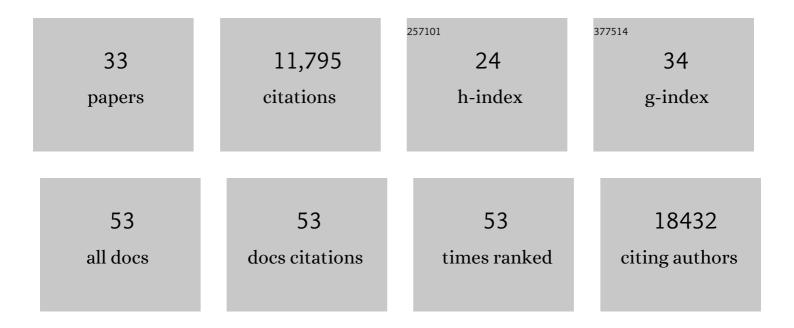
## Lawrence A David

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4105202/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Diet rapidly and reproducibly alters the human gut microbiome. Nature, 2014, 505, 559-563.	13.7	7,592
2	Ecology drives a global network of gene exchange connecting the human microbiome. Nature, 2011, 480, 241-244.	13.7	788
3	Host lifestyle affects human microbiota on daily timescales. Genome Biology, 2014, 15, R89.	13.9	735
4	Resource Partitioning and Sympatric Differentiation Among Closely Related Bacterioplankton. Science, 2008, 320, 1081-1085.	6.0	472
5	Rapid evolutionary innovation during an Archaean genetic expansion. Nature, 2011, 469, 93-96.	13.7	344
6	A phylogenetic transform enhances analysis of compositional microbiota data. ELife, 2017, 6, .	2.8	247
7	Gut Microbial Succession Follows Acute Secretory Diarrhea in Humans. MBio, 2015, 6, e00381-15.	1.8	150
8	Antibiotic-induced changes in the microbiota disrupt redox dynamics in the gut. ELife, 2018, 7, .	2.8	121
9	Quantification of Cell Edge Velocities and Traction Forces Reveals Distinct Motility Modules during Cell Spreading. PLoS ONE, 2008, 3, e3735.	1.1	112
10	Microbial nitrogen limitation in the mammalian large intestine. Nature Microbiology, 2018, 3, 1441-1450.	5.9	107
11	Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. PeerJ, 2017, 5, e2969.	0.9	105
12	Ontogenetic Differences in Dietary Fat Influence Microbiota Assembly in the Zebrafish Gut. MBio, 2015, 6, e00687-15.	1.8	101
13	Looking for Darwin's footprints in the microbial world. Trends in Microbiology, 2009, 17, 196-204.	3.5	94
14	Naught all zeros in sequence count data are the same. Computational and Structural Biotechnology Journal, 2020, 18, 2789-2798.	1.9	87
15	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. Environmental Microbiology, 2011, 13, 265-275.	1.8	76
16	Human Gut Microbiota Predicts Susceptibility to Vibrio cholerae Infection. Journal of Infectious Diseases, 2018, 218, 645-653.	1.9	60
17	Genotypic and Phenotypic Diversity among Human Isolates of Akkermansia muciniphila. MBio, 2021, 12, .	1.8	60
18	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. Microbiome, 2018, 6, 202.	4.9	54

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#	Article	IF	CITATIONS
19	Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. Ecological Monographs, 2019, 89, e01353.	2.4	52
20	Reproducibility of <i>Vibrionaceae</i> population structure in coastal bacterioplankton. ISME Journal, 2013, 7, 509-519.	4.4	50
21	Short-Chain Fatty Acid Production by Gut Microbiota from Children with Obesity Differs According to Prebiotic Choice and Bacterial Community Composition. MBio, 2020, 11, .	1.8	49
22	Measuring and mitigating PCR bias in microbiota datasets. PLoS Computational Biology, 2021, 17, e1009113.	1.5	43
23	Conserved anti-inflammatory effects and sensing of butyrate in zebrafish. Gut Microbes, 2020, 12, 1824563.	4.3	41
24	Interindividual Variation in Dietary Carbohydrate Metabolism by Gut Bacteria Revealed with Droplet Microfluidic Culture. MSystems, 2020, 5, .	1.7	34
25	Plant community and soil conditions individually affect soil microbial community assembly in experimental mesocosms. Ecology and Evolution, 2018, 8, 1196-1205.	0.8	31
26	Predicting <i>Vibrio cholerae</i> Infection and Disease Severity Using Metagenomics in a Prospective Cohort Study. Journal of Infectious Diseases, 2021, 223, 342-351.	1.9	25
27	Modulation of microbial community dynamics by spatial partitioning. Nature Chemical Biology, 2022, 18, 394-402.	3.9	23
28	The Pediatric Obesity Microbiome and Metabolism Study (POMMS): Methods, Baseline Data, and Early Insights. Obesity, 2021, 29, 569-578.	1.5	19
29	Using DNA Metabarcoding To Evaluate the Plant Component of Human Diets: a Proof of Concept. MSystems, 2019, 4, .	1.7	18
30	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	5.9	13
31	Benchmarking of Dynamic Bayesian Networks Inferred from Stochastic Time-Series Data. Annals of the New York Academy of Sciences, 2007, 1115, 90-101.	1.8	11
32	Conceptual Exchanges for Understanding Free-Living and Host-Associated Microbiomes. MSystems, 2022, 7, e0137421.	1.7	3
33	Toward Personalized Control of Human Gut Bacterial Communities. MSystems, 2018, 3, .	1.7	2