Chongle Pan

List of Publications by Year
in descending order

81 papers	4,464 citations	94433 37 h-index	110387 64 g-index
85 all docs	85 docs citations	85 times ranked	6722 citing authors

#	Article	IF	Citations
1	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138.	2.5	374
2	Systematic Comparison of Label-Free, Metabolic Labeling, and Isobaric Chemical Labeling for Quantitative Proteomics on LTQ Orbitrap Velos. Journal of Proteome Research, 2012, 11, 1582-1590.	3.7	301
3	Effects of Diet on Resource Utilization by a Model Human Gut Microbiota Containing Bacteroides cellulosilyticus WH2, a Symbiont with an Extensive Glycobiome. PLoS Biology, 2013, 11, e1001637.	5.6	244
4	Impact of Pretreated Switchgrass and Biomass Carbohydrates on Clostridium thermocellum ATCC 27405 Cellulosome Composition: A Quantitative Proteomic Analysis. PLoS ONE, 2009, 4, e5271.	2.5	206
5	Mediterranean grassland soil C–N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. Nature Microbiology, 2019, 4, 1356-1367.	13.3	170
6	Efficient and Specific Trypsin Digestion of Microgram to Nanogram Quantities of Proteins in Organic–Aqueous Solvent Systems. Analytical Chemistry, 2006, 78, 125-134.	6.5	168
7	*Metaproteomics*: Harnessing the Power of High Performance Mass Spectrometry to Identify the Suite of Proteins That Control Metabolic Activities in Microbial Communities. Analytical Chemistry, 2013, 85, 4203-4214.	6.5	165
8	Microbial metaproteomics for characterizing the range of metabolic functions and activities of human gut microbiota. Proteomics, 2015, 15, 3424-3438.	2.2	126
9	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. PeerJ, 2016, 4, e2687.	2.0	124
10	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. Nature Ecology and Evolution, 2018, 2, 499-509.	7.8	116
11	Improved genome annotation for Zymomonas mobilis. Nature Biotechnology, 2009, 27, 893-894.	17.5	107
12	ProRata: A Quantitative Proteomics Program for Accurate Protein Abundance Ratio Estimation with Confidence Interval Evaluation. Analytical Chemistry, 2006, 78, 7121-7131.	6.5	97
13	MIDAS: A Database-Searching Algorithm for Metabolite Identification in Metabolomics. Analytical Chemistry, 2014, 86, 9496-9503.	6.5	97
14	Sigma: Strain-level inference of genomes from metagenomic analysis for biosurveillance. Bioinformatics, 2015, 31, 170-177.	4.1	90
15	Phage-Induced Expression of CRISPR-Associated Proteins Is Revealed by Shotgun Proteomics in Streptococcus thermophilus. PLoS ONE, 2012, 7, e38077.	2.5	88
16	Selenium-Assisted Nucleic Acid Crystallography: Use of Phosphoroselenoates for MAD Phasing of a DNA Structure. Journal of the American Chemical Society, 2002, 124, 14910-14916.	13.7	83
17	Omega: an Overlap-graph *de novo* Assembler for Metagenomics. Bioinformatics, 2014, 30, 2717-2722.	4.1	83
18	Phylogenetically conserved resource partitioning in the coastal microbial loop. ISME Journal, 2017, 11, 2781-2792.	9.8	82

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19	Quantitative Tracking of Isotope Flows in Proteomes of Microbial Communities. Molecular and Cellular Proteomics, 2011, 10, M110.006049.	3.8	77
20	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Frontiers in Microbiology, 2016, 7, 238.	3.5	66
21	Cultivation and quantitative proteomic analyses of acidophilic microbial communities. ISME Journal, 2010, 4, 520-530.	9.8	65
22	Characterization of Anaerobic Catabolism of p-Coumarate in Rhodopseudomonas palustris by Integrating Transcriptomics and Quantitative Proteomics. Molecular and Cellular Proteomics, 2008, 7, 938-948.	3.8	64
23	Systems Biology Analysis of Zymomonas mobilis ZM4 Ethanol Stress Responses. PLoS ONE, 2013, 8, e68886.	2.5	64
24	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. PLoS ONE, 2011, 6, e27173.	2.5	58
25	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. ISME Journal, 2015, 9, 180-194.	9.8	57
26	Elucidation of Zymomonas mobilis physiology and stress responses by quantitative proteomics and transcriptomics. Frontiers in Microbiology, 2014, 5, 246.	3.5	54
27	Metaproteomics reveals functional shifts in microbial and human proteins during a preterm infant gut colonization case. Proteomics, 2015, 15, 3463-3473.	2.2	54
28	Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. ISME Journal, 2011, 5, 1152-1161.	9.8	53
29	A high-throughput de novo sequencing approach for shotgun proteomics using high-resolution tandem mass spectrometry. BMC Bioinformatics, 2010, 11, 118.	2.6	52
30	Heterotrophic Archaea Contribute to Carbon Cycling in Low-pH, Suboxic Biofilm Communities. Applied and Environmental Microbiology, 2012, 78, 8321-8330.	3.1	52
31	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. Nature Communications, 2014, 5, 4405.	12.8	51
32	Proteome changes in the initial bacterial colonist during ecological succession in an acid mine drainage biofilm community. Environmental Microbiology, 2011, 13, 2279-2292.	3.8	49
33	^{15}N and ^{2}H proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. Environmental Microbiology, 2014, 16, 3224-3237.	3.8	48
34	Microbial Community Structure–Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. Frontiers in Microbiology, 2018, 9, 1282.	3.5	48
35	Geochemical, metagenomic and metaproteomic insights into trace metal utilization by methane-oxidizing microbial consortia in sulphidic marine sediments. Environmental Microbiology, 2014, 16, 1592-1611.	3.8	47
36	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. MSystems, 2016, 1, .	3.8	43

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37	A graph-theoretic approach for the separation of b and y ions in tandem mass spectra. Bioinformatics, 2005, 21, 563-574.	4.1	42
38	Robust Estimation of Peptide Abundance Ratios and Rigorous Scoring of Their Variability and Bias in Quantitative Shotgun Proteomics. Analytical Chemistry, 2006, 78, 7110-7120.	6.5	40
39	Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungal–endobacterial system. Environmental Microbiology, 2017, 19, 1041-1053.	3.8	38
40	Phytoplankton exudates and lysates support distinct microbial consortia with specialized metabolic and ecophysiological traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
41	Sipros Ensemble improves database searching and filtering for complex metaproteomics. Bioinformatics, 2018, 34, 795-802.	4.1	35
42	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. Frontiers in Microbiology, 2016, 7, 563.	3.5	34
43	Deep neural network improves the estimation of polygenic risk scores for breast cancer. Journal of Human Genetics, 2021, 66, 359-369.	2.3	31
44	Structural Rationalization of a Large Difference in RNA Affinity Despite a Small Difference in Chemistry between Two 2′-O-Modified Nucleic Acid Analogues. Journal of the American Chemical Society, 2004, 126, 15006-15007.	13.7	30
45	Stable-Isotope Probing Reveals That Hydrogen Isotope Fractionation in Proteins and Lipids in a Microbial Community Are Different and Species-Specific. ACS Chemical Biology, 2013, 8, 1755-1763.	3.4	30
46	Sipros/ProRata: a versatile informatics system for quantitative community proteomics. Bioinformatics, 2013, 29, 2064-2065.	4.1	30
47	Complete genome sequence of the aquatic bacterium Runella slithyformis type strain (LSU 4T). Standards in Genomic Sciences, 2012, 6, 145-154.	1.5	24
48	Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in <i>Arabidopsis</i>. Journal of Proteome Research, 2014, 13, 1359-1372.	3.7	24
49	Proteomic and Mutant Analysis of the CO_2 Concentrating Mechanism of Hydrothermal Vent Chemolithoautotroph Thiomicrospira crunogena. Journal of Bacteriology, 2017, 199, .	2.2	24
50	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute Sulfobacillus acidophilus type strain (NALT). Standards in Genomic Sciences, 2012, 6, 293-303.	1.5	23
51	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using 13CO2 and 13C-Methanol. Frontiers in Microbiology, 2019, 10, 2706.	3.5	23
52	Isolation and chemical analysis of nanoparticles from English ivy (<i>Hedera helix</i> L.). Journal of the Royal Society Interface, 2013, 10, 20130392.	3.4	22
53	Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. BMC Evolutionary Biology, 2014, 14, 207.	3.2	22
54	Mass spectrometric approaches for characterizing bacterial proteomes. Expert Review of Proteomics, 2004, 1, 433-447.	3.0	17

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55	Phenotype Fingerprinting Suggests the Involvement of Single-Genotype Consortia in Degradation of Aromatic Compounds by Rhodopseudomonas palustris. PLoS ONE, 2009, 4, e4615.	2.5	17
56	Quantitative Metaproteomics: Functional Insights into Microbial Communities. Methods in Molecular Biology, 2014, 1096, 231-240.	0.9	16
57	Exhaustive database searching for amino acid mutations in proteomes. Bioinformatics, 2012, 28, 1895-1901.	4.1	14
58	Deep-learning-aided forward optical coherence tomography endoscope for percutaneous nephrostomy guidance. Biomedical Optics Express, 2021, 12, 2404.	2.9	12
59	Complete genome sequence of the thermophilic sulfur-reducer Desulfurobacterium thermolithotrophum type strain (BSAT) from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 2011, 5, 407-415.	1.5	11
60	Sample Handling and Mass Spectrometry for Microbial Metaproteomic Analyses. Methods in Enzymology, 2013, 531, 289-303.	1.0	11
61	Genome sequence of the free-living aerobic spirochete Turneriella parva type strain (HT), and emendation of the species Turneriella parva. Standards in Genomic Sciences, 2013, 8, 228-238.	1.5	11
62	Complete genome sequence of the facultatively anaerobic, appendaged bacterium Muricauda ruestringensis type strain (B1T). Standards in Genomic Sciences, 2012, 6, 185-193.	1.5	10
63	Multipole-Storage-Assisted Dissociation for the Characterization of Large Proteins and Simple Protein Mixtures by ESI-FTICR-MS. Analytical Chemistry, 2005, 77, 3072-3082.	6.5	9
64	High performance statistical computing with parallel R: applications to biology and climate modelling. Journal of Physics: Conference Series, 2006, 46, 505-509.	0.4	9
65	The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in Populus trichocarpa. Genome Biology and Evolution, 2021, 13, .	2.5	9
66	Epidural anesthesia needle guidance by forward-view endoscopic optical coherence tomography and deep learning. Scientific Reports, 2022, 12, .	3.3	9
67	Complete genome sequence of the aerobic, heterotroph Marinithermus hydrothermalis type strain (T1T) from a deep-sea hydrothermal vent chimney. Standards in Genomic Sciences, 2012, 6, 21-30.	1.5	8
68	Genomic Features and Pervasive Negative Selection in <i>Rhodanobacter</i> Strains Isolated from Nitrate and Heavy Metal Contaminated Aquifer. Microbiology Spectrum, 2022, 10, e0259121.	3.0	8
69	Islet autoantibody seroconversion in type-1 diabetes is associated with metagenome-assembled genomes in infant gut microbiomes. Nature Communications, 2022, 13, .	12.8	8
70	Metagenome Sequencing of a Coastal Marine Microbial Community from Monterey Bay, California. Genome Announcements, 2015, 3, .	0.8	6
71	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing Î³-proteobacterium Thioalkalimicrobium cyclicum type strain ALM 1 (DSM 14477T). Standards in Genomic Sciences, 2016, 11, 38.	1.5	6
72	Measuring Dissociation Rate Constants of Protein Complexes through Subunit Exchange: Experimental Design and Theoretical Modeling. PLoS ONE, 2011, 6, e28827.	2.5	5

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73	*Rhodopseudomonas palustris* CGA010 Proteome Implicates Extracytoplasmic Function Sigma Factor in Stress Response. Journal of Proteome Research, 2015, 14, 2158-2168.	3.7	5
74	Computer‐aided Veress needle guidance using endoscopic optical coherence tomography and convolutional neural networks. Journal of Biophotonics, 2022, 15, e202100347.	2.3	5
75	LINA: A Linearizing Neural Network Architecture for Accurate First-Order and Second-Order Interpretations. IEEE Access, 2022, 10, 36166-36176.	4.2	5
76	Phenylpropanoid Biosynthesis Gene Expression Precedes Lignin Accumulation During Shoot Development in Lowland and Upland Switchgrass Genotypes. Frontiers in Plant Science, 2021, 12, 640930.	3.6	4
77	SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud. , 2018, , .		2
78	Using Apache Spark on genome assembly for scalable overlap-graph reduction. Human Genomics, 2019, 13, 48.	2.9	2
79	Conceptualizing a Genomics Software Institute (GSI). Standards in Genomic Sciences, 2012, 6, 136-144.	1.5	1
80	Genome Sequences of 42 Bacteria Isolated from Sorghum bicolor Roots. Microbiology Resource Announcements, 2020, 9, .	0.6	1
81	In Silico Recognition of Protein-Protein Interaction. , 2006, , 248-268.		0