

Jian Xu

List of Publications by Year in Descending Order

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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.

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	Species-resolved sequencing of low-biomass or degraded microbiomes using 2bRAD-M.. <i>Genome Biology</i> , 2022 , 23, 36	18.3	2
138	JIB-04 Has Broad-Spectrum Antiviral Activity and Inhibits SARS-CoV-2 Replication and Coronavirus Pathogenesis.. <i>MBio</i> , 2022 , e0337721	7.8	2
137	Comprehensive understanding to the public health risk of environmental microbes via a microbiome-based index.. <i>Journal of Genetics and Genomics</i> , 2022 ,	4	1
136	Assessing Efficacy of Clinical Disinfectants for Pathogenic Fungi by Single-Cell Raman Microspectroscopy.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 772378	5.9	
135	Species-Resolved Metagenomics of Kindergarten Microbiomes Reveal Microbial Admixture Within Sites and Potential Microbial Hazards.. <i>Frontiers in Microbiology</i> , 2022 , 13, 871017	5.7	0
134	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	17.4	0
133	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> , 2021 , 200, 113925	11.8	4
132	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,	11.5	2
131	Developing a medium combination to attain similar glycosylation profile to originator by DoE and cluster analysis method. <i>Scientific Reports</i> , 2021 , 11, 7103	4.9	
130	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. <i>MBio</i> , 2021 , 12,	7.8	9
129	Genome engineering of <i>Nannochloropsis</i> with hundred-kilobase fragment deletions by Cas9 cleavages. <i>Plant Journal</i> , 2021 , 106, 1148-1162	6.9	6
128	One-Cell Metabolic Phenotyping and Sequencing of Soil Microbiome by Raman-Activated Gravity-Driven Encapsulation (RAGE). <i>MSystems</i> , 2021 , 6, e0018121	7.6	6
127	Culture-Free Identification and Metabolic Profiling of Microalgal Single Cells via Ensemble Learning of Ramanomes. <i>Analytical Chemistry</i> , 2021 , 93, 8872-8880	7.8	3
126	Predicting Selective RNA Processing and Stabilization Operons in spp. <i>Frontiers in Microbiology</i> , 2021 , 12, 673349	5.7	
125	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	9.7	4
124	Integrated Addressable Dynamic Droplet Array (aDDA) as Sub-Nanoliter Reactors for High-Coverage Genome Sequencing of Single Yeast Cells. <i>Small</i> , 2021 , 17, e2100325	11	0
123	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	7.9	2

122	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. <i>BMC Genomics</i> , 2021 , 22, 9	4.5	5
121	DO-Probed Raman Microspectroscopy Distinguishes the Metabolic Dynamics of Macromolecules in Organellar Anticancer Drug Response. <i>Analytical Chemistry</i> , 2021 , 93, 2125-2134	7.8	5
120	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. <i>MSystems</i> , 2021 , 6,	7.6	10
119	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , 2021 , 6, e0039421	7.6	1
118	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Population of Cells. <i>MBio</i> , 2021 , 12, e0147021	7.8	1
117	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	11	
116	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	8.5	1
115	The NanDeSyn database for Nannochloropsis systems and synthetic biology. <i>Plant Journal</i> , 2020 , 104, 1736-1745	6.9	12
114	Rational Optimization of Raman-Activated Cell Ejection and Sequencing for Bacteria. <i>Analytical Chemistry</i> , 2020 , 92, 8081-8089	7.8	6
113	Integration of proteome and transcriptome refines key molecular processes underlying oil production in. <i>Biotechnology for Biofuels</i> , 2020 , 13, 109	7.8	10
112	Phenome-Genome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing. <i>Small</i> , 2020 , 16, e2001172	11	13
111	Efficient and Low-Cost Error Removal in DNA Synthesis by a High-Durability MutS. <i>ACS Synthetic Biology</i> , 2020 , 9, 940-952	5.7	2
110	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020 , 5,	7.6	12
109	The Oral Microbiome Bank of China 2020 , 287-300		0
108	Dynamic Meta-Storms enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. <i>Bioinformatics</i> , 2020 , 36, 2308-2310	7.2	8
107	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	14.3	25
106	PhenomeGenome Profiling: PhenomeGenome Profiling of Single Bacterial Cell by Raman-Activated Gravity-Driven Encapsulation and Sequencing (Small 30/2020). <i>Small</i> , 2020 , 16, 2070165	11	1
105	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	10.2	8

104	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. <i>MSystems</i> , 2019 , 4,	7.6	12
103	Biosynthesis of Triacylglycerol Molecules with a Tailored PUFA Profile in Industrial Microalgae. <i>Molecular Plant</i> , 2019 , 12, 474-488	14.4	37
102	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	5.7	6
101	Ramanome technology platform for label-free screening and sorting of microbial cell factories at single-cell resolution. <i>Biotechnology Advances</i> , 2019 , 37, 107388	17.8	33
100	Knockdown of carbonate anhydrase elevates <i>Nannochloropsis</i> productivity at high CO level. <i>Metabolic Engineering</i> , 2019 , 54, 96-108	9.7	34
99	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
98	Genome assembly of provides evidence of host nucleus overthrow by the symbiont nucleus during speciation. <i>Communications Biology</i> , 2019 , 2, 249	6.7	15
97	Transcriptomic and proteomic responses to very low CO suggest multiple carbon concentrating mechanisms in. <i>Biotechnology for Biofuels</i> , 2019 , 12, 168	7.8	23
96	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	3	3
95	Regulation of biomass degradation by alternative Γ factors in cellulolytic clostridia. <i>Scientific Reports</i> , 2018 , 8, 11036	4.9	10
94	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. <i>Microbiome</i> , 2018 , 6, 200	16.6	38
93	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018 , 9,	7.8	21
92	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. <i>Scientific Reports</i> , 2018 , 8, 16321	4.9	74
91	Raman-activated cell sorting and metagenomic sequencing revealing carbon-fixing bacteria in the ocean. <i>Environmental Microbiology</i> , 2018 , 20, 2241-2255	5.2	41
90	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	5	13
89	Development of a facile droplet-based single-cell isolation platform for cultivation and genomic analysis in microorganisms. <i>Scientific Reports</i> , 2017 , 7, 41192	4.9	51
88	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
87	Metabolic-Activity-Based Assessment of Antimicrobial Effects by DO-Labeled Single-Cell Raman Microspectroscopy. <i>Analytical Chemistry</i> , 2017 , 89, 4108-4115	7.8	87

86	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. <i>Engineering</i> , 2017 , 3, 66-70	9.7	19
85	Producing Designer Oils in Industrial Microalgae by Rational Modulation of Co-evolving Type-2 Diacylglycerol Acyltransferases. <i>Molecular Plant</i> , 2017 , 10, 1523-1539	14.4	78
84	Label-free, simultaneous quantification of starch, protein and triacylglycerol in single microalgal cells. <i>Biotechnology for Biofuels</i> , 2017 , 10, 275	7.8	30
83	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. <i>Microbiome</i> , 2017 , 5, 91	16.6	104
82	Enhancing photosynthetic biomass productivity of industrial oleaginous microalgae by overexpression of RuBisCO activase. <i>Algal Research</i> , 2017 , 27, 366-375	5	57
81	Raman-Activated Droplet Sorting (RADS) for Label-Free High-Throughput Screening of Microalgal Single-Cells. <i>Analytical Chemistry</i> , 2017 , 89, 12569-12577	7.8	76
80	RNAi-based targeted gene knockdown in the model oleaginous microalgae <i>Nannochloropsis oceanica</i> . <i>Plant Journal</i> , 2017 , 89, 1236-1250	6.9	51
79	Lotus Leaf Aqueous Extract Reduces Visceral Fat Mass and Ameliorates Insulin Resistance in HFD-Induced Obese Rats by Regulating PPAR α Expression. <i>Frontiers in Pharmacology</i> , 2017 , 8, 409	5.6	17
78	Metabolic Remodeling of Membrane Glycerolipids in the Microalga <i>Nannochloropsis oceanica</i> under Nitrogen Deprivation. <i>Frontiers in Marine Science</i> , 2017 , 4,	4.5	26
77	Genome editing of model oleaginous microalgae <i>Nannochloropsis</i> spp. by CRISPR/Cas9. <i>Plant Journal</i> , 2016 , 88, 1071-1081	6.9	170
76	Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. <i>Scientific Reports</i> , 2016 , 6, 20602	4.9	142
75	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. <i>Journal of Insect Science</i> , 2016 , 16,	2	31
74	Microbiota-based Signature of Gingivitis Treatments: A Randomized Study. <i>Scientific Reports</i> , 2016 , 6, 24705	4.9	17
73	Label-free, rapid and quantitative phenotyping of stress response in <i>E. coli</i> via ramanome. <i>Scientific Reports</i> , 2016 , 6, 34359	4.9	58
72	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	7.8	52
71	Cetylpyridinium chloride mouth rinses alleviate experimental gingivitis by inhibiting dental plaque maturation. <i>International Journal of Oral Science</i> , 2016 , 8, 182-90	27.9	20
70	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
69	Cellulosome stoichiometry in <i>Clostridium cellulolyticum</i> is regulated by selective RNA processing and stabilization. <i>Nature Communications</i> , 2015 , 6, 6900	17.4	27

68	A self-powered microfluidic monodispersed droplet generator with capability of multi-sample introduction. <i>Microfluidics and Nanofluidics</i> , 2015 , 18, 1067-1073	2.8	14
67	Single-Cell Biotechnology for Uncultured Microorganisms. <i>Springer Protocols</i> , 2015 , 119-131	0.3	
66	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp. <i>Plant Physiology</i> , 2015 , 169, 2444-61	6.6	89
65	Towards high-throughput microfluidic Raman-activated cell sorting. <i>Analyst, The</i> , 2015 , 140, 6163-74	5	55
64	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015 , 18, 296-306	23.4	123
63	In vitro method for prediction of plaque reduction by dentifrice. <i>Journal of Microbiological Methods</i> , 2015 , 118, 85-92	2.8	1
62	Single-Cell and Systems Biology Tools for Biofuel Production. <i>Springer Protocols</i> , 2015 , 133-144	0.3	
61	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	5	145
60	Magnetic nanoparticle-mediated isolation of functional bacteria in a complex microbial community. <i>ISME Journal</i> , 2015 , 9, 603-14	11.9	63
59	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	6.4	15
58	Near-Complete Genome Sequence of the Cellulolytic Bacterium <i>Bacteroides</i> (<i>Pseudobacteroides</i>) <i>cellulosolvens</i> ATCC 35603. <i>Genome Announcements</i> , 2015 , 3,		10
57	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	2.8	23
56	Single-Cell Metabolomics. <i>Springer Protocols</i> , 2015 , 77-90	0.3	
55	Phytohormones in microalgae: a new opportunity for microalgal biotechnology?. <i>Trends in Plant Science</i> , 2015 , 20, 273-282	13.1	183
54	Single cell biotechnology to shed a light on biological dark matter in nature. <i>Microbial Biotechnology</i> , 2015 , 8, 15-6	6.3	19
53	Raman-activated cell sorting based on dielectrophoretic single-cell trap and release. <i>Analytical Chemistry</i> , 2015 , 87, 2282-9	7.8	106
52	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
51	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

50	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
49	Raman spectroscopy provides a rapid, non-invasive method for quantitation of starch in live, unicellular microalgae. <i>Biotechnology Journal</i> , 2014 , 9, 1512-8	5.6	41
48	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	6.9	75
47	Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. <i>Biotechnology for Biofuels</i> , 2014 , 7, 58	7.8	53
46	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	7.8	58
45	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. <i>ISME Journal</i> , 2014 , 8, 1768-80	11.9	70
44	DNA extraction protocol for biological ingredient analysis of Liuwei Dihuang Wan. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 137-43	6.5	16
43	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
42	Saliva microbiota carry caries-specific functional gene signatures. <i>PLoS ONE</i> , 2014 , 9, e76458	3.7	11
41	On-demand control of microfluidic flow via capillary-tuned solenoid microvalve suction. <i>Lab on a Chip</i> , 2014 , 14, 4599-603	7.2	11
40	<i>Nannochloropsis</i> genomes reveal evolution of microalgal oleaginous traits. <i>PLoS Genetics</i> , 2014 , 10, e1004094	10.4	173
39	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
38	Development of HuMiChip for functional profiling of human microbiomes. <i>PLoS ONE</i> , 2014 , 9, e90546	3.7	13
37	QSpec: online control and data analysis system for single-cell Raman spectroscopy. <i>PeerJ</i> , 2014 , 2, e4363	3.1	6
36	Structure and regulation of the cellulose degradome in <i>Clostridium cellulolyticum</i> . <i>Biotechnology for Biofuels</i> , 2013 , 6, 73	7.8	38
35	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU		1
34	Microevolution from shock to adaptation revealed strategies improving ethanol tolerance and production in <i>Thermoanaerobacter</i> . <i>Biotechnology for Biofuels</i> , 2013 , 6, 103	7.8	11
33	<i>Nannochloropsis</i> plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. <i>BMC Genomics</i> , 2013 , 14, 534	4.5	45

32	The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. <i>ISME Journal</i> , 2013 , 7, 1974-84	11.9	24
31	Dissecting and engineering metabolic and regulatory networks of thermophilic bacteria for biofuel production. <i>Biotechnology Advances</i> , 2013 , 31, 827-37	17.8	44
30	Raman activated cell ejection for isolation of single cells. <i>Analytical Chemistry</i> , 2013 , 85, 10697-701	7.8	80
29	QC-Chain: fast and holistic quality control method for next-generation sequencing data. <i>PLoS ONE</i> , 2013 , 8, e60234	3.7	49
28	Single cell Raman spectroscopy for cell sorting and imaging. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 56-63	11.4	154
27	Parallel-META: efficient metagenomic data analysis based on high-performance computation. <i>BMC Systems Biology</i> , 2012 , 6 Suppl 1, S16	3.5	29
26	A machine learning framework of functional biomarker discovery for different microbial communities based on metagenomic data 2012 ,		2
25	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012 , 6, 1-10	11.9	245
24	Microbial Community Changes Along a Land-Use Gradient of Desert Soil Origin. <i>Pedosphere</i> , 2012 , 22, 593-603	5	25
23	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
22	MetaSee: an interactive and extendable visualization toolbox for metagenomic sample analysis and comparison. <i>PLoS ONE</i> , 2012 , 7, e48998	3.7	13
21	Establishing oleaginous microalgae research models for consolidated bioprocessing of solar energy. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2012 , 128, 69-84	1.7	13
20	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
19	Metagenomic insights into the fibrolytic microbiome in yak rumen. <i>PLoS ONE</i> , 2012 , 7, e40430	3.7	71
18	Autotrophic growth of nitrifying community in an agricultural soil. <i>ISME Journal</i> , 2011 , 5, 1226-36	11.9	276
17	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. <i>BMC Oral Health</i> , 2011 , 11, 33	3.7	82
16	An Open-source Collaboration Environment for Metagenomics Research 2011 ,		1
15	Correlation of genomic and physiological traits of thermoanaerobacter species with biofuel yields. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7998-8008	4.8	36

14	The Thermoanaerobacter glyco biome reveals mechanisms of pentose and hexose co-utilization in bacteria. <i>PLoS Genetics</i> , 2011 , 7, e1002318	6	32
13	Factors influencing cellulosome activity in consolidated bioprocessing of cellulosic ethanol. <i>Bioresource Technology</i> , 2010 , 101, 9560-9	11	49
12	Ultrasound-mediated DNA transformation in thermophilic gram-positive anaerobes. <i>PLoS ONE</i> , 2010 , 5, e12582	3.7	27
11	Characterization of the central metabolic pathways in Thermoanaerobacter sp. strain X514 via isotopomer-assisted metabolite analysis. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5001-8	4.8	52
10	Novel features of the polysaccharide-digesting gliding bacterium Flavobacterium johnsoniae as revealed by genome sequence analysis. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6864-75	4.8	177
9	Evolution of symbiotic bacteria in the distal human intestine. <i>PLoS Biology</i> , 2007 , 5, e156	9.7	401
8	Glycan foraging in vivo by an intestine-adapted bacterial symbiont. <i>Science</i> , 2005 , 307, 1955-9	33.3	803
7	MapLinker: a software tool that aids physical map-linked whole genome shotgun assembly. <i>Bioinformatics</i> , 2005 , 21, 1265-6	7.2	4
6	Fosmid-based physical mapping of the Histoplasma capsulatum genome. <i>Genome Research</i> , 2004 , 14, 1603-9	9.7	20
5	Message from a human gut symbiont: sensitivity is a prerequisite for sharing. <i>Trends in Microbiology</i> , 2004 , 12, 21-8	12.4	77
4	Honor thy symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10452-9	11.5	687
3	A genomic view of the human-Bacteroides thetaiotaomicron symbiosis. <i>Science</i> , 2003 , 299, 2074-6	33.3	1005
2	A scale-free, fully connected global transition network underlies known microbiome diversity		1
1	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Cellular Population		1