

Chun Hang Au

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

1,336
citations

516710

16
h-index

414414

32
g-index

35
all docs

35
docs citations

35
times ranked

2625
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11889-11894.	7.1	389
2	Composition and genetic diversity of picoeukaryotes in subtropical coastal waters as revealed by 454 pyrosequencing. ISME Journal, 2010, 4, 1053-1059.	9.8	223
3	Sputum Microbiota in Tuberculosis as Revealed by 16S rRNA Pyrosequencing. PLoS ONE, 2013, 8, e54574.	2.5	85
4	Clinical evaluation of panel testing by next-generation sequencing (NGS) for gene mutations in myeloid neoplasms. Diagnostic Pathology, 2016, 11, 11.	2.0	77
5	5'-Serial Analysis of Gene Expression studies reveal a transcriptomic switch during fruiting body development in <i>Coprinopsis cinerea</i> . BMC Genomics, 2013, 14, 195.	2.8	65
6	Homoharringtonine (omacetaxine mepesuccinate) as an adjunct for <i>FLT3</i> ITD acute myeloid leukemia. Science Translational Medicine, 2016, 8, 359ra129.	12.4	53
7	Gene expression studies of the dikaryotic mycelium and primordium of <i>Lentinula edodes</i> by serial analysis of gene expression. Mycological Research, 2008, 112, 950-964.	2.5	44
8	The importance of analysis of long-range rearrangement of BRCA1 and BRCA2 in genetic diagnosis of familial breast cancer. Cancer Genetics, 2015, 208, 448-454.	0.4	43
9	A Novel <i>Lentinula edodes</i> Laccase and Its Comparative Enzymology Suggest Guaiacol-Based Laccase Engineering for Bioremediation. PLoS ONE, 2013, 8, e66426.	2.5	30
10	Next-generation sequencing with a myeloid gene panel in core-binding factor AML showed KIT activation loop and TET2 mutations predictive of outcome. Blood Cancer Journal, 2016, 6, e442-e442.	6.2	29
11	Prospective study on human fecal carriage of Enterobacteriaceae possessing <i>mcr-1</i> and <i>mcr-2</i> genes in a regional hospital in Hong Kong. BMC Infectious Diseases, 2018, 18, 81.	2.9	28
12	BAMClipper: removing primers from alignments to minimize false-negative mutations in amplicon next-generation sequencing. Scientific Reports, 2017, 7, 1567.	3.3	27
13	The genetic structure of the A mating-type locus of <i>Lentinula edodes</i> . Gene, 2014, 535, 184-190.	2.2	25
14	Rapid detection of chromosomal translocation and precise breakpoint characterization in acute myeloid leukemia by nanopore long-read sequencing. Cancer Genetics, 2019, 239, 22-25.	0.4	24
15	Rapid genotyping by low-coverage resequencing to construct genetic linkage maps of fungi: a case study in <i>Lentinula edodes</i> . BMC Research Notes, 2013, 6, 307.	1.4	21
16	Potential utility of targeted Nanopore sequencing for improving etiologic diagnosis of bacterial and fungal respiratory infection. Diagnostic Pathology, 2020, 15, 41.	2.0	20
17	INDELseek: detection of complex insertions and deletions from next-generation sequencing data. BMC Genomics, 2017, 18, 16.	2.8	19
18	Cataloging and profiling genes expressed in <i>Lentinula edodes</i> fruiting body by massive cDNA pyrosequencing and LongSAGE. Fungal Genetics and Biology, 2011, 48, 359-369.	2.1	17

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19	Evaluation on the use of Nanopore sequencing for direct characterization of coronaviruses from respiratory specimens, and a study on emerging missense mutations in partial RdRP gene of SARS-CoV-2. <i>Virology Journal</i> , 2020, 17, 183.	3.4	17
20	Germline Mutation in 1338 BRCA-Negative Chinese Hereditary Breast and/or Ovarian Cancer Patients. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 544-554.	2.8	17
21	Next-generation sequencing and molecular cytogenetic characterization of ETV6-LYN fusion due to chromosomes 1, 8 and 12 rearrangement in acute myeloid leukemia. <i>Cancer Genetics</i> , 2017, 218-219, 15-19.	0.4	14
22	Rapid and economical drug resistance profiling with Nanopore MinION for clinical specimens with low bacillary burden of <i>Mycobacterium tuberculosis</i> . <i>BMC Research Notes</i> , 2020, 13, 444.	1.4	13
23	Mutation screening of germline TP53 mutations in high-risk Chinese breast cancer patients. <i>BMC Cancer</i> , 2020, 20, 1053.	2.6	10
24	database.bio: a web application for interpreting human variations. <i>Bioinformatics</i> , 2015, 31, 4035-4037.	4.1	9
25	Germline PALB2 Mutation in High-Risk Chinese Breast and/or Ovarian Cancer Patients. <i>Cancers</i> , 2021, 13, 4195.	3.7	7
26	Genome sequence and genetic linkage analysis of Shiitake mushroom <i>Lentinula edodes</i> . <i>Nature Precedings</i> , 2012, , .	0.1	6
27	An economical Nanopore sequencing assay for human papillomavirus (HPV) genotyping. <i>Diagnostic Pathology</i> , 2020, 15, 45.	2.0	6
28	Genome Sequences of SARS-CoV-2 Strains Detected in Hong Kong. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
29	A Case Report of Germline Compound Heterozygous Mutations in the BRCA1 Gene of an Ovarian and Breast Cancer Patient. <i>International Journal of Molecular Sciences</i> , 2021, 22, 889.	4.1	5
30	A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. <i>BMC Research Notes</i> , 2012, 5, 80.	1.4	4
31	A Phase II Single-Arm Open-Labelled Study Evaluating Combination of Quizartinib and Omacetaxine Mepesuccinate (QUIZOM) in Newly Diagnosed or Relapsed/Refractory AML Carrying FLT3-ITD. <i>Blood</i> , 2019, 134, 3825-3825.	1.4	3
32	Rapid Breakpoint Mapping of a Novel Germline <i>PALB2</i> Duplication by PCR-Free Long-Read Sequencing for Interpretation of Its Pathogenicity. <i>JCO Precision Oncology</i> , 2021, 5, 1044-1047.	3.0	1
33	A Proposal of Genomic Analytical Workflow in a Bacterial Pathogen Outbreak Investigation. <i>Nature Precedings</i> , 2011, , .	0.1	0
34	Genome Sequences of <i>Salmonella enterica</i> Serotype Typhimurium Blood Clinical Isolate ST4848/06 and Stool Isolate ST1489/06. <i>Genome Announcements</i> , 2013, 1, .	0.8	0
35	Characterization of Genomic Landscape and Risk Stratification of De Novo Cytogenetically Normal Acute Myeloid Leukaemia. <i>Blood</i> , 2018, 132, 5267-5267.	1.4	0