

Jian Xu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2657346/publications.pdf>

Version: 2024-02-01

143
papers

11,247
citations

38660

50
h-index

31759

101
g-index

152
all docs

152
docs citations

152
times ranked

12853
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genomic View of the Human-Bacteroides thetaiotaomicron Symbiosis. <i>Science</i> , 2003, 299, 2074-2076.	6.0	1,186
2	Glycan Foraging in Vivo by an Intestine-Adapted Bacterial Symbiont. <i>Science</i> , 2005, 307, 1955-1959.	6.0	1,000
3	Honor thy symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10452-10459.	3.3	795
4	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	2.6	490
5	Autotrophic growth of nitrifying community in an agricultural soil. <i>ISME Journal</i> , 2011, 5, 1226-1236.	4.4	366
6	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012, 6, 1-10.	4.4	320
7	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
8	Phytohormones in microalgae: a new opportunity for microalgal biotechnology?. <i>Trends in Plant Science</i> , 2015, 20, 273-282.	4.3	268
9	Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. <i>Scientific Reports</i> , 2016, 6, 20602.	1.6	238
10	Genome editing of model oleaginous microalgae <i>Nannochloropsis</i> spp. by CRISPR/Cas9. <i>Plant Journal</i> , 2016, 88, 1071-1081.	2.8	229
11	<i>Nannochloropsis</i> Genomes Reveal Evolution of Microalgal Oleaginous Traits. <i>PLoS Genetics</i> , 2014, 10, e1004094.	1.5	217
12	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6864-6875.	1.4	212
13	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. <i>Microbiome</i> , 2017, 5, 91.	4.9	208
14	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015, 18, 296-306.	5.1	204
15	Molecular mechanisms for photosynthetic carbon partitioning into storage neutral lipids in <i>Nannochloropsis oceanica</i> under nitrogen-depletion conditions. <i>Algal Research</i> , 2015, 7, 66-77.	2.4	188
16	Single cell Raman spectroscopy for cell sorting and imaging. <i>Current Opinion in Biotechnology</i> , 2012, 23, 56-63.	3.3	180
17	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
18	Metabolic-Activity-Based Assessment of Antimicrobial Effects by D ₂ O-Labeled Single-Cell Raman Microspectroscopy. <i>Analytical Chemistry</i> , 2017, 89, 4108-4115.	3.2	129

#	ARTICLE	IF	CITATIONS
19	Raman-Activated Cell Sorting Based on Dielectrophoretic Single-Cell Trap and Release. <i>Analytical Chemistry</i> , 2015, 87, 2282-2289.	3.2	126
20	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. <i>Scientific Reports</i> , 2018, 8, 16321.	1.6	126
21	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. <i>ISME Journal</i> , 2014, 8, 1768-1780.	4.4	118
22	Raman-Activated Droplet Sorting (RADS) for Label-Free High-Throughput Screening of Microalgal Single-Cells. <i>Analytical Chemistry</i> , 2017, 89, 12569-12577.	3.2	113
23	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. <i>Plant Physiology</i> , 2015, 169, 2444-2461.	2.3	111
24	Producing Designer Oils in Industrial Microalgae by Rational Modulation of Co-evolving Type-2 Diacylglycerol Acyltransferases. <i>Molecular Plant</i> , 2017, 10, 1523-1539.	3.9	111
25	Raman Activated Cell Ejection for Isolation of Single Cells. <i>Analytical Chemistry</i> , 2013, 85, 10697-10701.	3.2	105
26	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. <i>BMC Oral Health</i> , 2011, 11, 33.	0.8	104
27	Antagonistic roles of abscisic acid and cytokinin during response to nitrogen depletion in oleaginous microalga <i>Nannochloropsis oceanica</i> expand the evolutionary breadth of phytohormone function. <i>Plant Journal</i> , 2014, 80, 52-68.	2.8	101
28	Enhancing photosynthetic biomass productivity of industrial oleaginous microalgae by overexpression of RuBisCO activase. <i>Algal Research</i> , 2017, 27, 366-375.	2.4	99
29	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. <i>PLoS ONE</i> , 2012, 7, e40430.	1.1	98
30	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
31	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. <i>Microbiome</i> , 2018, 6, 200.	4.9	88
32	Message from a human gut symbiont: sensitivity is a prerequisite for sharing. <i>Trends in Microbiology</i> , 2004, 12, 21-28.	3.5	87
33	Label-free, rapid and quantitative phenotyping of stress response in <i>E. coli</i> via ramanome. <i>Scientific Reports</i> , 2016, 6, 34359.	1.6	87
34	Regulation of the cholesterol biosynthetic pathway and its integration with fatty acid biosynthesis in the oleaginous microalga <i>Nannochloropsis oceanica</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 81.	6.2	81
35	Magnetic nanoparticle-mediated isolation of functional bacteria in a complex microbial community. <i>ISME Journal</i> , 2015, 9, 603-614.	4.4	75
36	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

#	ARTICLE	IF	CITATIONS
37	<sc>RNA</sc>-based targeted gene knockdown in the model oleaginous microalgae <i>Nannochloropsis oceanica</i> . <i>Plant Journal</i> , 2017, 89, 1236-1250.	2.8	74
38	Biosynthesis of Triacylglycerol Molecules with a Tailored PUFA Profile in Industrial Microalgae. <i>Molecular Plant</i> , 2019, 12, 474-488.	3.9	73
39	Reverse and Multiple Stable Isotope Probing to Study Bacterial Metabolism and Interactions at the Single Cell Level. <i>Analytical Chemistry</i> , 2016, 88, 9443-9450.	3.2	72
40	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
41	Ultralight, highly compressible, thermally stable MXene/aramid nanofiber anisotropic aerogels for electromagnetic interference shielding. <i>Journal of Materials Chemistry A</i> , 2022, 10, 6690-6700.	5.2	69
42	QC-Chain: Fast and Holistic Quality Control Method for Next-Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e60234.	1.1	68
43	Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. <i>Biotechnology for Biofuels</i> , 2014, 7, 58.	6.2	67
44	Towards high-throughput microfluidic Raman-activated cell sorting. <i>Analyst</i> , 2015, 140, 6163-6174.	1.7	67
45	Raman-activated cell sorting and metagenomic sequencing revealing carbon-fixing bacteria in the ocean. <i>Environmental Microbiology</i> , 2018, 20, 2241-2255.	1.8	62
46	Development of a facile droplet-based single-cell isolation platform for cultivation and genomic analysis in microorganisms. <i>Scientific Reports</i> , 2017, 7, 41192.	1.6	60
47	Characterization of the Central Metabolic Pathways in <i>Thermoanaerobacter</i> sp. Strain X514 via Isotopomer-Assisted Metabolite Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5001-5008.	1.4	57
48	<i>Nannochloropsis</i> plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. <i>BMC Genomics</i> , 2013, 14, 534.	1.2	55
49	Ramanome technology platform for label-free screening and sorting of microbial cell factories at single-cell resolution. <i>Biotechnology Advances</i> , 2019, 37, 107388.	6.0	55
50	Knockdown of carbonate anhydrase elevates <i>Nannochloropsis</i> productivity at high CO ₂ level. <i>Metabolic Engineering</i> , 2019, 54, 96-108.	3.6	55
51	Factors influencing cellulosome activity in Consolidated Bioprocessing of cellulosic ethanol. <i>Bioresource Technology</i> , 2010, 101, 9560-9569.	4.8	54
52	Raman spectroscopy provides a rapid, non-invasive method for quantitation of starch in live, unicellular microalgae. <i>Biotechnology Journal</i> , 2014, 9, 1512-1518.	1.8	50
53	Structure and regulation of the cellulose degradome in <i>Clostridium cellulolyticum</i> . <i>Biotechnology for Biofuels</i> , 2013, 6, 73.	6.2	49
54	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. <i>Journal of Insect Science</i> , 2016, 16, 97.	0.6	49

#	ARTICLE	IF	CITATIONS
55	Positive dielectrophoresis-based Raman-activated droplet sorting for culture-free and label-free screening of enzyme function in vivo. <i>Science Advances</i> , 2020, 6, eabb3521.	4.7	48
56	Dissecting and engineering metabolic and regulatory networks of thermophilic bacteria for biofuel production. <i>Biotechnology Advances</i> , 2013, 31, 827-837.	6.0	47
57	Transcriptomic and proteomic responses to very low CO ₂ suggest multiple carbon concentrating mechanisms in <i>Nannochloropsis oceanica</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 168.	6.2	46
58	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
59	Metabolic Remodeling of Membrane Glycerolipids in the Microalga <i>Nannochloropsis oceanica</i> under Nitrogen Deprivation. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	45
60	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
61	Label-free, simultaneous quantification of starch, protein and triacylglycerol in single microalgal cells. <i>Biotechnology for Biofuels</i> , 2017, 10, 275.	6.2	44
62	Cellulosome stoichiometry in <i>Clostridium cellulolyticum</i> is regulated by selective RNA processing and stabilization. <i>Nature Communications</i> , 2015, 6, 6900.	5.8	43
63	Correlation of Genomic and Physiological Traits of <i>Thermoanaerobacter</i> Species with Biofuel Yields. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7998-8008.	1.4	42
64	Cetylpyridinium chloride mouth rinses alleviate experimental gingivitis by inhibiting dental plaque maturation. <i>International Journal of Oral Science</i> , 2016, 8, 182-190.	3.6	41
65	Lotus Leaf Aqueous Extract Reduces Visceral Fat Mass and Ameliorates Insulin Resistance in HFD-Induced Obese Rats by Regulating PPAR γ Expression. <i>Frontiers in Pharmacology</i> , 2017, 8, 409.	1.6	39
66	The <i>Thermoanaerobacter</i> Glycobiome Reveals Mechanisms of Pentose and Hexose Co-Utilization in Bacteria. <i>PLoS Genetics</i> , 2011, 7, e1002318.	1.5	37
67	The NanDeSyn database for <i>Nannochloropsis</i> systems and synthetic biology. <i>Plant Journal</i> , 2020, 104, 1736-1745.	2.8	37
68	Parallel-META: efficient metagenomic data analysis based on high-performance computation. <i>BMC Systems Biology</i> , 2012, 6, S16.	3.0	36
69	Ultrasound-Mediated DNA Transformation in Thermophilic Gram-Positive Anaerobes. <i>PLoS ONE</i> , 2010, 5, e12582.	1.1	36
70	Microbial Community Changes Along a Land-Use Gradient of Desert Soil Origin. <i>Pedosphere</i> , 2012, 22, 593-603.	2.1	34
71	Phenome-Genome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing. <i>Small</i> , 2020, 16, e2001172.	5.2	33
72	The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. <i>ISME Journal</i> , 2013, 7, 1974-1984.	4.4	32

#	ARTICLE	IF	CITATIONS
73	Species-resolved sequencing of low-biomass or degraded microbiomes using 2bRAD-M. <i>Genome Biology</i> , 2022, 23, 36.	3.8	31
74	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. <i>Engineering</i> , 2017, 3, 66-70.	3.2	30
75	Genome assembly of <i>Nannochloropsis oceanica</i> provides evidence of host nucleus overthrow by the symbiont nucleus during speciation. <i>Communications Biology</i> , 2019, 2, 249.	2.0	29
76	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	1.8	28
77	Microbiota-based Signature of Gingivitis Treatments: A Randomized Study. <i>Scientific Reports</i> , 2016, 6, 24705.	1.6	27
78	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
79	DNA Extraction Protocol for Biological Ingredient Analysis of Liuwei Dihuang Wan. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 137-143.	3.0	26
80	Flavin mononucleotide (FMN)-based fluorescent protein (FbFP) as reporter for promoter screening in <i>Clostridium cellulolyticum</i> . <i>Journal of Microbiological Methods</i> , 2015, 119, 37-43.	0.7	26
81	Regulation of biomass degradation by alternative λ factors in cellulolytic clostridia. <i>Scientific Reports</i> , 2018, 8, 11036.	1.6	24
82	D_2 -O-Probed Raman Microspectroscopy Distinguishes the Metabolic Dynamics of Macromolecules in Organellar Anticancer Drug Response. <i>Analytical Chemistry</i> , 2021, 93, 2125-2134.	3.2	24
83	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. <i>MBio</i> , 2021, 12, .	1.8	24
84	Fosmid-Based Physical Mapping of the <i>Histoplasma capsulatum</i> Genome. <i>Genome Research</i> , 2004, 14, 1603-1609.	2.4	23
85	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. <i>MSystems</i> , 2019, 4, .	1.7	22
86	Integration of proteome and transcriptome refines key molecular processes underlying oil production in <i>Nannochloropsis oceanica</i> . <i>Biotechnology for Biofuels</i> , 2020, 13, 109.	6.2	22
87	Establishing Oleaginous Microalgae Research Models for Consolidated Bioprocessing of Solar Energy. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2011, 128, 69-84.	0.6	21
88	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in <i>Ettlia oleoabundans</i> . <i>Algal Research</i> , 2018, 33, 142-155.	2.4	21
89	One-Cell Metabolic Phenotyping and Sequencing of Soil Microbiome by Raman-Activated Gravity-Driven Encapsulation (RAGE). <i>MSystems</i> , 2021, 6, e0018121.	1.7	21
90	A preliminary study of the mechanism of nitrate-stimulated remarkable increase of rifamycin production in <i>Amycolatopsis mediterranei</i> U32 by RNA-seq. <i>Microbial Cell Factories</i> , 2015, 14, 75.	1.9	20

#	ARTICLE	IF	CITATIONS
91	Single cell biotechnology to shed a light on biological "dark matter"™ in nature. <i>Microbial Biotechnology</i> , 2015, 8, 15-16.	2.0	20
92	Transcriptomic and proteomic choreography in response to light quality variation reveals key adaption mechanisms in marine <i>Nannochloropsis oceanica</i> . <i>Science of the Total Environment</i> , 2020, 720, 137667.	3.9	20
93	On-demand control of microfluidic flow via capillary-tuned solenoid microvalve suction. <i>Lab on A Chip</i> , 2014, 14, 4599-4603.	3.1	19
94	Genome engineering of <i>Nannochloropsis</i> with hundred-kilobase fragment deletions by Cas9 cleavages. <i>Plant Journal</i> , 2021, 106, 1148-1162.	2.8	19
95	A Palm Germ-Radar (PaGeR) for rapid and simple COVID-19 detection by reverse transcription loop-mediated isothermal amplification (RT-LAMP). <i>Biosensors and Bioelectronics</i> , 2022, 200, 113925.	5.3	19
96	Development of HuMiChip for Functional Profiling of Human Microbiomes. <i>PLoS ONE</i> , 2014, 9, e90546.	1.1	18
97	Saliva Microbiota Carry Caries-Specific Functional Gene Signatures. <i>PLoS ONE</i> , 2014, 9, e76458.	1.1	16
98	A self-powered microfluidic monodispersed droplet generator with capability of multi-sample introduction. <i>Microfluidics and Nanofluidics</i> , 2015, 18, 1067-1073.	1.0	16
99	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	1.7	16
100	Culture-Free Identification and Metabolic Profiling of Microalgal Single Cells via Ensemble Learning of Ramanomes. <i>Analytical Chemistry</i> , 2021, 93, 8872-8880.	3.2	16
101	Single-Cell Identification, Drug Susceptibility Test, and Whole-genome Sequencing of <i>Helicobacter pylori</i> Directly from Gastric Biopsy by Clinical Antimicrobial Susceptibility Test Ramanometry. <i>Clinical Chemistry</i> , 2022, 68, 1064-1074.	1.5	16
102	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. <i>BMC Genomics</i> , 2021, 22, 9.	1.2	15
103	MetaSee: An Interactive and Extendable Visualization Toolbox for Metagenomic Sample Analysis and Comparison. <i>PLoS ONE</i> , 2012, 7, e48998.	1.1	14
104	Optimized methods of chromatin immunoprecipitation for profiling histone modifications in industrial microalgae <i>Nannochloropsis</i> spp.. <i>Journal of Phycology</i> , 2018, 54, 358-367.	1.0	14
105	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
106	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. <i>MSystems</i> , 2021, 6, .	1.7	14
107	Manipulating fatty-acid profile at unit chain-length resolution in the model industrial oleaginous microalgae <i>Nannochloropsis</i> . <i>Metabolic Engineering</i> , 2021, 66, 157-166.	3.6	14
108	JIB-04 Has Broad-Spectrum Antiviral Activity and Inhibits SARS-CoV-2 Replication and Coronavirus Pathogenesis. <i>MBio</i> , 2022, 13, e0337721.	1.8	14

#	ARTICLE	IF	CITATIONS
109	Microevolution from shock to adaptation revealed strategies improving ethanol tolerance and production in <i>Thermoanaerobacter</i> . <i>Biotechnology for Biofuels</i> , 2013, 6, 103.	6.2	12
110	Near-Complete Genome Sequence of the Cellulolytic Bacterium <i>Bacteroides</i> (<i>Bacteroides</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (<i>P	0.8	12
111	<i>Dynamic Meta-Storms</i> enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. <i>Bioinformatics</i> , 2020, 36, 2308-2310.	1.8	12
112	Exploring a blue-light-sensing transcription factor to double the peak productivity of oil in <i>Nannochloropsis oceanica</i> . <i>Nature Communications</i> , 2022, 13, 1664.	5.8	12
113	Species-Resolved Metagenomics of Kindergarten Microbiomes Reveal Microbial Admixture Within Sites and Potential Microbial Hazards. <i>Frontiers in Microbiology</i> , 2022, 13, 871017.	1.5	11
114	Hierarchical Multi-Core@Shell CoNi@Graphite Carbon@Carbon Nanoboxes for Highly Efficient Broadband Microwave Absorption. <i>ACS Applied Nano Materials</i> , 2022, 5, 7300-7311.	2.4	11
115	Protein expression analysis revealed a fine-tuned mechanism of in situ detoxification pathway for the tolerant industrial yeast <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5781-5796.	1.7	10
116	Rational Optimization of Raman-Activated Cell Ejection and Sequencing for Bacteria. <i>Analytical Chemistry</i> , 2020, 92, 8081-8089.	3.2	10
117	Structural insight into a GH1 β -glucosidase from the oleaginous microalga, <i>Nannochloropsis oceanica</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 170, 196-206.	3.6	10
118	Comprehensive understanding to the public health risk of environmental microbes via a microbiome-based index. <i>Journal of Genetics and Genomics</i> , 2022, 49, 685-688.	1.7	9
119	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Population of Cells. <i>MBio</i> , 2021, 12, e0147021.	1.8	8
120	Evolution of Ycf54-independent chlorophyll biosynthesis in cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
121	QSpec: online control and data analysis system for single-cell Raman spectroscopy. <i>PeerJ</i> , 2014, 2, e436.	0.9	6
122	Rapid, automated, and reliable antimicrobial susceptibility test from positive blood culture by CAST@R. , 2022, 1, 329-340.		6
123	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , 2021, 6, e0039421.	1.7	5
124	Single-cell Raman microspectroscopy-based assessment of three intracanal disinfectants' effect on <i>Enterococcus faecalis</i> . <i>Journal of Raman Spectroscopy</i> , 2022, 53, 902-910.	1.2	5
125	MapLinker: a software tool that aids physical map-linked whole genome shotgun assembly. <i>Bioinformatics</i> , 2005, 21, 1265-1266.	1.8	4
126	A machine learning framework of functional biomarker discovery for different microbial communities based on metagenomic data. , 2012, , .		4

#	ARTICLE	IF	CITATIONS
127	Efficient and Low-Cost Error Removal in DNA Synthesis by a High-Durability MutS. <i>ACS Synthetic Biology</i> , 2020, 9, 940-952.	1.9	4
128	Integrated Addressable Dynamic Droplet Array (aDDA) as Sub-nanoliter Reactors for High-Coverage Genome Sequencing of Single Yeast Cells. <i>Small</i> , 2021, 17, 2100325.	5.2	4
129	An Open-source Collaboration Environment for Metagenomics Research. , 2011, , .		3
130	Phenome-Genome Profiling: Phenome-Genome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing (Small 30/2020). <i>Small</i> , 2020, 16, 2070165.	5.2	3
131	A milliliter to picoliter-level centrifugal microfluidic concentrator for fast pathogen detection and antimicrobial susceptibility testing. <i>Sensors and Actuators B: Chemical</i> , 2021, 343, 130117.	4.0	3
132	Application of Meta-Mesh on the analysis of microbial communities from human associated habitats. <i>Quantitative Biology</i> , 2015, 3, 4-18.	0.3	2
133	In vitro method for prediction of plaque reduction by dentifrice. <i>Journal of Microbiological Methods</i> , 2015, 118, 85-92.	0.7	2
134	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU. , 2013, , .		1
135	Single-Cell Metabolomics. <i>Springer Protocols</i> , 2015, , 77-90.	0.1	1
136	The Oral Microbiome Bank of China. , 2020, , 287-300.		1
137	Assessing Efficacy of Clinical Disinfectants for Pathogenic Fungi by Single-Cell Raman Microspectroscopy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 772378.	1.8	1
138	Single-Cell Biotechnology for Uncultured Microorganisms. <i>Springer Protocols</i> , 2015, , 119-131.	0.1	0
139	Single-Cell and Systems Biology Tools for Biofuel Production. <i>Springer Protocols</i> , 2015, , 133-144.	0.1	0
140	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	1.8	0
141	Developing a medium combination to attain similar glycosylation profile to originator by DoE and cluster analysis method. <i>Scientific Reports</i> , 2021, 11, 7103.	1.6	0
142	Predicting Selective RNA Processing and Stabilization Operons in <i>Clostridium</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 673349.	1.5	0
143	Integrated Addressable Dynamic Droplet Array (aDDA) as Sub-nanoliter Reactors for High-Coverage Genome Sequencing of Single Yeast Cells (Small 37/2021). <i>Small</i> , 2021, 17, 2170191.	5.2	0