

Swee Hoe Ong

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4133524/publications.pdf>

Version: 2024-02-01

26
papers

1,479
citations

361413

20
h-index

552781

26
g-index

31
all docs

31
docs citations

31
times ranked

2865
citing authors

#	ARTICLE	IF	CITATIONS
1	IVA: accurate <i>de novo</i> assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015, 31, 2374-2376.	4.1	179
2	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. <i>Nature Genetics</i> , 2020, 52, 604-614.	21.4	107
3	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. <i>Nature</i> , 2021, 598, 510-514.	27.8	95
4	Species Identification and Profiling of Complex Microbial Communities Using Shotgun Illumina Sequencing of 16S rRNA Amplicon Sequences. <i>PLoS ONE</i> , 2013, 8, e60811.	2.5	93
5	Genomic Epidemiology of a Dengue Virus Epidemic in Urban Singapore. <i>Journal of Virology</i> , 2009, 83, 4163-4173.	3.4	89
6	Outcompeting p53-Mutant Cells in the Normal Esophagus by Redox Manipulation. <i>Cell Stem Cell</i> , 2019, 25, 329-341.e6.	11.1	88
7	Deep Sequencing of Norovirus Genomes Defines Evolutionary Patterns in an Urban Tropical Setting. <i>Journal of Virology</i> , 2014, 88, 11056-11069.	3.4	78
8	Genome-wide CRISPR-KO Screen Uncovers mTORC1-Mediated Gsk3 Regulation in Naive Pluripotency Maintenance and Dissolution. <i>Cell Reports</i> , 2018, 24, 489-502.	6.4	77
9	A method for full genome sequencing of all four serotypes of the dengue virus. <i>Journal of Virological Methods</i> , 2010, 169, 202-206.	2.1	72
10	Epidermal Tissue Adapts to Restrain Progenitors Carrying Clonal p53 Mutations. <i>Cell Stem Cell</i> , 2018, 23, 687-699.e8.	11.1	72
11	Plasmablasts Generated during Repeated Dengue Infection Are Virus Glycoprotein-Specific and Bind to Multiple Virus Serotypes. <i>Journal of Immunology</i> , 2012, 189, 5877-5885.	0.8	70
12	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. <i>Cancer Discovery</i> , 2021, 11, 340-361.	9.4	66
13	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	4.9	64
14	Periodic re-emergence of endemic strains with strong epidemic potential—A proposed explanation for the 2004 Indonesian dengue epidemic. <i>Infection, Genetics and Evolution</i> , 2008, 8, 191-204.	2.3	55
15	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
16	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017, 15, e2001855.	5.6	38
17	Optimised metrics for CRISPR-KO screens with second-generation gRNA libraries. <i>Scientific Reports</i> , 2017, 7, 7384.	3.3	37
18	Systems consequences of amplicon formation in human breast cancer. <i>Genome Research</i> , 2014, 24, 1559-1571.	5.5	32

#	ARTICLE	IF	CITATIONS
19	KAT7 is a genetic vulnerability of acute myeloid leukemias driven by MLL rearrangements. <i>Leukemia</i> , 2021, 35, 1012-1022.	7.2	26
20	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. <i>Virus Research</i> , 2017, 239, 10-16.	2.2	23
21	Patient-Based Transcriptome-Wide Analysis Identify Interferon and Ubiquitination Pathways as Potential Predictors of Influenza A Disease Severity. <i>PLoS ONE</i> , 2014, 9, e111640.	2.5	19
22	RNAmut: robust identification of somatic mutations in acute myeloid leukemia using RNA-sequencing. <i>Haematologica</i> , 2020, 105, e290-e293.	3.5	13
23	DengueInfo: A web portal to dengue information resources. <i>Infection, Genetics and Evolution</i> , 2007, 7, 540-541.	2.3	12
24	Accurate characterization of the IFITM locus using MiSeq and PacBio sequencing shows genetic variation in Galliformes. <i>BMC Genomics</i> , 2017, 18, 419.	2.8	9
25	Comparative analysis of the chicken IFITM locus by targeted genome sequencing reveals evolution of the locus and positive selection in IFITM1 and IFITM3. <i>BMC Genomics</i> , 2019, 20, 272.	2.8	6
26	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	4.9	1