

List of Publications by Year in
Descending Order

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Version: 2024-04-09

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22 papers	433 citations	10 h-index	20 g-index
22 ext. papers	681 ext. citations	5.8 avg, IF	3.3 L-index

#	Paper	IF	Citations
22	SARS-CoV-2 encoded microRNAs are involved in the process of virus infection and host immune response. <i>Journal of Biomedical Research</i> , 2021 , 35, 216-227	1.5	10
21	PM2RA: A Framework for Detecting and Quantifying Relationship Alterations in Microbial Community. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 , 19, 154-167	6.5	2
20	Gene variations in autism spectrum disorder are associated with alteration of gut microbiota, metabolites and cytokines. <i>Gut Microbes</i> , 2021 , 13, 1-16	8.8	10
19	Deviated and early unsustainable stunted development of gut microbiota in children with autism spectrum disorder.. <i>Gut</i> , 2021 ,	19.2	4
18	Alteration in gut microbiota is associated with dysregulation of cytokines and glucocorticoid therapy in systemic lupus erythematosus. <i>Gut Microbes</i> , 2020 , 11, 1758-1773	8.8	24
17	Acute Sleep-Wake Cycle Shift Results in Community Alteration of Human Gut Microbiome. <i>MSphere</i> , 2020 , 5,	5	19
16	Altered gut microbial profile is associated with abnormal metabolism activity of Autism Spectrum Disorder. <i>Gut Microbes</i> , 2020 , 11, 1246-1267	8.8	53
15	Lead exposure results in defective behavior as well as alteration of gut microbiota composition in flies and their offsprings. <i>International Journal of Developmental Neuroscience</i> , 2020 , 80, 699-708	2.7	3
14	Elevating H3K27me3 level sensitizes colorectal cancer to oxaliplatin. <i>Journal of Molecular Cell Biology</i> , 2020 , 12, 125-137	6.3	25
13	Systematic analysis reveals long noncoding RNAs regulating neighboring transcription factors in human cancers. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018 , 1864, 2785-2792	6.9	19
12	A Genome-Wide Study of Allele-Specific Expression in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2018 , 9, 570	4.5	12
11	Dataset for regulation between lncRNAs and their nearby protein-coding genes in human cancers. <i>Data in Brief</i> , 2018 , 19, 1902-1906	1.2	7
10	Alternative NF- κ B signaling promotes colorectal tumorigenesis through transcriptionally upregulating Bcl-3. <i>Oncogene</i> , 2018 , 37, 5887-5900	9.2	5
9	Heterologous expression, purification and function of the extracellular domain of human RANK. <i>BMC Biotechnology</i> , 2017 , 17, 87	3.5	2
8	miR-449a inhibits colorectal cancer progression by targeting SATB2. <i>Oncotarget</i> , 2017 , 8, 100975-100983	3.3	15
7	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , 2016 , 6, 26942	4.9	21
6	cisASE: a likelihood-based method for detecting putative cis-regulated allele-specific expression in RNA sequencing data. <i>Bioinformatics</i> , 2016 , 32, 3291-3297	7.2	6

5	The histone H3 lysine-27 demethylase Jmjd3 plays a critical role in specific regulation of Th17 cell differentiation. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 505-16	6.3	67
4	Comparing computational methods for identification of allele-specific expression based on next generation sequencing data. <i>Genetic Epidemiology</i> , 2014 , 38, 591-8	2.6	9
3	A microRNA 221- and 222-mediated feedback loop maintains constitutive activation of NF κ B and STAT3 in colorectal cancer cells. <i>Gastroenterology</i> , 2014 , 147, 847-859.e11	13.3	119
2	Investigating co-evolution of functionally associated phosphosites in human. <i>Molecular Genetics and Genomics</i> , 2014 , 289, 1217-23	3.1	
1	The de novo sequence origin of two long non-coding genes from an inter-genic region. <i>BMC Genomics</i> , 2013 , 14 Suppl 8, S6	4.5	1