# Chongle Pan

List of Publications by Year
in descending order

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|---|---|---|---|
| 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 | 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 |
| 2 | Computer‑aided Veress needle guidance using endoscopic optical coherence tomography and convolutional neural networks. Journal of Biophotonics, 2022, 15, e202100347. | 2.3 | 5 |
| 3 | LINA: A Linearizing Neural Network Architecture for Accurate First-Order and Second-Order Interpretations. IEEE Access, 2022, 10, 36166-36176. | 4.2 | 5 |
| 4 | Epidural anesthesia needle guidance by forward-view endoscopic optical coherence tomography and deep learning. Scientific Reports, 2022, 12, . | 3.3 | 9 |
| 5 | Islet autoantibody seroconversion in type-1 diabetes is associated with metagenome-assembled genomes in infant gut microbiomes. Nature Communications, 2022, 13, . | 12.8 | 8 |
| 6 | Deep neural network improves the estimation of polygenic risk scores for breast cancer. Journal of Human Genetics, 2021, 66, 359-369. | 2.3 | 31 |
| 7 | Deep-learning-aided forward optical coherence tomography endoscope for percutaneous nephrostomy guidance. Biomedical Optics Express, 2021, 12, 2404. | 2.9 | 12 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | Genome Sequences of 42 Bacteria Isolated from Sorghum bicolor Roots. Microbiology Resource Announcements, 2020, 9, . | 0.6 | 1 |
| 12 | Using Apache Spark on genome assembly for scalable overlap-graph reduction. Human Genomics, 2019, 13, 48. | 2.9 | 2 |
| 13 | 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 |
| 14 | Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using 13CO2 and 13C-Methanol. Frontiers in Microbiology, 2019, 10, 2706. | 3.5 | 23 |
| 15 | Sipros Ensemble improves database searching and filtering for complex metaproteomics. Bioinformatics, 2018, 34, 795-802. | 4.1 | 35 |
| 16 | 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 |
| 17 | SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud. , 2018, , . | | 2 |
| 18 | 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 |

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|---|---------|-----|-----------|
| 19 | Proteomic and Mutant Analysis of the $CO_2$ Concentrating Mechanism of Hydrothermal Vent Chemolithoautotroph Thiomicrospira crunogena. Journal of Bacteriology, 2017, 199, . | 2.2 | 24 |
| 20 | Phylogenetically conserved resource partitioning in the coastal microbial loop. ISME Journal, 2017, 11, 2781-2792. | 9.8 | 82 |
| 21 | Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungal€endobacterial system. Environmental Microbiology, 2017, 19, 1041-1053. | 3.8 | 38 |
| 22 | 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 |
| 23 | Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. Frontiers in Microbiology, 2016, 7, 563. | 3.5 | 34 |
| 24 | 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 |
| 25 | Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. MSystems, 2016, 1, . | 3.8 | 43 |
| 26 | Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. PeerJ, 2016, 4, e2687. | 2.0 | 124 |
| 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 | Sigma: Strain-level inference of genomes from metagenomic analysis for biosurveillance. Bioinformatics, 2015, 31, 170-177. | 4.1 | 90 |
| 29 | Metagenome Sequencing of a Coastal Marine Microbial Community from Monterey Bay, California. Genome Announcements, 2015, 3, . | 0.8 | 6 |
| 30 | *Rhodopseudomonas palustris* CGA010 Proteome Implicates Extracytoplasmic Function Sigma Factor in Stress Response. Journal of Proteome Research, 2015, 14, 2158-2168. | 3.7 | 5 |
| 31 | Microbial metaproteomics for characterizing the range of metabolic functions and activities of human gut microbiota. Proteomics, 2015, 15, 3424-3438. | 2.2 | 126 |
| 32 | Elevated temperature alters proteomic responses of individual organisms within a biofilm community. ISME Journal, 2015, 9, 180-194. | 9.8 | 57 |
| 33 | Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. BMC Evolutionary Biology, 2014, 14, 207. | 3.2 | 22 |
| 34 | Elucidation of Zymomonas mobilis physiology and stress responses by quantitative proteomics and transcriptomics. Frontiers in Microbiology, 2014, 5, 246. | 3.5 | 54 |
| 35 | Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. Nature Communications, 2014, 5, 4405. | 12.8 | 51 |
| 36 | Quantitative Metaproteomics: Functional Insights into Microbial Communities. Methods in Molecular Biology, 2014, 1096, 231-240. | 0.9 | 16 |

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|---|---------|----|-----------|
| 37 | $^{15}$N and $^{2}$H proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. Environmental Microbiology, 2014, 16, 3224-3237. | 3.8 | 48 |
| 38 | 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 |
| 39 | MIDAS: A Database-Searching Algorithm for Metabolite Identification in Metabolomics. Analytical Chemistry, 2014, 86, 9496-9503. | 6.5 | 97 |
| 40 | Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in *Arabidopsis*. Journal of Proteome Research, 2014, 13, 1359-1372. | 3.7 | 24 |
| 41 | Omega: an Overlap-graph *de novo* Assembler for Metagenomics. Bioinformatics, 2014, 30, 2717-2722. | 4.1 | 83 |
| 42 | Sample Handling and Mass Spectrometry for Microbial Metaproteomic Analyses. Methods in Enzymology, 2013, 531, 289-303. | 1.0 | 11 |
| 43 | *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 |
| 44 | 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 |
| 45 | Sipros/ProRata: a versatile informatics system for quantitative community proteomics. Bioinformatics, 2013, 29, 2064-2065. | 4.1 | 30 |
| 46 | 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 |
| 47 | Isolation and chemical analysis of nanoparticles from English ivy ( *Hedera helix* L.). Journal of the Royal Society Interface, 2013, 10, 20130392. | 3.4 | 22 |
| 48 | 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 |
| 49 | Systems Biology Analysis of Zymomonas mobilis ZM4 Ethanol Stress Responses. PLoS ONE, 2013, 8, e68886. | 2.5 | 64 |
| 50 | Heterotrophic Archaea Contribute to Carbon Cycling in Low-pH, Suboxic Biofilm Communities. Applied and Environmental Microbiology, 2012, 78, 8321-8330. | 3.1 | 52 |
| 51 | 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 |
| 52 | 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 |
| 53 | Conceptualizing a Genomics Software Institute (GSI). Standards in Genomic Sciences, 2012, 6, 136-144. | 1.5 | 1 |
| 54 | 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 |

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|---|---------|-----|-----------|
| 55 | Complete genome sequence of the aquatic bacterium Runella slithyformis type strain (LSU 4T). Standards in Genomic Sciences, 2012, 6, 145-154. | 1.5 | 24 |
| 56 | 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 |
| 57 | Phage-Induced Expression of CRISPR-Associated Proteins Is Revealed by Shotgun Proteomics in Streptococcus thermophilus. PLoS ONE, 2012, 7, e38077. | 2.5 | 88 |
| 58 | Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138. | 2.5 | 374 |
| 59 | Exhaustive database searching for amino acid mutations in proteomes. Bioinformatics, 2012, 28, 1895-1901. | 4.1 | 14 |
| 60 | Measuring Dissociation Rate Constants of Protein Complexes through Subunit Exchange: Experimental Design and Theoretical Modeling. PLoS ONE, 2011, 6, e28827. | 2.5 | 5 |
| 61 | Quantitative Tracking of Isotope Flows in Proteomes of Microbial Communities. Molecular and Cellular Proteomics, 2011, 10, M110.006049. | 3.8 | 77 |
| 62 | 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 |
| 63 | 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 |
| 64 | Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. ISME Journal, 2011, 5, 1152-1161. | 9.8 | 53 |
| 65 | Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. PLoS ONE, 2011, 6, e27173. | 2.5 | 58 |
| 66 | A high-throughput de novo sequencing approach for shotgun proteomics using high-resolution tandem mass spectrometry. BMC Bioinformatics, 2010, 11, 118. | 2.6 | 52 |
| 67 | Cultivation and quantitative proteomic analyses of acidophilic microbial communities. ISME Journal, 2010, 4, 520-530. | 9.8 | 65 |
| 68 | Improved genome annotation for Zymomonas mobilis. Nature Biotechnology, 2009, 27, 893-894. | 17.5 | 107 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | ProRata: Â A Quantitative Proteomics Program for Accurate Protein Abundance Ratio Estimation with Confidence Interval Evaluation. Analytical Chemistry, 2006, 78, 7121-7131. | 6.5 | 97 |

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|---|---------|----|-----------|
| 73 | Efficient and Specific Trypsin Digestion of Microgram to Nanogram Quantities of Proteins in Organicâˆ'Aqueous Solvent Systems. Analytical Chemistry, 2006, 78, 125-134. | 6.5 | 168 |
| 74 | 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 |
| 75 | 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 |
| 76 | In Silico Recognition of Protein-Protein Interaction. , 2006, , 248-268. | | 0 |
| 77 | A graph-theoretic approach for the separation of b and y ions in tandem mass spectra. Bioinformatics, 2005, 21, 563-574. | 4.1 | 42 |
| 78 | 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 |
| 79 | Mass spectrometric approaches for characterizing bacterial proteomes. Expert Review of Proteomics, 2004, 1, 433-447. | 3.0 | 17 |
| 80 | Structural Rationalization of a Large Difference in RNA Affinity Despite a Small Difference in Chemistry between Two 2â€²-O-Modified Nucleic Acid Analogues. Journal of the American Chemical Society, 2004, 126, 15006-15007. | 13.7 | 30 |
| 81 | Selenium-Assisted Nucleic Acid Crystallography:Â Use of Phosphoroselenoates for MAD Phasing of a DNA Structure. Journal of the American Chemical Society, 2002, 124, 14910-14916. | 13.7 | 83 |