

Kang Ning

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8772595/publications.pdf>

Version: 2024-02-01

126
papers

4,846
citations

126708

33
h-index

114278

63
g-index

142
all docs

142
docs citations

142
times ranked

6416
citing authors

#	ARTICLE	IF	CITATIONS
1	Network Pharmacology Databases for Traditional Chinese Medicine: Review and Assessment. <i>Frontiers in Pharmacology</i> , 2019, 10, 123.	1.6	731
2	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012, 6, 1-10.	4.4	320
3	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.	3.1	311
4	<i>Nannochloropsis</i> Genomes Reveal Evolution of Microalgal Oleaginous Traits. <i>PLoS Genetics</i> , 2014, 10, e1004094.	1.5	217
5	TCM-Mesh: The database and analytical system for network pharmacology analysis for TCM preparations. <i>Scientific Reports</i> , 2017, 7, 2821.	1.6	168
6	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.	6.5	154
7	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, 2261-2271.	1.8	150
8	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.	1.6	132
9	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 435-466.	0.3	123
10	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. <i>Plant Physiology</i> , 2015, 169, 2444-2461.	2.3	111
11	Stereotypes About Enterotype: the Old and New Ideas. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 4-12.	3.0	97
12	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. <i>Scientific Reports</i> , 2017, 7, 40371.	1.6	96
13	GMrepo: a database of curated and consistently annotated human gut metagenomes. <i>Nucleic Acids Research</i> , 2020, 48, D545-D553.	6.5	96
14	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.	1.2	78
15	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae <i>Nannochloropsis</i> . <i>Scientific Reports</i> , 2014, 4, 5454.	1.6	75
16	Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. <i>PLoS ONE</i> , 2014, 9, e89323.	1.1	70
17	QC-Chain: Fast and Holistic Quality Control Method for Next-Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e60234.	1.1	68
18	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.	1.2	63

#	ARTICLE	IF	CITATIONS
19	Pan-genome analyses of 24 <i>Shewanella</i> strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. <i>Biotechnology for Biofuels</i> , 2018, 11, 193.	6.2	59
20	Computational analysis of unassigned high-quality MS/MS spectra in proteomic data sets. <i>Proteomics</i> , 2010, 10, 2712-2718.	1.3	58
21	Computational Molecular Networks and Network Pharmacology. <i>BioMed Research International</i> , 2017, 2017, 1-1.	0.9	58
22	Nanochloropsis plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. <i>BMC Genomics</i> , 2013, 14, 534.	1.2	55
23	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, S14.	1.2	52
24	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, 2006-2014.	1.4	52
25	GMrepo v2: a curated human gut microbiome database with special focus on disease markers and cross-dataset comparison. <i>Nucleic Acids Research</i> , 2022, 50, D777-D784.	6.5	50
26	RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. <i>BMC Genomics</i> , 2018, 19, 144.	1.2	46
27	Assessment of quality control approaches for metagenomic data analysis. <i>Scientific Reports</i> , 2014, 4, 6957.	1.6	45
28	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.	1.6	45
29	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.	1.6	45
30	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. <i>Gut</i> , 2019, 68, 2254-2255.	6.1	45
31	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, 2493-2501.	1.8	44
32	The Human Gut Virome in Hypertension. <i>Frontiers in Microbiology</i> , 2018, 9, 3150.	1.5	40
33	Stratification of athletes' gut microbiota: the multifaceted hubs associated with dietary factors, physical characteristics and performance. <i>Gut Microbes</i> , 2020, 12, 1842991.	4.3	40
34	Parallel-META: efficient metagenomic data analysis based on high-performance computation. <i>BMC Systems Biology</i> , 2012, 6, S16.	3.0	36
35	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. <i>MSystems</i> , 2019, 4, .	1.7	36
36	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. <i>Bioinformatics</i> , 2016, 32, 462-464.	1.8	34

#	ARTICLE	IF	CITATIONS
37	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , .		33
38	Traditional Chinese Medicine and Gut Microbiome: Their Respective and Concert Effects on Healthcare. <i>Frontiers in Pharmacology</i> , 2020, 11, 538.	1.6	32
39	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 76-90.	3.0	31
40	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.	3.0	29
41	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019, 20, 229.	3.8	28
42	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.	5.3	28
43	A Culture-Independent Approach to Unravel Uncultured Bacteria and Functional Genes in a Complex Microbial Community. <i>PLoS ONE</i> , 2012, 7, e47530.	1.1	26
44	DNA Extraction Protocol for Biological Ingredient Analysis of Liuwei Dihuang Wan. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 137-143.	3.0	26
45	Microbiome Big-Data Mining and Applications Using Single-Cell Technologies and Metagenomics Approaches Toward Precision Medicine. <i>Frontiers in Genetics</i> , 2019, 10, 972.	1.1	26
46	SNP calling using genotype model selection on high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 643-650.	1.8	22
47	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.	1.8	21
48	Is rice-crayfish co-culture a better aquaculture model: From the perspective of antibiotic resistome profiles. <i>Environmental Pollution</i> , 2022, 292, 118450.	3.7	21
49	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. <i>Bioinformatics</i> , 2014, 30, 1031-1033.	1.8	20
50	Microbial Dark Matter: from Discovery to Applications. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 867-881.	3.0	20
51	Towards a better solution to the shortest common supersequence problem: the deposition and reduction algorithm. <i>BMC Bioinformatics</i> , 2006, 7, S12.	1.2	19
52	Meta-QC-Chain: Comprehensive and Fast Quality Control Method for Metagenomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 52-56.	3.0	17
53	Mechanisms of niche neutrality balancing can drive the assembling of microbial community. <i>Molecular Ecology</i> , 2021, 30, 1492-1504.	2.0	17
54	Saliva Microbiota Carry Caries-Specific Functional Gene Signatures. <i>PLoS ONE</i> , 2014, 9, e76458.	1.1	16

#	ARTICLE	IF	CITATIONS
55	The Tara Oceans Project: New Opportunities and Greater Challenges Ahead. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 275-277.	3.0	16
56	Meta-network: optimized species-species network analysis for microbial communities. <i>BMC Genomics</i> , 2019, 20, 187.	1.2	16
57	Integrating pan-genome with metagenome for microbial community profiling. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1458-1466.	1.9	16
58	REFINING MARKOV CLUSTERING FOR PROTEIN COMPLEX PREDICTION BY INCORPORATING CORE-ATTACHMENT STRUCTURE. , 2009, , .		16
59	Characterization of saliva microbiota's functional feature based on metagenomic sequencing. <i>SpringerPlus</i> , 2016, 5, 2098.	1.2	15
60	Biological ingredient complement chemical ingredient in the assessment of the quality of TCM preparations. <i>Scientific Reports</i> , 2019, 9, 5853.	1.6	15
61	Hidden link in gut-joint axis: gut microbes promote rheumatoid arthritis at early stage by enhancing ascorbate degradation. <i>Gut</i> , 2022, 71, 1041-1043.	6.1	15
62	MetaSee: An Interactive and Extendable Visualization Toolbox for Metagenomic Sample Analysis and Comparison. <i>PLoS ONE</i> , 2012, 7, e48998.	1.1	14
63	Single-cell SNP analyses and interpretations based on RNA-Seq data for colon cancer research. <i>Scientific Reports</i> , 2016, 6, 34420.	1.6	14
64	Proteomic study uncovers molecular principles of single-cell-level phenotypic heterogeneity in lipid storage of <i>Nannochloropsis oceanica</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 21.	6.2	14
65	Protist 10,000 Genomes Project. <i>Innovation(China)</i> , 2020, 1, 100058.	5.2	14
66	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. <i>PeerJ</i> , 2015, 3, e993.	0.9	13
67	Decoding herbal materials of TCM preparations with the multi-barcode sequencing approach. <i>Scientific Reports</i> , 2022, 12, 5988.	1.6	13
68	Condensing Raman spectrum for single-cell phenotype analysis. <i>BMC Bioinformatics</i> , 2015, 16, S15.	1.2	12
69	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, .	3.3	12
70	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. <i>BMC Genomics</i> , 2017, 18, 268.	1.2	11
71	A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2005, 33, e144-e144.	6.5	10
72	Microbial community pattern detection in human body habitats via ensemble clustering framework. <i>BMC Systems Biology</i> , 2014, 8, S7.	3.0	10

#	ARTICLE	IF	CITATIONS
73	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.	3.2	10
74	Predicting new indications of compounds with a network pharmacology approach: Liuwei Dihuang Wan as a case study. <i>Oncotarget</i> , 2017, 8, 93957-93968.	0.8	10
75	ON PREPROCESSING AND ANTISYMMETRY IN DE NOVO PEPTIDE SEQUENCING: IMPROVING EFFICIENCY AND ACCURACY. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 467-492.	0.3	9
76	Niche and Neutrality Work Differently in Microbial Communities in Fluidic and Non-fluidic Ecosystems. <i>Microbial Ecology</i> , 2020, 79, 527-538.	1.4	9
77	High biodiversity and distinct assembly patterns of microbial communities in groundwater compared with surface water. <i>Science of the Total Environment</i> , 2022, 834, 155345.	3.9	9
78	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.	3.6	9
79	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.	1.5	8
80	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.	3.9	8
81	Refining Markov Clustering for protein complex prediction by incorporating core-attachment structure. <i>Genome Informatics</i> , 2009, 23, 159-68.	0.4	8
82	MODELING AND CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1329-1352.	0.3	7
83	Deposition and extension approach to find longest common subsequence for thousands of long sequences. <i>Computational Biology and Chemistry</i> , 2010, 34, 149-157.	1.1	7
84	The Seasonal Dynamics and the Influence of Human Activities on Campus Outdoor Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1579.	1.5	7
85	SAW: A Method to Identify Splicing Events from RNA-Seq Data Based on Splicing Fingerprints. <i>PLoS ONE</i> , 2010, 5, e12047.	1.1	7
86	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.	1.2	7
87	<i>Glycyrrhiza uralensis</i> 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.	2.2	7
88	Sustainability of the rice-crayfish co-culture aquaculture model: microbiome profiles based on multi-kingdom analyses. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	7
89	Finding Patterns in Biological Sequences by Longest Common Subsequences and Shortest Common Supersequences. , 2006, , .		6
90	Correlation-Centric Network (CCN) representation for microbial co-occurrence patterns: new insights for microbial ecology. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa042.	1.5	6

#	ARTICLE	IF	CITATIONS
91	Utilizing microbiome approaches to assist source tracking, treatment and prevention of COVID-19: Review and assessment. Computational and Structural Biotechnology Journal, 2020, 18, 3615-3622.	1.9	6
92	Big data for biomedical research: Current status and prospective. Chinese Science Bulletin, 2015, 60, 534-546.	0.4	6
93	QSpec: online control and data analysis system for single-cell Raman spectroscopy. PeerJ, 2014, 2, e436.	0.9	6
94	Heterogeneous circRNA expression profiles and regulatory functions among HEK293T single cells. Scientific Reports, 2017, 7, 14393.	1.6	5
95	Strain-GeMS: optimized subspecies identification from microbiome data based on accurate variant modeling. Bioinformatics, 2019, 35, 1789-1791.	1.8	5
96	ALGORITHM FOR PEPTIDE SEQUENCING BY TANDEM MASS SPECTROMETRY BASED ON BETTER PREPROCESSING AND ANTI-SYMMETRIC COMPUTATIONAL MODEL. , 2007, , .		5
97	The multiple sequence sets: problem and heuristic algorithms. Journal of Combinatorial Optimization, 2011, 22, 778-796.	0.8	4
98	A machine learning framework of functional biomarker discovery for different microbial communities based on metagenomic data. , 2012, , .		4
99	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. Scientific Reports, 2015, 4, 6393.	1.6	4
100	A Living Eukaryotic Autocementation Kit from Surface Display of Silica Binding Peptides on <i>Yarrowia lipolytica</i> . ACS Synthetic Biology, 2016, 5, 1466-1474.	1.9	4
101	Pan-genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. Environmental Microbiology, 2021, 23, 3599-3613.	1.8	4
102	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. BMC Genomics, 2021, 22, 83.	1.2	4
103	Reliable and Interpretable Mortality Prediction With Strong Foresight in COVID-19 Patients: An International Study From China and Germany. Frontiers in Artificial Intelligence, 2021, 4, 672050.	2.0	4
104	An Open-source Collaboration Environment for Metagenomics Research. , 2011, , .		3
105	Analysis of the relationships among Longest Common Subsequences, Shortest Common Supersequences and patterns and its application on pattern discovery in biological sequences. International Journal of Data Mining and Bioinformatics, 2011, 5, 611.	0.1	3
106	Metagenomics and Single-Cell Omics Data Analysis for Human Microbiome Research. Advances in Experimental Medicine and Biology, 2016, 939, 117-137.	0.8	3
107	MultiGeMS: detection of SNVs from multiple samples using model selection on high-throughput sequencing data. Bioinformatics, 2016, 32, 1486-1492.	1.8	3
108	Microbiome Sample Comparison and Search: From Pair-Wise Calculations to Model-Based Matching. Frontiers in Microbiology, 2021, 12, 642439.	1.5	3

#	ARTICLE	IF	CITATIONS
109	How much metagenome data is needed for protein structure prediction: The advantages of targeted approach from the ecological and evolutionary perspectives. , 2022, 1, .		3
110	Towards a Better Solution to the Shortest Common Supersequence Problem: A Post. , 2006, , .		2
111	Detecting hubs and quasi cliques in scale-free networks. , 2008, , .		2
112	Parallel-META: A high-performance computational pipeline for metagenomic data analysis. , 2011, , .		2
113	Application of Metaâ€Mesh on the analysis of microbial communities from human associatedâ€habitats. Quantitative Biology, 2015, 3, 4-18.	0.3	2
114	The Fast Track for Microbiome Research. Genomics, Proteomics and Bioinformatics, 2019, 17, 1-3.	3.0	2
115	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. Journal of Genetics and Genomics, 2021, 48, 972-983.	1.7	2
116	PepSOM: an algorithm for peptide identification by tandem mass spectrometry based on SOM. Genome Informatics, 2006, 17, 194-205.	0.4	2
117	Algorithm for peptide sequencing by tandem mass spectrometry based on better preprocessing and anti-symmetric computational model. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 19-30.	0.4	2
118	An accurate and efficient algorithm for Peptide and ptm identification by tandem mass spectrometry. Genome Informatics, 2007, 19, 119-30.	0.4	2
119	Microbiome Resilience and Health Implications for People in Half-Year Travel. Frontiers in Immunology, 2022, 13, 848994.	2.2	2
120	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU. , 2013, , .		1
121	<i>MetaMed</i> : Linking Microbiota Functions with Medicine Therapeutics. MSystems, 2019, 4, .	1.7	1
122	Ontology-aware neural network: a general framework for pattern mining from microbiome data. Briefings in Bioinformatics, 2022, , .	3.2	1
123	The distribution and deposition algorithm for multiple oligo nucleotide arrays. Genome Informatics, 2006, 17, 89-99.	0.4	1
124	AN ACCURATE AND EFFICIENT ALGORITHM FOR PEPTIDE AND PTM IDENTIFICATION BY TANDEM MASS SPECTROMETRY. , 2007, , .		0
125	Session 12: Information security. , 2013, , .		0
126	Two-phase Filtering Strategy for Efficient Peptide Identification from Mass Spectrometry. Journal of Proteomics and Bioinformatics, 2010, 03, 121-129.	0.4	0