

Natapol Pornputtpong

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,433
citations

933447

10
h-index

610901

24
g-index

26
all docs

26
docs citations

26
times ranked

3243
citing authors

#	ARTICLE	IF	CITATIONS
1	A multi-epitope chimeric protein elicited a strong antibody response and partial protection against <i>Edwardsiella ictaluri</i> in Nile tilapia. <i>Journal of Fish Diseases</i> , 2022, 45, 1-18.	1.9	17
2	Is <i>Hyperdermium</i> Congeneric with <i>Ascopolyporus</i> ? Phylogenetic Relationships of <i>Ascopolyporus</i> spp. (<i>Cordycipitaceae</i> , <i>Hypocreales</i>) and a New Genus <i>Neohyperdermium</i> on Scale Insects in Thailand. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 516.	3.5	3
3	Using machine learning-based analytics of daily activities to identify modifiable risk factors for falling in Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2021, 82, 77-83.	2.2	3
4	Four Novel Phenanthrene Derivatives with β -Glucosidase Inhibitory Activity from <i>Gastrochilus bellinus</i> . <i>Molecules</i> , 2021, 26, 418.	3.8	5
5	Resurfacing receptor binding domain of Colicin N to enhance its cytotoxic effect on human lung cancer cells. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5225-5234.	4.1	3
6	Chemosensitizing activity of peptide from <i>Lentinus squarrosulus</i> (Mont.) on cisplatin-induced apoptosis in human lung cancer cells. <i>Scientific Reports</i> , 2021, 11, 4060.	3.3	8
7	Development and Qualification of a Physiologically Based Pharmacokinetic Model of Finasteride and Minoxidil Following Scalp Application. <i>Journal of Pharmaceutical Sciences</i> , 2021, 110, 2301-2310.	3.3	6
8	Novelties in <i>Fuscosporellaceae</i> (<i>Fuscosporellales</i>): Two New <i>Parafuscosporella</i> from Thailand Revealed by Morphology and Phylogenetic Analyses. <i>Diversity</i> , 2021, 13, 517.	1.7	7
9	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
10	In silico analysis for factors affecting anti-malarial penetration into red blood cells. <i>Malaria Journal</i> , 2020, 19, 215.	2.3	3
11	MHCSeqNet: a deep neural network model for universal MHC binding prediction. <i>BMC Bioinformatics</i> , 2019, 20, 270.	2.6	56
12	Accounting for biological variation with linear mixed-effects modelling improves the quality of clinical metabolomics data. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 611-618.	4.1	31
13	Spitz nevi and Spitzoid melanomas: exome sequencing and comparison with conventional melanocytic nevi and melanomas. <i>Modern Pathology</i> , 2017, 30, 640-649.	5.5	55
14	<i>Conioscypha nakagirii</i> , a new species from naturally submerged wood in Thailand based on morphological and molecular data. <i>Mycoscience</i> , 2017, 58, 424-431.	0.8	9
15	Distinct dominant T-cell receptors with a tissue resident memory phenotype in individual melanoma metastases. <i>Journal of Clinical Oncology</i> , 2017, 35, 3-3.	1.6	1
16	Germline MC1R status influences somatic mutation burden in melanoma. <i>Nature Communications</i> , 2016, 7, 12064.	12.8	103
17	Global copy number profiling of cancer genomes. <i>Bioinformatics</i> , 2016, 32, 926-928.	4.1	4
18	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

#	ARTICLE	IF	CITATIONS
19	Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas. <i>Nature Genetics</i> , 2015, 47, 996-1002.	21.4	348
20	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
21	Reconstruction of Genome-Scale Active Metabolic Networks for 69 Human Cell Types and 16 Cancer Types Using INIT. <i>PLoS Computational Biology</i> , 2012, 8, e1002518.	3.2	381
22	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
23	Prediction of Non-coding RNA and Their Targets in <i>Spirulina platensis</i> Genome. <i>Communications in Computer and Information Science</i> , 2010, , 106-117.	0.5	2
24	3D Structure Modeling of a Transmembrane Protein, Fatty Acid Elongase. <i>Communications in Computer and Information Science</i> , 2010, , 36-45.	0.5	1
25	Homology modeling of <i>Mycoplasma pneumoniae</i> enolase and its molecular interaction with human-plasminogen. <i>Bioinformatics</i> , 2008, 3, 18-23.	0.5	13
26	Adjusting an Invalid Correlation Matrix with Applications to High-Dimensional Biological Data. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0