

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
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108
all docs

108
docs citations

108
times ranked

12911
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Development of RIKEN Plant Metabolome MetaDatabase. <i>Plant and Cell Physiology</i> , 2022, 63, 433-440.	3.1	6
3	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
4	Open Access and Data Sharing of Nucleotide Sequence Data. <i>Data Science Journal</i> , 2021, 20, .	1.3	4
5	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
6	Genetic Markers of Genome Rearrangements in <i>Helicobacter pylori</i> . <i>Microorganisms</i> , 2021, 9, 621.	3.6	1
7	Host-Diet Effect on the Metabolism of <i>Bifidobacterium</i> . <i>Genes</i> , 2021, 12, 609.	2.4	17
8	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
9	Î±-Linolenic acid in <i>Papilio machaon</i> larvae regurgitant induces a defensive response in Apiaceae. <i>Phytochemistry</i> , 2021, 188, 112796.	2.9	2
10	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
11	The international nucleotide sequence database collaboration. <i>Nucleic Acids Research</i> , 2021, 49, D121-D124.	14.5	135
12	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
13	Systematic Multi-Omics Integration (MOI) Approach in Plant Systems Biology. <i>Frontiers in Plant Science</i> , 2020, 11, 944.	3.6	92
14	A lipidome atlas in MS-DIAL 4. <i>Nature Biotechnology</i> , 2020, 38, 1159-1163.	17.5	424
15	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
16	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
17	<i>Lactobacillus buchneri</i> subsp. <i>silagei</i> subsp. nov., isolated from rice grain silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3111-3116.	1.7	17
18	<i>Bifidobacteria</i> in two-toed sloths (<i>Choloepus didactylus</i>): phylogenetic characterization of the novel taxon <i>Bifidobacterium choloepi</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6115-6125.	1.7	13

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19	Bioinformaticsâ€”The Power of Integrated Platforms for Omics Mining. , 2020, , 211-221.		0
20	Development of the portal site of COVID-19 data in Japan. , 2020, , .		1
21	Mass Spectrometry Data Repository Enhances Novel Metabolite Discoveries with Advances in Computational Metabolomics. <i>Metabolites</i> , 2019, 9, 119.	2.9	31
22	Creating a Reliable Mass Spectralâ€”Retention Time Library for All Ion Fragmentation-Based Metabolomics. <i>Metabolites</i> , 2019, 9, 251.	2.9	30
23	Pseudofructophilic <i>Leuconostoc citreum</i> Strain F192-5, Isolated from Satsuma Mandarin Peel. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	7
24	Characterization of <i>Bifidobacterium</i> species in feaces 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
25	Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. <i>Methods in Molecular Biology</i> , 2019, 1962, 215-226.	0.9	7
26	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. <i>Nature Methods</i> , 2019, 16, 295-298.	19.0	194
27	Rearrangement analysis of multiple bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 631.	2.6	7
28	Isolation and Identification of Lactic Acid Bacteria from Environmental Samples. <i>Methods in Molecular Biology</i> , 2019, 1887, 3-13.	0.9	11
29	<i>Bifidobacterium jacchi</i> sp. nov., isolated from the faeces of a baby common marmoset (<i>Callithrix</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.7	23
30	Uncovering Ecdysozoa-specific Sphingomyelin Synthase by Phylogenetic Analysis of Metazoan Sequences. <i>Zoological Science</i> , 2019, 36, 316.	0.7	2
31	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
32	Knockout of the SREBP system increases production of the polyketide FR901512 in filamentous fungal sp. No. 14919 and lovastatin in <i>Aspergillus terreus</i> ATCC20542. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1393-1405.	3.6	16
33	Identification of small molecules using accurate mass MS/MS search. <i>Mass Spectrometry Reviews</i> , 2018, 37, 513-532.	5.4	292
34	Identifying metabolites by integrating metabolome databases with mass spectrometry cheminformatics. <i>Nature Methods</i> , 2018, 15, 53-56.	19.0	368
35	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
36	Fructophilic Lactic Acid Bacteria, a Unique Group of Fructose-Fermenting Microbes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	79

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37	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
38	Physicochemical Prediction of Metabolite Fragmentation in Tandem Mass Spectrometry. <i>Mass Spectrometry</i> , 2018, 7, A0066-A0066.	0.6	1
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	Visualization of consensus genome structure without using a reference genome. <i>BMC Genomics</i> , 2017, 18, 208.	2.8	9
41	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
42	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
43	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
44	Genome Sequence of the Fungal Strain 14919 Producing 3-Hydroxy-3-Methylglutarylâ€Coenzyme A Reductase Inhibitor FR901512. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
45	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
46	<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
47	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
48	Editorial: Metabolome Informatics and Statistics: Current State and Emerging Trends. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 63.	4.1	3
49	Critical Involvement of Environmental Carbon Dioxide Fixation to Drive Wax Ester Fermentation in <i>Euglena</i> . <i>PLoS ONE</i> , 2016, 11, e0162827.	2.5	8
50	Genome sequence of <i>Aspergillus luchuensis</i> NBRC 4314. <i>DNA Research</i> , 2016, 23, 507-515.	3.4	48
51	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
52	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
53	SPLASH, a hashed identifier for mass spectra. <i>Nature Biotechnology</i> , 2016, 34, 1099-1101.	17.5	61
54	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

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55	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
56	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
57	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
58	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
59	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 38.	4.1	39
60	Analysis of Chemical Properties of Edible and Medicinal Ginger by Metabolomics Approach. <i>BioMed Research International</i> , 2015, 2015, 1-7.	1.9	37
61	Targeted Integration of RNA-Seq and Metabolite Data to Elucidate Curcuminoid Biosynthesis in Four <i>Curcuma</i> Species. <i>Plant and Cell Physiology</i> , 2015, 56, 843-851.	3.1	9
62	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
63	MS-DIAL: data-independent MS/MS deconvolution for comprehensive metabolome analysis. <i>Nature Methods</i> , 2015, 12, 523-526.	19.0	1,955
64	Embedding standards in metabolomics: the Metabolomics Society data standards task group. <i>Metabolomics</i> , 2015, 11, 782-783.	3.0	13
65	Detriment of global ranking. <i>Journal of Information Processing and Management</i> , 2015, 57, 755-758.	0.0	0
66	MRMPROBS suite for metabolomics using large-scale MRM assays. <i>Bioinformatics</i> , 2014, 30, 2379-2380.	4.1	77
67	Exploration of polar lipid accumulation profiles in <i>Euglena gracilis</i> using LipidBlast, an MS/MS spectral library constructed <i>in silico</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 14-18.	1.3	10
68	Circadian clocks optimally adapt to sunlight for reliable synchronization. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131018.	3.4	25
69	Optimal Implementations for Reliable Circadian Clocks. <i>Physical Review Letters</i> , 2014, 113, 108101.	7.8	18
70	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
71	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
72	Enhanced entrainability of genetic oscillators by period mismatch. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20121020.	3.4	15

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73	Phylogenomic and Domain Analysis of Iterative Polyketide Synthases in <i>Aspergillus</i> Species. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9796.	1.2	11
74	Fluctuating noise drives Brownian transport. <i>Journal of the Royal Society Interface</i> , 2012, 9, 3554-3563.	3.4	6
75	Databases on Food Phytochemicals and Their Health-Promoting Effects. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 4331-4348.	5.2	183
76	Escape process and stochastic resonance under noise intensity fluctuation. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2011, 375, 3450-3458.	2.1	13
77	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
78	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
79	Covering Chemical Diversity of Genetically-Modified Tomatoes Using Metabolomics for Objective Substantial Equivalence Assessment. <i>PLoS ONE</i> , 2011, 6, e16989.	2.5	110
80	Database for crude drugs and Kampo medicine. <i>Genome Informatics</i> , 2011, 25, 1-11.	0.4	3
81	Nested structure acquired through simple evolutionary process. <i>Journal of Theoretical Biology</i> , 2010, 264, 782-786.	1.7	13
82	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
83	Bistable stochastic processes in the γ -exponential family. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 4450-4461.	2.6	7
84	Heterogeneous distribution of metabolites across plant species. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 2771-2780.	2.6	10
85	Properties of the maximum-likelihood estimator for independent random variables. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 3399-3412.	2.6	13
86	Integrated omics approaches in plant systems biology. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 532-538.	6.1	201
87	What can metabolomics learn from genomics and proteomics?. <i>Current Opinion in Biotechnology</i> , 2009, 20, 610-615.	6.6	16
88	Compensation for Systematic Cross-Contribution Improves Normalization of Mass Spectrometry Based Metabolomics Data. <i>Analytical Chemistry</i> , 2009, 81, 7974-7980.	6.5	173
89	Characterizing gene coexpression modules in <i>Oryza sativa</i> based on a graph-clustering approach. <i>Plant Biotechnology</i> , 2009, 26, 485-493.	1.0	12
90	A pitfall of wiki solution for biological databases. <i>Briefings in Bioinformatics</i> , 2008, 10, 295-296.	6.5	14

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91	SVD-based Anatomy of Gene Expressions for Correlation Analysis in Arabidopsis thaliana. DNA Research, 2008, 15, 367-374.	3.4	17
92	Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in Arabidopsis thaliana. BMC Systems Biology, 2007, 1, 53.	3.0	116
93	Comparison of Protein Complexes Predicted from PPI Networks by DPPlus and Newman Clustering Algorithms. IPSJ Digital Courier, 2006, 2, 674-684.	0.3	3
94	All systems go: launching cell simulation fueled by integrated experimental biology data. Current Opinion in Biotechnology, 2005, 16, 344-349.	6.6	27
95	Large-Scale Prediction of Cationic Metabolite Identity and Migration Time in Capillary Electrophoresis Mass Spectrometry Using Artificial Neural Networks. Analytical Chemistry, 2005, 77, 78-84.	6.5	55
96	Species-specific variation of alternative splicing and transcriptional initiation in six eukaryotes. Gene, 2005, 364, 53-62.	2.2	92
97	Scale-Freeness and Biological Networks. Journal of Biochemistry, 2005, 138, 1-4.	1.7	67
98	The metabolic world of Escherichia coli is not small. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1543-1547.	7.1	287
99	Biosynthesis of Camptothecin. In Silico and in Vivo Tracer Study from [1-13C]Glucose. Plant Physiology, 2004, 134, 161-170.	4.8	103
100	Secret Signatures Inside Genomic DNA. Biotechnology Progress, 2004, 20, 1605-1607.	2.6	76
101	From The Cover: Integration of transcriptomics and metabolomics for understanding of global responses to nutritional stresses in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10205-10210.	7.1	726
102	In Silico Atomic Tracing by Substrate-Product Relationships in Escherichia coli Intermediary Metabolism. Genome Research, 2003, 13, 2455-2466.	5.5	87
103	Processing sequence annotation data using the Lua programming language. Genome Informatics, 2003, 14, 154-63.	0.4	7
104	DNA sequence design using templates. New Generation Computing, 2002, 20, 263-277.	3.3	104
105	Metabolic reconstruction using shortest paths. Simulation Modelling Practice and Theory, 2000, 8, 109-125.	0.3	49