

Kazunori Murase

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

656
citations

840776

11
h-index

610901

24
g-index

27
all docs

27
docs citations

27
times ranked

1003
citing authors

#	ARTICLE	IF	CITATIONS
1	The Shiga toxin 2 production level in enterohemorrhagic <i>Escherichia coli</i> O157:H7 is correlated with the subtypes of toxin-encoding phage. <i>Scientific Reports</i> , 2015, 5, 16663.	3.3	112
2	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	12.8	102
3	Defining the genome features of <i>Escherichia albertii</i> , an emerging enteropathogen closely related to <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2015, 7, evv211.	2.5	83
4	Distinct interacting core taxa in co-occurrence networks enable discrimination of polymicrobial oral diseases with similar symptoms. <i>Scientific Reports</i> , 2016, 6, 30997.	3.3	70
5	TBC1D9 regulates TBK1 activation through Ca ²⁺ signaling in selective autophagy. <i>Nature Communications</i> , 2020, 11, 770.	12.8	39
6	Improved 18S and 28S rDNA primer sets for NGS-based parasite detection. <i>Scientific Reports</i> , 2019, 9, 15789.	3.3	37
7	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
8	Characterization of pig saliva as the major natural habitat of <i>Streptococcus suis</i> by analyzing oral, fecal, vaginal, and environmental microbiota. <i>PLoS ONE</i> , 2019, 14, e0215983.	2.5	29
9	Differential dynamics and impacts of prophages and plasmids on the pangenome and virulence factor repertoires of Shiga toxin-producing <i>Escherichia coli</i> O145:H28. <i>Microbial Genomics</i> , 2020, 6, .	2.0	28
10	Draft genome sequences of bacteria isolated from the <i>Deschampsia antarctica</i> phyllosphere. <i>Extremophiles</i> , 2018, 22, 537-552.	2.3	19
11	Haemolysin E- and enterohaemolysin-derived haemolytic activity of O55/O157 strains and other <i>Escherichia coli</i> lineages. <i>Microbiology (United Kingdom)</i> , 2012, 158, 746-758.	1.8	14
12	Phylogenetic relationship of prophages is affected by CRISPR selection in Group A <i>Streptococcus</i> . <i>BMC Microbiology</i> , 2019, 19, 24.	3.3	12
13	Intracellular Group A <i>Streptococcus</i> Induces Golgi Fragmentation To Impair Host Defenses through Streptolysin O and NAD-Glycohydrolase. <i>MBio</i> , 2021, 12, .	4.1	12
14	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
15	The global population structure and evolutionary history of the acquisition of major virulence factor-encoding genetic elements in Shiga toxin-producing <i>Escherichia coli</i> O121:H19. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
16	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
17	Global population structure of the <i>Serratia marcescens</i> complex and identification of hospital-adapted lineages in the complex. <i>Microbial Genomics</i> , 2022, 8, .	2.0	8
18	Genetic diversity of environmental <i>Vibrio cholerae</i> O1 strains isolated in Northern Vietnam. <i>Infection, Genetics and Evolution</i> , 2017, 54, 146-151.	2.3	7

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19	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. <i>Frontiers in Microbiology</i> , 2020, 11, 840.	3.5	7
20	Cytolysin A (ClyA): A Bacterial Virulence Factor with Potential Applications in Nanopore Technology, Vaccine Development, and Tumor Therapy. <i>Toxins</i> , 2022, 14, 78.	3.4	7
21	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
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	DNA-based culture-independent analysis detects the presence of group a streptococcus in throat samples from healthy adults in Japan. <i>BMC Microbiology</i> , 2016, 16, 237.	3.3	2
24	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
25	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
26	Complete Genome Sequences of Two <i>Streptococcus suis</i> Strains Isolated from Asymptomatic Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
27	Single-chain variable fragment (scFv) targeting streptolysin O controls group A <i>Streptococcus</i> infection. <i>Biochemical and Biophysical Research Communications</i> , 2021, 566, 177-183.	2.1	0