

Williams Turpin

List of Publications by Year in Descending Order

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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.

24
papers

1,287
citations

16
h-index

27
g-index

27
ext. papers

1,888
ext. citations

8.3
avg, IF

4.23
L-index

#	Paper	IF	Citations
24	Persistent Diarrhea in Patients With Crohn's Disease After Mucosal Healing Is Associated With Lower Diversity of the Intestinal Microbiome and Increased Dysbiosis. <i>Clinical Gastroenterology and Hepatology</i> , 2021 , 19, 296-304.e3	6.9	9
23	Novel Fecal Biomarkers That Precede Clinical Diagnosis of Ulcerative Colitis. <i>Gastroenterology</i> , 2021 , 160, 1532-1545	13.3	25
22	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
21	Increased Intestinal Permeability Is Associated With Later Development of Crohn's Disease. <i>Gastroenterology</i> , 2020 , 159, 2092-2100.e5	13.3	53
20	Comparison of Co-housing and Littermate Methods for Microbiota Standardization in Mouse Models. <i>Cell Reports</i> , 2019 , 27, 1910-1919.e2	10.6	80
19	Analysis of Genetic Association of Intestinal Permeability in Healthy First-degree Relatives of Patients with Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2019 , 25, 1796-1804	4.5	10
18	Mucosa-Associated Microbiota in Ileoanal Pouches May Contribute to Clinical Symptoms, Particularly Stool Frequency, Independent of Endoscopic Disease Activity. <i>Clinical and Translational Gastroenterology</i> , 2019 , 10, 1-7	4.2	4
17	Nod2 influences microbial resilience and susceptibility to colitis following antibiotic exposure. <i>Mucosal Immunology</i> , 2019 , 12, 720-732	9.2	21
16	Determinants of IBD Heritability: Genes, Bugs, and More. <i>Inflammatory Bowel Diseases</i> , 2018 , 24, 1133-1148	14.8	57
15	FUT2 genotype and secretory status are not associated with fecal microbial composition and inferred function in healthy subjects. <i>Gut Microbes</i> , 2018 , 9, 357-368	8.8	27
14	The genomic and transcriptomic basis of the potential of <i>Lactobacillus plantarum</i> A6 to improve the nutritional quality of a cereal based fermented food. <i>International Journal of Food Microbiology</i> , 2018 , 266, 346-354	5.8	8
13	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
12	Fecal microbiota manipulation prevents dysbiosis and alcohol-induced liver injury in mice. <i>Journal of Hepatology</i> , 2017 , 66, 806-815	13.4	167
11	PCR of crtNM combined with analytical biochemistry: An efficient way to identify carotenoid producing lactic acid bacteria. <i>Systematic and Applied Microbiology</i> , 2016 , 39, 115-21	4.2	7
10	Association of host genome with intestinal microbial composition in a large healthy cohort. <i>Nature Genetics</i> , 2016 , 48, 1413-1417	36.3	257
9	Determinants of intestinal permeability in healthy first-degree relatives of individuals with Crohn's disease. <i>Inflammatory Bowel Diseases</i> , 2015 , 21, 879-87	4.5	38
8	Assessment and Selection of Competing Models for Zero-Inflated Microbiome Data. <i>PLoS ONE</i> , 2015 , 10, e0129606	3.7	93

7	Determination of expression and activity of genes involved in starch metabolism in <i>Lactobacillus plantarum</i> A6 during fermentation of a cereal-based gruel. <i>International Journal of Food Microbiology</i> , 2014 , 185, 103-11	5.8	19
6	Microbiome analysis - from technical advances to biological relevance. <i>F1000prime Reports</i> , 2014 , 6, 51		9
5	Behavior of lactobacilli isolated from fermented slurry (ben-saalga) in gnotobiotic rats. <i>PLoS ONE</i> , 2013 , 8, e57711	3.7	12
4	Lactobacillaceae and cell adhesion: genomic and functional screening. <i>PLoS ONE</i> , 2012 , 7, e38034	3.7	78
3	Genetic screening of functional properties of lactic acid bacteria in a fermented pearl millet slurry and in the metagenome of fermented starchy foods. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8722-34	4.8	93
2	Lactobacilli as multifaceted probiotics with poorly disclosed molecular mechanisms. <i>International Journal of Food Microbiology</i> , 2010 , 143, 87-102	5.8	74
1	Large-scale association analyses identify host factors influencing human gut microbiome composition		9