Young-Mo Kim

List of Publications by Year
in descending order

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95 papers	5,596 citations	61945 43 h-index	85498 71 g-index
108 all docs	108 docs citations	108 times ranked	8847 citing authors

#	Article	IF	Citations
1	Bulk and Spatially Resolved Extracellular Metabolome of Free-Living Nitrogen Fixation. Applied and Environmental Microbiology, 2022, 88, .	1.4	1
2	Cryptococcus neoformans-Infected Macrophages Release Proinflammatory Extracellular Vesicles: Insight into Their Components by Multi-omics. MBio, 2021, 12, .	1.8	14
3	Integration of Proteomics and Metabolomics Into the Design, Build, Test, Learn Cycle to Improve 3-Hydroxypropionic Acid Production in Aspergillus pseudoterreus. Frontiers in Bioengineering and Biotechnology, 2021, 9, 603832.	2.0	12
4	A resource of lipidomics and metabolomics data from individuals with undiagnosed diseases. Scientific Data, 2021, 8, 114.	2.4	12
5	A Histoplasma capsulatum Lipid Metabolic Map Identifies Antifungal Targets. MBio, 2021, 12, e0297221.	1.8	6
6	Deciphering the microbial and molecular responses of geographically diverse Setaria accessions grown in a nutrient-poor soil. PLoS ONE, 2021, 16, e0259937.	1.1	0
7	Editorial: Multi-Omics Technologies for Optimizing Synthetic Biomanufacturing. Frontiers in Bioengineering and Biotechnology, 2021, 9, 818010.	2.0	1
8	Statistically Driven Metabolite and Lipid Profiling of Patients from the Undiagnosed Diseases Network. Analytical Chemistry, 2020, 92, 1796-1803.	3.2	7
9	Colonies of the fungus Aspergillus niger are highly differentiated to adapt to local carbon source variation. Environmental Microbiology, 2020, 22, 1154-1166.	1.8	15
10	Soil microbial EPS resiliency is influenced by carbon source accessibility. Soil Biology and Biochemistry, 2020, 151, 108037.	4.2	17
11	Lignin induced iron reduction by novel sp., Tolumonas lignolytic BRL6-1. PLoS ONE, 2020, 15, e0233823.	1.1	8
12	Synthetic microbial communities of heterotrophs and phototrophs facilitate sustainable growth. Nature Communications, 2020, 11, 3803.	5.8	55
13	High-Throughput Large-Scale Targeted Proteomics Assays for Quantifying Pathway Proteins in Pseudomonas putida KT2440. Frontiers in Bioengineering and Biotechnology, 2020, 8, 603488.	2.0	10
14	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohnâ€™s Disease: A Randomized Diet Controlled Trial. Nutrients, 2020, 12, 3749.	1.7	62
15	Polystyrene nano- and microplastic accumulation at Arabidopsis and wheat root cap cells, but no evidence for uptake into roots. Environmental Science: Nano, 2020, 7, 1942-1953.	2.2	102
16	Temporospatial shifts in the human gut microbiome and metabolome after gastric bypass surgery. Npj Biofilms and Microbiomes, 2020, 6, 12.	2.9	57
17	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. Scientific Reports, 2020, 10, 10882.	1.6	9
18	Genetic and metabolic links between the murine microbiome and memory. Microbiome, 2020, 8, 53.	4.9	56

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19	Multi-Omics Driven Metabolic Network Reconstruction and Analysis of Lignocellulosic Carbon Utilization in Rhodosporidium toruloides. Frontiers in Bioengineering and Biotechnology, 2020, 8, 612832.	2.0	25
20	Metabolite, Protein, and Lipid Extraction (MPLEx): A Method that Simultaneously Inactivates Middle East Respiratory Syndrome Coronavirus and Allows Analysis of Multiple Host Cell Components Following Infection. Methods in Molecular Biology, 2020, 2099, 173-194.	0.4	15
21	Lignin induced iron reduction by novel sp., Tolumonas lignolytic BRL6-1. , 2020, 15, e0233823.		0
22	Lignin induced iron reduction by novel sp., Tolumonas lignolytic BRL6-1. , 2020, 15, e0233823.		0
23	Lignin induced iron reduction by novel sp., Tolumonas lignolytic BRL6-1. , 2020, 15, e0233823.		0
24	Lignin induced iron reduction by novel sp., Tolumonas lignolytic BRL6-1. , 2020, 15, e0233823.		0
25	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. Frontiers in Molecular Biosciences, 2019, 6, 108.	1.6	26
26	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. Cell, 2019, 177, 1600-1618.e17.	13.5	701
27	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. MSystems, 2019, 4, .	1.7	56
28	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. Nature Microbiology, 2019, 4, 864-875.	5.9	68
29	Atmo-ecometabolomics: a novel atmospheric particle chemical characterization methodology for ecological research. Environmental Monitoring and Assessment, 2019, 191, 78.	1.3	7
30	Salmonella-Mediated Inflammation Eliminates Competitors for Fructose-Asparagine in the Gut. Infection and Immunity, 2018, 86, .	1.0	12
31	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. American Journal of Human Genetics, 2018, 102, 494-504.	2.6	59
32	Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4284-E4293.	3.3	391
33	Temporal dynamics of CO2 and CH4 loss potentials in response to rapid hydrological shifts in tidal freshwater wetland soils. Ecological Engineering, 2018, 114, 104-114.	1.6	13
34	Dichomitus squalens partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	1.8	36
35	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. Journal of Visualized Experiments, 2018, , .	0.2	19
36	A Cobalamin Activity-Based Probe Enables Microbial Cell Growth and Finds New Cobalamin-Protein Interactions across Domains. Applied and Environmental Microbiology, 2018, 84, .	1.4	15

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37	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in Aspergillus nidulans. BMC Genomics, 2018, 19, 214.	1.2	11
38	Time-resolved proteome profiling of normal lung development. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L11-L24.	1.3	25
39	Mass Spectrometry-Based Metabolomics. Methods in Molecular Biology, 2018, 1775, 107-118.	0.4	38
40	Salinivirga fredricksonii gen. nov., sp. nov., a heterotrophic halophile isolated from a photosynthetic mat, a member of a novel lineage (Salinarimonadaceae fam. nov.) within the order Rhizobiales, and reclassification of the genus Salinarimonas Liu et al. 2010 into Salinarimonadaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1591-1598.	0.8	25
41	MPLEx: a method for simultaneous pathogen inactivation and extraction of samples for multi-omics profiling. Analyst, The, 2017, 142, 442-448.	1.7	43
42	Elucidation of roles for vitamin B ₁₂ in regulation of folate, ubiquinone, and methionine metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1205-E1214.	3.3	75
43	The state of rhizospheric science in the era of multi-omics: A practical guide to omics technologies. Rhizosphere, 2017, 3, 212-221.	1.4	66
44	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in Yarrowia lipolytica. MBio, 2017, 8, .	1.8	38
45	Indirect Interspecies Regulation: Transcriptional and Physiological Responses of a Cyanobacterium to Heterotrophic Partnership. MSystems, 2017, 2, .	1.7	20
46	Comparing identified and statistically significant lipids and polar metabolites in 15â€year old serum and dried blood spot samples for longitudinal studies. Rapid Communications in Mass Spectrometry, 2017, 31, 447-456.	0.7	31
47	Multi-platform â€™Omics Analysis of Human Ebola Virus Disease Pathogenesis. Cell Host and Microbe, 2017, 22, 817-829.e8.	5.1	88
48	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. Nature Microbiology, 2017, 2, 16221.	5.9	138
49	Lipidomics reveals dramatic lipid compositional changes in the maturing postnatal lung. Scientific Reports, 2017, 7, 40555.	1.6	67
50	Are the metabolomic responses to folivory of closely related plant species linked to macroevolutionary and plantâ€“folivore coevolutionary processes?. Ecology and Evolution, 2016, 6, 4372-4386.	0.8	15
51	MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. MSystems, 2016, 1, .	1.7	166
52	SPE-IMS-MS: An automated platform for sub-sixty second surveillance of endogenous metabolites and xenobiotics in biofluids. Clinical Mass Spectrometry, 2016, 2, 1-10.	1.9	63
53	Multi-omics analysis reveals regulators of the response to nitrogen limitation in Yarrowia lipolytica. BMC Genomics, 2016, 17, 138.	1.2	62
54	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. Cell Host and Microbe, 2016, 19, 254-266.	5.1	75

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55	Enhanced Performance in Bulk Heterojunction Polymer Solar Cell Using Water Soluble Conjugated Polymer. Journal of Nanoscience and Nanotechnology, 2015, 15, 1683-1686.	0.9	2
56	Silymarin Suppresses Cellular Inflammation By Inducing Reparative Stress Signaling. Journal of Natural Products, 2015, 78, 1990-2000.	1.5	53
57	Diel metabolomics analysis of a hot spring chlorophototrophic microbial mat leads to new hypotheses of community member metabolisms. Frontiers in Microbiology, 2015, 6, 209.	1.5	104
58	Comprehensive Metabolomic, Lipidomic and Microscopic Profiling of Yarrowia lipolytica during Lipid Accumulation Identifies Targets for Increased Lipogenesis. PLoS ONE, 2015, 10, e0123188.	1.1	54
59	Silymarin suppresses cellular inflammation by inducing reparative stress signaling. Planta Medica, 2015, 81, .	0.7	0
60	Phototrophic biofilm assembly in microbial-mat-derived unicyanobacterial consortia: model systems for the study of autotroph-heterotroph interactions. Frontiers in Microbiology, 2014, 5, 109.	1.5	97
61	Integrated â€˜omics analysis for studying the microbial community response to a pH perturbation of a cellulose-degrading bioreactor culture. FEMS Microbiology Ecology, 2014, 90, 802-815.	1.3	10
62	The fungus gardens of leafâ€cutter ants undergo a distinct physiological transition during biomass degradation. Environmental Microbiology Reports, 2014, 6, 389-395.	1.0	21
63	A statistical analysis of the effects of urease pre-treatment on the measurement of the urinary metabolome by gas chromatographyâ€“mass spectrometry. Metabolomics, 2014, 10, 897-908.	1.4	28
64	Decreased abundance of type III secretion system-inducing signals in Arabidopsis mkp1 enhances resistance against Pseudomonas syringae. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6846-6851.	3.3	97
65	A multi-omic systems approach to elucidating Yersinia virulence mechanisms. Molecular BioSystems, 2013, 9, 44-54.	2.9	29
66	Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes. Molecular BioSystems, 2013, 9, 1522.	2.9	49
67	A Multi-Omic View of Host-Pathogen-Commensal Interplay in Salmonella-Mediated Intestinal Infection. PLoS ONE, 2013, 8, e67155.	1.1	81
68	Modelâ€driven multiâ€omic data analysis elucidates metabolic immunomodulators of macrophage activation. Molecular Systems Biology, 2012, 8, 558.	3.2	142
69	Microbial Diversity and Biogeochemical Function of the Phototrophic Microbial Mats of Epsomitic Hot Lake, WA. Microscopy and Microanalysis, 2012, 18, 10-11.	0.2	3
70	Metabolomic response of human skin tissue to low dose ionizing radiation. Molecular BioSystems, 2012, 8, 1979.	2.9	31
71	Studying Salmonellae and Yersiniae Hostâ€“Pathogen Interactions Using Integrated â€˜Omics and Modeling. Current Topics in Microbiology and Immunology, 2012, 363, 21-41.	0.7	10
72	Degradation of polybrominated diphenyl ethers by a sequential treatment with nanoscale zero valent iron and aerobic biodegradation. Journal of Chemical Technology and Biotechnology, 2012, 87, 216-224.	1.6	93

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73	A Catabolic Activity of Sphingomonas wittichii RW1 in the Biotransformation of Carbazole. Water, Air, and Soil Pollution, 2012, 223, 943-949.	1.1	3
74	Formation of dehydroalanine from mimosine and cysteine: artifacts in gas chromatography/mass spectrometry based metabolomics. Rapid Communications in Mass Spectrometry, 2011, 25, 2561-2564.	0.7	14
75	Triclosan susceptibility and co-metabolism â€“ A comparison for three aerobic pollutant-degrading bacteria. Bioresource Technology, 2011, 102, 2206-2212.	4.8	122
76	Mineralization and transformation of monofluorophenols by Pseudonocardia benzenivorans. Applied Microbiology and Biotechnology, 2010, 87, 1569-1577.	1.7	24
77	Laccaseâ€catalysed polymeric dye synthesis from plantâ€derived phenols for potential application in hair dyeing: Enzymatic colourations driven by homoâ€or heteroâ€polymer synthesis. Microbial Biotechnology, 2010, 3, 324-335.	2.0	82
78	Degradation of triclosan by an integrated nano-bio redox process. Bioresource Technology, 2010, 101, 6354-6360.	4.8	89
79	Enhanced transformation of triclosan by laccase in the presence of redox mediators. Water Research, 2010, 44, 298-308.	5.3	118
80	Biodegradation of 1,4-dioxane and transformation of related cyclic compounds by a newly isolated Mycobacterium sp. PH-06. Biodegradation, 2009, 20, 511-519.	1.5	96
81	Enhanced transformation of malachite green by laccase of Ganoderma lucidum in the presence of natural phenolic compounds. Applied Microbiology and Biotechnology, 2009, 82, 341-350.	1.7	87
82	Effect of metal ions on reactive dye decolorization by laccase from Ganoderma lucidum. Journal of Hazardous Materials, 2009, 168, 523-529.	6.5	138
83	Use of grape seed and its natural polyphenol extracts as a natural organic coagulant for removal of cationic dyes. Chemosphere, 2009, 77, 1090-1098.	4.2	70
84	Synergistic effect of laccase mediators on pentachlorophenol removal by Ganoderma lucidum laccase. Applied Microbiology and Biotechnology, 2008, 81, 783-790.	1.7	60
85	Bioremediation of PCDD/Fs-contaminated municipal solid waste incinerator fly ash by a potent microbial biocatalyst. Journal of Hazardous Materials, 2008, 157, 114-121.	6.5	46
86	Decolourization of reactive black 5 by laccase: Optimization by response surface methodology. Dyes and Pigments, 2007, 75, 176-184.	2.0	145
87	Decolorization of reactive dyes by a thermostable laccase produced by Ganoderma lucidum in solid state culture. Enzyme and Microbial Technology, 2007, 40, 1662-1672.	1.6	232
88	Effect of heavy metals on the biodegradation of dibenzofuran in liquid medium. Journal of Hazardous Materials, 2007, 140, 145-148.	6.5	28
89	Biodegradation of diphenyl ether and transformation of selected brominated congeners by Sphingomonas sp. PH-07. Applied Microbiology and Biotechnology, 2007, 77, 187-194.	1.7	125
90	Author's reply to comment on â€œBiological removal of polychlorinated dibenzo-p-dioxins from incinerator fly ash by sphingomonas wittichii RW1â€•by Rolf U. Halden. Water Research, 2006, 40, 2246-2247.	5.3	2

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91	Mass spectrometric analysis of isotope effects in bioconversion of benzene to cyclohexanone. International Journal of Mass Spectrometry, 2006, 252, 256-260.	0.7	3
92	Purification and characterization of laccase produced by a white rot fungus Pleurotus sajor-caju under submerged culture condition and its potential in decolorization of azo dyes. Applied Microbiology and Biotechnology, 2006, 72, 939-946.	1.7	100
93	Biotransformation of 1,2,3-Tri- and 1,2,3,4,7,8-Hexachlorodibenzo- p - Dioxin by Sphingomonas wittichii Strain RW1. Applied and Environmental Microbiology, 2006, 72, 112-116.	1.4	68
94	Biological removal of polychlorinated dibenzo-p-dioxins from incinerator fly ash by Sphingomonas wittichii RW1. Water Research, 2005, 39, 4651-4660.	5.3	43
95	Biodegradation of Dibenzo-p-dioxin, Dibenzofuran, and Chlorodibenzo-p-dioxins by Pseudomonas veronii PH-03. Biodegradation, 2004, 15, 303-313.	1.5	48