Hinrich Schulenburg

List of Publications by Year
in descending order

98 papers	6,061 citations	71102 41 h-index	91884 69 g-index
112 all docs	112 docs citations	112 times ranked	5824 citing authors

#	Article	IF	Citations
1	The Natural Biotic Environment of<i>Caenorhabditis elegans</i>. Genetics, 2017, 206, 55-86.	2.9	339
2	The native microbiome of the nematode Caenorhabditis elegans: gateway to a new host-microbiome model. BMC Biology, 2016, 14, 38.	3.8	330
3	Introduction. Ecological immunology. Philosophical Transactions of the Royal Society B: Biological Sciences, 2009, 364, 3-14.	4.0	225
4	Anti-Fungal Innate Immunity in C. elegans Is Enhanced by Evolutionary Diversification of Antimicrobial Peptides. PLoS Pathogens, 2008, 4, e1000105.	4.7	212
5	Evolution of the innate immune system: the worm perspective. Immunological Reviews, 2004, 198, 36-58.	6.0	195
6	When the Most Potent Combination of Antibiotics Selects for the Greatest Bacterial Load: The Smile-Frown Transition. PLoS Biology, 2013, 11, e1001540.	5.6	182
7	Specificity of the innate immune system and diversity of C-type lectin domain (CTLD) proteins in the nematode Caenorhabditis elegans. Immunobiology, 2008, 213, 237-250.	1.9	178
8	Caenorhabditis elegans as a Model for Microbiome Research. Frontiers in Microbiology, 2017, 8, 485.	3.5	177
9	Multiple reciprocal adaptations and rapid genetic change upon experimental coevolution of an animal host and its microbial parasite. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7359-7364.	7.1	170
10	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. Microbiome, 2019, 7, 133.	11.1	141
11	How do invertebrates generate a highly specific innate immune response?. Molecular Immunology, 2007, 44, 3338-3344.	2.2	138
12	Alternative Evolutionary Paths to Bacterial Antibiotic Resistance Cause Distinct Collateral Effects. Molecular Biology and Evolution, 2017, 34, 2229-2244.	8.9	133
13	Diversity and specificity in the interaction between Caenorhabditis elegans and the pathogen Serratia marcescens. BMC Evolutionary Biology, 2004, 4, 49.	3.2	126
14	High Innate Immune Specificity through Diversified C-Type Lectin-Like Domain Proteins in Invertebrates. Journal of Innate Immunity, 2016, 8, 129-142.	3.8	126
15	Evolutionary History of Caenorhabditis elegans Inferred from Microsatellites: Evidence for Spatial and Temporal Genetic Differentiation and the Occurrence of Outbreeding. Molecular Biology and Evolution, 2004, 22, 160-173.	8.9	123
16	The Role of Integrative and Conjugative Elements in Antibiotic Resistance Evolution. Trends in Microbiology, 2021, 29, 8-18.	7.7	118
17	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
18	CeMbio - The<i>Caenorhabditis elegans</i>Microbiome Resource. G3: Genes, Genomes, Genetics, 2020, 10, 3025-3039.	1.8	96

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19	WormExp: a web-based application for a <i>Caenorhabditis elegans</i>-specific gene expression enrichment analysis. Bioinformatics, 2016, 32, 943-945.	4.1	93
20	Hostâ€"parasite coevolution: why changing population size matters. Zoology, 2016, 119, 330-338.	1.2	88
21	Using a Sequential Regimen to Eliminate Bacteria at Sublethal Antibiotic Dosages. PLoS Biology, 2015, 13, e1002104.	5.6	82
22	The genetics of pathogen avoidance in <i>Caenorhabditis elegans</i>. Molecular Microbiology, 2007, 66, 563-570.	2.5	81
23	Antimicrobial effectors in the nematode <i>Caenorhabditis elegans</i> : an outgroup to the Arthropoda. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150299.	4.0	81
24	Cellular hysteresis as a principle to maximize the efficacy of antibiotic therapy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9767-9772.	7.1	81
25	Lotkaâ€"Volterra dynamics kills the Red Queen: population size fluctuations and associated stochasticity dramatically change host-parasite coevolution. BMC Evolutionary Biology, 2013, 13, 254.	3.2	78
26	Antibiotic combination efficacy (ACE) networks for a Pseudomonas aeruginosa model. PLoS Biology, 2018, 16, e2004356.	5.6	72
27	Hostâ€"Pathogen Coevolution: The Selective Advantage of Bacillus thuringiensis Virulence and Its Cry Toxin Genes. PLoS Biology, 2015, 13, e1002169.	5.6	69
28	The functional repertoire contained within the native microbiota of the model nematode <i>Caenorhabditis elegans</i>. ISME Journal, 2020, 14, 26-38.	9.8	68
29	Diversification and adaptive sequence evolution of Caenorhabditis lysozymes (Nematoda: Rhabditidae). BMC Evolutionary Biology, 2008, 8, 114.	3.2	67
30	Why we need more ecology for genetic models such as C. elegans. Trends in Genetics, 2015, 31, 120-127.	6.7	67
31	The role of Caenorhabditis elegans insulinâ€like signaling in the behavioral avoidance of pathogenic Bacillus thuringiensis. FASEB Journal, 2007, 21, 1801-1812.	0.5	65
32	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
33	Oral immune priming with Bacillus thuringiensis induces a shift in the gene expression of Tribolium castaneum larvae. BMC Genomics, 2017, 18, 329.	2.8	61
34	Neutrality in the Metaorganism. PLoS Biology, 2019, 17, e3000298.	5.6	61
35	Infection routes matter in population-specific responses of the red flour beetle to the entomopathogen Bacillus thuringiensis. BMC Genomics, 2014, 15, 445.	2.8	60
36	Evolutionary stability of collateral sensitivity to antibiotics in the model pathogen Pseudomonas aeruginosa. ELife, 2019, 8, .	6.0	59

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37	The prevalence of Caenorhabditis elegans across 1.5Âyears in selected North German locations: the importance of substrate type, abiotic parameters, and Caenorhabditis competitors. BMC Ecology, 2014, 14, 4.	3.0	58
38	Protist-Type Lysozymes of the Nematode Caenorhabditis elegans Contribute to Resistance against Pathogenic Bacillus thuringiensis. PLoS ONE, 2011, 6, e24619.	2.5	57
39	Temporal variation in antibiotic environments slows down resistance evolution in pathogenic <i>Pseudomonas aeruginosa</i>. Evolutionary Applications, 2015, 8, 945-955.	3.1	55
40	Gene-environment and protein-degradation signatures characterize genomic and phenotypic diversity in wild Caenorhabditis eleganspopulations. BMC Biology, 2013, 11, 93.	3.8	53
41	Evolutionary Transition from Pathogenicity to Commensalism: Global Regulator Mutations Mediate Fitness Gains through Virulence Attenuation. Molecular Biology and Evolution, 2015, 32, 2883-2896.	8.9	52
42	Contrasting invertebrate immune defense behaviors caused by a single gene, the Caenorhabditis elegans neuropeptide receptor gene npr-1. BMC Genomics, 2016, 17, 280.	2.8	52
43	Genomics of Rapid Adaptation to Antibiotics: Convergent Evolution and Scalable Sequence Amplification. Genome Biology and Evolution, 2014, 6, 1287-1301.	2.5	50
44	The effect of Photorhabdus luminescens (Enterobacteriaceae) on the survival, development, reproduction and behaviour of Caenorhabditis elegans (Nematoda: Rhabditidae). Environmental Microbiology, 2007, 9, 12-25.	3.8	49
45	Hostâ€“parasite local adaptation after experimental coevolution of <i>Caenorhabditis elegans</i> and its microparasite <i>Bacillus thuringiensis</i>. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2832-2839.	2.6	49
46	Overlapping and unique signatures in the proteomic and transcriptomic responses of the nematode Caenorhabditis elegans toward pathogenic Bacillus thuringiensis. Developmental and Comparative Immunology, 2015, 51, 1-9.	2.3	49
47	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
48	Sex differences in host defence interfere with parasiteâ€mediated selection for outcrossing during hostâ€“parasite coevolution. Ecology Letters, 2013, 16, 461-468.	6.4	46
49	Travelling at a slugâ€™s pace: possible invertebrate vectors of Caenorhabditis nematodes. BMC Ecology, 2015, 15, 19.	3.0	46
50	Evolutionary ecology meets the antibiotic crisis. Evolution, Medicine and Public Health, 2019, 2019, 37-45.	2.5	43
51	Experimental evolution as an efficient tool to dissect adaptive paths to antibiotic resistance. Drug Resistance Updates, 2013, 16, 96-107.	14.4	42
52	Complete Genome Sequence of Bacillus thuringiensis Strain 407 Cry-. Genome Announcements, 2013, 1, .	0.8	40
53	A multi-parent recombinant inbred line population of C. elegans allows identification of novel QTLs for complex life history traits. BMC Biology, 2019, 17, 24.	3.8	40
54	Experimental insight into the proximate causes of male persistence variation among two strains of the androdioecious Caenorhabditis elegans (Nematoda). BMC Ecology, 2008, 8, 12.	3.0	39

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55	Community assembly of the native <scp><i>C</i>. <i>elegans</i></scp> microbiome is influenced by time, substrate and individual bacterial taxa. Environmental Microbiology, 2020, 22, 1265-1279.	3.8	39
56	Bdellovibrio and Like Organisms Are Predictors of Microbiome Diversity in Distinct Host Groups. Microbial Ecology, 2020, 79, 252-257.	2.8	35
57	Evolutionary Approaches to Combat Antibiotic Resistance: Opportunities and Challenges for Precision Medicine. Frontiers in Immunology, 2020, 11, 1938.	4.8	35
58	GATA transcription factor as a likely key regulator of the Caenorhabditis elegans innate immune response against gut pathogens. Zoology, 2016, 119, 244-253.	1.2	34
59	Association between clinical antibiotic resistance and susceptibility of<i>Pseudomonas</i>in the cystic fibrosis lung. Evolution, Medicine and Public Health, 2016, 2016, 182-194.	2.5	34
60	Bottleneck size and selection level reproducibly impact evolution of antibiotic resistance. Nature Ecology and Evolution, 2021, 5, 1233-1242.	7.8	32
61	ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences. BMC Genomics, 2016, 17, 541.	2.8	31
62	Ten years of life in compost: temporal and spatial variation of North German <i><scp>C</scp>aenorhabditis elegans</i> populations. Ecology and Evolution, 2015, 5, 3250-3263.	1.9	30
63	Host-parasite coevolution in populations of constant and variable size. BMC Evolutionary Biology, 2015, 15, 212.	3.2	30
64	High potency of sequential therapy with only Î²-lactam antibiotics. ELife, 2021, 10, .	6.0	29
65	Development and characterization of novel microsatellite markers for the common earthworm (Lumbricus terrestris L.). Molecular Ecology Notes, 2007, 7, 1060-1062.	1.7	28
66	Evolution of Microbiotaâ€"Host Associations: The Microbeâ€™s Perspective. Trends in Microbiology, 2021, 29, 779-787.	7.7	28
67	Rapid evolution of virulence leading to host extinction under host-parasite coevolution. BMC Evolutionary Biology, 2015, 15, 112.	3.2	27
68	The Inducible Response of the Nematode Caenorhabditis elegans to Members of Its Natural Microbiota Across Development and Adult Life. Frontiers in Microbiology, 2019, 10, 1793.	3.5	26
69	Activation of the Caenorhabditis elegans FOXO family transcription factor DAF-16 by pathogenic Bacillus thuringiensis. Developmental and Comparative Immunology, 2012, 37, 193-201.	2.3	24
70	Gene sharing among plasmids and chromosomes reveals barriers for antibiotic resistance gene transfer. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200467.	4.0	23
71	The C. elegans GATA transcription factor elt-2 mediates distinct transcriptional responses and opposite infection outcomes towards different Bacillus thuringiensis strains. PLoS Pathogens, 2020, 16, e1008826.	4.7	22
72	Effector and regulator: Diverse functions of C. elegans C-type lectin-like domain proteins. PLoS Pathogens, 2021, 17, e1009454.	4.7	22

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73	The Genomic Basis of Rapid Adaptation to Antibiotic Combination Therapy in <i>Pseudomonas aeruginosa</i>. Molecular Biology and Evolution, 2021, 38, 449-464.	8.9	21
74	The <i>Caenorhabditis elegans</i> Proteome Response to Naturally Associated Microbiome Members of the Genus <i>Ochrobactrum</i>. Proteomics, 2018, 18, e1700426.	2.2	20
75	Exploring Effects of C. elegans Protective Natural Microbiota on Host Physiology. Frontiers in Cellular and Infection Microbiology, 2022, 12, 775728.	3.9	20
76	On the evolutionary origins of hostâ€"microbe associations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
77	Pseudomonas aeruginosa populations in the cystic fibrosis lung lose susceptibility to newly applied Î²-lactams within 3 days. Journal of Antimicrobial Chemotherapy, 2019, 74, 2916-2925.	3.0	17
78	Hostâ€"parasite coevolutionâ€"rapid reciprocal adaptation and its genetic basis. Zoology, 2016, 119, 241-243.	1.2	16
79	Increased responsiveness in feeding behaviour of Caenorhabditis elegans after experimental coevolution with its microparasite Bacillus thuringiensis. Biology Letters, 2012, 8, 234-236.	2.3	15
80	Modeling host-associating microbes under selection. ISME Journal, 2021, 15, 3648-3656.	9.8	15
81	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
82	When experimental selection for virulence leads to loss of virulence. Trends in Parasitology, 2015, 31, 426-434.	3.3	12
83	Highly potent host external immunity acts as a strong selective force enhancing rapid parasite virulence evolution. Environmental Microbiology, 2017, 19, 2090-2100.	3.8	11
84	Population size impacts hostâ€"pathogen coevolution. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20212269.	2.6	11
85	Complete Genome sequence of the nematicidal Bacillus thuringiensis MYBT18246. Standards in Genomic Sciences, 2017, 12, 48.	1.5	10
86	aFold â€" using polynomial uncertainty modelling for differential gene expression estimation from RNA sequencing data. BMC Genomics, 2019, 20, 364.	2.8	9
87	Complete genome sequence of the nematicidal Bacillus thuringiensis MYBT18247. Journal of Biotechnology, 2017, 260, 48-52.	3.8	8
88	The genetics of gene expression in a <i>Caenorhabditis elegans</i> multiparental recombinant inbred line population. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	8
89	Do males facilitate the spread of novel phenotypes within populations of the androdioecious nematode Caenorhabditis elegans?. Journal of Nematology, 2009, 41, 247-54.	0.9	6
90	High instability of a nematicidal Cry toxin plasmid in Bacillus thuringiensis. Journal of Invertebrate Pathology, 2016, 133, 34-40.	3.2	5

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91	Experimental evolution in silico: a custom-designed mathematical model for virulence evolution of Bacillus thuringiensis. Zoology, 2016, 119, 359-365.	1.2	3
92	The effects of nested miRNAs and their host genes on immune defense against Bacillus thuringiensis infection in Caenorhabditis elegans. Developmental and Comparative Immunology, 2021, 123, 104144.	2.3	3
93	The Antibiotic Dosage of Fastest Resistance Evolution: Gene Amplifications Underpinning the Inverted-U. Molecular Biology and Evolution, 2021, 38, 3847-3863.	8.9	1
94	Infection Models: Novel Potato Blight-like Pathogens in Worms. Current Biology, 2018, 28, R273-R275.	3.9	0
95	Title is missing!. , 2020, 16, e1008826.		0
96	Title is missing!. , 2020, 16, e1008826.		0
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98	Title is missing!. , 2020, 16, e1008826.		0