

Weiwei Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12161201/publications.pdf>

Version: 2024-02-01

19
papers

1,223
citations

687363

13
h-index

794594

19
g-index

22
all docs

22
docs citations

22
times ranked

2527
citing authors

#	ARTICLE	IF	CITATIONS
1	Isolation of a Human Betaretrovirus from Patients with Primary Biliary Cholangitis. <i>Viruses</i> , 2022, 14, 886.	3.3	7
2	Enrichment of low abundance DNA/RNA by oligonucleotide-clicked iron oxide nanoparticles. <i>Scientific Reports</i> , 2021, 11, 13053.	3.3	7
3	Genome profiles of pathologist-defined cell clusters by multiregional LCM and G&T-seq in one triple-negative breast cancer patient. <i>Cell Reports Medicine</i> , 2021, 2, 100404.	6.5	5
4	Independent evolution of cutaneous lymphoma subclones in different microenvironments of the skin. <i>Scientific Reports</i> , 2020, 10, 15483.	3.3	3
5	Branched evolution and genomic intratumor heterogeneity in the pathogenesis of cutaneous T-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 2489-2500.	5.2	45
6	Skin colonization by circulating neoplastic clones in cutaneous T-cell lymphoma. <i>Blood</i> , 2019, 134, 1517-1527.	1.4	44
7	Clonotypic heterogeneity in cutaneous T-cell lymphoma (mycosis fungoides) revealed by comprehensive whole-exome sequencing. <i>Blood Advances</i> , 2019, 3, 1175-1184.	5.2	39
8	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. <i>Gut</i> , 2018, 67, 1517-1524.	12.1	42
9	Novel mutations involving β II, β IIA, or β IVB-tubulin isotypes with functional resemblance to β III-tubulin in breast cancer. <i>Protoplasma</i> , 2017, 254, 1163-1173.	2.1	22
10	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 459.	3.5	659
11	Gamma-Retrovirus Integration Marks Cell Type-Specific Cancer Genes: A Novel Profiling Tool in Cancer Genomics. <i>PLoS ONE</i> , 2016, 11, e0154070.	2.5	8
12	Cerebrospinal Fluid in a Small Cohort of Patients with Multiple Sclerosis Was Generally Free of Microbial DNA. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 198.	3.9	9
13	Metagenomic Analysis of Microbiome in Colon Tissue from Subjects with Inflammatory Bowel Diseases Reveals Interplay of Viruses and Bacteria. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	1.9	100
14	Mitochondrial genome sequences of <i>Artemia tibetiana</i> and <i>Artemia urmiana</i> : assessing molecular changes for high plateau adaptation. <i>Science China Life Sciences</i> , 2013, 56, 440-452.	4.9	37
15	Identification of Hepatotropic Viruses from Plasma Using Deep Sequencing: A Next Generation Diagnostic Tool. <i>PLoS ONE</i> , 2013, 8, e60595.	2.5	53
16	Diverse LEA (late embryogenesis abundant) and LEA-like genes and their responses to hypersaline stress in post-diapause embryonic development of <i>Artemia franciscana</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2011, 160, 32-39.	1.6	32
17	A gene catalogue for post-diapause development of an anhydrobiotic arthropod <i>Artemia franciscana</i> . <i>BMC Genomics</i> , 2009, 10, 52.	2.8	36
18	Phylogenetic Analysis of Brine Shrimp (<i>Artemia</i>) in China Using DNA Barcoding. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 155-162.	6.9	20

#	ARTICLE	IF	CITATIONS
19	A proteomic study on postdiapaused embryonic development of brine shrimp (<i>Artemia</i>) Tj ETQq1 1 0.784314.rgBT /Overlock 10	2.2	50