

Masanori Arita, æœç”°æ-£è|•

List of Publications by Year in descending order

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105
papers

10,306
citations

87888

38
h-index

36028

97
g-index

108
all docs

108
docs citations

108
times ranked

12911
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | MS-DIAL: data-independent MS/MS deconvolution for comprehensive metabolome analysis. <i>Nature Methods</i> , 2015, 12, 523-526. | 19.0 | 1,955 |
| 2 | MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010, 45, 703-714. | 1.6 | 1,831 |
| 3 | From The Cover: Integration of transcriptomics and metabolomics for understanding of global responses to nutritional stresses in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10205-10210. | 7.1 | 726 |
| 4 | Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. <i>Analytical Chemistry</i> , 2016, 88, 7946-7958. | 6.5 | 441 |
| 5 | A lipidome atlas in MS-DIAL 4. <i>Nature Biotechnology</i> , 2020, 38, 1159-1163. | 17.5 | 424 |
| 6 | Identifying metabolites by integrating metabolome databases with mass spectrometry cheminformatics. <i>Nature Methods</i> , 2018, 15, 53-56. | 19.0 | 368 |
| 7 | Identification of small molecules using accurate mass MS/MS search. <i>Mass Spectrometry Reviews</i> , 2018, 37, 513-532. | 5.4 | 292 |
| 8 | The metabolic world of <i>Escherichia coli</i> is not small. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1543-1547. | 7.1 | 287 |
| 9 | MS-based lipidomics of human blood plasma: a community-initiated position paper to develop accepted guidelines. <i>Journal of Lipid Research</i> , 2018, 59, 2001-2017. | 4.2 | 231 |
| 10 | Metabolomic correlation-network modules in <i>Arabidopsis</i> based on a graph-clustering approach. <i>BMC Systems Biology</i> , 2011, 5, 1. | 3.0 | 215 |
| 11 | Integrated omics approaches in plant systems biology. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 532-538. | 6.1 | 201 |
| 12 | DFAST and DAGA: web-based integrated genome annotation tools and resources. <i>Bioscience of Microbiota, Food and Health</i> , 2016, 35, 173-184. | 1.8 | 194 |
| 13 | A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. <i>Nature Methods</i> , 2019, 16, 295-298. | 19.0 | 194 |
| 14 | Databases on Food Phytochemicals and Their Health-Promoting Effects. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 4331-4348. | 5.2 | 183 |
| 15 | Compensation for Systematic Cross-Contribution Improves Normalization of Mass Spectrometry Based Metabolomics Data. <i>Analytical Chemistry</i> , 2009, 81, 7974-7980. | 6.5 | 173 |
| 16 | The international nucleotide sequence database collaboration. <i>Nucleic Acids Research</i> , 2021, 49, D121-D124. | 14.5 | 135 |
| 17 | Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2007, 1, 53. | 3.0 | 116 |
| 18 | Covering Chemical Diversity of Genetically-Modified Tomatoes Using Metabolomics for Objective Substantial Equivalence Assessment. <i>PLoS ONE</i> , 2011, 6, e16989. | 2.5 | 110 |

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|----|---|------|-----------|
| 19 | DNA sequence design using templates. <i>New Generation Computing</i> , 2002, 20, 263-277. | 3.3 | 104 |
| 20 | Biosynthesis of Camptothecin. In Silico and in Vivo Tracer Study from [1-13C]Glucose. <i>Plant Physiology</i> , 2004, 134, 161-170. | 4.8 | 103 |
| 21 | MRMPROBS: A Data Assessment and Metabolite Identification Tool for Large-Scale Multiple Reaction Monitoring Based Widely Targeted Metabolomics. <i>Analytical Chemistry</i> , 2013, 85, 5191-5199. | 6.5 | 102 |
| 22 | Data standards can boost metabolomics research, and if there is a will, there is a way. <i>Metabolomics</i> , 2016, 12, 14. | 3.0 | 97 |
| 23 | Species-specific variation of alternative splicing and transcriptional initiation in six eukaryotes. <i>Gene</i> , 2005, 364, 53-62. | 2.2 | 92 |
| 24 | Systematic Multi-Omics Integration (MOI) Approach in Plant Systems Biology. <i>Frontiers in Plant Science</i> , 2020, 11, 944. | 3.6 | 92 |
| 25 | In Silico Atomic Tracing by Substrate-Product Relationships in <i>Escherichia coli</i> Intermediary Metabolism. <i>Genome Research</i> , 2003, 13, 2455-2466. | 5.5 | 87 |
| 26 | Fructophilic Lactic Acid Bacteria, a Unique Group of Fructose-Fermenting Microbes. <i>Applied and Environmental Microbiology</i> , 2018, 84, . | 3.1 | 79 |
| 27 | MRMPROBS suite for metabolomics using large-scale MRM assays. <i>Bioinformatics</i> , 2014, 30, 2379-2380. | 4.1 | 77 |
| 28 | Secret Signatures Inside Genomic DNA. <i>Biotechnology Progress</i> , 2004, 20, 1605-1607. | 2.6 | 76 |
| 29 | Scale-Freeness and Biological Networks. <i>Journal of Biochemistry</i> , 2005, 138, 1-4. | 1.7 | 67 |
| 30 | SPLASH, a hashed identifier for mass spectra. <i>Nature Biotechnology</i> , 2016, 34, 1099-1101. | 17.5 | 61 |
| 31 | Large-Scale Prediction of Cationic Metabolite Identity and Migration Time in Capillary Electrophoresis Mass Spectrometry Using Artificial Neural Networks. <i>Analytical Chemistry</i> , 2005, 77, 78-84. | 6.5 | 55 |
| 32 | Comprehensive identification of sphingolipid species by in silico retention time and tandem mass spectral library. <i>Journal of Cheminformatics</i> , 2017, 9, 19. | 6.1 | 54 |
| 33 | Comparative genomics of <i>Fructobacillus</i> spp. and <i>Leuconostoc</i> spp. reveals niche-specific evolution of <i>Fructobacillus</i> spp.. <i>BMC Genomics</i> , 2015, 16, 1117. | 2.8 | 53 |
| 34 | Genomic characterization of a fructophilic bee symbiont <i>Lactobacillus kunkeei</i> reveals its niche-specific adaptation. <i>Systematic and Applied Microbiology</i> , 2016, 39, 516-526. | 2.8 | 51 |
| 35 | Metabolic reconstruction using shortest paths. <i>Simulation Modelling Practice and Theory</i> , 2000, 8, 109-125. | 0.3 | 49 |
| 36 | Genome sequence of <i>Aspergillus luchuensis</i> NBRC 4314. <i>DNA Research</i> , 2016, 23, 507-515. | 3.4 | 48 |

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|----|---|-----|-----------|
| 37 | Correlation-Based Deconvolution (CorrDec) To Generate High-Quality MS2 Spectra from Data-Independent Acquisition in Multisample Studies. <i>Analytical Chemistry</i> , 2020, 92, 11310-11317. | 6.5 | 46 |
| 38 | Complete genome sequence and analysis of <i>Lactobacillus hokkaidonensis</i> LOOC260T, a psychrotrophic lactic acid bacterium isolated from silage. <i>BMC Genomics</i> , 2015, 16, 240. | 2.8 | 44 |
| 39 | <i>Lactobacillus paragasseri</i> sp. nov., a sister taxon of <i>Lactobacillus gasseri</i> , based on whole-genome sequence analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3512-3517. | 1.7 | 43 |
| 40 | Metablonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 38. | 4.1 | 39 |
| 41 | Analysis of Chemical Properties of Edible and Medicinal Ginger by Metabolomics Approach. <i>BioMed Research International</i> , 2015, 2015, 1-7. | 1.9 | 37 |
| 42 | Mass Spectrometry Data Repository Enhances Novel Metabolite Discoveries with Advances in Computational Metabolomics. <i>Metabolites</i> , 2019, 9, 119. | 2.9 | 31 |
| 43 | Creating a Reliable Mass Spectral Retention Time Library for All Ion Fragmentation-Based Metabolomics. <i>Metabolites</i> , 2019, 9, 251. | 2.9 | 30 |
| 44 | MRM-DIFF: data processing strategy for differential analysis in large scale MRM-based lipidomics studies. <i>Frontiers in Genetics</i> , 2014, 5, 471. | 2.3 | 29 |
| 45 | All systems go: launching cell simulation fueled by integrated experimental biology data. <i>Current Opinion in Biotechnology</i> , 2005, 16, 344-349. | 6.6 | 27 |
| 46 | The effect of rapamycin on biodiesel-producing protist <i>Euglena gracilis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 1223-1229. | 1.3 | 26 |
| 47 | Circadian clocks optimally adapt to sunlight for reliable synchronization. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131018. | 3.4 | 25 |
| 48 | <i>Bifidobacterium jacchi</i> sp. nov., isolated from the faeces of a baby common marmoset (<i>Callithrix</i>). <i>Journal of Microbiology and Biotechnology</i> , 2017, 17, 23. | 1.7 | 23 |
| 49 | Characterization of <i>Bifidobacterium</i> species in faeces of the Egyptian fruit bat: Description of <i>B. vespertilionis</i> sp. nov. and <i>B. roussetti</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 126017. | 2.8 | 22 |
| 50 | Unique niche-specific adaptation of fructophilic lactic acid bacteria and proposal of three <i>Apilactobacillus</i> species as novel members of the group. <i>BMC Microbiology</i> , 2021, 21, 41. | 3.3 | 19 |
| 51 | <i>Lactobacillus silagincola</i> sp. nov. and <i>Lactobacillus pentosiphilus</i> sp. nov., isolated from silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3639-3644. | 1.7 | 19 |
| 52 | Optimal Implementations for Reliable Circadian Clocks. <i>Physical Review Letters</i> , 2014, 113, 108101. | 7.8 | 18 |
| 53 | SVD-based Anatomy of Gene Expressions for Correlation Analysis in <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2008, 15, 367-374. | 3.4 | 17 |
| 54 | Host-Diet Effect on the Metabolism of <i>Bifidobacterium</i> . <i>Genes</i> , 2021, 12, 609. | 2.4 | 17 |

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|----|---|-----|-----------|
| 55 | Lactobacillus buchneri subsp. silagei subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116. | 1.7 | 17 |
| 56 | What can metabolomics learn from genomics and proteomics?. Current Opinion in Biotechnology, 2009, 20, 610-615. | 6.6 | 16 |
| 57 | Knockout of the SREBP system increases production of the polyketide FR901512 in filamentous fungal sp. No. 14919 and lovastatin in Aspergillus terreus ATCC20542. Applied Microbiology and Biotechnology, 2018, 102, 1393-1405. | 3.6 | 16 |
| 58 | Enhanced entrainability of genetic oscillators by period mismatch. Journal of the Royal Society Interface, 2013, 10, 20121020. | 3.4 | 15 |
| 59 | A pitfall of wiki solution for biological databases. Briefings in Bioinformatics, 2008, 10, 295-296. | 6.5 | 14 |
| 60 | Properties of the maximum -likelihood estimator for independent random variables. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 3399-3412. | 2.6 | 13 |
| 61 | Nested structure acquired through simple evolutionary process. Journal of Theoretical Biology, 2010, 264, 782-786. | 1.7 | 13 |
| 62 | Escape process and stochastic resonance under noise intensity fluctuation. Physics Letters, Section A: General, Atomic and Solid State Physics, 2011, 375, 3450-3458. | 2.1 | 13 |
| 63 | Embedding standards in metabolomics: the Metabolomics Society data standards task group. Metabolomics, 2015, 11, 782-783. | 3.0 | 13 |
| 64 | Bifidobacteria in two-toed sloths (Choloepus didactylus): phylogenetic characterization of the novel taxon Bifidobacterium choloepi sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6115-6125. | 1.7 | 13 |
| 65 | Characterizing gene coexpression modules in Oryza sativa based on a graph-clustering approach. Plant Biotechnology, 2009, 26, 485-493. | 1.0 | 12 |
| 66 | Phylogenomic and Domain Analysis of Iterative Polyketide Synthases in Aspergillus Species. Evolutionary Bioinformatics, 2012, 8, EBO.S9796. | 1.2 | 11 |
| 67 | Isolation and Identification of Lactic Acid Bacteria from Environmental Samples. Methods in Molecular Biology, 2019, 1887, 3-13. | 0.9 | 11 |
| 68 | Heterogeneous distribution of metabolites across plant species. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 2771-2780. | 2.6 | 10 |
| 69 | Exploration of polar lipid accumulation profiles in <i>Euglena gracilis</i> using LipidBlast, an MS/MS spectral library constructed <i>in silico</i>. Bioscience, Biotechnology and Biochemistry, 2014, 78, 14-18. | 1.3 | 10 |
| 70 | Targeted Integration of RNA-Seq and Metabolite Data to Elucidate Curcuminoid Biosynthesis in Four Curcuma Species. Plant and Cell Physiology, 2015, 56, 843-851. | 3.1 | 9 |
| 71 | Visualization of consensus genome structure without using a reference genome. BMC Genomics, 2017, 18, 208. | 2.8 | 9 |
| 72 | Critical Involvement of Environmental Carbon Dioxide Fixation to Drive Wax Ester Fermentation in Euglena. PLoS ONE, 2016, 11, e0162827. | 2.5 | 8 |

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|----|---|-----|-----------|
| 73 | Revealing the genomic differences between two subgroups in <i>Lactobacillus gasseri</i>. <i>Bioscience of Microbiota, Food and Health</i> , 2017, 36, 155-159. | 1.8 | 8 |
| 74 | Comparative analysis of probiotic bacteria based on a new definition of core genome. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840012. | 0.8 | 8 |
| 75 | Biosynthesis of Novel Statins by Combining Heterologous Genes from <i>Xylaria</i> and <i>Aspergillus</i>. <i>ACS Synthetic Biology</i> , 2018, 7, 2783-2789. | 3.8 | 8 |
| 76 | Bistable stochastic processes in the -exponential family. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 4450-4461. | 2.6 | 7 |
| 77 | Noise-intensity fluctuation in Langevin model and its higher-order Fokker-Planck equation. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011, 390, 1051-1063. | 2.6 | 7 |
| 78 | Pseudofrucophilic <i>Leuconostoc citreum</i> Strain F192-5, Isolated from Satsuma Mandarin Peel. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 3.1 | 7 |
| 79 | Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. <i>Methods in Molecular Biology</i> , 2019, 1962, 215-226. | 0.9 | 7 |
| 80 | Rearrangement analysis of multiple bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 631. | 2.6 | 7 |
| 81 | Differential annotation of converted metabolites (DAC-Met): Exploration of Maoto (Ma-huang-tang)-derived metabolites in plasma using high-resolution mass spectrometry. <i>Metabolomics</i> , 2020, 16, 63. | 3.0 | 7 |
| 82 | Oligosaccharide Metabolism and Lipoteichoic Acid Production in <i>Lactobacillus gasseri</i> and <i>Lactobacillus paragasseri</i> . <i>Microorganisms</i> , 2021, 9, 1590. | 3.6 | 7 |
| 83 | Processing sequence annotation data using the Lua programming language. <i>Genome Informatics</i> , 2003, 14, 154-63. | 0.4 | 7 |
| 84 | Comprehensive Metabolomic Comparison of Five Cereal Vinegars Using Non-Targeted and Chemical Isotope Labeling LC-MS Analysis. <i>Metabolites</i> , 2022, 12, 427. | 2.9 | 7 |
| 85 | Fluctuating noise drives Brownian transport. <i>Journal of the Royal Society Interface</i> , 2012, 9, 3554-3563. | 3.4 | 6 |
| 86 | Phylogenetic characterization of two novel species of the genus <i>Bifidobacterium</i> : <i>Bifidobacterium saimiriisciurei</i> sp. nov. and <i>Bifidobacterium platyrrhinorum</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126111. | 2.8 | 6 |
| 87 | Development of RIKEN Plant Metabolome MetaDatabase. <i>Plant and Cell Physiology</i> , 2022, 63, 433-440. | 3.1 | 6 |
| 88 | Isolation of a Highly Thermostable Bile Salt Hydrolase With Broad Substrate Specificity From <i>Lactobacillus paragasseri</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 810872. | 3.5 | 5 |
| 89 | Genome Sequence of the Fungal Strain 14919 Producing 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase Inhibitor FR901512. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 4 |
| 90 | Open Access and Data Sharing of Nucleotide Sequence Data. <i>Data Science Journal</i> , 2021, 20, . | 1.3 | 4 |

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|-----|---|------|-----------|
| 91 | Comparison of Protein Complexes Predicted from PPI Networks by DPCLus and Newman Clustering Algorithms. <i>IPSI Digital Courier</i> , 2006, 2, 674-684. | 0.3 | 3 |
| 92 | Editorial: Metabolome Informatics and Statistics: Current State and Emerging Trends. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 63. | 4.1 | 3 |
| 93 | Database for crude drugs and Kampo medicine. <i>Genome Informatics</i> , 2011, 25, 1-11. | 0.4 | 3 |
| 94 | Metabolomic Characterization of a Low Phytic Acid and High Anti-oxidative Cultivar of Turmeric. <i>Natural Product Communications</i> , 2015, 10, 1934578X1501000. | 0.5 | 2 |
| 95 | Genomic characterization reconfirms the taxonomic status of <i>Lactobacillus parakefiri</i> . <i>Bioscience of Microbiota, Food and Health</i> , 2017, 36, 129-134. | 1.8 | 2 |
| 96 | \pm -Linolenic acid in <i>Papilio machaon</i> larvae regurgitant induces a defensive response in Apiaceae. <i>Phytochemistry</i> , 2021, 188, 112796. | 2.9 | 2 |
| 97 | Uncovering Ecdysozoa-specific Sphingomyelin Synthase by Phylogenetic Analysis of Metazoan Sequences. <i>Zoological Science</i> , 2019, 36, 316. | 0.7 | 2 |
| 98 | PASMet: a web-based platform for prediction, modelling and analyses of metabolic systems. <i>Nucleic Acids Research</i> , 2016, 44, W205-W211. | 14.5 | 1 |
| 99 | Physicochemical Prediction of Metabolite Fragmentation in Tandem Mass Spectrometry. <i>Mass Spectrometry</i> , 2018, 7, A0066-A0066. | 0.6 | 1 |
| 100 | Genetic Markers of Genome Rearrangements in <i>Helicobacter pylori</i> . <i>Microorganisms</i> , 2021, 9, 621. | 3.6 | 1 |
| 101 | A sugar utilization phenotype contributes to the formation of genetic exchange communities in lactic acid bacteria. <i>FEMS Microbiology Letters</i> , 2021, 368, . | 1.8 | 1 |
| 102 | Development of the portal site of COVID-19 data in Japan. , 2020, , . | | 1 |
| 103 | Genome Sequence of <i>Lactobacillus paracasei</i> Strain LC-Ikematsu, Isolated from a Pineapple in Okinawa, Japan. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 0 |
| 104 | Detriment of global ranking. <i>Journal of Information Processing and Management</i> , 2015, 57, 755-758. | 0.0 | 0 |
| 105 | Bioinformaticsâ€”The Power of Integrated Platforms for Omics Mining. , 2020, , 211-221. | | 0 |