

Amirhossein Shamsaddini

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

294
citations

1163117

8
h-index

1199594

12
g-index

12
all docs

12
docs citations

12
times ranked

355
citing authors

#	ARTICLE	IF	CITATIONS
1	Interaction of Microbiome, Diet, and Hospitalizations Between Brazilian and American Patients With Cirrhosis. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 930-940.	4.4	7
2	Stool microbiota are superior to saliva in distinguishing cirrhosis and hepatic encephalopathy using machine learning. <i>Journal of Hepatology</i> , 2022, 76, 600-607.	3.7	12
3	Sex is associated with differences in gut microbial composition and function in hepatic encephalopathy. <i>Journal of Hepatology</i> , 2021, 74, 80-88.	3.7	10
4	Interaction of bacterial metagenome and virome in patients with cirrhosis and hepatic encephalopathy. <i>Gut</i> , 2021, 70, 1162-1173.	12.1	53
5	Fecal Microbiota Transplant in Cirrhosis Reduces Gut Microbial Antibiotic Resistance Genes: Analysis of Two Trials. <i>Hepatology Communications</i> , 2021, 5, 258-271.	4.3	41
6	Gut Microbial Signature of Hepatocellular Cancer in Men With Cirrhosis. <i>Liver Transplantation</i> , 2021, 27, 629-640.	2.4	14
7	Impact of Antibiotic Resistance Genes in Gut Microbiome of Patients With Cirrhosis. <i>Gastroenterology</i> , 2021, 161, 508-521.e7.	1.3	33
8	Distinct gut microbial compositional and functional changes associated with impaired inhibitory control in patients with cirrhosis. <i>Gut Microbes</i> , 2021, 13, 1953247.	9.8	16
9	Multiple bacterial virulence factors focused on adherence and biofilm formation associate with outcomes in cirrhosis. <i>Gut Microbes</i> , 2021, 13, 1993584.	9.8	5
10	BiomMiner: An advanced exploratory microbiome analysis and visualization pipeline. <i>PLoS ONE</i> , 2020, 15, e0234860.	2.5	19
11	Human germline and pan-cancer variomes and their distinct functional profiles. <i>Nucleic Acids Research</i> , 2014, 42, 11570-11588.	14.5	22
12	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau022.	3.0	62