

# Taisei Kikuchi

## List of Publications by Year in descending order

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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	Possible stochastic sex determination in <i>Bursaphelenchus</i> nematodes. <i>Nature Communications</i> , 2022, 13, 2574.	12.8	13
2	piRNA-like small RNAs target transposable elements in a Clade IV parasitic nematode. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
3	Additional description and genome analyses of <i>Caenorhabditis auriculariae</i> representing the basal lineage of genus <i>Caenorhabditis</i> . <i>Scientific Reports</i> , 2021, 11, 6720.	3.3	10
4	Genome of the fatal tapeworm <i>Sparganum proliferum</i> uncovers mechanisms for cryptic life cycle and aberrant larval proliferation. <i>Communications Biology</i> , 2021, 4, 649.	4.4	9
5	Diversity of the Tellurite Resistance Gene Operon in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 681175.	3.5	17
6	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
7	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
8	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
9	Biological Effect of <i>Streptococcus pyogenes</i> -Released Extracellular Vesicles on Human Monocytic Cells, Induction of Cytotoxicity, and Inflammatory Response. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 711144.	3.9	8
10	Phylogeography of Blue Corals (Genus <i>Heliopora</i> ) Across the Indo-West Pacific. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	5
11	Human proliferative sparganosis update. <i>Parasitology International</i> , 2020, 75, 102036.	1.3	21
12	Complete Genome Sequences of Two <i>Streptococcus suis</i> Strains Isolated from Asymptomatic Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
13	Additional Og-Typing PCR Techniques Targeting <i>Escherichia coli</i> -Novel and <i>Shigella</i> -Unique O-Antigen Biosynthesis Gene Clusters. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	8
14	Nearly Complete Genome Assembly of the Pinewood Nematode <i>Bursaphelenchus xylophilus</i> Strain Ka4C1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	14
15	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
16	Reduced Genome of the Gut Symbiotic Bacterium <i>Candidatus Benitsuchiophilus tojoi</i> Provides Insight Into Its Possible Roles in Ecology and Adaptation of the Host Insect. <i>Frontiers in Microbiology</i> , 2020, 11, 840.	3.5	7
17	Telomere-to-Telomere Genome Assembly of <i>Bursaphelenchus okinawaensis</i> Strain SH1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
18	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

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19	Improved 18S and 28S rDNA primer sets for NGS-based parasite detection. <i>Scientific Reports</i> , 2019, 9, 15789.	3.3	37
20	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
21	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
22	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
23	Complete Genome Sequences of Eight Methicillin-Resistant <i>Staphylococcus aureus</i> Strains Isolated from Patients in Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	9
24	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
25	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
26	Multiplexed ISSR genotyping by sequencing distinguishes two precious coral species (Anthozoa:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	2.0	21
27	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
28	<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
29	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
30	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
31	Assessment of the behaviour and survival of nematodes under low oxygen concentrations. <i>PLoS ONE</i> , 2018, 13, e0197122.	2.5	18
32	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
33	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	12.8	102
34	<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
35	Insights into the phylogeny of Northern Hemisphere <i>Armillaria</i> : Neighbor-net and Bayesian analyses of translation elongation factor 1- $\beta$ gene sequences. <i>Mycologia</i> , 2017, 109, 75-91.	1.9	30
36	Genome Evolution of Plant-Parasitic Nematodes. <i>Annual Review of Phytopathology</i> , 2017, 55, 333-354.	7.8	71

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37	Venestatin, a Ca ++ -binding protein from the parasitic nematode <i>Strongyloides venezuelensis</i> , is involved in the larval migration process. <i>International Journal for Parasitology</i> , 2017, 47, 501-509.	3.1	13
38	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
39	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
40	Study of intra- and inter species protein-protein interactions for potential drug targets identification and subsequent drug design for <i>Escherichia coli</i> O104:H4 C277-11. <i>In Silico Pharmacology</i> , 2017, 5, 1.	3.3	13
41	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	13.3	107
42	An untypeable enterotoxigenic <i>Escherichia coli</i> represents one of the dominant types causing human disease. <i>Microbial Genomics</i> , 2017, 3, e000121.	2.0	13
43	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
44	An expressed, endogenous Nodavirus-like element captured by a retrotransposon in the genome of the plant parasitic nematode <i>Bursaphelenchus xylophilus</i> . <i>Scientific Reports</i> , 2016, 6, 39749.	3.3	11
45	Venison, another source of <i>Paragonimus westermani</i> infection. <i>Parasitology International</i> , 2016, 65, 607-612.	1.3	26
46	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
47	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
48	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
49	Complete mitochondrial genomes of four entomopathogenic nematode species of the genus <i>Steinernema</i> . <i>Parasites and Vectors</i> , 2016, 9, 430.	2.5	8
50	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
51	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	21.4	226
52	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
53	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
54	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

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55	Signatures of adaptation to plant parasitism in nematode genomes. <i>Parasitology</i> , 2015, 142, S71-S84.	1.5	68
56	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
57	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
58	Assessment of Helminth Biodiversity in Wild Rats Using 18S rDNA Based Metagenomics. <i>PLoS ONE</i> , 2014, 9, e110769.	2.5	49
59	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
60	Summarizing Specific Profiles in Illumina Sequencing from Whole-Genome Amplified DNA. <i>DNA Research</i> , 2014, 21, 243-254.	3.4	20
61	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
62	Distribution and evolution of glycoside hydrolase family 45 cellulases in nematodes and fungi. <i>BMC Evolutionary Biology</i> , 2014, 14, 69.	3.2	37
63	Karyotype and reproduction mode of the rodent parasite <i>Strongyloides venezuelensis</i> . <i>Parasitology</i> , 2014, 141, 1736-1745.	1.5	17
64	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
65	Top 10 plant-parasitic nematodes in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2013, 14, 946-961.	4.2	1,454
66	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
67	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
68	Simple and quick methods for nematode DNA preparation. <i>Applied Entomology and Zoology</i> , 2012, 47, 291-294.	1.2	82
69	Degradation of the Plant Cell Wall by Nematodes. , 2011, , 255-272.		31
70	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
71	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
72	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

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73	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
74	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
75	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
76	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
77	<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
78	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
79	Parasitism Genes of the Pine Wood Nematode. , 2008, , 67-80.		3
80	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
81	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
82	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
83	Molecular and biochemical characterization of an endo- $\beta$ -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
84	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
85	Fungicide activity through activation of a fungal signalling pathway. <i>Molecular Microbiology</i> , 2004, 53, 1785-1796.	2.5	215
86	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
87	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
88	The Mitogen-Activated Protein Kinase Gene MAF1 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
89	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