

Taisei Kikuchi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8502493/publications.pdf>

Version: 2024-02-01

89
papers

6,013
citations

136950

32
h-index

76900

74
g-index

94
all docs

94
docs citations

94
times ranked

5380
citing authors

#	ARTICLE	IF	CITATIONS
1	Top 10 plant-parasitic nematodes in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2013, 14, 946-961.	4.2	1,454
2	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	4.7	351
3	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88.	9.6	293
4	The <i>Colletotrichum lagenarium</i> MAP Kinase Gene <i>CMK1</i> Regulates Diverse Aspects of Fungal Pathogenesis. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 374-383.	2.6	244
5	The genomic basis of parasitism in the Strongyloides clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	21.4	226
6	Fungicide activity through activation of a fungal signalling pathway. <i>Molecular Microbiology</i> , 2004, 53, 1785-1796.	2.5	215
7	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	9.6	212
8	A family of glycosyl hydrolase family 45 cellulases from the pine wood nematode <i>Bursaphelenchus xylophilus</i> . <i>FEBS Letters</i> , 2004, 572, 201-205.	2.8	178
9	A Rapid and Precise Diagnostic Method for Detecting the Pinewood Nematode <i>Bursaphelenchus xylophilus</i> by Loop-Mediated Isothermal Amplification. <i>Phytopathology</i> , 2009, 99, 1365-1369.	2.2	175
10	A complete view of the genetic diversity of the <i>Escherichia coli</i> O-antigen biosynthesis gene cluster. <i>DNA Research</i> , 2015, 22, 101-107.	3.4	155
11	<i>Bursaphelenchus xylophilus</i> : opportunities in comparative genomics and molecular host-parasite interactions. <i>Molecular Plant Pathology</i> , 2008, 9, 357-368.	4.2	131
12	Molecular and biochemical characterization of an endo- β -1,3-glucanase from the pinewood nematode <i>Bursaphelenchus xylophilus</i> acquired by horizontal gene transfer from bacteria. <i>Biochemical Journal</i> , 2005, 389, 117-125.	3.7	121
13	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	13.3	107
14	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	12.8	102
15	The Mitogen-Activated Protein Kinase Gene <i>MAF1</i> Is Essential for the Early Differentiation Phase of Appressorium Formation in <i>Colletotrichum lagenarium</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 1268-1276.	2.6	100
16	Cloning and Characterization of Pectate Lyases Expressed in the Esophageal Gland of the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 280-287.	2.6	99
17	Secretome Analysis of the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> Reveals the Tangled Roots of Parasitism and Its Potential for Molecular Mimicry. <i>PLoS ONE</i> , 2013, 8, e67377.	2.5	98
18	Expressed sequence tag (EST) analysis of the pine wood nematode <i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 9-17.	1.1	83

#	ARTICLE	IF	CITATIONS
19	Simple and quick methods for nematode DNA preparation. <i>Applied Entomology and Zoology</i> , 2012, 47, 291-294.	1.2	82
20	Horizontal gene transfer from bacteria and fungi as a driving force in the evolution of plant parasitism in nematodes. <i>Nematology</i> , 2005, 7, 641-646.	0.6	76
21	Genome Evolution of Plant-Parasitic Nematodes. <i>Annual Review of Phytopathology</i> , 2017, 55, 333-354.	7.8	71
22	Signatures of adaptation to plant parasitism in nematode genomes. <i>Parasitology</i> , 2015, 142, S71-S84.	1.5	68
23	A possible origin population of pathogenic intestinal nematodes, <i>Strongyloides stercoralis</i> , unveiled by molecular phylogeny. <i>Scientific Reports</i> , 2017, 7, 4844.	3.3	62
24	<i>Strongyloides ratti</i> and <i>S. venezuelensis</i> – rodent models of <i>Strongyloides</i> infection. <i>Parasitology</i> , 2017, 144, 285-294.	1.5	56
25	Longicorn beetle that vectors pinewood nematode carries many <i>Wolbachia</i> genes on an autosome. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 3791-3798.	2.6	55
26	Gut bacterial and fungal communities in ground-dwelling beetles are associated with host food habit and habitat. <i>ISME Journal</i> , 2019, 13, 676-685.	9.8	54
27	Assessment of Helminth Biodiversity in Wild Rats Using 18S rDNA Based Metagenomics. <i>PLoS ONE</i> , 2014, 9, e110769.	2.5	49
28	Identification of putative expansin-like genes from the pine wood nematode, <i>Bursaphelenchus xylophilus</i> , and evolution of the expansin gene family within the Nematoda. <i>Nematology</i> , 2009, 11, 355-364.	0.6	47
29	Sequence-based identification of Japanese <i>Armillaria</i> species using the elongation factor-1 alpha gene. <i>Mycologia</i> , 2010, 102, 898-910.	1.9	40
30	Comparative and population genomic landscape of <i>Phellinus noxius</i> : A hypervariable fungus causing root rot in trees. <i>Molecular Ecology</i> , 2017, 26, 6301-6316.	3.9	40
31	Distribution and evolution of glycoside hydrolase family 45 cellulases in nematodes and fungi. <i>BMC Evolutionary Biology</i> , 2014, 14, 69.	3.2	37
32	Improved 18S and 28S rDNA primer sets for NGS-based parasite detection. <i>Scientific Reports</i> , 2019, 9, 15789.	3.3	37
33	Estimation of virulence of <i>Bursaphelenchus xylophilus</i> (Nematoda: Aphelenchoididae) based on its reproductive ability. <i>Nematology</i> , 2007, 9, 371-377.	0.6	36
34	Comparative Genomics of <i>Taphrina</i> Fungi Causing Varying Degrees of Tumorous Deformity in Plants. <i>Genome Biology and Evolution</i> , 2014, 6, 861-872.	2.5	33
35	Transcriptional and morphological changes in the transition from mycetophagous to phytophagous phase in the plant-parasitic nematode <i>Bursaphelenchus xylophilus</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 77-83.	4.2	33
36	Analysis of expressed sequence tags and identification of genes encoding cell-wall-degrading enzymes from the fungivorous nematode <i>Aphelenchus avenae</i> . <i>BMC Genomics</i> , 2009, 10, 525.	2.8	32

#	ARTICLE	IF	CITATIONS
37	Demonstration of interbreeding between virulent and avirulent populations of <i>Bursaphelenchus xylophilus</i> (Nematoda: Aphelenchoididae) by PCR-RFLP method. <i>Applied Entomology and Zoology</i> , 2003, 38, 565-569.	1.2	31
38	Degradation of the Plant Cell Wall by Nematodes. , 2011, , 255-272.		31
39	Genome-Wide Analyses of Individual <i>Strongyloides stercoralis</i> (Nematoda: Rhabditoidea) Provide Insights into Population Structure and Reproductive Life Cycles. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005253.	3.0	31
40	Sequential Changes in the Host Gut Microbiota During Infection With the Intestinal Parasitic Nematode <i>Strongyloides venezuelensis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 217.	3.9	31
41	Insights into the phylogeny of Northern Hemisphere <i>Armillaria</i> : Neighbor-net and Bayesian analyses of translation elongation factor 1- β gene sequences. <i>Mycologia</i> , 2017, 109, 75-91.	1.9	30
42	A novel method to assess the biodiversity of parasites using 18S rDNA Illumina sequencing; parasitome analysis method. <i>Parasitology International</i> , 2016, 65, 572-575.	1.3	28
43	Genome-wide variation in the pinewood nematode <i>Bursaphelenchus xylophilus</i> and its relationship with pathogenic traits. <i>BMC Genomics</i> , 2015, 16, 845.	2.8	27
44	Integrated evidence reveals a new species in the ancient blue coral genus <i>Heliopora</i> (Octocorallia). <i>Scientific Reports</i> , 2018, 8, 15875.	3.3	27
45	Venison, another source of <i>Paragonimus westermani</i> infection. <i>Parasitology International</i> , 2016, 65, 607-612.	1.3	26
46	<i>Escherichia coli</i> H-Genotyping PCR: a Complete and Practical Platform for Molecular H Typing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	26
47	Stage-specific transcriptome of <i>Bursaphelenchus xylophilus</i> reveals temporal regulation of effector genes and roles of the dauer-like stages in the lifecycle. <i>Scientific Reports</i> , 2019, 9, 6080.	3.3	26
48	Genetic Differentiation and Spatial Structure of <i>Phellinus noxius</i> , the Causal Agent of Brown Root Rot of Woody Plants in Japan. <i>PLoS ONE</i> , 2015, 10, e0141792.	2.5	25
49	Purification and Characterization of Recombinant Endoglucanases from the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 1325-1332.	1.3	24
50	Comparative transcriptomics gives insights into the evolution of parasitism in <i>Strongyloides</i> nematodes at the genus, subclade and species level. <i>Scientific Reports</i> , 2018, 8, 5192.	3.3	24
51	Secretome analysis of <i>Strongyloides venezuelensis</i> parasitic stages reveals that soluble and insoluble proteins are involved in its parasitism. <i>Parasites and Vectors</i> , 2019, 12, 21.	2.5	23
52	Treatment of larva migrans syndrome with long-term administration of albendazole. <i>Journal of Microbiology, Immunology and Infection</i> , 2019, 52, 100-105.	3.1	23
53	Evidence for an Opportunistic and Endophytic Lifestyle of the <i>Bursaphelenchus xylophilus</i> -Associated Bacteria <i>Serratia marcescens</i> PWN146 Isolated from Wilting <i>Pinus pinaster</i> . <i>Microbial Ecology</i> , 2016, 72, 669-681.	2.8	22
54	Human proliferative sparganosis update. <i>Parasitology International</i> , 2020, 75, 102036.	1.3	21

#	ARTICLE	IF	CITATIONS
55	Multiplexed ISSR genotyping by sequencing distinguishes two precious coral species (Anthozoa: Tj ETQq1 1 0.784314 rgBT /Overloc	2.0	21
56	Summarizing Specific Profiles in Illumina Sequencing from Whole-Genome Amplified DNA. DNA Research, 2014, 21, 243-254.	3.4	20
57	Assessment of the behaviour and survival of nematodes under low oxygen concentrations. PLoS ONE, 2018, 13, e0197122.	2.5	18
58	Karyotype and reproduction mode of the rodent parasite <i>Strongyloides venezuelensis</i> . Parasitology, 2014, 141, 1736-1745.	1.5	17
59	Diversity of the Tellurite Resistance Gene Operon in Escherichia coli. Frontiers in Microbiology, 2021, 12, 681175.	3.5	17
60	Nearly Complete Genome Assembly of the Pinewood Nematode Bursaphelenchus xylophilus Strain Ka4C1. Microbiology Resource Announcements, 2020, 9, .	0.6	14
61	Venestatin, a Ca ⁺⁺ -binding protein from the parasitic nematode Strongyloides venezuelensis, is involved in the larval migration process. International Journal for Parasitology, 2017, 47, 501-509.	3.1	13
62	Study of intra- and inter species protein-protein interactions for potential drug targets identification and subsequent drug design for Escherichia coli O104:H4 C277-11. In Silico Pharmacology, 2017, 5, 1.	3.3	13
63	An untypeable enterotoxigenic Escherichia coli represents one of the dominant types causing human disease. Microbial Genomics, 2017, 3, e000121.	2.0	13
64	Possible stochastic sex determination in Bursaphelenchus nematodes. Nature Communications, 2022, 13, 2574.	12.8	13
65	An expressed, endogenous Nodavirus-like element captured by a retrotransposon in the genome of the plant parasitic nematode Bursaphelenchus xylophilus. Scientific Reports, 2016, 6, 39749.	3.3	11
66	Additional description and genome analyses of Caenorhabditis auriculariae representing the basal lineage of genus Caenorhabditis. Scientific Reports, 2021, 11, 6720.	3.3	10
67	Complete Genome Sequences of Eight Methicillin-Resistant Staphylococcus aureus Strains Isolated from Patients in Japan. Microbiology Resource Announcements, 2019, 8, .	0.6	9
68	Genome of the fatal tapeworm Sparganum proliferum uncovers mechanisms for cryptic life cycle and aberrant larval proliferation. Communications Biology, 2021, 4, 649.	4.4	9
69	Complete mitochondrial genomes of four entomopathogenic nematode species of the genus Steinernema. Parasites and Vectors, 2016, 9, 430.	2.5	8
70	Additional Og-Typing PCR Techniques Targeting Escherichia coli-Novel and <i>Shigella</i> -Unique O-Antigen Biosynthesis Gene Clusters. Journal of Clinical Microbiology, 2020, 58, .	3.9	8
71	Biological Effect of Streptococcus pyogenes-Released Extracellular Vesicles on Human Monocytic Cells, Induction of Cytotoxicity, and Inflammatory Response. Frontiers in Cellular and Infection Microbiology, 2021, 11, 711144.	3.9	8
72	Reduced Genome of the Gut Symbiotic Bacterium <i>Candidatus Benitsuchiphilus tojoii</i> Provides Insight Into Its Possible Roles in Ecology and Adaptation of the Host Insect. Frontiers in Microbiology, 2020, 11, 840.	3.5	7

#	ARTICLE	IF	CITATIONS
73	Telomere-to-Telomere Genome Assembly of <i>Bursaphelenchus okinawaensis</i> Strain SH1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
74	Optimal ELISA antigen for the diagnosis of <i>Ascaris suum</i> infection in humans. <i>Parasitology Research</i> , 2016, 115, 4701-4705.	1.6	6
75	Genome-Wide SNP Data Revealed Notable Spatial Genetic Structure in the Deep-Sea Precious Coral <i>Corallium japonicum</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	6
76	Venestatin from parasitic helminths interferes with receptor for advanced glycation end products (RAGE)-mediated immune responses to promote larval migration. <i>PLoS Pathogens</i> , 2021, 17, e1009649.	4.7	6
77	Evaluation of magnetic cellulose bead-based DNA extraction from faecal materials for high-throughput bacterial community analyses. <i>Applied Entomology and Zoology</i> , 2018, 53, 281-286.	1.2	5
78	Phylogeography of Blue Corals (Genus <i>Heliopora</i>) Across the Indo-West Pacific. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	5
79	piRNA-like small RNAs target transposable elements in a Clade IV parasitic nematode. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
80	Complete Genome Sequences of <i>Streptococcus pneumoniae</i> Strains HU-OH (Serotype 3, Sequence Type) Tj ETQq0 0 0 rgBT /Overlock 1 Announcements, 2019, 8, .	0.6	3
81	Spatial Autocorrelation Analysis Using MIG-seq Data Indirectly Estimated the Gamete and Larval Dispersal Range of the Blue Coral, <i>Heliopora coerulea</i> , Within Reefs. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	3
82	Parasitism Genes of the Pine Wood Nematode. , 2008, , 67-80.		3
83	Complete Genome Sequence of <i>Streptococcus agalactiae</i> Serotype III, Multilocus Sequence Type 335 Strain HU-GS5823, Isolated from a Human Patient in Japan with Severe Invasive Infection. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
84	Development and validation of SSR markers for the plant-parasitic nematode <i>Subanguina moxae</i> using genome assembly of Illumina pair-end reads. <i>Nematology</i> , 2015, 17, 515-522.	0.6	1
85	Complete Genome Sequences of <i>Streptococcus pyogenes</i> Serotype M3, M28, and M89 Strains Isolated from Human Patients in Japan, 1994 to 2009. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
86	The nucleotide sequence analysis of ITS1-5.8SrDNA- ITS2 region of <i>Subanguina moxae</i> collected in Japan. <i>Nihon Senchu Gakkai Shi = Japanese Journal of Nematology</i> , 2014, 44, 49-53.	0.3	1
87	New Insights to Develop Studies on Witch's Broom Caused by <i>Taphrina wiesneri</i> . <i>Journal of the Japanese Forest Society</i> , 2015, 97, 153-157.	0.2	1
88	Complete Genome Sequences of Two <i>Streptococcus suis</i> Strains Isolated from Asymptomatic Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
89	Detection of <i>Armillaria</i> spp. by the Bait Method Using Oak Logs in a Cherry Stand Damaged by <i>Armillaria tabescens</i> .. <i>Journal of the Japanese Forest Society</i> , 2009, 91, 201-207.	0.2	0