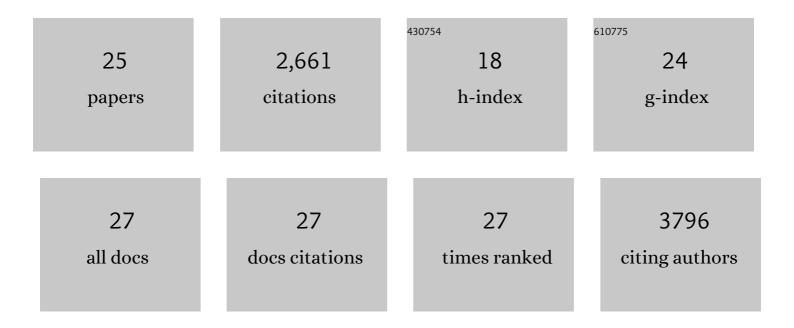
## Williams Turpin

List of Publications by Year in descending order

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WILLIAMS THODIN

#	Article	IF	CITATIONS
1	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
2	Association of host genome with intestinal microbial composition in a large healthy cohort. Nature Genetics, 2016, 48, 1413-1417.	9.4	388
3	Fecal microbiota manipulation prevents dysbiosis and alcohol-induced liver injury in mice. Journal of Hepatology, 2017, 66, 806-815.	1.8	247
4	Increased Intestinal Permeability Is Associated With Later Development of Crohn's Disease. Gastroenterology, 2020, 159, 2092-2100.e5.	0.6	156
5	Assessment and Selection of Competing Models for Zero-Inflated Microbiome Data. PLoS ONE, 2015, 10, e0129606.	1.1	134
6	Comparison of Co-housing and Littermate Methods for Microbiota Standardization in Mouse Models. Cell Reports, 2019, 27, 1910-1919.e2.	2.9	134
7	Genetic Screening of Functional Properties of Lactic Acid Bacteria in a Fermented Pearl Millet Slurry and in the Metagenome of Fermented Starchy Foods. Applied and Environmental Microbiology, 2011, 77, 8722-8734.	1.4	129
8	Determinants of IBD Heritability: Genes, Bugs, and More. Inflammatory Bowel Diseases, 2018, 24, 1133-1148.	0.9	122
9	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. Microbiome, 2018, 6, 101.	4.9	109
10	Lactobacillaceae and Cell Adhesion: Genomic and Functional Screening. PLoS ONE, 2012, 7, e38034.	1.1	99
11	Novel Fecal Biomarkers That Precede Clinical Diagnosis of Ulcerative Colitis. Gastroenterology, 2021, 160, 1532-1545.	0.6	94
12	Lactobacilli as multifaceted probiotics with poorly disclosed molecular mechanisms. International Journal of Food Microbiology, 2010, 143, 87-102.	2.1	91
13	Determinants of Intestinal Permeability in Healthy First-Degree Relatives of Individuals with Crohn's Disease. Inflammatory Bowel Diseases, 2015, 21, 879-887.	0.9	49
14	Mediterranean-Like Dietary Pattern Associations With Gut Microbiome Composition and Subclinical Gastrointestinal Inflammation. Gastroenterology, 2022, 163, 685-698.	0.6	37
15	FUT2 genotype and secretory status are not associated with fecal microbial composition and inferred function in healthy subjects. Gut Microbes, 2018, 9, 1-12.	4.3	33
16	Nod2 influences microbial resilience and susceptibility to colitis following antibiotic exposure. Mucosal Immunology, 2019, 12, 720-732.	2.7	31
17	Determination of expression and activity of genes involved in starch metabolism in Lactobacillus plantarum A6 during fermentation of a cereal-based gruel. International Journal of Food Microbiology, 2014, 185, 103-111.	2.1	22
18	Analysis of Genetic Association of Intestinal Permeability in Healthy First-degree Relatives of Patients with Crohn's Disease. Inflammatory Bowel Diseases, 2019, 25, 1796-1804.	0.9	21

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#	Article	IF	CITATIONS
19	Persistent Diarrhea in Patients With Crohn's Disease After Mucosal Healing Is Associated With Lower Diversity of the Intestinal Microbiome and Increased Dysbiosis. Clinical Gastroenterology and Hepatology, 2021, 19, 296-304.e3.	2.4	19
20	PCR of crtNM combined with analytical biochemistry: An efficient way to identify carotenoid producing lactic acid bacteria. Systematic and Applied Microbiology, 2016, 39, 115-121.	1.2	15
21	Behavior of Lactobacilli Isolated from Fermented Slurry (ben-saalga) in Gnotobiotic Rats. PLoS ONE, 2013, 8, e57711.	1.1	15
22	The genomic and transcriptomic basis of the potential of Lactobacillus plantarum A6 to improve the nutritional quality of a cereal based fermented food. International Journal of Food Microbiology, 2018, 266, 346-354.	2.1	10
23	Mucosa-Associated Microbiota in Ileoanal Pouches May Contribute to Clinical Symptoms, Particularly Stool Frequency, Independent of Endoscopic Disease Activity. Clinical and Translational Gastroenterology, 2019, 10, e00038.	1.3	9
24	Microbiome analysis – from technical advances to biological relevance. F1000prime Reports, 2014, 6, 51.	5.9	9
25	Too much hygiene: CD in later life?. , 0, , .		0