

Chun Hang Au

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3212732/publications.pdf>

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	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
2	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
3	Germline PALB2 Mutation in High-Risk Chinese Breast and/or Ovarian Cancer Patients. <i>Cancers</i> , 2021, 13, 4195.	3.7	7
4	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
5	Genome Sequences of SARS-CoV-2 Strains Detected in Hong Kong. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
6	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
7	Mutation screening of germline TP53 mutations in high-risk Chinese breast cancer patients. <i>BMC Cancer</i> , 2020, 20, 1053.	2.6	10
8	An economical Nanopore sequencing assay for human papillomavirus (HPV) genotyping. <i>Diagnostic Pathology</i> , 2020, 15, 45.	2.0	6
9	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
10	Potential utility of targeted Nanopore sequencing for improving etiologic diagnosis of bacterial and fungal respiratory infection. <i>Diagnostic Pathology</i> , 2020, 15, 41.	2.0	20
11	Rapid detection of chromosomal translocation and precise breakpoint characterization in acute myeloid leukemia by nanopore long-read sequencing. <i>Cancer Genetics</i> , 2019, 239, 22-25.	0.4	24
12	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
13	Prospective study on human fecal carriage of Enterobacteriaceae possessing mcr-1 and mcr-2 genes in a regional hospital in Hong Kong. <i>BMC Infectious Diseases</i> , 2018, 18, 81.	2.9	28
14	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
15	BAMClipper: removing primers from alignments to minimize false-negative mutations in amplicon next-generation sequencing. <i>Scientific Reports</i> , 2017, 7, 1567.	3.3	27
16	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
17	INDELseek: detection of complex insertions and deletions from next-generation sequencing data. <i>BMC Genomics</i> , 2017, 18, 16.	2.8	19
18	Next-generation sequencing with a myeloid gene panel in core-binding factor AML showed KIT activation loop and TET2 mutations predictive of outcome. <i>Blood Cancer Journal</i> , 2016, 6, e442-e442.	6.2	29

#	ARTICLE	IF	CITATIONS
19	Clinical evaluation of panel testing by next-generation sequencing (NGS) for gene mutations in myeloid neoplasms. <i>Diagnostic Pathology</i> , 2016, 11, 11.	2.0	77
20	Homoharringtonine (omacetaxine mepesuccinate) as an adjunct for <i>FLT3</i> ITD acute myeloid leukemia. <i>Science Translational Medicine</i> , 2016, 8, 359ra129.	12.4	53
21	The importance of analysis of long-range rearrangement of BRCA1 and BRCA2 in genetic diagnosis of familial breast cancer. <i>Cancer Genetics</i> , 2015, 208, 448-454.	0.4	43
22	database.bio: a web application for interpreting human variations. <i>Bioinformatics</i> , 2015, 31, 4035-4037.	4.1	9
23	The genetic structure of the A mating-type locus of <i>Lentinula edodes</i> . <i>Gene</i> , 2014, 535, 184-190.	2.2	25
24	5'-Serial Analysis of Gene Expression studies reveal a transcriptomic switch during fruiting body development in <i>Coprinopsis cinerea</i> . <i>BMC Genomics</i> , 2013, 14, 195.	2.8	65
25	Rapid genotyping by low-coverage resequencing to construct genetic linkage maps of fungi: a case study in <i>Lentinula edodes</i> . <i>BMC Research Notes</i> , 2013, 6, 307.	1.4	21
26	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
27	Sputum Microbiota in Tuberculosis as Revealed by 16S rRNA Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e54574.	2.5	85
28	A Novel <i>Lentinula edodes</i> Laccase and Its Comparative Enzymology Suggest Guaiacol-Based Laccase Engineering for Bioremediation. <i>PLoS ONE</i> , 2013, 8, e66426.	2.5	30
29	Genome sequence and genetic linkage analysis of Shiitake mushroom <i>Lentinula edodes</i> . <i>Nature Precedings</i> , 2012, , .	0.1	6
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	Cataloging and profiling genes expressed in <i>Lentinula edodes</i> fruiting body by massive cDNA pyrosequencing and LongSAGE. <i>Fungal Genetics and Biology</i> , 2011, 48, 359-369.	2.1	17
32	A Proposal of Genomic Analytical Workflow in a Bacterial Pathogen Outbreak Investigation. <i>Nature Precedings</i> , 2011, , .	0.1	0
33	Composition and genetic diversity of picoeukaryotes in subtropical coastal waters as revealed by 454 pyrosequencing. <i>ISME Journal</i> , 2010, 4, 1053-1059.	9.8	223
34	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11889-11894.	7.1	389
35	Gene expression studies of the dikaryotic mycelium and primordium of <i>Lentinula edodes</i> by serial analysis of gene expression. <i>Mycological Research</i> , 2008, 112, 950-964.	2.5	44