

Kelly Quek

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6277828/publications.pdf>

Version: 2024-02-01

22
papers

6,914
citations

687363

13
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

13094
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
2	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	27.8	2,132
3	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	27.8	1,206
4	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	12.8	236
5	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. <i>Cancer Discovery</i> , 2017, 7, 1088-1097.	9.4	160
6	Comprehensive T cell repertoire characterization of non-small cell lung cancer. <i>Nature Communications</i> , 2020, 11, 603.	12.8	140
7	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. <i>Gastroenterology</i> , 2021, 160, 362-377.e13.	1.3	90
8	High prevalence of relapse in children with Philadelphia-like acute lymphoblastic leukemia despite risk-adapted treatment. <i>Haematologica</i> , 2017, 102, e490-e493.	3.5	52
9	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. <i>Oncotarget</i> , 2017, 8, 21994-22002.	1.8	39
10	Distinct co-acquired alterations and genomic evolution during TKI treatment in non-small-cell lung cancer patients with or without acquired T790M mutation. <i>Oncogene</i> , 2020, 39, 1846-1859.	5.9	29
11	Expression of the SARS-CoV-2 receptor ACE2 reveals the susceptibility of COVID-19 in non-small cell lung cancer. <i>Journal of Cancer</i> , 2020, 11, 5289-5292.	2.5	28
12	Antimicrobial susceptibility and clarithromycin resistance patterns of <i>Helicobacter pylori</i> clinical isolates in Vietnam. <i>Frontiers in Microbiology</i> , 2016, 5, 671.	1.6	25
13	TRACERx: Tracking tumor evolution to impact the course of lung cancer. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2018, 155, 1199-1202.	0.8	14
14	Integrated Bioinformatics Analysis Reveals Key Candidate Genes and Pathways Associated With Clinical Outcome in Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 814.	2.3	11
15	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020, 12, 1952-1959.	1.4	6
16	Association of the T-cell receptor landscape with survival in non-small cell lung cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 140-140.	1.6	4
17	Abstract 213: Exome sequencing of paired primary and relapsed small cell lung cancers reveals increased copy number aberration complexity to be associated with disease relapse. , 2018, , .		3
18	Immunogenomic intertumor heterogeneity across primary and metastatic sites in a patient with lung adenocarcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 172.	8.6	2

#	ARTICLE	IF	CITATIONS
19	High Prevalence of Relapse in Australian Children with Ph-like Acute Lymphoblastic Leukemia Despite Risk Adapted Treatment. <i>Blood</i> , 2015, 126, 1419-1419.	1.4	1
20	Intratumor heterogeneity of stage IA lung adenocarcinoma by multiregion whole exome sequencing and association with survival.. <i>Journal of Clinical Oncology</i> , 2017, 35, 8545-8545.	1.6	1
21	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , 2014, 57, 31-38.	1.8	0
22	Co-fuse: a new class discovery analysis tool to identify and prioritize recurrent fusion genes from RNA-sequencing data. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1217-1229.	2.1	0