

Hinrich Schulenburg

List of Publications by Year in descending order

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98
papers

6,061
citations

71102

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91884

69
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112
all docs

112
docs citations

112
times ranked

5824
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene sharing among plasmids and chromosomes reveals barriers for antibiotic resistance gene transfer. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200467.	4.0	23
2	Exploring Effects of <i>C. elegans</i> Protective Natural Microbiota on Host Physiology. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 775728.	3.9	20
3	The Role of Integrative and Conjugative Elements in Antibiotic Resistance Evolution. <i>Trends in Microbiology</i> , 2021, 29, 8-18.	7.7	118
4	The Genomic Basis of Rapid Adaptation to Antibiotic Combination Therapy in <i>Pseudomonas aeruginosa</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 449-464.	8.9	21
5	On the evolutionary origins of host-microbe associations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
6	The Antibiotic Dosage of Fastest Resistance Evolution: Gene Amplifications Underpinning the Inverted-U. <i>Molecular Biology and Evolution</i> , 2021, 38, 3847-3863.	8.9	1
7	Effector and regulator: Diverse functions of <i>C. elegans</i> C-type lectin-like domain proteins. <i>PLoS Pathogens</i> , 2021, 17, e1009454.	4.7	22
8	Modeling host-associating microbes under selection. <i>ISME Journal</i> , 2021, 15, 3648-3656.	9.8	15
9	Bottleneck size and selection level reproducibly impact evolution of antibiotic resistance. <i>Nature Ecology and Evolution</i> , 2021, 5, 1233-1242.	7.8	32
10	High potency of sequential therapy with only β -lactam antibiotics. <i>ELife</i> , 2021, 10, .	6.0	29
11	The genetics of gene expression in a <i>Caenorhabditis elegans</i> multiparental recombinant inbred line population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	8
12	Evolution of Microbiota-Host Associations: The Microbe's Perspective. <i>Trends in Microbiology</i> , 2021, 29, 779-787.	7.7	28
13	The effects of nested miRNAs and their host genes on immune defense against <i>Bacillus thuringiensis</i> infection in <i>Caenorhabditis elegans</i> . <i>Developmental and Comparative Immunology</i> , 2021, 123, 104144.	2.3	3
14	Population size impacts host-pathogen coevolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212269.	2.6	11
15	<i>Bdellovibrio</i> and Like Organisms Are Predictors of Microbiome Diversity in Distinct Host Groups. <i>Microbial Ecology</i> , 2020, 79, 252-257.	2.8	35
16	The functional repertoire contained within the native microbiota of the model nematode <i>Caenorhabditis elegans</i> . <i>ISME Journal</i> , 2020, 14, 26-38.	9.8	68
17	The <i>C. elegans</i> GATA transcription factor <i>elt-2</i> mediates distinct transcriptional responses and opposite infection outcomes towards different <i>Bacillus thuringiensis</i> strains. <i>PLoS Pathogens</i> , 2020, 16, e1008826.	4.7	22
18	Community assembly of the native <i>C. elegans</i> microbiome is influenced by time, substrate and individual bacterial taxa. <i>Environmental Microbiology</i> , 2020, 22, 1265-1279.	3.8	39

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19	CeMbio - The <i>Caenorhabditis elegans</i> Microbiome Resource. G3: Genes, Genomes, Genetics, 2020, 10, 3025-3039.	1.8	96
20	Evolutionary Approaches to Combat Antibiotic Resistance: Opportunities and Challenges for Precision Medicine. Frontiers in Immunology, 2020, 11, 1938.	4.8	35
21	Microbiome-mediated plasticity directs host evolution along several distinct time scales. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190589.	4.0	62
22	How long do Red Queen dynamics survive under genetic drift? A comparative analysis of evolutionary and eco-evolutionary models. BMC Evolutionary Biology, 2020, 20, 8.	3.2	13
23	Title is missing!. , 2020, 16, e1008826.		0
24	Title is missing!. , 2020, 16, e1008826.		0
25	Title is missing!. , 2020, 16, e1008826.		0
26	Title is missing!. , 2020, 16, e1008826.		0
27	<i>Pseudomonas aeruginosa</i> populations in the cystic fibrosis lung lose susceptibility to newly applied β -lactams within 3 days. Journal of Antimicrobial Chemotherapy, 2019, 74, 2916-2925.	3.0	17
28	The Inducible Response of the Nematode <i>Caenorhabditis elegans</i> to Members of Its Natural Microbiota Across Development and Adult Life. Frontiers in Microbiology, 2019, 10, 1793.	3.5	26
29	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. Microbiome, 2019, 7, 133.	11.1	141
30	Neutrality in the Metaorganism. PLoS Biology, 2019, 17, e3000298.	5.6	61
31	aFold â€“ using polynomial uncertainty modelling for differential gene expression estimation from RNA sequencing data. BMC Genomics, 2019, 20, 364.	2.8	9
32	Evolutionary ecology meets the antibiotic crisis. Evolution, Medicine and Public Health, 2019, 2019, 37-45.	2.5	43
33	A multi-parent recombinant inbred line population of <i>C. elegans</i> allows identification of novel QTLs for complex life history traits. BMC Biology, 2019, 17, 24.	3.8	40
34	Experimental evolution of immunological specificity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20598-20604.	7.1	49
35	The genomic basis of Red Queen dynamics during rapid reciprocal hostâ€“pathogen coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 923-928.	7.1	102
36	Evolutionary stability of collateral sensitivity to antibiotics in the model pathogen <i>Pseudomonas aeruginosa</i> . ELife, 2019, 8, .	6.0	59

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37	The <i>Caenorhabditis elegans</i> Proteome Response to Naturally Associated Microbiome Members of the Genus <i>Ochrobactrum</i> . <i>Proteomics</i> , 2018, 18, e1700426.	2.2	20
38	Infection Models: Novel Potato Blight-like Pathogens in Worms. <i>Current Biology</i> , 2018, 28, R273-R275.	3.9	0
39	Cellular hysteresis as a principle to maximize the efficacy of antibiotic therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9767-9772.	7.1	81
40	Antibiotic combination efficacy (ACE) networks for a <i>Pseudomonas aeruginosa</i> model. <i>PLoS Biology</i> , 2018, 16, e2004356.	5.6	72
41	Alternative Evolutionary Paths to Bacterial Antibiotic Resistance Cause Distinct Collateral Effects. <i>Molecular Biology and Evolution</i> , 2017, 34, 2229-2244.	8.9	133
42	Oral immune priming with <i>Bacillus thuringiensis</i> induces a shift in the gene expression of <i>Tribolium castaneum</i> larvae. <i>BMC Genomics</i> , 2017, 18, 329.	2.8	61
43	The Natural Biotic Environment of <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2017, 206, 55-86.	2.9	339
44	Highly potent host external immunity acts as a strong selective force enhancing rapid parasite virulence evolution. <i>Environmental Microbiology</i> , 2017, 19, 2090-2100.	3.8	11
45	Complete genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18247. <i>Journal of Biotechnology</i> , 2017, 260, 48-52.	3.8	8
46	<i>Caenorhabditis elegans</i> as a Model for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 485.	3.5	177
47	Complete Genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18246. <i>Standards in Genomic Sciences</i> , 2017, 12, 48.	1.5	10
48	ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences. <i>BMC Genomics</i> , 2016, 17, 541.	2.8	31
49	GATA transcription factor as a likely key regulator of the <i>Caenorhabditis elegans</i> innate immune response against gut pathogens. <i>Zoology</i> , 2016, 119, 244-253.	1.2	34
50	Host-parasite coevolution-rapid reciprocal adaptation and its genetic basis. <i>Zoology</i> , 2016, 119, 241-243.	1.2	16
51	Contrasting invertebrate immune defense behaviors caused by a single gene, the <i>Caenorhabditis elegans</i> neuropeptide receptor gene <i>npr-1</i> . <i>BMC Genomics</i> , 2016, 17, 280.	2.8	52
52	Antimicrobial effectors in the nematode <i>Caenorhabditis elegans</i> : an outgroup to the Arthropoda. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150299.	4.0	81
53	Association between clinical antibiotic resistance and susceptibility of <i>Pseudomonas</i> in the cystic fibrosis lung. <i>Evolution, Medicine and Public Health</i> , 2016, 2016, 182-194.	2.5	34
54	The native microbiome of the nematode <i>Caenorhabditis elegans</i> : gateway to a new host-microbiome model. <i>BMC Biology</i> , 2016, 14, 38.	3.8	330

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55	High Innate Immune Specificity through Diversified C-Type Lectin-Like Domain Proteins in Invertebrates. <i>Journal of Innate Immunity</i> , 2016, 8, 129-142.	3.8	126
56	Experimental evolution in silico: a custom-designed mathematical model for virulence evolution of <i>Bacillus thuringiensis</i> . <i>Zoology</i> , 2016, 119, 359-365.	1.2	3
57	High instability of a nematocidal Cry toxin plasmid in <i>Bacillus thuringiensis</i> . <i>Journal of Invertebrate Pathology</i> , 2016, 133, 34-40.	3.2	5
58	Host-parasite coevolution: why changing population size matters. <i>Zoology</i> , 2016, 119, 330-338.	1.2	88
59	WormExp: a web-based application for a <i>Caenorhabditis elegans</i> -specific gene expression enrichment analysis. <i>Bioinformatics</i> , 2016, 32, 943-945.	4.1	93
60	Ten years of life in compost: temporal and spatial variation of North German <i>Caenorhabditis elegans</i> populations. <i>Ecology and Evolution</i> , 2015, 5, 3250-3263.	1.9	30
61	Temporal variation in antibiotic environments slows down resistance evolution in pathogenic <i>Pseudomonas aeruginosa</i> . <i>Evolutionary Applications</i> , 2015, 8, 945-955.	3.1	55
62	Host-parasite coevolution in populations of constant and variable size. <i>BMC Evolutionary Biology</i> , 2015, 15, 212.	3.2	30
63	Evolutionary Transition from Pathogenicity to Commensalism: Global Regulator Mutations Mediate Fitness Gains through Virulence Attenuation. <i>Molecular Biology and Evolution</i> , 2015, 32, 2883-2896.	8.9	52
64	Why we need more ecology for genetic models such as <i>C. elegans</i> . <i>Trends in Genetics</i> , 2015, 31, 120-127.	6.7	67
65	Overlapping and unique signatures in the proteomic and transcriptomic responses of the nematode <i>Caenorhabditis elegans</i> toward pathogenic <i>Bacillus thuringiensis</i> . <i>Developmental and Comparative Immunology</i> , 2015, 51, 1-9.	2.3	49
66	Using a Sequential Regimen to Eliminate Bacteria at Sublethal Antibiotic Dosages. <i>PLoS Biology</i> , 2015, 13, e1002104.	5.6	82
67	When experimental selection for virulence leads to loss of virulence. <i>Trends in Parasitology</i> , 2015, 31, 426-434.	3.3	12
68	Rapid evolution of virulence leading to host extinction under host-parasite coevolution. <i>BMC Evolutionary Biology</i> , 2015, 15, 112.	3.2	27
69	Travelling at a slug's pace: possible invertebrate vectors of <i>Caenorhabditis</i> nematodes. <i>BMC Ecology</i> , 2015, 15, 19.	3.0	46
70	Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015, 13, e1002169.	5.6	69
71	Genomics of Rapid Adaptation to Antibiotics: Convergent Evolution and Scalable Sequence Amplification. <i>Genome Biology and Evolution</i> , 2014, 6, 1287-1301.	2.5	50
72	The prevalence of <i>Caenorhabditis elegans</i> across 1.5 years in selected North German locations: the importance of substrate type, abiotic parameters, and <i>Caenorhabditis</i> competitors. <i>BMC Ecology</i> , 2014, 14, 4.	3.0	58

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73	Infection routes matter in population-specific responses of the red flour beetle to the entomopathogen <i>Bacillus thuringiensis</i> . <i>BMC Genomics</i> , 2014, 15, 445.	2.8	60
74	Experimental evolution as an efficient tool to dissect adaptive paths to antibiotic resistance. <i>Drug Resistance Updates</i> , 2013, 16, 96-107.	14.4	42
75	Gene-environment and protein-degradation signatures characterize genomic and phenotypic diversity in wild <i>Caenorhabditis elegans</i> populations. <i>BMC Biology</i> , 2013, 11, 93.	3.8	53
76	Complete Genome Sequence of <i>Bacillus thuringiensis</i> Strain 407 Cry-. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
77	Lotkaâ€œVolterra dynamics kills the Red Queen: population size fluctuations and associated stochasticity dramatically change host-parasite coevolution. <i>BMC Evolutionary Biology</i> , 2013, 13, 254.	3.2	78
78	When the Most Potent Combination of Antibiotics Selects for the Greatest Bacterial Load: The Smile-Frown Transition. <i>PLoS Biology</i> , 2013, 11, e1001540.	5.6	182
79	Sex differences in host defence interfere with parasiteâ€œmediated selection for outcrossing during hostâ€œparasite coevolution. <i>Ecology Letters</i> , 2013, 16, 461-468.	6.4	46
80	Increased responsiveness in feeding behaviour of <i>Caenorhabditis elegans</i> after experimental coevolution with its microparasite <i>Bacillus thuringiensis</i> . <i>Biology Letters</i> , 2012, 8, 234-236.	2.3	15
81	Activation of the <i>Caenorhabditis elegans</i> FOXO family transcription factor DAF-16 by pathogenic <i>Bacillus thuringiensis</i> . <i>Developmental and Comparative Immunology</i> , 2012, 37, 193-201.	2.3	24
82	Protist-Type Lysozymes of the Nematode <i>Caenorhabditis elegans</i> Contribute to Resistance against Pathogenic <i>Bacillus thuringiensis</i> . <i>PLoS ONE</i> , 2011, 6, e24619.	2.5	57
83	Hostâ€œparasite local adaptation after experimental coevolution of <i>Caenorhabditis elegans</i> and its microparasite <i>Bacillus thuringiensis</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2832-2839.	2.6	49
84	Multiple reciprocal adaptations and rapid genetic change upon experimental coevolution of an animal host and its microbial parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7359-7364.	7.1	170
85	Introduction. <i>Ecological immunology</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 3-14.	4.0	225
86	Do males facilitate the spread of novel phenotypes within populations of the androdioecious nematode <i>Caenorhabditis elegans</i> ?. <i>Journal of Nematology</i> , 2009, 41, 247-54.	0.9	6
87	Experimental insight into the proximate causes of male persistence variation among two strains of the androdioecious <i>Caenorhabditis elegans</i> (Nematoda). <i>BMC Ecology</i> , 2008, 8, 12.	3.0	39
88	Diversification and adaptive sequence evolution of <i>Caenorhabditis</i> lysozymes (Nematoda: Rhabditidae). <i>BMC Evolutionary Biology</i> , 2008, 8, 114.	3.2	67
89	Specificity of the innate immune system and diversity of C-type lectin domain (CTLD) proteins in the nematode <i>Caenorhabditis elegans</i> . <i>Immunobiology</i> , 2008, 213, 237-250.	1.9	178
90	Anti-Fungal Innate Immunity in <i>C. elegans</i> Is Enhanced by Evolutionary Diversification of Antimicrobial Peptides. <i>PLoS Pathogens</i> , 2008, 4, e1000105.	4.7	212

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91	The role of <i>Caenorhabditis elegans</i> insulin-like signaling in the behavioral avoidance of pathogenic <i>Bacillus thuringiensis</i> . <i>FASEB Journal</i> , 2007, 21, 1801-1812.	0.5	65
92	How do invertebrates generate a highly specific innate immune response?. <i>Molecular Immunology</i> , 2007, 44, 3338-3344.	2.2	138
93	The effect of <i>Photorhabdus luminescens</i> (Enterobacteriaceae) on the survival, development, reproduction and behaviour of <i>Caenorhabditis elegans</i> (Nematoda: Rhabditidae). <i>Environmental Microbiology</i> , 2007, 9, 12-25.	3.8	49
94	The genetics of pathogen avoidance in <i>Caenorhabditis elegans</i> . <i>Molecular Microbiology</i> , 2007, 66, 563-570.	2.5	81
95	Development and characterization of novel microsatellite markers for the common earthworm (<i>Lumbricus terrestris</i> L.). <i>Molecular Ecology Notes</i> , 2007, 7, 1060-1062.	1.7	28
96	Evolutionary History of <i>Caenorhabditis elegans</i> Inferred from Microsatellites: Evidence for Spatial and Temporal Genetic Differentiation and the Occurrence of Outbreeding. <i>Molecular Biology and Evolution</i> , 2004, 22, 160-173.	8.9	123
97	Evolution of the innate immune system: the worm perspective. <i>Immunological Reviews</i> , 2004, 198, 36-58.	6.0	195
98	Diversity and specificity in the interaction between <i>Caenorhabditis elegans</i> and the pathogen <i>Serratia marcescens</i> . <i>BMC Evolutionary Biology</i> , 2004, 4, 49.	3.2	126