

Karsten Zengler

List of Publications by Year in descending order

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Version: 2024-02-01

118
papers

11,804
citations

50566

48
h-index

34195

103
g-index

127
all docs

127
docs citations

127
times ranked

16590
citing authors

#	ARTICLE	IF	CITATIONS
1	Flux balance analysis of the ammonia-oxidizing bacterium <i>Nitrosomonas europaea</i> ATCC19718 unravels specific metabolic activities while degrading toxic compounds. <i>PLoS Computational Biology</i> , 2022, 18, e1009828.	1.5	4
2	Genome-Scale Metabolic Modeling Enables In-Depth Understanding of Big Data. <i>Metabolites</i> , 2022, 12, 14.	1.3	37
3	Linking anaerobic gut bacteria and cardiovascular disease. <i>Nature Microbiology</i> , 2022, 7, 14-15.	5.9	3
4	The Ubiquitous Human Skin Commensal <i>Staphylococcus hominis</i> Protects against Opportunistic Pathogens. <i>MBio</i> , 2022, 13, .	1.8	24
5	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , 2021, 2327, 87-92.	0.4	1
6	Carbohydrates great and small, from dietary fiber to sialic acids: How glycans influence the gut microbiome and affect human health. <i>Gut Microbes</i> , 2021, 13, 1-18.	4.3	41
7	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	1.7	19
8	The sum is greater than the parts: exploiting microbial communities to achieve complex functions. <i>Current Opinion in Biotechnology</i> , 2021, 67, 149-157.	3.3	25
9	Analysis of the cyanobacterial amino acid metabolism with a precise genome-scale metabolic reconstruction of <i>Anabaena</i> sp. UTEX 2576. <i>Biochemical Engineering Journal</i> , 2021, 171, 108008.	1.8	8
10	Dietary Neu5Ac Intervention Protects Against Atherosclerosis Associated With Human-Like Neu5Gc Lossâ€”Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2730-2739.	1.1	10
11	Biotechnology for secure biocontainment designs in an emerging bioeconomy. <i>Current Opinion in Biotechnology</i> , 2021, 71, 25-31.	3.3	23
12	Examining the impact of carbon dioxide levels and modulation of resulting hydrogen peroxide in <i>Chlorella vulgaris</i> . <i>Algal Research</i> , 2021, 60, 102492.	2.4	4
13	Microbiome Signatures in a Fast- and Slow-Progressing Gastric Cancer Murine Model and Their Contribution to Gastric Carcinogenesis. <i>Microorganisms</i> , 2021, 9, 189.	1.6	13
14	Intestinal Î±1-2-Fucosylation Contributes to Obesity and Steatohepatitis in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 293-320.	2.3	14
15	Creating a synthetic lichen: Mutualistic co-culture of fungi and extracellular polysaccharide-secreting cyanobacterium <i>Nostoc</i> PCC 7413. <i>Algal Research</i> , 2020, 45, 101755.	2.4	24
16	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020, 5, .	1.7	40
17	Synthetic microbial communities of heterotrophs and phototrophs facilitate sustainable growth. <i>Nature Communications</i> , 2020, 11, 3803.	5.8	55
18	Linking metabolic phenotypes to pathogenic traits among <i>Candidatus Liberibacter asiaticus</i> and its hosts. <i>Npj Systems Biology and Applications</i> , 2020, 6, 24.	1.4	20

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19	Modeling of nitrogen fixation and polymer production in the heterotrophic diazotroph <i>Azotobacter vinelandii</i> DJ. <i>Metabolic Engineering Communications</i> , 2020, 11, e00132.	1.9	17
20	Transcriptional profiling of lung macrophages identifies a predictive signature for inflammatory lung disease in preterm infants. <i>Communications Biology</i> , 2020, 3, 259.	2.0	25
21	Genomic and Transcriptomic Evidence Supports Methane Metabolism in <i>Archaeoglobi</i> . <i>MSystems</i> , 2020, 5, .	1.7	33
22	Interplay of Staphylococcal and Host Proteases Promotes Skin Barrier Disruption in Netherton Syndrome. <i>Cell Reports</i> , 2020, 30, 2923-2933.e7.	2.9	56
23	Dynamic resource allocation drives growth under nitrogen starvation in eukaryotes. <i>Npj Systems Biology and Applications</i> , 2020, 6, 14.	1.4	18
24	Functional and Proteomic Analysis of <i>Streptococcus pyogenes</i> Virulence Upon Loss of Its Native Cas9 Nuclease. <i>Frontiers in Microbiology</i> , 2019, 10, 1967.	1.5	11
25	Modelling approaches for studying the microbiome. <i>Nature Microbiology</i> , 2019, 4, 1253-1267.	5.9	114
26	Utilizing genome-scale models to optimize nutrient supply for sustained algal growth and lipid productivity. <i>Npj Systems Biology and Applications</i> , 2019, 5, 33.	1.4	21
27	Environmental stimuli drive a transition from cooperation to competition in synthetic phototrophic communities. <i>Nature Microbiology</i> , 2019, 4, 2184-2191.	5.9	54
28	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. <i>Nature Microbiology</i> , 2019, 4, 2082-2089.	5.9	56
29	A computational knowledge-base elucidates the response of <i>Staphylococcus aureus</i> to different media types. <i>PLoS Computational Biology</i> , 2019, 15, e1006644.	1.5	41
30	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	5.8	428
31	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. <i>Nature Methods</i> , 2019, 16, 567-571.	9.0	90
32	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019, 17, 47.	1.7	101
33	Quorum sensing between bacterial species on the skin protects against epidermal injury in atopic dermatitis. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	185
34	Mast cell recruitment is modulated by the hairless skin microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 330-333.e6.	1.5	6
35	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. <i>PLoS Computational Biology</i> , 2019, 15, e1006848.	1.5	46
36	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	295

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37	The nonlesional skin surface distinguishes atopic dermatitis with food allergy as a unique endotype. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	159
38	Anaerobic degradation of hexadecane and phenanthrene coupled to sulfate reduction by enriched consortia from northern Gulf of Mexico seafloor sediment. <i>Scientific Reports</i> , 2019, 9, 1239.	1.6	31
39	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	5.9	590
40	The Role of Intestinal Cα-type Regenerating Islet Derivedα3 Lectins for Nonalcoholic Steatohepatitis. <i>Hepatology Communications</i> , 2018, 2, 393-406.	2.0	35
41	The social network of microorganisms â€” how auxotrophies shape complex communities. <i>Nature Reviews Microbiology</i> , 2018, 16, 383-390.	13.6	311
42	Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote <i>Chlorella vulgaris</i> . <i>Plant Physiology</i> , 2018, 176, 450-462.	2.3	49
43	Optimization of carbon and energy utilization through differential translational efficiency. <i>Nature Communications</i> , 2018, 9, 4474.	5.8	35
44	Advances in metabolic modeling of oleaginous microalgae. <i>Biotechnology for Biofuels</i> , 2018, 11, 241.	6.2	49
45	Need for Laboratory Ecosystems To Unravel the Structures and Functions of Soil Microbial Communities Mediated by Chemistry. <i>MBio</i> , 2018, 9, .	1.8	34
46	Genome Sequence of the Oleaginous Green Alga, <i>Chlorella vulgaris</i> UTEX 395. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 37.	2.0	21
47	Improving saliva shotgun metagenomics by chemical host DNA depletion. <i>Microbiome</i> , 2018, 6, 42.	4.9	218
48	Metabolic capability and in situ activity of microorganisms in an oil reservoir. <i>Microbiome</i> , 2018, 6, 5.	4.9	70
49	Group B Streptococcus Biofilm Regulatory Protein A Contributes to Bacterial Physiology and Innate Immune Resistance. <i>Journal of Infectious Diseases</i> , 2018, 218, 1641-1652.	1.9	38
50	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. <i>PLoS ONE</i> , 2018, 13, e0197272.	1.1	20
51	Production of organics from CO_2 by microbial electrosynthesis (MES) at high temperature. <i>Journal of Chemical Technology and Biotechnology</i> , 2017, 92, 375-381.	1.6	50
52	Integrated Regulatory and Metabolic Networks of the Marine Diatom <i>Phaeodactylum tricornutum</i> Predict the Response to Rising CO_2 Levels. <i>MSystems</i> , 2017, 2, .	1.7	40
53	Antimicrobials from human skin commensal bacteria protect against <i>Staphylococcus aureus</i> and are deficient in atopic dermatitis. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	744
54	Elucidation of complexity and prediction of interactions in microbial communities. <i>Microbial Biotechnology</i> , 2017, 10, 1500-1522.	2.0	117

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55	Evidence for fungal and chemodenitrification based N ₂ O flux from nitrogen impacted coastal sediments. <i>Nature Communications</i> , 2017, 8, 15595.	5.8	103
56	Efficient Synergistic Single-Cell Genome Assembly. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 42.	2.0	3
57	Genome-Scale Model Reveals Metabolic Basis of Biomass Partitioning in a Model Diatom. <i>PLoS ONE</i> , 2016, 11, e0155038.	1.1	104
58	Genome-Scale Metabolic Model for the Green Alga <i>Chlorella vulgaris</i> UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. <i>Plant Physiology</i> , 2016, 172, 589-602.	2.3	86
59	FRT - FONDATION RENE TOURAINE. <i>Experimental Dermatology</i> , 2016, 25, 917-932.	1.4	0
60	A Phaeodactylum tricornutum literature database for interactive annotation of content. <i>Algal Research</i> , 2016, 18, 241-243.	2.4	0
61	A streamlined ribosome profiling protocol for the characterization of microorganisms. <i>BioTechniques</i> , 2015, 58, 329-32.	0.8	33
62	A logical data representation framework for electricity-driven bioproduction processes. <i>Biotechnology Advances</i> , 2015, 33, 736-744.	6.0	174
63	Adaptive Evolution of Thermotoga maritima Reveals Plasticity of the ABC Transporter Network. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5477-5485.	1.4	16
64	Investigating Moorella thermoacetica metabolism with a genome-scale constraint-based metabolic model. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 869-882.	0.6	33
65	Unraveling interactions in microbial communities - from co-cultures to microbiomes. <i>Journal of Microbiology</i> , 2015, 53, 295-305.	1.3	57
66	Engineering of oleaginous organisms for lipid production. <i>Current Opinion in Biotechnology</i> , 2015, 36, 32-39.	3.3	43
67	Networks of energetic and metabolic interactions define dynamics in microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15450-15455.	3.3	208
68	Supplementation of Saturated Long-Chain Fatty Acids Maintains Intestinal Eubiosis and Reduces Ethanol-induced Liver Injury in Mice. <i>Gastroenterology</i> , 2015, 148, 203-214.e16.	0.6	266
69	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. <i>PLoS Genetics</i> , 2014, 10, e1004264.	1.5	67
70	Protocols for High-Throughput Isolation and Cultivation. <i>Springer Protocols</i> , 2014, , 27-35.	0.1	3
71	Constraint-Based Modeling of Carbon Fixation and the Energetics of Electron Transfer in Geobacter metallireducens. <i>PLoS Computational Biology</i> , 2014, 10, e1003575.	1.5	38
72	Reconstruction and modeling protein translocation and compartmentalization in Escherichia coli at the genome-scale. <i>BMC Systems Biology</i> , 2014, 8, 110.	3.0	81

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73	The Iron Stimulon and Fur Regulon of <i>Geobacter sulfurreducens</i> and Their Role in Energy Metabolism. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2918-2927.	1.4	42
74	Genome-scale reconstruction of the sigma factor network in <i>Escherichia coli</i> : topology and functional states. <i>BMC Biology</i> , 2014, 12, 4.	1.7	111
75	Single-cell genome and metatranscriptome sequencing reveal metabolic interactions of an alkane-degrading methanogenic community. <i>ISME Journal</i> , 2014, 8, 757-767.	4.4	133
76	A new model for electron flow during anaerobic digestion: direct interspecies electron transfer to <i>Methanosaeta</i> for the reduction of carbon dioxide to methane. <i>Energy and Environmental Science</i> , 2014, 7, 408-415.	15.6	1,074
77	Trash to treasure: production of biofuels and commodity chemicals via syngas fermenting microorganisms. <i>Current Opinion in Biotechnology</i> , 2014, 27, 79-87.	3.3	175
78	Characterization and modelling of interspecies electron transfer mechanisms and microbial community dynamics of a syntrophic association. <i>Nature Communications</i> , 2013, 4, 2809.	5.8	103
79	Genomes and Post-genome Technology. , 2013, , 329-344.		0
80	Crystal ball " 2013. <i>Microbial Biotechnology</i> , 2013, 6, 3-16.	2.0	6
81	Characterizing the interplay between multiple levels of organization within bacterial sigma factor regulatory networks. <i>Nature Communications</i> , 2013, 4, 1755.	5.8	15
82	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of <i>Clostridium ljungdahlii</i> . <i>Microbial Cell Factories</i> , 2013, 12, 118.	1.9	145
83	Sulfide-Driven Microbial Electrosynthesis. <i>Environmental Science & Technology</i> , 2013, 47, 568-573.	4.6	101
84	The Genome Organization of <i>Thermotoga maritima</i> Reflects Its Lifestyle. <i>PLoS Genetics</i> , 2013, 9, e1003485.	1.5	38
85	Transcriptional regulation of the carbohydrate utilization network in <i>Thermotoga maritima</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 244.	1.5	48
86	Transcriptional Regulation of Central Carbon and Energy Metabolism in Bacteria by Redox-Responsive Repressor Rex. <i>Journal of Bacteriology</i> , 2012, 194, 1145-1157.	1.0	120
87	Anaerobic utilization of toluene by marine alpha- and gammaproteobacteria reducing nitrate. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2946-2957.	0.7	31
88	In silico method for modelling metabolism and gene product expression at genome scale. <i>Nature Communications</i> , 2012, 3, 929.	5.8	238
89	A road map for the development of community systems (CoSy) biology. <i>Nature Reviews Microbiology</i> , 2012, 10, 366-372.	13.6	135
90	Deciphering the transcriptional regulatory logic of amino acid metabolism. <i>Nature Chemical Biology</i> , 2012, 8, 65-71.	3.9	83

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91	A cät type cytochrome and a transcriptional regulator responsible for enhanced extracellular electron transfer in <i>Geobacter sulfurreducens</i> revealed by adaptive evolution. Environmental Microbiology, 2011, 13, 13-23.	1.8	89
92	Deciphering the regulatory codes in bacterial genomes. Biotechnology Journal, 2011, 6, 1052-1063.	1.8	9
93	Adaptive laboratory evolutionÉc; harnessing the power of biology for metabolic engineering. Current Opinion in Biotechnology, 2011, 22, 590-594.	3.3	246
94	Production of pilus-like filaments in <i>Geobacter sulfurreducens</i> in the absence of the type IV pilin protein PilA. FEMS Microbiology Letters, 2010, 310, 62-68.	0.7	27
95	The challenges of integrating multi-omic data sets. Nature Chemical Biology, 2010, 6, 787-789.	3.9	154
96	De Novo Assembly of the Complete Genome of an Enhanced Electricity-Producing Variant of <i>Geobacter sulfurreducens</i> Using Only Short Reads. PLoS ONE, 2010, 5, e10922.	1.1	29
97	Structural and operational complexity of the <i>Geobacter sulfurreducens</i> genome. Genome Research, 2010, 20, 1304-1311.	2.4	75
98	Isotopic fingerprinting of methane and CO2 formation from aliphatic and aromatic hydrocarbons. Organic Geochemistry, 2010, 41, 482-490.	0.9	40
99	The transcription unit architecture of the <i>Escherichia coli</i> genome. Nature Biotechnology, 2009, 27, 1043-1049.	9.4	251
100	Central Role of the Cell in Microbial Ecology. Microbiology and Molecular Biology Reviews, 2009, 73, 712-729.	2.9	78
101	Targeted Access to the Genomes of Low-Abundance Organisms in Complex Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 3205-3214.	1.4	225
102	<i>Anoxybacillus kamchatkensis</i> sp. nov., a novel thermophilic facultative aerobic bacterium with a broad pH optimum from the Geyser valley, Kamchatka. Extremophiles, 2005, 9, 391-398.	0.9	55
103	High-throughput Cultivation of Microorganisms Using Microcapsules. Methods in Enzymology, 2005, 397, 124-130.	0.4	90
104	New Methods to Access Microbial Diversity for Small Molecule Discovery. , 2005, , 275-293.		15
105	Tapping into microbial diversity. Nature Reviews Microbiology, 2004, 2, 141-150.	13.6	272
106	Nonlinear partial differential equations and applications: Cultivating the uncultured. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15681-15686.	3.3	721
107	Anaerobic degradation and carbon isotopic fractionation of alkylbenzenes in crude oil by sulphate-reducing bacteria. Organic Geochemistry, 2000, 31, 101-115.	0.9	106
108	Anaerobic Oxidation of o-Xylene, m-Xylene, and Homologous Alkylbenzenes by New Types of Sulfate-Reducing Bacteria. Applied and Environmental Microbiology, 1999, 65, 999-1004.	1.4	202

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109	Methane formation from long-chain alkanes by anaerobic microorganisms. Nature, 1999, 401, 266-269.	13.7	591
110	New Cultivation Strategies for Terrestrial Microorganisms. , 0, , 171-192.		8
111	Methods To Study Consortia and Mixed Cultures. , 0, , 205-219.		4
112	The Human Intestinal Microbiota and Its Impact on Health. , 0, , 11-32.		1
113	The Diversity of Free-Living Protists Seen and Unseen, Cultured and Uncultured. , 0, , 67-93.		5
114	The Least Common Denominator: Species or Operational Taxonomic Units?. , 0, , 117-130.		7
115	Metagenomics as a Tool To Study Biodiversity. , 0, , 153-169.		4
116	Cultivation of Marine Symbiotic Microorganisms. , 0, , 193-204.		0
117	Does Cultivation Still Matter?. , 0, , 1-10.		1
118	Single-Cell Genomics. , 0, , 267-278.		0