

# 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	Gut metagenome in European women with normal, impaired and diabetic glucose control. <i>Nature</i> , 2013, 498, 99-103.	27.8	2,401
2	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
3	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015, 15, 141-161.	3.5	580
4	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
5	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
6	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
7	Stimulation of Piezo1 by mechanical signals promotes bone anabolism. <i>ELife</i> , 2019, 8, .	6.0	185
8	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, e7-e7.	14.5	149
9	Site-specific programming of the host epithelial transcriptome by the gut microbiota. <i>Genome Biology</i> , 2015, 16, 62.	8.8	131
10	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.	14.5	116
11	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
12	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
13	Human metabolic atlas: an online resource for human metabolism. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav068.	3.0	76
14	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
15	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
16	Molecular Mechanism of Flocculation Self-Recognition in Yeast and Its Role in Mating and Survival. <i>MBio</i> , 2015, 6, .	4.1	62
17	Simplified Intestinal Microbiota to Study Microbe-Diet-Host Interactions in a Mouse Model. <i>Cell Reports</i> , 2019, 26, 3772-3783.e6.	6.4	61
18	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

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19	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
20	<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
21	Comparative Systems Analyses Reveal Molecular Signatures of Clinically tested Vaccine Adjuvants. <i>Scientific Reports</i> , 2016, 6, 39097.	3.3	53
22	Safety Assessment of a Nham Starter Culture <i>Lactobacillus plantarum</i> BCC9546 via Whole-genome Analysis. <i>Scientific Reports</i> , 2020, 10, 10241.	3.3	53
23	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
24	Veillonella, Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , 2013, 9, 431-448.	1.5	47
25	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , 2019, 10, 260.	3.5	46
26	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
27	BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. <i>Nucleic Acids Research</i> , 2014, 42, W175-W181.	14.5	40
28	Crosshatch nanofiber networks of tunable interfiber spacing induce plasticity in cell migration and cytoskeletal response. <i>FASEB Journal</i> , 2019, 33, 10618-10632.	0.5	40
29	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
30	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
31	Circular DNA in the human germline and its association with recombination. <i>Molecular Cell</i> , 2022, 82, 209-217.e7.	9.7	37
32	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
33	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
34	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
35	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
36	Genome Characterization of Oleaginous <i>Aspergillus oryzae</i> BCC7051: A Potential Fungal-Based Platform for Lipid Production. <i>Current Microbiology</i> , 2018, 75, 57-70.	2.2	30

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37	Distinctive molecular signature and activated signaling pathways in aortic smooth muscle cells of patients with myocardial infarction. <i>Atherosclerosis</i> , 2018, 271, 237-244.	0.8	29
38	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. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5895.	4.1	29
39	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
40	Low-complexity microbiota in the duodenum of children with newly diagnosed ulcerative colitis. <i>PLoS ONE</i> , 2017, 12, e0186178.	2.5	27
41	dBBQs: dataBase of Bacterial Quality scores. <i>BMC Bioinformatics</i> , 2017, 18, 483.	2.6	27
42	Effective CRISPR interference of an endogenous gene via a single transgene in mice. <i>Scientific Reports</i> , 2019, 9, 17312.	3.3	25
43	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
44	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
45	Profiles of urine and blood metabolomics in autism spectrum disorders. <i>Metabolic Brain Disease</i> , 2021, 36, 1641-1671.	2.9	24
46	Sample storage conditions induce post-collection biases in microbiome profiles. <i>BMC Microbiology</i> , 2018, 18, 227.	3.3	23
47	Neonatal gut colonization by <i>Bifidobacterium</i> is associated with higher childhood cytokine responses. <i>Gut Microbes</i> , 2020, 12, 1847628.	9.8	22
48	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
49	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , 2017, 18, 471.	2.6	20
50	Genome-Scale Metabolic Models of <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2011, 759, 445-463.	0.9	18
51	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. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E961-E972.	3.5	18
52	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
53	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F1 Mice. <i>Nutrients</i> , 2019, 11, 776.	4.1	17
54	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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55	Transcriptome analyses reveal the synergistic effects of feeding and eyestalk ablation on ovarian maturation in black tiger shrimp. <i>Scientific Reports</i> , 2020, 10, 3239.	3.3	16
56	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
57	Optimization of high molecular weight DNA extraction methods in shrimp for a long-read sequencing platform. <i>PeerJ</i> , 2020, 8, e10340.	2.0	15
58	Dietary Polyunsaturated Fatty Acids Promote Neutrophil Accumulation in the Spleen by Altering Chemotaxis and Delaying Cell Death. <i>Infection and Immunity</i> , 2019, 87, .	2.2	14
59	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
60	yStreX: yeast stress expression database. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	3.0	13
61	Eicosapentaenoic and Docosahexaenoic Acid-Enriched High Fat Diet Delays Skeletal Muscle Degradation in Mice. <i>Nutrients</i> , 2016, 8, 543.	4.1	13
62	Six Tissue Transcriptomics Reveals Specific Immune Suppression in Spleen by Dietary Polyunsaturated Fatty Acids. <i>PLoS ONE</i> , 2016, 11, e0155099.	2.5	13
63	Transcriptome alterations of vascular smooth muscle cells in aortic wall of myocardial infarction patients. <i>Data in Brief</i> , 2018, 17, 1112-1135.	1.0	13
64	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.	1.6	13
65	Global metabolite profiles of rice brown planthopper-resistant traits reveal potential secondary metabolites for both constitutive and inducible defenses. <i>Metabolomics</i> , 2019, 15, 151.	3.0	13
66	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
67	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
68	<i>Clostridium manihottivorum</i> sp. nov., a novel mesophilic anaerobic bacterium that produces cassava pulp-degrading enzymes. <i>PeerJ</i> , 2020, 8, e10343.	2.0	12
69	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	2.3	11
70	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
71	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
72	Genetic Aberration Analysis in Thai Colorectal Adenoma and Early-Stage Adenocarcinoma Patients by Whole-Exome Sequencing. <i>Cancers</i> , 2019, 11, 977.	3.7	10

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73	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
74	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
75	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
76	R-loop-forming Sequences Analysis in Thousands of Viral Genomes Identify A New Common Element in Herpesviruses. <i>Scientific Reports</i> , 2020, 10, 6389.	3.3	8
77	UPLC-ESI-MRM/MS for Absolute Quantification and MS/MS Structural Elucidation of Six Specialized Pyranonaphthoquinone Metabolites From <i>Ventilago harmandiana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 602993.	3.6	8
78	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
79	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
80	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
81	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
82	Genome-Based Comparison of <i>Clostridioides difficile</i> : Average Amino Acid Identity Analysis of Core Genomes. <i>Microbial Ecology</i> , 2018, 76, 801-813.	2.8	6
83	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, .	0.6	6
84	Assessment of genome annotation using gene function similarity within the gene neighborhood. <i>BMC Bioinformatics</i> , 2017, 18, 345.	2.6	5
85	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, .	0.6	5
86	Complete Genome and Plasmid Sequences of <i>Escherichia coli</i> Type Strain ATCC 11775. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
87	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
88	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
89	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
90	Network Proteomics: From Protein Structure to Protein-Protein Interaction. <i>BioMed Research International</i> , 2017, 2017, 1-1.	1.9	4

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91	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
92	Current and Future Methodology for Quantitation and Site-Specific Mapping the Location of DNA Adducts. <i>Toxics</i> , 2022, 10, 45.	3.7	4
93	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, .	0.6	3
94	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
95	Genome-wide Cas9 binding specificity in <i>Saccharomyces cerevisiae</i> . <i>PeerJ</i> , 2020, 8, e9442.	2.0	3
96	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
97	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
98	Spleen proteomics data from high fat diet fed mice. <i>Data in Brief</i> , 2020, 32, 106110.	1.0	2
99	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
100	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
101	Nanopore Sequencing for Detection and Characterization of Phosphorothioate Modifications in Native DNA Sequences. <i>Frontiers in Microbiology</i> , 2022, 13, 871937.	3.5	2
102	Exercise suppresses tumor growth through epinephrine- and IL-6-dependent mobilization and redistribution of NK cells. , 2015, 3, P246.		1
103	Green Tea Extract as a Safe and Effective Dietary Supplement: Lessons Learned from Mice. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa045_052.	0.3	1
104	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
105	487. Severity and Clinical Outcomes of <i>Clostridium difficile</i> Infection Based on Toxin B Assay Results. <i>Open Forum Infectious Diseases</i> , 2018, 5, S180-S181.	0.9	0
106	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.	1.2	0
107	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.	1.2	0
108	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

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109	Cannabidiol: From Drug Interaction Potential to Modulation of the Gut Microbiome. Current Developments in Nutrition, 2020, 4, nzaa045_051.	0.3	0
110	Characteristics and Network Influence of Providers Involved in the Treatment of Patients With Chronic Back, Neck or Joint Pain in Arkansas. Journal of Pain, 2021, 22, 1681-1695.	1.4	0
111	Host diabetes status is the major regulator of gut microbiome in the UCDâ€™2DM Rat. FASEB Journal, 2017, 31, .	0.5	0
112	Direct Sequencing of RNA and RNA Modification Identification Using Nanopore. Methods in Molecular Biology, 2022, 2477, 71-77.	0.9	0