

# Floris Imhann

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/133506/publications.pdf>

Version: 2024-02-01

22  
papers

6,981  
citations

393982

19  
h-index

610482

24  
g-index

25  
all docs

25  
docs citations

25  
times ranked

11270  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.   | 6.0 | 1,398     |
| 2  | Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.   | 5.9 | 1,094     |
| 3  | Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , 2016, 65, 740-748.   | 6.1 | 885       |
| 4  | The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016, 48, 1407-1412.  | 9.4 | 672       |
| 5  | Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , 2018, 67, 108-119.                           | 6.1 | 590       |
| 6  | The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. <i>Circulation Research</i> , 2015, 117, 817-824.  | 2.0 | 534       |
| 7  | Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. <i>Nature Communications</i> , 2020, 11, 362.  | 5.8 | 416       |
| 8  | Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .                     | 5.8 | 351       |
| 9  | Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.  | 3.6 | 322       |
| 10 | Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021, 70, 1287-1298.                               | 6.1 | 246       |
| 11 | Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019, 10, 358-366.   | 4.3 | 118       |
| 12 | The 1000IBD project: multi-omics data of 1000 inflammatory bowel disease patients; data release 1. <i>BMC Gastroenterology</i> , 2019, 19, 5.   | 0.8 | 68        |
| 13 | MOLGENIS research: advanced bioinformatics data software for non-bioinformaticians. <i>Bioinformatics</i> , 2019, 35, 1076-1078.  | 1.8 | 58        |
| 14 | Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 1439-1449.                             | 0.6 | 39        |
| 15 | Cohort profile: design and first results of the Dutch IBD Biobank: a prospective, nationwide biobank of patients with inflammatory bowel disease. <i>BMJ Open</i> , 2017, 7, e016695. | 0.8 | 33        |
| 16 | Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD. <i>Gut</i> , 2021, 70, gutjnl-2019-319706.   | 6.1 | 26        |
| 17 | Habitual dietary intake of IBD patients differs from population controls: a case-control study. <i>European Journal of Nutrition</i> , 2021, 60, 345-356.                             | 1.8 | 22        |
| 18 | Pooled Resequencing of 122 Ulcerative Colitis Genes in a Large Dutch Cohort Suggests Population-Specific Associations of Rare Variants in MUC2. <i>PLoS ONE</i> , 2016, 11, e0159609. | 1.1 | 21        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | HSPA6 is an ulcerative colitis susceptibility factor that is induced by cigarette smoke and protects intestinal epithelial cells by stabilizing anti-apoptotic Bcl-XL. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 788-796. | 1.8 | 16        |
| 20 | Genomic and Expression Analyses Identify a Disease-Modifying Variant for Fibrostenotic Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2018, 12, 582-588.  | 0.6 | 16        |
| 21 | SLC39A8 missense variant is associated with Crohn's disease but does not have a major impact on gut microbiome composition in healthy subjects. <i>PLoS ONE</i> , 2019, 14, e0211328.   | 1.1 | 10        |
| 22 | Patient attitudes towards faecal sampling for gut microbiome studies and clinical care reveal positive engagement and room for improvement. <i>PLoS ONE</i> , 2021, 16, e0249405.   | 1.1 | 4         |