Kanthida Kusonmano

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5522049/publications.pdf

Version: 2024-02-01

		687363	752698
20	627	13	20
papers	citations	h-index	g-index

20	20	20	1522
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Microbial community structure in aquifers associated with arsenic: analysis of 16S rRNA and arsenite oxidase genes. PeerJ, 2021, 9, e10653.	2.0	12
2	Arsenic speciation, the abundance of arsenite-oxidizing bacteria and microbial community structures in groundwater, surface water, and soil from a gold mine. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2021, 56, 769-785.	1.7	6
3	Diverse Microbial Community Profiles of Propionate-Degrading Cultures Derived from Different Sludge Sources of Anaerobic Wastewater Treatment Plants. Microorganisms, 2020, 8, 277.	3.6	21
4	Genetic Aberration Analysis in Thai Colorectal Adenoma and Early-Stage Adenocarcinoma Patients by Whole-Exome Sequencing. Cancers, 2019, 11, 977.	3.7	10
5	<i>PIK3CA</i> Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. Clinical Cancer Research, 2019, 25, 334-345.	7.0	17
6	HER2 expression patterns in paired primary and metastatic endometrial cancer lesions. British Journal of Cancer, 2018, 118, 378-387.	6.4	43
7	Identification of highly connected and differentially expressed gene subnetworks in metastasizing endometrial cancer. PLoS ONE, 2018, 13, e0206665.	2.5	11
8	PIK3CA exon9 mutations associate with reduced survival, and are highly concordant between matching primary tumors and metastases in endometrial cancer. Scientific Reports, 2017, 7, 10240.	3.3	19
9	Clinicopathologic and molecular markers in cervical carcinoma: a prospective cohort study. American Journal of Obstetrics and Gynecology, 2017, 217, 432.e1-432.e17.	1.3	38
10	Aneuploidy related transcriptional changes in endometrial cancer link low expression of chromosome 15q genes to poor survival. Oncotarget, 2017, 8, 9696-9707.	1.8	4
11	Gene Expression Analysis Through Network Biology: Bioinformatics Approaches. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 15-32.	1.1	2
12	Informatics for Metabolomics. Advances in Experimental Medicine and Biology, 2016, 939, 91-115.	1.6	28
13	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. Nature Genetics, 2016, 48, 848-855.	21.4	174
14	ATAD2 overexpression links to enrichment of B-MYB-translational signatures and development of aggressive endometrial carcinoma. Oncotarget, 2015, 6, 28440-28452.	1.8	37
15	Molecular profiling of endometrial carcinoma precursor, primary and metastatic lesions suggests different targets for treatment in obese compared to non-obese patients. Oncotarget, 2015, 6, 1327-1339.	1.8	50
16	Increased angiogenesis is associated with a 32-gene expression signature and 6p21 amplification in aggressive endometrial cancer. Oncotarget, 2015, 6, 10634-10645.	1.8	15
17	Loss of progesterone receptor links to high proliferation and increases from primary to metastatic endometrial cancer lesions. European Journal of Cancer, 2014, 50, 3003-3010.	2.8	73
18	Dip in the gene pool: Metagenomic survey of natural coccolithovirus communities. Virology, 2014, 466-467, 129-137.	2.4	10

#	ARTICLE	IF	CITATIONS
19	Switch in FOXA1 Status Associates with Endometrial Cancer Progression. PLoS ONE, 2014, 9, e98069.	2.5	22
20	High Phospho-Stathmin(Serine38) Expression Identifies Aggressive Endometrial Cancer and Suggests an Association with PI3K Inhibition. Clinical Cancer Research, 2013, 19, 2331-2341.	7.0	35