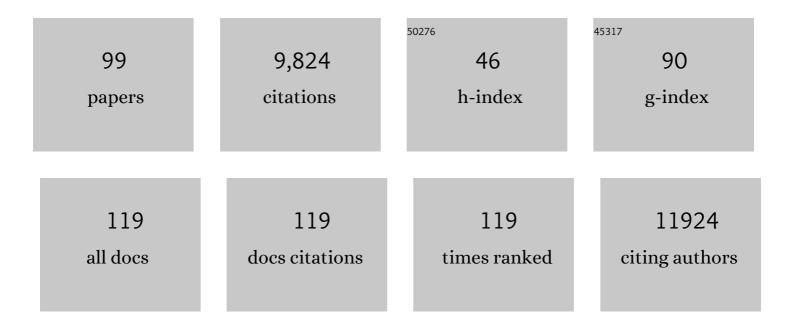
## Martin Ackermann

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Global dynamics of microbial communities emerge from local interaction rules. PLoS Computational Biology, 2022, 18, e1009877.	3.2	13
2	Dynamic character displacement among a pair of bacterial phyllosphere commensals in situ. Nature Communications, 2022, 13, .	12.8	15
3	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. ISME Journal, 2021, 15, 862-878.	9.8	66
4	Rapid evolution destabilizes species interactions in a fluctuating environment. ISME Journal, 2021, 15, 450-460.	9.8	24
5	Nutrient complexity triggers transitions between solitary and colonial growth in bacterial populations. ISME Journal, 2021, 15, 2614-2626.	9.8	36
6	Short-range quorum sensing controls horizontal gene transfer at micron scale in bacterial communities. Nature Communications, 2021, 12, 2324.	12.8	57
7	A distinct growth physiology enhances bacterial growth under rapid nutrient fluctuations. Nature Communications, 2021, 12, 3662.	12.8	40
8	Microbiota-derived metabolites inhibit <i>Salmonella</i> virulent subpopulation development by acting on single-cell behaviors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	20
9	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. Epidemics, 2021, 37, 100480.	3.0	34
10	Microfluidics for Single-Cell Study of Antibiotic Tolerance and Persistence Induced by Nutrient Limitation. Methods in Molecular Biology, 2021, 2357, 107-124.	0.9	3
11	Stochastic Gene Expression Influences the Selection of Antibiotic Resistance Mutations. Molecular Biology and Evolution, 2020, 37, 58-70.	8.9	8
12	Environmental drivers of metabolic heterogeneity in clonal microbial populations. Current Opinion in Biotechnology, 2020, 62, 202-211.	6.6	40
13	Wide lag time distributions break a trade-off between reproduction and survival in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18729-18736.	7.1	72
14	Understanding the evolution of interspecies interactions in microbial communities. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190256.	4.0	68
15	Short-range interactions govern the dynamics and functions of microbial communities. Nature Ecology and Evolution, 2020, 4, 366-375.	7.8	172
16	Dissection of the mutation accumulation process during bacterial range expansions. BMC Genomics, 2020, 21, 253.	2.8	8
17	Microbial life cycles link global modularity in regulation to mosaic evolution. Nature Ecology and Evolution, 2019, 3, 1184-1196.	7.8	18
18	Mutational and Selective Processes Involved in Evolution during Bacterial Range Expansions. Molecular Biology and Evolution, 2019, 36, 2313-2327.	8.9	11

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19	Metabolic activity affects the response of single cells to a nutrient switch in structured populations. Journal of the Royal Society Interface, 2019, 16, 20190182.	3.4	36
20	Emergent microscale gradients give rise to metabolic cross-feeding and antibiotic tolerance in clonal bacterial populations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190080.	4.0	74
21	Disseminating antibiotic resistance during treatment. Science, 2019, 364, 737-738.	12.6	36
22	Why microbes secrete molecules to modify their environment: the case of iron-chelating siderophores. Journal of the Royal Society Interface, 2019, 16, 20180674.	3.4	61
23	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	28.6	748
24	Individual―versus groupâ€optimality in the production of secreted bacterial compounds. Evolution; International Journal of Organic Evolution, 2019, 73, 675-688.	2.3	21
25	The rate of environmental fluctuations shapes ecological dynamics in a twoâ€species microbial system. Ecology Letters, 2019, 22, 838-846.	6.4	35
26	Spatially Correlated Gene Expression in Bacterial Groups: The Role of Lineage History, Spatial Gradients, and Cell-Cell Interactions. Cell Systems, 2018, 6, 496-507.e6.	6.2	59
27	Function and functional redundancy in microbial systems. Nature Ecology and Evolution, 2018, 2, 936-943.	7.8	912
28	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. ISME Journal, 2018, 12, 1344-1359.	9.8	84
29	Prolonged bacterial lag time results in small colony variants that represent a sub-population of persisters. Nature Communications, 2018, 9, 4074.	12.8	109
30	Division of labor in bacteria. ELife, 2018, 7, .	6.0	7
31	Effective polyploidy causes phenotypic delay and influences bacterial evolvability. PLoS Biology, 2018, 16, e2004644.	5.6	37
32	Thiouridine residues in tRNAs are responsible for a synergistic effect of UVA and UVB light in photoinactivation of <i>Escherichia coli</i> . Environmental Microbiology, 2017, 19, 434-442.	3.8	33
33	Inflammation boosts bacteriophage transfer between <i>Salmonella</i> spp Science, 2017, 355, 1211-1215.	12.6	160
34	Accumulation of Deleterious Mutations During Bacterial Range Expansions. Genetics, 2017, 207, 669-684.	2.9	74
35	Stochastic gene expression: bacterial elites in chemotaxis. Molecular Systems Biology, 2017, 13, 909.	7.2	4
36	Asymmetric cellular memory in bacteria exposed to antibiotics. BMC Evolutionary Biology, 2017, 17, 73.	3.2	12

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37	A passive mutualistic interaction promotes the evolution of spatial structure within microbial populations. BMC Evolutionary Biology, 2017, 17, 106.	3.2	41
38	Magnitude and Mechanism of Siderophore-Mediated Competition at Low Iron Solubility in the Pseudomonas aeruginosa Pyochelin System. Frontiers in Microbiology, 2017, 8, 1964.	3.5	32
39	Cell-to-cell variation and specialization in sugar metabolism in clonal bacterial populations. PLoS Genetics, 2017, 13, e1007122.	3.5	58
40	Genetic Manipulation of Glycogen Allocation Affects Replicative Lifespan in E. coli. PLoS Genetics, 2016, 12, e1005974.	3.5	10
41	How type 1 fimbriae help Escherichia coli to evade extracellular antibiotics. Scientific Reports, 2016, 6, 18109.	3.3	47
42	The Microbial Olympics 2016. Nature Microbiology, 2016, 1, 16122.	13.3	7
43	Phenotypic heterogeneity driven by nutrient limitation promotes growth in fluctuating environments. Nature Microbiology, 2016, 1, 16055.	13.3	154
44	Response of single bacterial cells to stress gives rise to complex history dependence at the population level. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4224-4229.	7.1	58
45	A growing focus on bacterial individuality. Environmental Microbiology, 2015, 17, 2193-2195.	3.8	14
46	Phenotypic heterogeneity in metabolic traits among single cells of a rare bacterial species in its natural environment quantified with a combination of flow cell sorting and NanoSIMS. Frontiers in Microbiology, 2015, 06, 243.	3.5	72
47	Bacterial Ventures into Multicellularity: Collectivism through Individuality. PLoS Biology, 2015, 13, e1002162.	5.6	22
48	Association of Biodiversity with the Rates of Micropollutant Biotransformations among Full-Scale Wastewater Treatment Plant Communities. Applied and Environmental Microbiology, 2015, 81, 666-675.	3.1	98
49	A functional perspective on phenotypic heterogeneity in microorganisms. Nature Reviews Microbiology, 2015, 13, 497-508.	28.6	709
50	The usefulness of evolutionary principles: predicting the unexpected. Environmental Microbiology Reports, 2015, 7, 4-5.	2.4	0
51	Costs of antibiotic resistance – separating trait effects and selective effects. Evolutionary Applications, 2015, 8, 261-272.	3.1	39
52	Bistable Expression of Virulence Genes in Salmonella Leads to the Formation of an Antibiotic-Tolerant Subpopulation. PLoS Biology, 2014, 12, e1001928.	5.6	172
53	Cecum Lymph Node Dendritic Cells Harbor Slow-Growing Bacteria Phenotypically Tolerant to Antibiotic Treatment. PLoS Biology, 2014, 12, e1001793.	5.6	139
54	A Synthetic Community Approach Reveals Plant Genotypes Affecting the Phyllosphere Microbiota. PLoS Genetics, 2014, 10, e1004283.	3.5	369

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55	Phenotypic plasticity influences the ecoâ€evolutionary dynamics of a predator–prey system. Ecology, 2014, 95, 3080-3092.	3.2	39
56	Antibiotic Treatment Selects for Cooperative Virulence of Salmonella Typhimurium. Current Biology, 2014, 24, 2000-2005.	3.9	87
57	Habitat structure and the evolution of diffusible siderophores in bacteria. Ecology Letters, 2014, 17, 1536-1544.	6.4	98
58	The predictability of molecular evolution during functional innovation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3044-3049.	7.1	69
59	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. Antimicrobial Agents and Chemotherapy, 2014, 58, 4573-4582.	3.2	198
60	Analysis of fluorescent reporters indicates heterogeneity in glucose uptake and utilization in clonal bacterial populations. BMC Microbiology, 2013, 13, 258.	3.3	77
61	Microbial individuality in the natural environment. ISME Journal, 2013, 7, 465-467.	9.8	56
62	Stabilization of cooperative virulence by the expression of an avirulent phenotype. Nature, 2013, 494, 353-356.	27.8	289
63	The role of bacteriocins as selfish genetic elements. Biology Letters, 2013, 9, 20121173.	2.3	45
64	Resolution of Conflicting Signals at the Single-Cell Level in the Regulation of Cyanobacterial Photosynthesis and Nitrogen Fixation. PLoS ONE, 2013, 8, e66060.	2.5	25
65	Patterns of Evolutionary Conservation of Essential Genes Correlate with Their Compensability. PLoS Genetics, 2012, 8, e1002803.	3.5	74
66	A Genome-Wide Analysis of Promoter-Mediated Phenotypic Noise in Escherichia coli. PLoS Genetics, 2012, 8, e1002443.	3.5	155
67	The optimal deployment of synergistic antibiotics: a control-theoretic approach. Journal of the Royal Society Interface, 2012, 9, 2488-2502.	3.4	22
68	Gut inflammation can boost horizontal gene transfer between pathogenic and commensal <i>Enterobacteriaceae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1269-1274.	7.1	398
69	The activity level of a microbial community function can be predicted from its metatranscriptome. ISME Journal, 2012, 6, 902-904.	9.8	70
70	Division of labour and the evolution of multicellularity. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1768-1776.	2.6	87
71	Metabolic specialization and the assembly of microbial communities. ISME Journal, 2012, 6, 1985-1991.	9.8	113
72	Selecting Against Antibiotic-Resistant Pathogens: Optimal Treatments in the Presence of Commensal Bacteria. Bulletin of Mathematical Biology, 2012, 74, 908-934.	1.9	17

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73	Evolution of Stress Response in the Face of Unreliable Environmental Signals. PLoS Computational Biology, 2012, 8, e1002627.	3.2	59
74	Framework for Using Quantitative PCR as a Nonculture Based Method To Estimate Virus Infectivity. Environmental Science & Technology, 2011, 45, 2257-2263.	10.0	82
75	Single-cell time-lapse analysis of depletion of the universally conserved essential protein YgjD. BMC Microbiology, 2011, 11, 118.	3.3	19
76	Pole Age Affects Cell Size and the Timing of Cell Division in Methylobacterium extorquens AM1. Journal of Bacteriology, 2011, 193, 5216-5221.	2.2	20
77	The Cost of Virulence: Retarded Growth of Salmonella Typhimurium Cells Expressing Type III Secretion System 1. PLoS Pathogens, 2011, 7, e1002143.	4.7	213
78	Second Messenger-Mediated Adjustment of Bacterial Swimming Velocity. Cell, 2010, 141, 107-116.	28.9	412
79	The constancy of gene conservation across divergent bacterial orders. BMC Research Notes, 2009, 2, 2.	1.4	17
80	Bacterial growth properties at low optical densities. Antonie Van Leeuwenhoek, 2009, 96, 267-274.	1.7	10
81	Second messenger signalling governs <i>Escherichia coli</i> biofilm induction upon ribosomal stress. Molecular Microbiology, 2009, 72, 1500-1516.	2.5	183
82	Self-destructive cooperation mediated by phenotypic noise. Nature, 2008, 454, 987-990.	27.8	384
83	Stabilization of the genome of the mismatch repair deficient Mycobacterium tuberculosis by context-dependent codon choice. BMC Genomics, 2008, 9, 249.	2.8	15
84	A Simple Screen to Identify Promoters Conferring High Levels of Phenotypic Noise. PLoS Genetics, 2008, 4, e1000307.	3.5	74
85	Bacteria as a New Model System for Aging Studies: Investigations Using Light Microscopy. BioTechniques, 2008, 44, 564-567.	1.8	12
86	On the evolutionary origin of aging. Aging Cell, 2007, 6, 235-244.	6.7	139
87	Experimental evolution of aging in a bacterium. BMC Evolutionary Biology, 2007, 7, 126.	3.2	48
88	The Effect of Multifunctionality on the Rate of Evolution in Yeast. Molecular Biology and Evolution, 2006, 23, 721-722.	8.9	52
89	DNA Sequences Shaped by Selection for Stability. PLoS Genetics, 2006, 2, e22.	3.5	40
90	EVOLUTION OF NICHE WIDTH AND ADAPTIVE DIVERSIFICATION. Evolution; International Journal of Organic Evolution, 2004, 58, 2599.	2.3	4

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91	Evolution of cooperation: Two for One?. Current Biology, 2004, 14, R73-R74.	3.9	10
92	Senescence in a Bacterium with Asymmetric Division. Science, 2003, 300, 1920-1920.	12.6	296
93	Effect of Low- and High-Virulence Yersinia enterocolitica Strains on the Inflammatory Response of Human Umbilical Vein Endothelial Cells. Infection and Immunity, 2002, 70, 3510-3520.	2.2	51
94	Effects of assay conditions in life history experiments with Drosophila melanogaster. Journal of Evolutionary Biology, 2001, 14, 199-209.	1.7	62
95	DECLINE IN OFFSPRING VIABILITY AS A MANIFESTATION OF AGING IN DROSOPHILA MELANOGASTER. Evolution; International Journal of Organic Evolution, 2001, 55, 1822-1831.	2.3	86
96	Experimental evolution of aging, growth, and reproduction in fruitflies. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 3309-3313.	7.1	176
97	The experimental evolution of aging in fruitflies. Experimental Gerontology, 1998, 33, 785-792.	2.8	17
98	Population dynamics, demographic stochasticity, and the evolution of cooperation. Proceedings of the United States of America, 1997, 94, 5167-5171.	7.1	18
99	Local Interactions Contribute to Spatial Correlations in Gene Expression Levels in Bacterial Groups. SSRN Electronic Journal, 0, , .	0.4	Ο