Jian Xu

List of Publications by Citations

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139 papers	8,198 citations	45 h-index	89 g-index
152 ext. papers	9,907 ext. citations	7.7 avg, IF	5.93 L-index

#	Paper	IF	Citations
139	A genomic view of the human-Bacteroides thetaiotaomicron symbiosis. *Science*, **2003**, 299, 2074-6	33.3	1005
138	Glycan foraging in vivo by an intestine-adapted bacterial symbiont. *Science*, **2005**, 307, 1955-9	33.3	803
137	Honor thy symbionts. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 10452-9	11.5	687
136	Evolution of symbiotic bacteria in the distal human intestine. *PLoS Biology*, **2007**, 5, e156	9.7	401
135	Autotrophic growth of nitrifying community in an agricultural soil. *ISME Journal*, **2011**, 5, 1226-36	11.9	276
134	Saliva microbiomes distinguish caries-active from healthy human populations. *ISME Journal*, **2012**, 6, 1-10	11.9	245
133	Choreography of Transcriptomes and Lipidomes of Nannochloropsis Reveals the Mechanisms of Oil Synthesis in Microalgae. *Plant Cell*, **2014**, 26, 1645-1665	11.6	243
132	Phytohormones in microalgae: a new opportunity for microalgal biotechnology?. *Trends in Plant Science*, **2015**, 20, 273-282	13.1	183
131	Novel features of the polysaccharide-digesting gliding bacterium Flavobacterium johnsoniae as revealed by genome sequence analysis. *Applied and Environmental Microbiology*, **2009**, 75, 6864-75	4.8	177
130	Nannochloropsis genomes reveal evolution of microalgal oleaginous traits. *PLoS Genetics*, **2014**, 10, e1004094	6	173
129	Genome editing of model oleaginous microalgae Nannochloropsis spp. by CRISPR/Cas9. *Plant Journal*, **2016**, 88, 1071-1081	6.9	170
128	Single cell Raman spectroscopy for cell sorting and imaging. *Current Opinion in Biotechnology*, **2012**, 23, 56-63	11.4	154
127	Molecular mechanisms for photosynthetic carbon partitioning into storage neutral lipids in Nannochloropsis oceanica under nitrogen-depletion conditions. *Algal Research*, **2015**, 7, 66-77	5	145
126	Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. *Scientific Reports*, **2016**, 6, 20602	4.9	142
125	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. *Cell Host and Microbe*, **2015**, 18, 296-306	23.4	123
124	Raman-activated cell sorting based on dielectrophoretic single-cell trap and release. *Analytical Chemistry*, **2015**, 87, 2282-9	7.8	106
123	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. *Microbiome*, **2017**, 5, 91	16.6	104

122	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous Chlorella spp. *Plant Physiology*, **2015**, 169, 2444-61	6.6	89
121	Metabolic-Activity-Based Assessment of Antimicrobial Effects by DO-Labeled Single-Cell Raman Microspectroscopy. *Analytical Chemistry*, **2017**, 89, 4108-4115	7.8	87
120	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. *BMC Oral Health*, **2011**, 11, 33	3.7	82
119	Raman activated cell ejection for isolation of single cells. *Analytical Chemistry*, **2013**, 85, 10697-701	7.8	80
118	Producing Designer Oils in Industrial Microalgae by Rational Modulation of Co-evolving Type-2 Diacylglycerol Acyltransferases. *Molecular Plant*, **2017**, 10, 1523-1539	14.4	78
117	Message from a human gut symbiont: sensitivity is a prerequisite for sharing. *Trends in Microbiology* , **2004**, 12, 21-8	12.4	77
116	Biological ingredient analysis of traditional Chinese medicine preparation based on high-throughput sequencing: the story for Liuwei Dihuang Wan. *Scientific Reports*, **2014**, 4, 5147	4.9	76
115	Raman-Activated Droplet Sorting (RADS) for Label-Free High-Throughput Screening of Microalgal Single-Cells. *Analytical Chemistry*, **2017**, 89, 12569-12577	7.8	76
114	Antagonistic roles of abscisic acid and cytokinin during response to nitrogen depletion in oleaginous microalga Nannochloropsis oceanica expand the evolutionary breadth of phytohormone function. *Plant Journal*, **2014**, 80, 52-68	6.9	75
113	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. *Scientific Reports*, **2018**, 8, 16321	4.9	74
112	Metagenomic insights into the fibrolytic microbiome in yak rumen. *PLoS ONE*, **2012**, 7, e40430	3.7	71
111	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. *ISME Journal*, **2014**, 8, 1768-80	11.9	70
110	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. *Scientific Reports*, **2017**, 7, 40371	4.9	64
109	Magnetic nanoparticle-mediated isolation of functional bacteria in a complex microbial community. *ISME Journal*, **2015**, 9, 603-14	11.9	63
108	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae Nannochloropsis. *Scientific Reports*, **2014**, 4, 5454	4.9	61
107	Label-free, rapid and quantitative phenotyping of stress response in E. coli via ramanome. *Scientific Reports*, **2016**, 6, 34359	4.9	58
106	Regulation of the cholesterol biosynthetic pathway and its integration with fatty acid biosynthesis in the oleaginous microalga Nannochloropsis oceanica. *Biotechnology for Biofuels*, **2014**, 7, 81	7.8	58
105	Enhancing photosynthetic biomass productivity of industrial oleaginous microalgae by overexpression of RuBisCO activase. *Algal Research*, **2017**, 27, 366-375	5	57

104	Towards high-throughput microfluidic Raman-activated cell sorting. *Analyst, The*, **2015**, 140, 6163-74	5	55
103	Parallel-META 2.0: enhanced metagenomic data analysis with functional annotation, high performance computing and advanced visualization. *PLoS ONE*, **2014**, 9, e89323	3.7	54
102	Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. *Biotechnology for Biofuels*, **2014**, 7, 58	7.8	53
101	Characterization of the central metabolic pathways in Thermoanaerobacter sp. strain X514 via isotopomer-assisted metabolite analysis. *Applied and Environmental Microbiology*, **2009**, 75, 5001-8	4.8	52
100	Reverse and Multiple Stable Isotope Probing to Study Bacterial Metabolism and Interactions at the Single Cell Level. *Analytical Chemistry*, **2016**, 88, 9443-9450	7.8	52
99	Development of a facile droplet-based single-cell isolation platform for cultivation and genomic analysis in microorganisms. *Scientific Reports*, **2017**, 7, 41192	4.9	51
98	RNAi-based targeted gene knockdown in the model oleaginous microalgae Nannochloropsis oceanica. *Plant Journal*, **2017**, 89, 1236-1250	6.9	51
97	QC-Chain: fast and holistic quality control method for next-generation sequencing data. *PLoS ONE*, **2013**, 8, e60234	3.7	49
96	Factors influencing cellulosome activity in consolidated bioprocessing of cellulosic ethanol. *Bioresource Technology*, **2010**, 101, 9560-9	11	49
95	Nannochloropsis plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. *BMC Genomics*, **2013**, 14, 534	4.5	45
94	Dissecting and engineering metabolic and regulatory networks of thermophilic bacteria for biofuel production. *Biotechnology Advances*, **2013**, 31, 827-37	17.8	44
93	Raman spectroscopy provides a rapid, non-invasive method for quantitation of starch in live, unicellular microalgae. *Biotechnology Journal*, **2014**, 9, 1512-8	5.6	41
92	Raman-activated cell sorting and metagenomic sequencing revealing carbon-fixing bacteria in the ocean. *Environmental Microbiology*, **2018**, 20, 2241-2255	5.2	41
91	Structure and regulation of the cellulose degradome in Clostridium cellulolyticum. *Biotechnology for Biofuels*, **2013**, 6, 73	7.8	38
90	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. *Microbiome*, **2018**, 6, 200	16.6	38
89	Biosynthesis of Triacylglycerol Molecules with a Tailored PUFA Profile in Industrial Microalgae. *Molecular Plant*, **2019**, 12, 474-488	14.4	37
88	Correlation of genomic and physiological traits of thermoanaerobacter species with biofuel yields. *Applied and Environmental Microbiology*, **2011**, 77, 7998-8008	4.8	36
87	Knockdown of carbonate anhydrase elevates Nannochloropsis productivity at high CO level. *Metabolic Engineering*, **2019**, 54, 96-108	9.7	34

86	Meta-Storms: efficient search for similar microbial communities based on a novel indexing scheme and similarity score for metagenomic data. *Bioinformatics*, **2012**, 28, 2493-501	7.2	34
85	Ramanome technology platform for label-free screening and sorting of microbial cell factories at single-cell resolution. *Biotechnology Advances*, **2019**, 37, 107388	17.8	33
84	The Thermoanaerobacter glycobiome reveals mechanisms of pentose and hexose co-utilization in bacteria. *PLoS Genetics*, **2011**, 7, e1002318	6	32
83	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. *Journal of Insect Science*, **2016**, 16,	2	31
82	Label-free, simultaneous quantification of starch, protein and triacylglycerol in single microalgal cells. *Biotechnology for Biofuels*, **2017**, 10, 275	7.8	30
81	Genomic and transcriptome analyses reveal that MAPK- and phosphatidylinositol-signaling pathways mediate tolerance to 5-hydroxymethyl-2-furaldehyde for industrial yeast Saccharomyces cerevisiae. *Scientific Reports*, **2014**, 4, 6556	4.9	29
80	Parallel-META: efficient metagenomic data analysis based on high-performance computation. *BMC Systems Biology*, **2012**, 6 Suppl 1, S16	3.5	29
79	Cellulosome stoichiometry in Clostridium cellulolyticum is regulated by selective RNA processing and stabilization. *Nature Communications*, **2015**, 6, 6900	17.4	27
78	Ultrasound-mediated DNA transformation in thermophilic gram-positive anaerobes. *PLoS ONE*, **2010**, 5, e12582	3.7	27
77	Metabolic Remodeling of Membrane Glycerolipids in the Microalga Nannochloropsis oceanica under Nitrogen Deprivation. *Frontiers in Marine Science*, **2017**, 4,	4.5	26
76	Microbial Community Changes Along a Land-Use Gradient of Desert Soil Origin. *Pedosphere*, **2012**, 22, 593-603	5	25
75	Positive dielectrophoresis-based Raman-activated droplet sorting for culture-free and label-free screening of enzyme function in vivo. *Science Advances*, **2020**, 6, eabb3521	14.3	25
74	The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. *ISME Journal*, **2013**, 7, 1974-84	11.9	24
73	Transcriptomic and proteomic responses to very low CO suggest multiple carbon concentrating mechanisms in. *Biotechnology for Biofuels*, **2019**, 12, 168	7.8	23
72	Flavin mononucleotide (FMN)-based fluorescent protein (FbFP) as reporter for promoter screening in Clostridium cellulolyticum. *Journal of Microbiological Methods*, **2015**, 119, 37-43	2.8	23
71	Identifying and Predicting Novelty in Microbiome Studies. *MBio*, **2018**, 9,	7.8	21
70	A culture-independent approach to unravel uncultured bacteria and functional genes in a complex microbial community. *PLoS ONE*, **2012**, 7, e47530	3.7	20
69	Fosmid-based physical mapping of the Histoplasma capsulatum genome. *Genome Research*, **2004**, 14, 1603-9	9.7	20

68	Cetylpyridinium chloride mouth rinses alleviate experimental gingivitis by inhibiting dental plaque maturation. *International Journal of Oral Science*, **2016**, 8, 182-90	27.9	20
67	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. *Engineering*, **2017**, 3, 66-70	9.7	19
66	Single cell biotechnology to shed a light on biological Sdark matterSin nature. *Microbial Biotechnology*, **2015**, 8, 15-6	6.3	19
65	Microbiota-based Signature of Gingivitis Treatments: A Randomized Study. *Scientific Reports*, **2016**, 6, 24705	4.9	17
64	Lotus Leaf Aqueous Extract Reduces Visceral Fat Mass and Ameliorates Insulin Resistance in HFD-Induced Obese Rats by Regulating PPAR□ Expression. *Frontiers in Pharmacology*, **2017**, 8, 409	5.6	17
63	DNA extraction protocol for biological ingredient analysis of Liuwei Dihuang Wan. *Genomics, Proteomics and Bioinformatics*, **2014**, 12, 137-43	6.5	16
62	Genome assembly of provides evidence of host nucleus overthrow by the symbiont nucleus during speciation. *Communications Biology*, **2019**, 2, 249	6.7	15
61	A preliminary study of the mechanism of nitrate-stimulated remarkable increase of rifamycin production in Amycolatopsis mediterranei U32 by RNA-seq. *Microbial Cell Factories*, **2015**, 14, 75	6.4	15
60	A self-powered microfluidic monodispersed droplet generator with capability of multi-sample introduction. *Microfluidics and Nanofluidics*, **2015**, 18, 1067-1073	2.8	14
59	Phenome-Genome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing. *Small*, **2020**, 16, e2001172	11	13
58	MetaSee: an interactive and extendable visualization toolbox for metagenomic sample analysis and comparison. *PLoS ONE*, **2012**, 7, e48998	3.7	13
57	Establishing oleaginous microalgae research models for consolidated bioprocessing of solar energy. *Advances in Biochemical Engineering/Biotechnology*, **2012**, 128, 69-84	1.7	13
56	Development of HuMiChip for functional profiling of human microbiomes. *PLoS ONE*, **2014**, 9, e90546	3.7	13
55	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in Ettlia oleoabundans. *Algal Research*, **2018**, 33, 142-155	5	13
54	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. *MSystems*, **2019**, 4,	7.6	12
53	The NanDeSyn database for Nannochloropsis systems and synthetic biology. *Plant Journal*, **2020**, 104, 1736-1745	6.9	12
52	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. *MSystems*, **2020**, 5,	7.6	12
51	Microevolution from shock to adaptation revealed strategies improving ethanol tolerance and production in Thermoanaerobacter. *Biotechnology for Biofuels*, **2013**, 6, 103	7.8	11

50	Saliva microbiota carry caries-specific functional gene signatures. *PLoS ONE*, **2014**, 9, e76458	3.7	11
49	On-demand control of microfluidic flow via capillary-tuned solenoid microvalve suction. *Lab on A Chip*, **2014**, 14, 4599-603	7.2	11
48	Proteomic study uncovers molecular principles of single-cell-level phenotypic heterogeneity in lipid storage of. *Biotechnology for Biofuels*, **2019**, 12, 21	7.8	10
47	Integration of proteome and transcriptome refines key molecular processes underlying oil production in. *Biotechnology for Biofuels*, **2020**, 13, 109	7.8	10
46	Regulation of biomass degradation by alternative σfactors in cellulolytic clostridia. *Scientific Reports*, **2018**, 8, 11036	4.9	10
45	Near-Complete Genome Sequence of the Cellulolytic Bacterium Bacteroides (Pseudobacteroides) cellulosolvens ATCC 35603. *Genome Announcements*, **2015**, 3,		10
44	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. *MSystems*, **2021**, 6,	7.6	10
43	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. *MBio*, **2021**, 12,	7.8	9
42	Dynamic Meta-Storms enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. *Bioinformatics*, **2020**, 36, 2308-2310	7.2	8
41	Transcriptomic and proteomic choreography in response to light quality variation reveals key adaption mechanisms in marine Nannochloropsis oceanica. *Science of the Total Environment*, **2020**, 720, 137667	10.2	8
40	Protein expression analysis revealed a fine-tuned mechanism of in situ detoxification pathway for the tolerant industrial yeast Saccharomyces cerevisiae. *Applied Microbiology and Biotechnology*, **2019**, 103, 5781-5796	5.7	6
39	Rational Optimization of Raman-Activated Cell Ejection and Sequencing for Bacteria. *Analytical Chemistry*, **2020**, 92, 8081-8089	7.8	6
38	QSpec: online control and data analysis system for single-cell Raman spectroscopy. *PeerJ*, **2014**, 2, e436	3.1	6
37	Genome engineering of Nannochloropsis with hundred-kilobase fragment deletions by Cas9 cleavages. *Plant Journal*, **2021**, 106, 1148-1162	6.9	6
36	One-Cell Metabolic Phenotyping and Sequencing of Soil Microbiome by Raman-Activated Gravity-Driven Encapsulation (RAGE). *MSystems*, **2021**, 6, e0018121	7.6	6
35	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. *BMC Genomics*, **2021**, 22, 9	4.5	5
34	DO-Probed Raman Microspectroscopy Distinguishes the Metabolic Dynamics of Macromolecules in Organellar Anticancer Drug Response. *Analytical Chemistry*, **2021**, 93, 2125-2134	7.8	5
33	MapLinker: a software tool that aids physical map-linked whole genome shotgun assembly. *Bioinformatics*, **2005**, 21, 1265-6	7.2	4

32	A Palm Germ-Radar (PaGeR) for rapid and simple COVID-19 detection by reverse transcription loop-mediated isothermal amplification (RT-LAMP).. *Biosensors and Bioelectronics*, **2021**, 200, 113925	11.8	4
31	Manipulating fatty-acid profile at unit chain-length resolution in the model industrial oleaginous microalgae Nannochloropsis. *Metabolic Engineering*, **2021**, 66, 157-166	9.7	4
30	Optimized methods of chromatin immunoprecipitation for profiling histone modifications in industrial microalgae Nannochloropsis spp. *Journal of Phycology*, **2018**, 54, 358-367	3	3
29	Culture-Free Identification and Metabolic Profiling of Microalgal Single Cells via Ensemble Learning of Ramanomes. *Analytical Chemistry*, **2021**, 93, 8872-8880	7.8	3
28	Application of Meta-Mesh on the analysis of microbial communities from human associated-habitats. *Quantitative Biology*, **2015**, 3, 4-18	3.9	2
27	Efficient and Low-Cost Error Removal in DNA Synthesis by a High-Durability MutS. *ACS Synthetic Biology*, **2020**, 9, 940-952	5.7	2
26	A machine learning framework of functional biomarker discovery for different microbial communities based on metagenomic data **2012**,		2
25	Species-resolved sequencing of low-biomass or degraded microbiomes using 2bRAD-M.. *Genome Biology*, **2022**, 23, 36	18.3	2
24	JIB-04 Has Broad-Spectrum Antiviral Activity and Inhibits SARS-CoV-2 Replication and Coronavirus Pathogenesis.. *MBio*, **2022**, e0337721	7.8	2
23	Evolution of Ycf54-independent chlorophyll biosynthesis in cyanobacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2
22	Structural insight into a GH1 βglucosidase from the oleaginous microalga, Nannochloropsis oceanica. *International Journal of Biological Macromolecules*, **2021**, 170, 196-206	7.9	2
21	In vitro method for prediction of plaque reduction by dentifrice. *Journal of Microbiological Methods*, **2015**, 118, 85-92	2.8	1
20	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU **2013**,		1
19	An Open-source Collaboration Environment for Metagenomics Research **2011**,		1
18	Comprehensive understanding to the public health risk of environmental microbes via a microbiome-based index.. *Journal of Genetics and Genomics*, **2022**,	4	1
17	A scale-free, fully connected global transition network underlies known microbiome diversity		1
16	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Cellular Population		1
15	Phenome‐Genome Profiling: Phenome‐Genome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing (Small 30/2020). *Small*, **2020**, 16, 2070165	11	1

14	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. *MSystems*, **2021**, 6, e0039421	7.6	1
13	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Population of Cells. *MBio*, **2021**, 12, e0147021	7.8	1
12	A milliliter to picoliter-level centrifugal microfluidic concentrator for fast pathogen detection and antimicrobial susceptibility testing. *Sensors and Actuators B: Chemical*, **2021**, 343, 130117	8.5	1
11	The Oral Microbiome Bank of China **2020**, 287-300		0
10	Integrated Addressable Dynamic Droplet Array (aDDA) as Sub-Nanoliter Reactors for High-Coverage Genome Sequencing of Single Yeast Cells. *Small*, **2021**, 17, e2100325	11	0
9	Species-Resolved Metagenomics of Kindergarten Microbiomes Reveal Microbial Admixture Within Sites and Potential Microbial Hazards.. *Frontiers in Microbiology*, **2022**, 13, 871017	5.7	0
8	Exploring a blue-light-sensing transcription factor to double the peak productivity of oil in Nannochloropsis oceanica.. *Nature Communications*, **2022**, 13, 1664	17.4	0
7	Single-Cell Biotechnology for Uncultured Microorganisms. *Springer Protocols*, **2015**, 119-131	0.3	
6	Single-Cell and Systems Biology Tools for Biofuel Production. *Springer Protocols*, **2015**, 133-144	0.3	
5	Single-Cell Metabolomics. *Springer Protocols*, **2015**, 77-90	0.3	
4	Developing a medium combination to attain similar glycosylation profile to originator by DoE and cluster analysis method. *Scientific Reports*, **2021**, 11, 7103	4.9	
3	Predicting Selective RNA Processing and Stabilization Operons in spp. *Frontiers in Microbiology*, **2021**, 12, 673349	5.7	
2	Integrated Addressable Dynamic Droplet Array (aDDA) as Sub-Nanoliter Reactors for High-Coverage Genome Sequencing of Single Yeast Cells (Small 37/2021). *Small*, **2021**, 17, 2170191	11	
1	Assessing Efficacy of Clinical Disinfectants for Pathogenic Fungi by Single-Cell Raman Microspectroscopy.. *Frontiers in Cellular and Infection Microbiology*, **2022**, 12, 772378	5.9	