14	4.8	40
99	Meta-Storms: efficient search for similar microbial communities based on a novel indexing scheme and similarity score for metagenomic data. <i>Bioinformatics</i> , 2012 , 28, 2493-501	7.2	34
98	Assessment of quality control approaches for metagenomic data analysis. <i>Scientific Reports</i> , 2014 , 4, 6957	4.9	31
97	Genomic and transcriptome analyses reveal that MAPK- and phosphatidylinositol-signaling pathways mediate tolerance to 5-hydroxymethyl-2-furaldehyde for industrial yeast <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2014 , 4, 6556	4.9	29
96	Parallel-META: efficient metagenomic data analysis based on high-performance computation. <i>BMC Systems Biology</i> , 2012 , 6 Suppl 1, S16	3.5	29
95	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. <i>Gut</i> , 2019 , 68, 2254-2255	19.2	28
94	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. <i>Bioinformatics</i> , 2016 , 32, 462-4	7.2	25
93	RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. <i>BMC Genomics</i> , 2018 , 19, 144	4.5	24
92	The Human Gut Virome in Hypertension. <i>Frontiers in Microbiology</i> , 2018 , 9, 3150	5.7	24
91	Pan-genome analyses of 24 strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. <i>Biotechnology for Biofuels</i> , 2018 , 11, 193	7.8	22
90	SNP calling using genotype model selection on high-throughput sequencing data. <i>Bioinformatics</i> , 2012 , 28, 643-50	7.2	20
89	A culture-independent approach to unravel uncultured bacteria and functional genes in a complex microbial community. <i>PLoS ONE</i> , 2012 , 7, e47530	3.7	20
88	Stratification of athletes' gut microbiota: the multifaceted hubs associated with dietary factors, physical characteristics and performance. <i>Gut Microbes</i> , 2020 , 12, 1-18	8.8	19
87	Microbiome Big-Data Mining and Applications Using Single-Cell Technologies and Metagenomics Approaches Toward Precision Medicine. <i>Frontiers in Genetics</i> , 2019 , 10, 972	4.5	17

86	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019 , 20, 229	18.3	17
85	Comparison and Interpretation of Taxonomical Structure of Bacterial Communities in Two Types of Lakes on Yun-Gui plateau of China. <i>Scientific Reports</i> , 2016 , 6, 30616	4.9	17
84	DNA extraction protocol for biological ingredient analysis of Liuwei Dihuang Wan. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 137-43	6.5	16
83	Towards a better solution to the shortest common supersequence problem: the deposition and reduction algorithm. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 4, S12	3.6	16
82	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. <i>Bioinformatics</i> , 2014 , 30, 1031-3	7.2	15
81	Meta-QC-Chain: comprehensive and fast quality control method for metagenomic data. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 52-6	6.5	15
80	Traditional Chinese Medicine and Gut Microbiome: Their Respective and Concert Effects on Healthcare. <i>Frontiers in Pharmacology</i> , 2020 , 11, 538	5.6	14
79	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION 2007 ,		14
78	Meta-network: optimized species-species network analysis for microbial communities. <i>BMC Genomics</i> , 2019 , 20, 187	4.5	13
77	MetaSee: an interactive and extendable visualization toolbox for metagenomic sample analysis and comparison. <i>PLoS ONE</i> , 2012 , 7, e48998	3.7	13
76	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 76-90	6.5	12
75	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. <i>PeerJ</i> , 2015 , 3, e993	3.1	12
74	Comprehensive Analysis Reveals the Evolution and Pathogenicity of , Viewed from Both Single Isolated Species and Microbial Communities. <i>MSystems</i> , 2019 , 4,	7.6	12
73	The Tara Oceans Project: New Opportunities and Greater Challenges Ahead. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 275-7	6.5	11
72	Saliva microbiota carry caries-specific functional gene signatures. <i>PLoS ONE</i> , 2014 , 9, e76458	3.7	11
71	Biological ingredient complement chemical ingredient in the assessment of the quality of TCM preparations. <i>Scientific Reports</i> , 2019 , 9, 5853	4.9	10
70	Proteomic study uncovers molecular principles of single-cell-level phenotypic heterogeneity in lipid storage of. <i>Biotechnology for Biofuels</i> , 2019 , 12, 21	7.8	10
69	Single-cell SNP analyses and interpretations based on RNA-Seq data for colon cancer research. <i>Scientific Reports</i> , 2016 , 6, 34420	4.9	10

68	Characterization of saliva microbiota's functional feature based on metagenomic sequencing. <i>SpringerPlus</i> , 2016 , 5, 2098		10
67	On preprocessing and antisymmetry in de novo peptide sequencing: improving efficiency and accuracy. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 467-92	1	8
66	Predicting new indications of compounds with a network pharmacology approach: Liuwei Dihuang Wan as a case study. <i>Oncotarget</i> , 2017 , 8, 93957-93968	3.3	8
65	Classification of the Gut Microbiota of Patients in Intensive Care Units During Development of Sepsis and Septic Shock. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 696-707	6.5	8
64	Refining Markov Clustering for protein complex prediction by incorporating core-attachment structure. <i>Genome Informatics</i> , 2009 , 23, 159-68		8
63	Microbial community pattern detection in human body habitats via ensemble clustering framework. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 4, S7	3.5	7
62	Deposition and extension approach to find longest common subsequence for thousands of long sequences. <i>Computational Biology and Chemistry</i> , 2010 , 34, 149-57	3.6	7
61	A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2005 , 33, e144	20.1	7
60	SAW: a method to identify splicing events from RNA-Seq data based on splicing fingerprints. <i>PLoS ONE</i> , 2010 , 5, e12047	3.7	7
59	Meta-Prism: Ultra-fast and highly accurate microbial community structure search utilizing dual indexing and parallel computation. <i>Briefings in Bioinformatics</i> , 2021 , 22, 557-567	13.4	7
58	Utilizing microbiome approaches to assist source tracking, treatment and prevention of COVID-19: Review and assessment. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 3615-3622	6.8	6
57	Condensing Raman spectrum for single-cell phenotype analysis. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 18, S15	3.6	6
56	Modeling and characterization of multi-charge mass spectra for peptide sequencing. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 1329-52	1	6
55	QSpec: online control and data analysis system for single-cell Raman spectroscopy. <i>PeerJ</i> , 2014 , 2, e436	3.1	6
54	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. <i>BMC Genomics</i> , 2017 , 18, 268	4.5	5
53	Finding Patterns in Biological Sequences by Longest Common Subsequences and Shortest Common Supersequences 2006 ,		5
52	Heterogeneous circRNA expression profiles and regulatory functions among HEK293T single cells. <i>Scientific Reports</i> , 2017 , 7, 14393	4.9	4
51	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. <i>Scientific Reports</i> , 2014 , 4, 6393	4.9	4

50	ALGORITHM FOR PEPTIDE SEQUENCING BY TANDEM MASS SPECTROMETRY BASED ON BETTER PREPROCESSING AND ANTI-SYMMETRIC COMPUTATIONAL MODEL 2007 ,		4
49	Big data for biomedical research: Current status and prospective. <i>Chinese Science Bulletin</i> , 2015 , 60, 534-546		4
48	Data-mining of Antibiotic Resistance Genes Provides Insight into the Community Structure of Ocean Microbiome		4
47	A Living Eukaryotic Autocementation Kit from Surface Display of Silica Binding Peptides on <i>Yarrowia lipolytica</i> . <i>ACS Synthetic Biology</i> , 2016 , 5, 1466-1474	5.7	4
46	Mechanisms of niche-neutrality balancing can drive the assembling of microbial community. <i>Molecular Ecology</i> , 2021 , 30, 1492-1504	5.7	4
45	Integrating pan-genome with metagenome for microbial community profiling. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 1458-1466	6.8	4
44	Using QC-Blind for Quality Control and Contamination Screening of Bacteria DNA Sequencing Data Without Reference Genome. <i>Frontiers in Microbiology</i> , 2019 , 10, 1560	5.7	3
43	The Seasonal Dynamics and the Influence of Human Activities on Campus Outdoor Microbial Communities. <i>Frontiers in Microbiology</i> , 2019 , 10, 1579	5.7	3
42	Analysis of the relationships among Longest Common Subsequences, Shortest Common Supersequences and patterns and its application on pattern discovery in biological sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2011 , 5, 611-25	0.5	3
41	Is rice-crayfish co-culture a better aquaculture model: From the perspective of antibiotic resistome profiles. <i>Environmental Pollution</i> , 2022 , 292, 118450	9.3	3
40	REFINING MARKOV CLUSTERING FOR PROTEIN COMPLEX PREDICTION BY INCORPORATING CORE-ATTACHMENT STRUCTURE 2009 ,		3
39	Association of Gut Microbiota during Early Pregnancy with Risk of Incident Gestational Diabetes Mellitus. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, e4128-e4141	5.6	3
38	Hidden link in gut-joint axis: gut microbes promote rheumatoid arthritis at early stage by enhancing ascorbate degradation. <i>Gut</i> , 2021 ,	19.2	3
37	Application of Meta-Mesh on the analysis of microbial communities from human associated-habitats. <i>Quantitative Biology</i> , 2015 , 3, 4-18	3.9	2
36	Metagenomics and Single-Cell Omics Data Analysis for Human Microbiome Research. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 939, 117-137	3.6	2
35	MultiGeMS: detection of SNVs from multiple samples using model selection on high-throughput sequencing data. <i>Bioinformatics</i> , 2016 , 32, 1486-92	7.2	2
34	A machine learning framework of functional biomarker discovery for different microbial communities based on metagenomic data 2012 ,		2
33	Detecting hubs and quasi cliques in scale-free networks 2008 ,		2

32	Decoding the link of microbiome niches with homologous sequences enables accurately targeted protein structure prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
31	Decoding herbal materials of representative TCM preparations with the multi-barcoding approach		2
30	Ontology-Aware Deep Learning Enables Ultrafast, Accurate and Interpretable Source Tracking among Sub-Million Microbial Community Samples from Hundreds of Niches		2
29	Holmes-ITS2: Consolidated ITS2 resources and search engines for plant DNA-based marker analyses		2
28	Strain-GeMS: optimized subspecies identification from microbiome data based on accurate variant modeling. <i>Bioinformatics</i> , 2019 , 35, 1789-1791	7.2	2
27	PepSOM: an algorithm for peptide identification by tandem mass spectrometry based on SOM. <i>Genome Informatics</i> , 2006 , 17, 194-205		2
26	Algorithm for peptide sequencing by tandem mass spectrometry based on better preprocessing and anti-symmetric computational model. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007 , 6, 19-30		2
25	An accurate and efficient algorithm for Peptide and ptm identification by tandem mass spectrometry. <i>Genome Informatics</i> , 2007 , 19, 119-30		2
24	Decoding herbal materials of TCM preparations with the multi-barcode sequencing approach.. <i>Scientific Reports</i> , 2022 , 12, 5988	4.9	2
23	Glycyrrhiza uralensis Fisch. Root-associated microbiota: the multifaceted hubs associated with environmental factors, growth status and accumulation of secondary metabolites.. <i>Environmental Microbiomes</i> , 2022 , 17, 23	5.6	2
22	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU 2013 ,		1
21	Parallel-META: A high-performance computational pipeline for metagenomic data analysis 2011 ,		1
20	An Open-source Collaboration Environment for Metagenomics Research 2011 ,		1
19	Correlation-Centric Network (CCN) representation for microbial co-occurrence patterns: new insights for microbial ecology. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa042	3.7	1
18	Pan-genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. <i>Environmental Microbiology</i> , 2021 , 23, 3599-3613	5.2	1
17	Microbiome Sample Comparison and Search: From Pair-Wise Calculations to Model-Based Matching. <i>Frontiers in Microbiology</i> , 2021 , 12, 642439	5.7	1
16	Niche and Neutrality Work Differently in Microbial Communities in Fluidic and Non-fluidic Ecosystems. <i>Microbial Ecology</i> , 2020 , 79, 527-538	4.4	1
15	Reliable and Interpretable Mortality Prediction With Strong Foresight in COVID-19 Patients: An International Study From China and Germany. <i>Frontiers in Artificial Intelligence</i> , 2021 , 4, 672050	3	1

14	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 972-983	4	1
13	Microbiome Resilience and Health Implications for People in Half-Year Travel.. <i>Frontiers in Immunology</i> , 2022 , 13, 848994	8.4	1
12	High biodiversity and distinct assembly patterns of microbial communities in groundwater compared with surface water.. <i>Science of the Total Environment</i> , 2022 , 155345	10.2	1
11	The multiple sequence sets: problem and heuristic algorithms. <i>Journal of Combinatorial Optimization</i> , 2011 , 22, 778-796	0.9	0
10	Analysis of antibiotic resistance genes reveals their important roles in influencing the community structure of ocean microbiome.. <i>Science of the Total Environment</i> , 2022 , 823, 153731	10.2	0
9	The seasonal changes of the gut microbiome of the population living in traditional lifestyles are represented by characteristic species-level and functional-level SNP enrichment patterns. <i>BMC Genomics</i> , 2021 , 22, 83	4.5	0
8	The distribution and deposition algorithm for multiple oligo nucleotide arrays. <i>Genome Informatics</i> , 2006 , 17, 89-99		0
7	How much metagenome data is needed for protein structure prediction: The advantages of targeted approach from the ecological and evolutionary perspectives 2022 , 1,		0
6	Linkage and driving mechanisms of antibiotic resistome in surface and ground water: Their responses to land use and seasonal variation.. <i>Water Research</i> , 2022 , 215, 118279	12.5	0
5	Understanding of the Site-Specific Microbial Patterns towards Accurate Identification for Patients with Diarrhea-Predominant Irritable Bowel Syndrome.. <i>Microbiology Spectrum</i> , 2021 , 9, e0125521	8.9	0
4	Ontology-aware deep learning enables ultrafast and interpretable source tracking among sub-million microbial community samples from hundreds of niches.. <i>Genome Medicine</i> , 2022 , 14, 43	14.4	0
3	Automated Identification of Protein Classification and Detection of Annotation Errors in Protein Databases Using Statistical Approaches. <i>Lecture Notes in Computer Science</i> , 2006 , 123-138	0.9	
2	Two-phase Filtering Strategy for Efficient Peptide Identification from Mass Spectrometry. <i>Journal of Proteomics and Bioinformatics</i> , 2010 , 3, 121-129	2.1	
1	Microbiome and Big-Data Mining 2022 , 197-222		