

Thidathip Wongsurawat

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

1,261
citations

471061

17
h-index

433756

31
g-index

69
all docs

69
docs citations

69
times ranked

1926
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, e7-e7.	6.5	149
2	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018, 46, e38-e38.	6.5	116
3	Quantitative model of R-loop forming structures reveals a novel level of RNA-DNA interactome complexity. <i>Nucleic Acids Research</i> , 2012, 40, e16-e16.	6.5	78
4	PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. <i>Frontiers in Microbiology</i> , 2018, 9, 1757.	1.5	76
5	Safety Assessment of a Nham Starter Culture <i>Lactobacillus plantarum</i> BCC9546 via Whole-genome Analysis. <i>Scientific Reports</i> , 2020, 10, 10241.	1.6	53
6	QmRLFS-finder: a model, web server and stand-alone tool for prediction and analysis of R-loop forming sequences. <i>Nucleic Acids Research</i> , 2015, 43, W527-W534.	6.5	50
7	R-Loops in Proliferating Cells but Not in the Brain: Implications for AOA2 and Other Autosomal Recessive Ataxias. <i>PLoS ONE</i> , 2014, 9, e90219.	1.1	50
8	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , 2019, 10, 260.	1.5	46
9	A chromosome-level assembly of the black tiger shrimp (<i>Penaeus monodon</i>) genome facilitates the identification of growth-associated genes. <i>Molecular Ecology Resources</i> , 2021, 21, 1620-1640.	2.2	43
10	Circular DNA in the human germline and its association with recombination. <i>Molecular Cell</i> , 2022, 82, 209-217.e7.	4.5	37
11	R-loopDB: a database for R-loop forming sequences (RLFS) and R-loops. <i>Nucleic Acids Research</i> , 2017, 45, D119-D127.	6.5	36
12	Chest imaging representing a COVID-19 positive rural U.S. population. <i>Scientific Data</i> , 2020, 7, 414.	2.4	33
13	The Interaction between 30b-5p miRNA and MBNL1 mRNA is Involved in Vascular Smooth Muscle Cell Differentiation in Patients with Coronary Atherosclerosis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 11.	1.8	31
14	Distinctive molecular signature and activated signaling pathways in aortic smooth muscle cells of patients with myocardial infarction. <i>Atherosclerosis</i> , 2018, 271, 237-244.	0.4	29
15	Multidrug-resistant <i>Neisseria gonorrhoeae</i> infection in heterosexual men with reduced susceptibility to ceftriaxone, first report in Thailand. <i>Scientific Reports</i> , 2021, 11, 21659.	1.6	29
16	Potential Probiotic or Trigger of Gut Inflammation – The Janus-Faced Nature of Cannabidiol-Rich Cannabis Extract. <i>Journal of Dietary Supplements</i> , 2020, 17, 543-560.	1.4	25
17	A novel Cas9-targeted long-read assay for simultaneous detection of IDH1/2 mutations and clinically relevant MGMT methylation in fresh biopsies of diffuse glioma. <i>Acta Neuropathologica Communications</i> , 2020, 8, 87.	2.4	24
18	Gene expression profile analysis of aortic vascular smooth muscle cells reveals upregulation of cadherin genes in myocardial infarction patients. <i>Physiological Genomics</i> , 2018, 50, 648-657.	1.0	18

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19	Oligosarcomas, IDH-mutant are distinct and aggressive. <i>Acta Neuropathologica</i> , 2022, 143, 263-281.	3.9	18
20	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F1 Mice. <i>Nutrients</i> , 2019, 11, 776.	1.7	17
21	Amplicon-Based, Next-Generation Sequencing Approaches to Characterize Single Nucleotide Polymorphisms of Orthohantavirus Species. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 565591.	1.8	15
22	Optimization of high molecular weight DNA extraction methods in shrimp for a long-read sequencing platform. <i>PeerJ</i> , 2020, 8, e10340.	0.9	15
23	Activation-induced cytidine deaminase localizes to G-quadruplex motifs at mutation hotspots in lymphoma. <i>NAR Cancer</i> , 2020, 2, zcaa029.	1.6	14
24	Detection and Discrimination of DNA Adducts Differing in Size, Regiochemistry, and Functional Group by Nanopore Sequencing. <i>Chemical Research in Toxicology</i> , 2020, 33, 2944-2952.	1.7	14
25	Genomic Analysis of <i>Aeromonas veronii</i> C198, a Novel Mcr-3.41-Harboring Isolate from a Patient with Septicemia in Thailand. <i>Pathogens</i> , 2020, 9, 1031.	1.2	14
26	Characterization of BPSS1521 (bprD), a Regulator of <i>Burkholderia pseudomallei</i> Virulence Gene Expression in the Mouse Model. <i>PLoS ONE</i> , 2014, 9, e104313.	1.1	13
27	An assessment of Oxford Nanopore sequencing for human gut metagenome profiling: A pilot study of head and neck cancer patients. <i>Journal of Microbiological Methods</i> , 2019, 166, 105739.	0.7	13
28	Cell-Free DNA Analysis by Whole-Exome Sequencing for Hepatocellular Carcinoma: A Pilot Study in Thailand. <i>Cancers</i> , 2021, 13, 2229.	1.7	13
29	<i>Clostridium manihotivorum</i> sp. nov., a novel mesophilic anaerobic bacterium that produces cassava pulp-degrading enzymes. <i>PeerJ</i> , 2020, 8, e10343.	0.9	12
30	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	1.0	11
31	KITSUNE: A Tool for Identifying Empirically Optimal K-mer Length for Alignment-Free Phylogenomic Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 556413.	2.0	11
32	Two Cases of Vancomycin-Resistant <i>Enterococcus faecium</i> Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa180.	0.4	11
33	Genetic Aberration Analysis in Thai Colorectal Adenoma and Early-Stage Adenocarcinoma Patients by Whole-Exome Sequencing. <i>Cancers</i> , 2019, 11, 977.	1.7	10
34	Genomic Islands as a Marker to Differentiate between Clinical and Environmental <i>Burkholderia pseudomallei</i> . <i>PLoS ONE</i> , 2012, 7, e37762.	1.1	10
35	A Glioblastoma Genomics Primer for Clinicians. <i>Medical Research Archives</i> , 2020, 8, .	0.1	10
36	Genome sequences of antibiotic-resistant <i>Streptococcus suis</i> strains isolated from human patients and diseased and asymptomatic pigs in Thailand. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104674.	1.0	9

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37	Two SARS-CoV-2 Genome Sequences of Isolates from Rural U.S. Patients Harboring the D614G Mutation, Obtained Using Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	9
38	R-loop-forming Sequences Analysis in Thousands of Viral Genomes Identify A New Common Element in Herpesviruses. <i>Scientific Reports</i> , 2020, 10, 6389.	1.6	8
39	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
40	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	1.1	7
41	Association of TNF-alpha, TNF-beta, IFN-gamma and IL-1Ra gene polymorphisms with Graves' disease in the Thai population. <i>Asian Pacific Journal of Allergy and Immunology</i> , 2006, 24, 207-11.	0.2	7
42	Genomic Characterization of <i>Streptococcus suis</i> Serotype 24 Clonal Complex 221/234 From Human Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 812436.	1.5	7
43	Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 Outbreak in Arkansas, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
44	Genome-Based Comparison of <i>Clostridioides difficile</i> : Average Amino Acid Identity Analysis of Core Genomes. <i>Microbial Ecology</i> , 2018, 76, 801-813.	1.4	6
45	Complete Genome Sequences of Four Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Isolates from Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
46	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant <i>Enterococcus faecium</i> with the <i>vanA</i> Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
47	Genome Sequences of Zika Virus Strains Recovered from Amniotic Fluid, Placenta, and Fetal Brain of a Microcephaly Patient in Thailand, 2017. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
48	Complete Genome and Plasmid Sequences of <i>Escherichia coli</i> Type Strain ATCC 11775. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
49	Complete Genome Sequences of Three <i>Neisseria gonorrhoeae</i> Isolates from Thailand with Multidrug Resistance and Multilocus Sequence Type 1903. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
50	Draft Genome Sequences of 48 Vancomycin-Resistant <i>Enterococcus faecium</i> Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
51	Systematic genome analysis of a novel arachidonic acid-producing strain uncovered unique metabolic traits in the production of acetyl-CoA-derived products in <i>Mortierella</i> fungi. <i>Gene</i> , 2020, 741, 144559.	1.0	3
52	Draft Genome Sequence of Methicillin-Resistant <i>Staphylococcus aureus</i> Harboring Staphylococcal Cassette Chromosome <i>mec</i> Type IX, Isolated from a Fatal Bacteremic Pneumonia Case. <i>Microbiology Resource Announcements</i> , 2021, 10, e0061621.	0.3	3
53	Native RNA or cDNA Sequencing for Transcriptomic Analysis: A Case Study on <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 842299.	2.0	3
54	Distinctive pattern of LET-7B and MIR-30B in human aortic smooth muscle cells of myocardial infarction patients. <i>Atherosclerosis</i> , 2017, 263, e63.	0.4	2

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55	Complete Genome Sequence of <i>Schaalia turicensis</i> Strain CT001, Isolated from a Patient with Gonococcal Urethritis in Thailand. <i>Microbiology Resource Announcements</i> , 2021, 10, e0083621.	0.3	2
56	Complete Genome Sequences of Mannanase-Producing <i>Bacillus</i> and <i>Niallia</i> Strains Isolated from the Intestine of the Black Tiger Shrimp (<i>Penaeus monodon</i>). <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
57	Is amplification bias consequential in transposon sequencing (TnSeq) assays? A case study with a <i>Staphylococcus aureus</i> TnSeq library subjected to PCR-based and amplification-free enrichment methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
58	Novel Organization of the Staphylococcal Cassette Chromosome <i>mec</i> Composite Island in Clinical <i>Staphylococcus haemolyticus</i> and <i>Staphylococcus hominis</i> Subspecies <i>hominis</i> Isolates from Dogs. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
59	GENE-18. TRANSCRIPTOME-WIDE ANALYSIS USING NANOPORE THIRD GENERATION SEQUENCING IN A RAT GLIOBLASTOMA MODEL: PROOF OF PRINCIPLE. <i>Neuro-Oncology</i> , 2019, 21, vi101-vi101.	0.6	0
60	PATH-05. RAPID SIMULTANEOUS IDH MUTATION AND MGMT METHYLATION STATUS ASSESSMENT IN GLIOMA PATIENTS USING CRISPR-Cas9-TARGETED NANOPORE SEQUENCING. <i>Neuro-Oncology</i> , 2019, 21, vi143-vi144.	0.6	0
61	RNA Sequencing Data Sets and Their Whole-Genome Sequence Assembly of Dengue Virus from Three Serial Passages in Vero Cells. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
62	Complete Genome Sequence of <i>Neisseria gonorrhoeae</i> Multilocus Sequence Type ST7363 Isolated from Thailand. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057321.	0.3	0
63	Complete Genome Sequences of <i>Mycobacterium farcinogenes</i> Strains Isolated from Clinical Specimens from Patients in Thailand. <i>Microbiology Resource Announcements</i> , 2021, 10, e0100521.	0.3	0
64	1355. Cluster of Multi-drug Resistance <i>Neisseria gonorrhoeae</i> Isolates with Reduce Ceftriaxone Susceptibility, First Report in Thailand. <i>Open Forum Infectious Diseases</i> , 2021, 8, S764-S764.	0.4	0
65	Direct Sequencing of RNA and RNA Modification Identification Using Nanopore. <i>Methods in Molecular Biology</i> , 2022, 2477, 71-77.	0.4	0