

# Alex R Hall

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

2,132  
citations

257450

24  
h-index

265206

42  
g-index

68  
all docs

68  
docs citations

68  
times ranked

2621  
citing authors

#	ARTICLE	IF	CITATIONS
1	Community composition of bacteria isolated from Swiss banknotes varies depending on collection environment. <i>Molecular Ecology</i> , 2023, 32, 2619-2632.	3.9	2
2	Exposure to lysed bacteria can promote or inhibit growth of neighboring live bacteria depending on local abiotic conditions. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	7
3	Rapid decline of adaptation of <i>Pseudomonas fluorescens</i> to soil biotic environment. <i>Biology Letters</i> , 2022, 18, 20210593.	2.3	6
4	Estimating plasmid conjugation rates: A new computational tool and a critical comparison of methods. <i>Plasmid</i> , 2022, 121, 102627.	1.4	19
5	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. <i>ISME Journal</i> , 2021, 15, 862-878.	9.8	66
6	Fitness benefits to bacteria of carrying prophages and prophage-encoded antibiotic-resistance genes peak in different environments. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 515-528.	2.3	61
7	Species interactions drive the spread of ampicillin resistance in human-associated gut microbiota. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 256-266.	2.5	5
8	Using ecological coexistence theory to understand antibiotic resistance and microbial competition. <i>Nature Ecology and Evolution</i> , 2021, 5, 431-441.	7.8	46
9	Human-associated microbiota suppress invading bacteria even under disruption by antibiotics. <i>ISME Journal</i> , 2021, 15, 2809-2812.	9.8	12
10	Evolution of honey resistance in experimental populations of bacteria depends on the type of honey and has no major side effects for antibiotic susceptibility. <i>Evolutionary Applications</i> , 2021, 14, 1314-1327.	3.1	6
11	Microbial community composition interacts with local abiotic conditions to drive colonization resistance in human gut microbiome samples. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203106.	2.6	12
12	<i>In Vitro</i> Gut Modeling as a Tool for Adaptive Evolutionary Engineering of <i>Lactiplantibacillus plantarum</i> . <i>MSystems</i> , 2021, 6, .	3.8	9
13	Collateral Sensitivity Interactions between Antibiotics Depend on Local Abiotic Conditions. <i>MSystems</i> , 2021, 6, e0105521.	3.8	7
14	Strong effects of lab-to-field environmental transitions on the bacterial intestinal microbiota of <i>Mus musculus</i> are modulated by <i>Trichuris muris</i> infection. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	17
15	Associations between sensitivity to antibiotics, disinfectants and heavy metals in natural, clinical and laboratory isolates of <i>Escherichia coli</i> . <i>Environmental Microbiology</i> , 2020, 22, 2664-2679.	3.8	9
16	Measuring Coevolutionary Dynamics in Species-Rich Communities. <i>Trends in Ecology and Evolution</i> , 2020, 35, 539-550.	8.7	28
17	Resident microbial communities inhibit growth and antibiotic-resistance evolution of <i>Escherichia coli</i> in human gut microbiome samples. <i>PLoS Biology</i> , 2020, 18, e3000465.	5.6	47
18	Title is missing!. , 2020, 18, e3000465.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 18, e3000465.		0
20	Title is missing!. , 2020, 18, e3000465.		0
21	Title is missing!. , 2020, 18, e3000465.		0
22	Title is missing!. , 2020, 18, e3000465.		0
23	Title is missing!. , 2020, 18, e3000465.		0
24	Impact of bile salts on coevolutionary dynamics between the gut bacterium <i>Escherichia coli</i> and its lytic phage PP01. <i>Infection, Genetics and Evolution</i> , 2019, 73, 425-432.	2.3	13
25	Transition bias influences the evolution of antibiotic resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS Biology</i> , 2019, 17, e3000265.	5.6	50
26	Coevolutionary dynamics shape the structure of bacteria–phage infection networks. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1001-1011.	2.3	36
27	Resistance Gene Carriage Predicts Growth of Natural and Clinical <i>Escherichia coli</i> Isolates in the Absence of Antibiotics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	9
28	Effects of prior exposure to antibiotics on bacterial adaptation to phages. <i>Journal of Evolutionary Biology</i> , 2018, 31, 277-286.	1.7	3
29	Modification of <i>Escherichia coli</i> –bacteriophage interactions by surfactants and antibiotics <i>in vitro</i> . <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw211.	2.7	19
30	Reversing resistance: different routes and common themes across pathogens. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171619.	2.6	22
31	Associations among Antibiotic and Phage Resistance Phenotypes in Natural and Clinical <i>Escherichia coli</i> Isolates. <i>MBio</i> , 2017, 8, .	4.1	37
32	Parasite genetic distance and local adaptation in coevolving bacteria–bacteriophage populations. <i>Molecular Ecology</i> , 2017, 26, 1747-1755.	3.9	8
33	Effects of antibiotic resistance alleles on bacterial evolutionary responses to viral parasites. <i>Biology Letters</i> , 2016, 12, 20160064.	2.3	4
34	Adaptation to Parasites and Costs of Parasite Resistance in Mutator and Nonmutator Bacteria. <i>Molecular Biology and Evolution</i> , 2016, 33, 770-782.	8.9	22
35	Experimental evolution and bacterial resistance: (co)evolutionary costs and trade-offs as opportunities in phage therapy research. <i>Bacteriophage</i> , 2015, 5, e1050153.	1.9	47
36	Coevolution with Bacteriophages Drives Genome-Wide Host Evolution and Constrains the Acquisition of Abiotic-Beneficial Mutations. <i>Molecular Biology and Evolution</i> , 2015, 32, 1425-1435.	8.9	94

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37	Costs of antibiotic resistance – separating trait effects and selective effects. <i>Evolutionary Applications</i> , 2015, 8, 261-272.	3.1	39
38	Lytic phages obscure the cost of antibiotic resistance in <i>Escherichia coli</i> . <i>ISME Journal</i> , 2015, 9, 809-820.	9.8	17
39	Interspecific interactions drive chitin and cellulose degradation by aquatic microorganisms. <i>Aquatic Microbial Ecology</i> , 2015, 76, 27-37.	1.8	23
40	Higher resources decrease fluctuating selection during host-parasite coevolution. <i>Ecology Letters</i> , 2014, 17, 1380-1388.	6.4	55
41	Tetracycline modifies competitive interactions in experimental microcosms containing bacteria isolated from freshwater. <i>FEMS Microbiology Ecology</i> , 2014, 90, 168-174.	2.7	6
42	The cost of antibiotic resistance depends on evolutionary history in <i>Escherichia coli</i> . <i>BMC Evolutionary Biology</i> , 2013, 13, 163.	3.2	42
43	No effect of host-parasite coevolution on host range expansion. <i>Journal of Evolutionary Biology</i> , 2013, 26, 205-209.	1.7	13
44	Genotype-by-environment interactions due to antibiotic resistance and adaptation in <i>Escherichia coli</i> . <i>Journal of Evolutionary Biology</i> , 2013, 26, 1655-1664.	1.7	29
45	The role of “soaking” in spiteful toxin production in <i>Pseudomonas aeruginosa</i> . <i>Biology Letters</i> , 2013, 9, 20120569.	2.3	10
46	Effects of Sequential and Simultaneous Applications of Bacteriophages on Populations of <i>Pseudomonas aeruginosa</i> <i>In Vitro</i> and in Wax Moth Larvae. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5646-5652.	3.1	139
47	Diversity-disturbance relationships: frequency and intensity interact. <i>Biology Letters</i> , 2012, 8, 768-771.	2.3	71
48	Multiplicity of infection does not accelerate infectivity evolution of viral parasites in laboratory microcosms. <i>Journal of Evolutionary Biology</i> , 2012, 25, 409-415.	1.7	7
49	Bacteria-Phage Coevolution and the Emergence of Generalist Pathogens. <i>American Naturalist</i> , 2011, 177, 44-53.	2.1	87
50	Host-parasite coevolutionary arms races give way to fluctuating selection. <i>Ecology Letters</i> , 2011, 14, 635-642.	6.4	243
51	Genetic basis of infectivity evolution in a bacteriophage. <i>Molecular Ecology</i> , 2011, 20, 981-989.	3.9	93
52	EPISTASIS BUFFERS THE FITNESS EFFECTS OF RIFAMPICIN- RESISTANCE MUTATIONS IN PSEUDOMONAS AERUGINOSA. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 2370-2379.	2.3	65
53	The Fitness Cost of Rifampicin Resistance in <i>Pseudomonas aeruginosa</i> Depends on Demand for RNA Polymerase. <i>Genetics</i> , 2011, 187, 817-822.	2.9	77
54	Mutational neighbourhood and mutation supply rate constrain adaptation in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 643-650.	2.6	42

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55	The population genetics of antibiotic resistance: integrating molecular mechanisms and treatment contexts. <i>Nature Reviews Genetics</i> , 2010, 11, 405-414.	16.3	181
56	Hypermutable and Compensatory Adaptation in Antibiotic-Resistant Bacteria. <i>American Naturalist</i> , 2010, 176, 303-311.	2.1	52
57	The evolution of antibiotic resistance: insight into the roles of molecular mechanisms of resistance and treatment context. <i>Discovery Medicine</i> , 2010, 10, 112-8.	0.5	13
58	Decay of unused characters by selection and drift. <i>Journal of Evolutionary Biology</i> , 2008, 21, 610-617.	1.7	57
59	How does resource supply affect evolutionary diversification?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 73-78.	2.6	38