

Karsten Zengler

List of Publications by Year in descending order

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118
papers

11,804
citations

44069

48
h-index

30087

103
g-index

127
all docs

127
docs citations

127
times ranked

14874
citing authors

#	ARTICLE	IF	CITATIONS
1	A new model for electron flow during anaerobic digestion: direct interspecies electron transfer to Methanosaeta for the reduction of carbon dioxide to methane. Energy and Environmental Science, 2014, 7, 408-415.	30.8	1,074
2	Antimicrobials from human skin commensal bacteria protect against <i>Staphylococcus aureus</i> and are deficient in atopic dermatitis. Science Translational Medicine, 2017, 9, .	12.4	744
3	Cultivating the uncultured. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15681-15686.	7.1	721
4	Methane formation from long-chain alkanes by anaerobic microorganisms. Nature, 1999, 401, 266-269.	27.8	591
5	GABA-modulating bacteria of the human gut microbiota. Nature Microbiology, 2019, 4, 396-403.	13.3	590
6	Establishing microbial composition measurement standards with reference frames. Nature Communications, 2019, 10, 2719.	12.8	428
7	The social network of microorganisms – how auxotrophies shape complex communities. Nature Reviews Microbiology, 2018, 16, 383-390.	28.6	311
8	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. MSystems, 2019, 4, .	3.8	295
9	Tapping into microbial diversity. Nature Reviews Microbiology, 2004, 2, 141-150.	28.6	272
10	Supplementation of Saturated Long-Chain Fatty Acids Maintains Intestinal Eubiosis and Reduces Ethanol-induced Liver Injury in Mice. Gastroenterology, 2015, 148, 203-214.e16.	1.3	266
11	The transcription unit architecture of the Escherichia coli genome. Nature Biotechnology, 2009, 27, 1043-1049.	17.5	251
12	Adaptive laboratory evolution – harnessing the power of biology for metabolic engineering. Current Opinion in Biotechnology, 2011, 22, 590-594.	6.6	246
13	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	12.8	238
14	Targeted Access to the Genomes of Low-Abundance Organisms in Complex Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 3205-3214.	3.1	225
15	Improving saliva shotgun metagenomics by chemical host DNA depletion. Microbiome, 2018, 6, 42.	11.1	218
16	Networks of energetic and metabolic interactions define dynamics in microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15450-15455.	7.1	208
17	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.	3.1	202
18	Quorum sensing between bacterial species on the skin protects against epidermal injury in atopic dermatitis. Science Translational Medicine, 2019, 11, .	12.4	185

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19	Trash to treasure: production of biofuels and commodity chemicals via syngas fermenting microorganisms. <i>Current Opinion in Biotechnology</i> , 2014, 27, 79-87.	6.6	175
20	A logical data representation framework for electricity-driven bioproduction processes. <i>Biotechnology Advances</i> , 2015, 33, 736-744.	11.7	174
21	The nonlesional skin surface distinguishes atopic dermatitis with food allergy as a unique endotype. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	159
22	The challenges of integrating multi-omic data sets. <i>Nature Chemical Biology</i> , 2010, 6, 787-789.	8.0	154
23	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of <i>Clostridium ljungdahlii</i> . <i>Microbial Cell Factories</i> , 2013, 12, 118.	4.0	145
24	A road map for the development of community systems (CoSy) biology. <i>Nature Reviews Microbiology</i> , 2012, 10, 366-372.	28.6	135
25	Single-cell genome and metatranscriptome sequencing reveal metabolic interactions of an alkane-degrading methanogenic community. <i>ISME Journal</i> , 2014, 8, 757-767.	9.8	133
26	Transcriptional Regulation of Central Carbon and Energy Metabolism in Bacteria by Redox-Responsive Repressor Rex. <i>Journal of Bacteriology</i> , 2012, 194, 1145-1157.	2.2	120
27	Elucidation of complexity and prediction of interactions in microbial communities. <i>Microbial Biotechnology</i> , 2017, 10, 1500-1522.	4.2	117
28	Modelling approaches for studying the microbiome. <i>Nature Microbiology</i> , 2019, 4, 1253-1267.	13.3	114
29	Genome-scale reconstruction of the sigma factor network in <i>Escherichia coli</i> : topology and functional states. <i>BMC Biology</i> , 2014, 12, 4.	3.8	111
30	Anaerobic degradation and carbon isotopic fractionation of alkylbenzenes in crude oil by sulphate-reducing bacteria. <i>Organic Geochemistry</i> , 2000, 31, 101-115.	1.8	106
31	Genome-Scale Model Reveals Metabolic Basis of Biomass Partitioning in a Model Diatom. <i>PLoS ONE</i> , 2016, 11, e0155038.	2.5	104
32	Characterization and modelling of interspecies electron transfer mechanisms and microbial community dynamics of a syntrophic association. <i>Nature Communications</i> , 2013, 4, 2809.	12.8	103
33	Evidence for fungal and chemodenitrification based N ₂ O flux from nitrogen impacted coastal sediments. <i>Nature Communications</i> , 2017, 8, 15595.	12.8	103
34	Sulfide-Driven Microbial Electrosynthesis. <i>Environmental Science & Technology</i> , 2013, 47, 568-573.	10.0	101
35	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019, 17, 47.	3.8	101
36	High-Throughput Cultivation of Microorganisms Using Microcapsules. <i>Methods in Enzymology</i> , 2005, 397, 124-130.	1.0	90

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37	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. <i>Nature Methods</i> , 2019, 16, 567-571.	19.0	90
38	A cé type cytochrome and a transcriptional regulator responsible for enhanced extracellular electron transfer in <i>Geobacter sulfurreducens</i> revealed by adaptive evolution. <i>Environmental Microbiology</i> , 2011, 13, 13-23.	3.8	89
39	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.	4.8	86
40	Deciphering the transcriptional regulatory logic of amino acid metabolism. <i>Nature Chemical Biology</i> , 2012, 8, 65-71.	8.0	83
41	Reconstruction and modeling protein translocation and compartmentalization in <i>Escherichia coli</i> at the genome-scale. <i>BMC Systems Biology</i> , 2014, 8, 110.	3.0	81
42	Central Role of the Cell in Microbial Ecology. <i>Microbiology and Molecular Biology Reviews</i> , 2009, 73, 712-729.	6.6	78
43	Structural and operational complexity of the <i>Geobacter sulfurreducens</i> genome. <i>Genome Research</i> , 2010, 20, 1304-1311.	5.5	75
44	Metabolic capability and in situ activity of microorganisms in an oil reservoir. <i>Microbiome</i> , 2018, 6, 5.	11.1	70
45	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. <i>PLoS Genetics</i> , 2014, 10, e1004264.	3.5	67
46	Unraveling interactions in microbial communities - from co-cultures to microbiomes. <i>Journal of Microbiology</i> , 2015, 53, 295-305.	2.8	57
47	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. <i>Nature Microbiology</i> , 2019, 4, 2082-2089.	13.3	56
48	Interplay of Staphylococcal and Host Proteases Promotes Skin Barrier Disruption in Netherton Syndrome. <i>Cell Reports</i> , 2020, 30, 2923-2933.e7.	6.4	56
49	<i>Anoxybacillus kamchatkensis</i> sp. nov., a novel thermophilic facultative aerobic bacterium with a broad pH optimum from the Geyser valley, Kamchatka. <i>Extremophiles</i> , 2005, 9, 391-398.	2.3	55
50	Synthetic microbial communities of heterotrophs and phototrophs facilitate sustainable growth. <i>Nature Communications</i> , 2020, 11, 3803.	12.8	55
51	Environmental stimuli drive a transition from cooperation to competition in synthetic phototrophic communities. <i>Nature Microbiology</i> , 2019, 4, 2184-2191.	13.3	54
52	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.	3.2	50
53	Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote <i>Chlorella vulgaris</i> . <i>Plant Physiology</i> , 2018, 176, 450-462.	4.8	49
54	Advances in metabolic modeling of oleaginous microalgae. <i>Biotechnology for Biofuels</i> , 2018, 11, 241.	6.2	49

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55	Transcriptional regulation of the carbohydrate utilization network in <i>Thermotoga maritima</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 244.	3.5	48
56	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. <i>PLoS Computational Biology</i> , 2019, 15, e1006848.	3.2	46
57	Engineering of oleaginous organisms for lipid production. <i>Current Opinion in Biotechnology</i> , 2015, 36, 32-39.	6.6	43
58	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.	3.1	42
59	A computational knowledge-base elucidates the response of <i>Staphylococcus aureus</i> to different media types. <i>PLoS Computational Biology</i> , 2019, 15, e1006644.	3.2	41
60	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.	9.8	41
61	Isotopic fingerprinting of methane and CO ₂ formation from aliphatic and aromatic hydrocarbons. <i>Organic Geochemistry</i> , 2010, 41, 482-490.	1.8	40
62	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, .	3.8	40
63	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020, 5, .	3.8	40
64	The Genome Organization of <i>Thermotoga maritima</i> Reflects Its Lifestyle. <i>PLoS Genetics</i> , 2013, 9, e1003485.	3.5	38
65	Constraint-Based Modeling of Carbon Fixation and the Energetics of Electron Transfer in <i>Geobacter metallireducens</i> . <i>PLoS Computational Biology</i> , 2014, 10, e1003575.	3.2	38
66	Group B <i>Streptococcus</i> Biofilm Regulatory Protein A Contributes to Bacterial Physiology and Innate Immune Resistance. <i>Journal of Infectious Diseases</i> , 2018, 218, 1641-1652.	4.0	38
67	Genome-Scale Metabolic Modeling Enables In-Depth Understanding of Big Data. <i>Metabolites</i> , 2022, 12, 14.	2.9	37
68	The Role of Intestinal α -Type Regenerating Islet Derived α 3 Lectins for Nonalcoholic Steatohepatitis. <i>Hepatology Communications</i> , 2018, 2, 393-406.	4.3	35
69	Optimization of carbon and energy utilization through differential translational efficiency. <i>Nature Communications</i> , 2018, 9, 4474.	12.8	35
70	Need for Laboratory Ecosystems To Unravel the Structures and Functions of Soil Microbial Communities Mediated by Chemistry. <i>MBio</i> , 2018, 9, .	4.1	34
71	A streamlined ribosome profiling protocol for the characterization of microorganisms. <i>BioTechniques</i> , 2015, 58, 329-32.	1.8	33
72	Investigating <i>Moorella thermoacetica</i> metabolism with a genome-scale constraint-based metabolic model. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 869-882.	1.3	33

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73	Genomic and Transcriptomic Evidence Supports Methane Metabolism in <i>Archaeoglobi</i> . <i>MSystems</i> , 2020, 5, .	3.8	33
74	Anaerobic utilization of toluene by marine alpha- and gammaproteobacteria reducing nitrate. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2946-2957.	1.8	31
75	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.	3.3	31
76	De Novo Assembly of the Complete Genome of an Enhanced Electricity-Producing Variant of <i>Geobacter sulfurreducens</i> Using Only Short Reads. <i>PLoS ONE</i> , 2010, 5, e10922.	2.5	29
77	Production of pilus-like filaments in <i>Geobacter sulfurreducens</i> in the absence of the type IV pilin protein PiiA. <i>FEMS Microbiology Letters</i> , 2010, 310, 62-68.	1.8	27
78	Transcriptional profiling of lung macrophages identifies a predictive signature for inflammatory lung disease in preterm infants. <i>Communications Biology</i> , 2020, 3, 259.	4.4	25
79	The sum is greater than the parts: exploiting microbial communities to achieve complex functions. <i>Current Opinion in Biotechnology</i> , 2021, 67, 149-157.	6.6	25
80	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.	4.6	24
81	The Ubiquitous Human Skin Commensal <i>Staphylococcus hominis</i> Protects against Opportunistic Pathogens. <i>MBio</i> , 2022, 13, .	4.1	24
82	Biotechnology for secure biocontainment designs in an emerging bioeconomy. <i>Current Opinion in Biotechnology</i> , 2021, 71, 25-31.	6.6	23
83	Genome Sequence of the Oleaginous Green Alga, <i>Chlorella vulgaris</i> UTEX 395. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 37.	4.1	21
84	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.	3.0	21
85	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. <i>PLoS ONE</i> , 2018, 13, e0197272.	2.5	20
86	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.	3.0	20
87	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	3.8	19
88	Dynamic resource allocation drives growth under nitrogen starvation in eukaryotes. <i>Npj Systems Biology and Applications</i> , 2020, 6, 14.	3.0	18
89	Modeling of nitrogen fixation and polymer production in the heterotrophic diazotroph <i>Azotobacter vinelandii</i> DJ. <i>Metabolic Engineering Communications</i> , 2020, 11, e00132.	3.6	17
90	Adaptive Evolution of <i>Thermotoga maritima</i> Reveals Plasticity of the ABC Transporter Network. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5477-5485.	3.1	16

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91	Characterizing the interplay between multiple levels of organization within bacterial sigma factor regulatory networks. <i>Nature Communications</i> , 2013, 4, 1755.	12.8	15
92	New Methods to Access Microbial Diversity for Small Molecule Discovery. , 2005, , 275-293.		15
93	Intestinal α 1-2-Fucosylation Contributes to Obesity and Steatohepatitis in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 293-320.	4.5	14
94	Microbiome Signatures in a Fast- and Slow-Progressing Gastric Cancer Murine Model and Their Contribution to Gastric Carcinogenesis. <i>Microorganisms</i> , 2021, 9, 189.	3.6	13
95	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.	3.5	11
96	Dietary Neu5Ac Intervention Protects Against Atherosclerosis Associated With Human-Like Neu5Gc Loss – Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2730-2739.	2.4	10
97	Deciphering the regulatory codes in bacterial genomes. <i>Biotechnology Journal</i> , 2011, 6, 1052-1063.	3.5	9
98	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.	3.6	8
99	New Cultivation Strategies for Terrestrial Microorganisms. , 0, , 171-192.		8
100	The Least Common Denominator: Species or Operational Taxonomic Units?. , 0, , 117-130.		7
101	Crystal ball – 2013. <i>Microbial Biotechnology</i> , 2013, 6, 3-16.	4.2	6
102	Mast cell recruitment is modulated by the hairless skin microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 330-333.e6.	2.9	6
103	The Diversity of Free-Living Protists Seen and Unseen, Cultured and Uncultured. , 0, , 67-93.		5
104	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.	4.6	4
105	Methods To Study Consortia and Mixed Cultures. , 0, , 205-219.		4
106	Metagenomics as a Tool To Study Biodiversity. , 0, , 153-169.		4
107	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.	3.2	4
108	Protocols for High-Throughput Isolation and Cultivation. <i>Springer Protocols</i> , 2014, , 27-35.	0.3	3

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109	Efficient Synergistic Single-Cell Genome Assembly. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 42.	4.1	3
110	Linking anaerobic gut bacteria and cardiovascular disease. <i>Nature Microbiology</i> , 2022, 7, 14-15.	13.3	3
111	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , 2021, 2327, 87-92.	0.9	1
112	The Human Intestinal Microbiota and Its Impact on Health. , 0, , 11-32.		1
113	Does Cultivation Still Matter?. , 0, , 1-10.		1
114	Genomes and Post-genome Technology. , 2013, , 329-344.		0
115	FRT - FONDATION RENE TOURAINE. <i>Experimental Dermatology</i> , 2016, 25, 917-932.	2.9	0
116	A <i>Phaeodactylum tricornutum</i> literature database for interactive annotation of content. <i>Algal Research</i> , 2016, 18, 241-243.	4.6	0
117	Cultivation of Marine Symbiotic Microorganisms. , 0, , 193-204.		0
118	Single-Cell Genomics. , 0, , 267-278.		0