

Michael Shapira

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7818652/publications.pdf>

Version: 2024-02-01

26
papers

3,349
citations

535685

17
h-index

759306

22
g-index

27
all docs

27
docs citations

27
times ranked

4794
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>miR-71</i> mediates age-dependent opposing contributions of the stress-activated kinase KGB-1 in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2021, 218, .	1.2	5
2	CeMbio - The <i>Caenorhabditis elegans</i> Microbiome Resource. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3025-3039.	0.8	96
3	Interactions with a Complex Microbiota Mediate a Trade-Off between the Host Development Rate and Heat Stress Resistance. <i>Microorganisms</i> , 2020, 8, 1781.	1.6	9
4	TGF β 2/BMP immune signaling affects abundance and function of <i>C. elegans</i> gut commensals. <i>Nature Communications</i> , 2019, 10, 604.	5.8	64
5	Integration of Stress Signaling in <i>Caenorhabditis elegans</i> Through Cell-Nonautonomous Contributions of the JNK Homolog KGB-1. <i>Genetics</i> , 2018, 210, 1317-1328.	1.2	8
6	Host-microbiota interactions in <i>Caenorhabditis elegans</i> and their significance. <i>Current Opinion in Microbiology</i> , 2017, 38, 142-147.	2.3	35
7	Adaptation from Within or from Without: A Reply to Rodrigo et al.. <i>Trends in Ecology and Evolution</i> , 2017, 32, 85.	4.2	2
8	FOS-1 functions as a transcriptional activator downstream of the <i>C. elegans</i> JNK homolog KGB-1. <i>Cellular Signalling</i> , 2017, 30, 1-8.	1.7	16
9	<i>Caenorhabditis elegans</i> as a Model for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 485.	1.5	177
10	Host-Specific Functional Significance of <i>Caenorhabditis</i> Gut Commensals. <i>Frontiers in Microbiology</i> , 2016, 7, 1622.	1.5	79
11	The nematode <i>Caenorhabditis elegans</i> survives subfreezing temperatures in an isochoric system. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 401-405.	1.0	24
12	Gut Microbiotas and Host Evolution: Scaling Up Symbiosis. <i>Trends in Ecology and Evolution</i> , 2016, 31, 539-549.	4.2	308
13	Assembly of the <i>Caenorhabditis elegans</i> gut microbiota from diverse soil microbial environments. <i>ISME Journal</i> , 2016, 10, 1998-2009.	4.4	296
14	GATA transcription factors as tissue-specific master regulators for induced responses. <i>Worm</i> , 2015, 4, e1118607.	1.0	32
15	The Developmental Intestinal Regulator ELT-2 Controls p38-Dependent Immune Responses in Adult <i>C. elegans</i> . <i>PLoS Genetics</i> , 2015, 11, e1005265.	1.5	48
16	Automated Separation of <i>C. elegans</i> Variably Colonized by a Bacterial Pathogen. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	0
17	Association with Soil Bacteria Enhances p38-Dependent Infection Resistance in <i>Caenorhabditis elegans</i> . <i>Infection and Immunity</i> , 2013, 81, 514-520.	1.0	121
18	An age-dependent reversal in the protective capacities of JNK signaling shortens <i>Caenorhabditis elegans</i> lifespan. <i>Aging Cell</i> , 2012, 11, 659-667.	3.0	41

#	ARTICLE	IF	CITATIONS
19	Dissociation of Immune Responses from Pathogen Colonization Supports Pattern Recognition in <i>C. elegans</i> . PLoS ONE, 2012, 7, e35400.	1.1	21
20	Genetic and molecular analysis of nematode-microbe interactions. Cellular Microbiology, 2011, 13, 497-507.	1.1	48
21	Genetic Analysis of <i>Caenorhabditis elegans</i> Innate Immunity. , 2008, 415, 429-442.		33
22	A conserved role for a GATA transcription factor in regulating epithelial innate immune responses. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14086-14091.	3.3	259
23	Disruption of Yeast Forkhead-associated Cell Cycle Transcription by Oxidative Stress. Molecular Biology of the Cell, 2004, 15, 5659-5669.	0.9	71
24	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	9.4	1,543
25	Stress Effects on Immunity in Vertebrates and Invertebrates. , 0, , 207-227.		1
26	Host Preference of Beneficial Commensals in a Microbially-Diverse Environment. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	11