

Intawat Nookaew

List of Publications by Year in descending order

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Version: 2024-02-01

112
papers

7,598
citations

159585

30
h-index

58581

82
g-index

122
all docs

122
docs citations

122
times ranked

14330
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolite profiles of brown planthopper-susceptible and resistant rice (<i>Oryza sativa</i>) varieties associated with infestation and mechanical stimuli. <i>Phytochemistry</i> , 2022, 194, 113044.	2.9	2
2	Circular DNA in the human germline and its association with recombination. <i>Molecular Cell</i> , 2022, 82, 209-217.e7.	9.7	37
3	Current and Future Methodology for Quantitation and Site-Specific Mapping the Location of DNA Adducts. <i>Toxics</i> , 2022, 10, 45.	3.7	4
4	Notch3 signaling between myeloma cells and osteocytes in the tumor niche promotes tumor growth and bone destruction. <i>Neoplasia</i> , 2022, 28, 100785.	5.3	5
5	Nanopore Sequencing for Detection and Characterization of Phosphorothioate Modifications in Native DNA Sequences. <i>Frontiers in Microbiology</i> , 2022, 13, 871937.	3.5	2
6	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.	4.1	3
7	Direct Sequencing of RNA and RNA Modification Identification Using Nanopore. <i>Methods in Molecular Biology</i> , 2022, 2477, 71-77.	0.9	0
8	Transcriptomic Analyses Reveal Long Non-Coding RNA in Peripheral Blood Mononuclear Cells as a Novel Biomarker for Diagnosis and Prognosis of Hepatocellular Carcinoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7882.	4.1	8
9	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, e7-e7.	14.5	149
10	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.	2.3	9
11	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, .	0.6	9
12	Improvement of Gut Diversity and Composition After Direct-Acting Antivirals in Hepatitis C Virus-Infected Patients With or Without Human Immunodeficiency Virus Coinfection. <i>Journal of Infectious Diseases</i> , 2021, 224, 1410-1421.	4.0	2
13	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.	4.8	43
14	Cell-Free DNA Analysis by Whole-Exome Sequencing for Hepatocellular Carcinoma: A Pilot Study in Thailand. <i>Cancers</i> , 2021, 13, 2229.	3.7	13
15	Identification of BHLHE40 expression in peripheral blood mononuclear cells as a novel biomarker for diagnosis and prognosis of hepatocellular carcinoma. <i>Scientific Reports</i> , 2021, 11, 11201.	3.3	4
16	Characteristics and Network Influence of Providers Involved in the Treatment of Patients With Chronic Back, Neck or Joint Pain in Arkansas. <i>Journal of Pain</i> , 2021, 22, 1681-1695.	1.4	0
17	Transcriptional Regulation of Plant Biomass Degradation and Carbohydrate Utilization Genes in the Extreme Thermophile <i>Caldicellulosiruptor bescii</i> . <i>MSystems</i> , 2021, 6, e0134520.	3.8	10
18	Neutralization of oxidized phospholipids attenuates age-associated bone loss in mice. <i>Aging Cell</i> , 2021, 20, e13442.	6.7	17

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19	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	2.4	7
20	Profiles of urine and blood metabolomics in autism spectrum disorders. <i>Metabolic Brain Disease</i> , 2021, 36, 1641-1671.	2.9	24
21	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, .	2.0	1
22	Metabolic Profiling and Compound-Class Identification Reveal Alterations in Serum Triglyceride Levels in Mice Immunized with Human Vaccine Adjuvant Alum. <i>Journal of Proteome Research</i> , 2020, 19, 269-278.	3.7	5
23	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.	4.1	31
24	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.	4.1	11
25	Metagenomics in bioflocs and their effects on gut microbiome and immune responses in Pacific white shrimp. <i>Fish and Shellfish Immunology</i> , 2020, 106, 733-741.	3.6	33
26	Estrogens decrease osteoclast number by attenuating mitochondria oxidative phosphorylation and ATP production in early osteoclast precursors. <i>Scientific Reports</i> , 2020, 10, 11933.	3.3	52
27	Neonatal gut colonization by <i>Bifidobacterium</i> is associated with higher childhood cytokine responses. <i>Gut Microbes</i> , 2020, 12, 1847628.	9.8	22
28	Spleen proteomics data from high fat diet fed mice. <i>Data in Brief</i> , 2020, 32, 106110.	1.0	2
29	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.	3.9	15
30	Are all faecal bacteria detected with equal efficiency? A study using next-generation sequencing and quantitative culture of infants' faecal samples. <i>Journal of Microbiological Methods</i> , 2020, 177, 106018.	1.6	5
31	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.	3.3	14
32	ProdMX: Rapid query and analysis of protein functional domain based on compressed sparse matrices. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3890-3896.	4.1	0
33	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.	2.6	25
34	Cannabidiol: From Drug Interaction Potential to Modulation of the Gut Microbiome. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa045_051.	0.3	0
35	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.	5.2	24
36	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.	2.2	3

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37	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. Microbiology Resource Announcements, 2020, 9, .	0.6	7
38	Safety Assessment of a Nham Starter Culture Lactobacillus plantarum BCC9546 via Whole-genome Analysis. Scientific Reports, 2020, 10, 10241.	3.3	53
39	Green Tea Extract as a Safe and Effective Dietary Supplement: Lessons Learned from Mice. Current Developments in Nutrition, 2020, 4, nzaa045_052.	0.3	1
40	Transcriptome analyses reveal the synergistic effects of feeding and eyestalk ablation on ovarian maturation in black tiger shrimp. Scientific Reports, 2020, 10, 3239.	3.3	16
41	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
42	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant Enterococcus faecium with the <i>vanA</i> Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. Microbiology Resource Announcements, 2020, 9, .	0.6	6
43	R-loop-forming Sequences Analysis in Thousands of Viral Genomes Identify A New Common Element in Herpesviruses. Scientific Reports, 2020, 10, 6389.	3.3	8
44	UPLC-ESI-MRM/MS for Absolute Quantification and MS/MS Structural Elucidation of Six Specialized Pyranonaphthoquinone Metabolites From Ventilago harmandiana. Frontiers in Plant Science, 2020, 11, 602993.	3.6	8
45	Optimization of high molecular weight DNA extraction methods in shrimp for a long-read sequencing platform. PeerJ, 2020, 8, e10340.	2.0	15
46	<i>Clostridium manihotivorum</i> sp. nov., a novel mesophilic anaerobic bacterium that produces cassava pulp-degrading enzymes. PeerJ, 2020, 8, e10343.	2.0	12
47	Genome-wide Cas9 binding specificity in Saccharomyces cerevisiae. PeerJ, 2020, 8, e9442.	2.0	3
48	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. Infection, Genetics and Evolution, 2019, 75, 103965.	2.3	11
49	Genetic Aberration Analysis in Thai Colorectal Adenoma and Early-Stage Adenocarcinoma Patients by Whole-Exome Sequencing. Cancers, 2019, 11, 977.	3.7	10
50	An assessment of Oxford Nanopore sequencing for human gut metagenome profiling: A pilot study of head and neck cancer patients. Journal of Microbiological Methods, 2019, 166, 105739.	1.6	13
51	Crosshatch nanofiber networks of tunable interfiber spacing induce plasticity in cell migration and cytoskeletal response. FASEB Journal, 2019, 33, 10618-10632.	0.5	40
52	Dietary Polyunsaturated Fatty Acids Promote Neutrophil Accumulation in the Spleen by Altering Chemotaxis and Delaying Cell Death. Infection and Immunity, 2019, 87, .	2.2	14
53	Draft Genome Sequences of 48 Vancomycin-Resistant Enterococcus faecium Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. Microbiology Resource Announcements, 2019, 8, .	0.6	3
54	Simplified Intestinal Microbiota to Study Microbe-Diet-Host Interactions in a Mouse Model. Cell Reports, 2019, 26, 3772-3783.e6.	6.4	61

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55	Complete Genome and Plasmid Sequences of Escherichia coli Type Strain ATCC 11775. Microbiology Resource Announcements, 2019, 8, .	0.6	5
56	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. Frontiers in Microbiology, 2019, 10, 260.	3.5	46
57	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F1 Mice. Nutrients, 2019, 11, 776.	4.1	17
58	Global metabolite profiles of rice brown planthopper-resistant traits reveal potential secondary metabolites for both constitutive and inducible defenses. Metabolomics, 2019, 15, 151.	3.0	13
59	GENE-18. TRANSCRIPTOME-WIDE ANALYSIS USING NANOPORE THIRD GENERATION SEQUENCING IN A RAT GLIOBLASTOMA MODEL: PROOF OF PRINCIPLE. Neuro-Oncology, 2019, 21, vi101-vi101.	1.2	0
60	The Omega-3 Fatty Acids EPA and DHA, as a Part of a Murine High-Fat Diet, Reduced Lipid Accumulation in Brown and White Adipose Tissues. International Journal of Molecular Sciences, 2019, 20, 5895.	4.1	29
61	Effective CRISPR interference of an endogenous gene via a single transgene in mice. Scientific Reports, 2019, 9, 17312.	3.3	25
62	PATH-05. RAPID SIMULTANEOUS IDH MUTATION AND MGMT METHYLATION STATUS ASSESSMENT IN GLIOMA PATIENTS USING CRISPR-Cas9-TARGETED NANOPORE SEQUENCING. Neuro-Oncology, 2019, 21, vi143-vi144.	1.2	0
63	Stimulation of Piezo1 by mechanical signals promotes bone anabolism. ELife, 2019, 8, .	6.0	185
64	Genome-Based Comparison of Clostridioides difficile: Average Amino Acid Identity Analysis of Core Genomes. Microbial Ecology, 2018, 76, 801-813.	2.8	6
65	Distinctive molecular signature and activated signaling pathways in aortic smooth muscle cells of patients with myocardial infarction. Atherosclerosis, 2018, 271, 237-244.	0.8	29
66	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of Saccharomyces cerevisiae CEN.PK113-7D. Nucleic Acids Research, 2018, 46, e38-e38.	14.5	116
67	Transcriptome alterations of vascular smooth muscle cells in aortic wall of myocardial infarction patients. Data in Brief, 2018, 17, 1112-1135.	1.0	13
68	Genome Characterization of Oleaginous Aspergillus oryzae BCC7051: A Potential Fungal-Based Platform for Lipid Production. Current Microbiology, 2018, 75, 57-70.	2.2	30
69	Sample storage conditions induce post-collection biases in microbiome profiles. BMC Microbiology, 2018, 18, 227.	3.3	23
70	Genome Sequences of Zika Virus Strains Recovered from Amniotic Fluid, Placenta, and Fetal Brain of a Microcephaly Patient in Thailand, 2017. Microbiology Resource Announcements, 2018, 7, .	0.6	5
71	487. Severity and Clinical Outcomes of Clostridium difficile Infection Based on Toxin B Assay Results. Open Forum Infectious Diseases, 2018, 5, S180-S181.	0.9	0
72	Diabetes-associated alterations in the cecal microbiome and metabolome are independent of diet or environment in the UC Davis Type 2 Diabetes Mellitus Rat model. American Journal of Physiology - Endocrinology and Metabolism, 2018, 315, E961-E972.	3.5	18

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73	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.	3.5	76
74	Viral Phylogenomics Using an Alignment-Free Method: A Three-Step Approach to Determine Optimal Length of k-mer. <i>Scientific Reports</i> , 2017, 7, 40712.	3.3	38
75	Evaluation and assessment of read-mapping by multiple next-generation sequencing aligners based on genome-wide characteristics. <i>Genomics</i> , 2017, 109, 186-191.	2.9	68
76	Single-cell gene expression analysis reveals regulators of distinct cell subpopulations among developing human neurons. <i>Genome Research</i> , 2017, 27, 1783-1794.	5.5	39
77	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
78	<i>In Vivo</i> Analysis of the Viable Microbiota and <i>Helicobacter pylori</i> Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. <i>Infection and Immunity</i> , 2017, 85, .	2.2	55
79	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , 2017, 18, 471.	2.6	20
80	Network Proteomics: From Protein Structure to Protein-Protein Interaction. <i>BioMed Research International</i> , 2017, 2017, 1-1.	1.9	4
81	Splenic Immune Response Is Down-Regulated in C57BL/6J Mice Fed Eicosapentaenoic Acid and Docosahexaenoic Acid Enriched High Fat Diet. <i>Nutrients</i> , 2017, 9, 50.	4.1	12
82	Low-complexity microbiota in the duodenum of children with newly diagnosed ulcerative colitis. <i>PLoS ONE</i> , 2017, 12, e0186178.	2.5	27
83	Assessment of genome annotation using gene function similarity within the gene neighborhood. <i>BMC Bioinformatics</i> , 2017, 18, 345.	2.6	5
84	dBBQs: dataBase of Bacterial Quality scores. <i>BMC Bioinformatics</i> , 2017, 18, 483.	2.6	27
85	Host diabetes status is the major regulator of gut microbiome in the UCDâ€¢2DM Rat. <i>FASEB Journal</i> , 2017, 31, .	0.5	0
86	Eicosapentaenoic and Docosahexaenoic Acid-Enriched High Fat Diet Delays Skeletal Muscle Degradation in Mice. <i>Nutrients</i> , 2016, 8, 543.	4.1	13
87	Comparative Analysis of Two <i>Helicobacter pylori</i> Strains using Genomics and Mass Spectrometry-Based Proteomics. <i>Frontiers in Microbiology</i> , 2016, 7, 1757.	3.5	10
88	Exploring complex cellular phenotypes and model-guided strain design with a novel genome-scale metabolic model of <i>Clostridium thermocellum</i> DSM 1313 implementing an adjustable cellulosome. <i>Biotechnology for Biofuels</i> , 2016, 9, 194.	6.2	32
89	Six Tissue Transcriptomics Reveals Specific Immune Suppression in Spleen by Dietary Polyunsaturated Fatty Acids. <i>PLoS ONE</i> , 2016, 11, e0155099.	2.5	13
90	Comparative Systems Analyses Reveal Molecular Signatures of Clinically tested Vaccine Adjuvants. <i>Scientific Reports</i> , 2016, 6, 39097.	3.3	53

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91	Glycosaminoglycan Profiling in Patientsâ€™ Plasma and Urine Predicts the Occurrence of Metastatic Clear Cell Renal Cell Carcinoma. <i>Cell Reports</i> , 2016, 15, 1822-1836.	6.4	55
92	Identification of a Latin American-specific BabA adhesin variant through whole genome sequencing of <i>Helicobacter pylori</i> patient isolates from Nicaragua. <i>BMC Evolutionary Biology</i> , 2016, 16, 53.	3.2	20
93	Voluntary Running Suppresses Tumor Growth through Epinephrine- and IL-6-Dependent NK Cell Mobilization and Redistribution. <i>Cell Metabolism</i> , 2016, 23, 554-562.	16.2	572
94	Human metabolic atlas: an online resource for human metabolism. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav068.	3.0	76
95	Eicosapentaenoic and docosahexaenoic acid-enriched high fat diet delays the development of fatty liver in mice. <i>Lipids in Health and Disease</i> , 2015, 14, 74.	3.0	27
96	Exercise suppresses tumor growth through epinephrine- and IL-6-dependent mobilization and redistribution of NK cells. , 2015, 3, P246.		1
97	Site-specific programming of the host epithelial transcriptome by the gut microbiota. <i>Genome Biology</i> , 2015, 16, 62.	8.8	131
98	Insights from 20Â½years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015, 15, 141-161.	3.5	580
99	Molecular Mechanism of Flocculation Self-Recognition in Yeast and Its Role in Mating and Survival. <i>MBio</i> , 2015, 6, .	4.1	62
100	Proteome- and Transcriptome-Driven Reconstruction of the Human Myocyte Metabolic Network and Its Use for Identification of Markers for Diabetes. <i>Cell Reports</i> , 2015, 11, 921-933.	6.4	112
101	Dietary Polyunsaturated Fatty Acids Increase Survival and Decrease Bacterial Load during Septic <i>Staphylococcus aureus</i> Infection and Improve Neutrophil Function in Mice. <i>Infection and Immunity</i> , 2015, 83, 514-521.	2.2	30
102	Metagenomic Data Utilization and Analysis (MEDUSA) and Construction of a Global Gut Microbial Gene Catalogue. <i>PLoS Computational Biology</i> , 2014, 10, e1003706.	3.2	55
103	BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. <i>Nucleic Acids Research</i> , 2014, 42, W175-W181.	14.5	40
104	A dedicated database system for handling multi-level data in systems biology. <i>Source Code for Biology and Medicine</i> , 2014, 9, 17.	1.7	2
105	yStreX: yeast stress expression database. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	13
106	Gut metagenome in European women with normal, impaired and diabetic glucose control. <i>Nature</i> , 2013, 498, 99-103.	27.8	2,401
107	Adipose Tissue Resting Energy Expenditure and Expression of Genes Involved in Mitochondrial Function Are Higher in Women than in Men. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E370-E378.	3.6	89
108	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. <i>Nucleic Acids Research</i> , 2013, 41, 4378-4391.	14.5	684

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109	Veillonella, Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , 2013, 9, 431-448.	1.5	47
110	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, 10084-10097.	14.5	285
111	Genome-Scale Metabolic Models of <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2011, 759, 445-463.	0.9	18
112	Identifying Molecular Effects of Diet through Systems Biology: Influence of Herring Diet on Sterol Metabolism and Protein Turnover in Mice. <i>PLoS ONE</i> , 2010, 5, e12361.	2.5	17