

# Marc Jan Bonder

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/6429990/marc-jan-bonder-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

78  
papers

9,054  
citations

43  
h-index

90  
g-index

90  
ext. papers

12,858  
ext. citations

18.4  
avg, IF

5.39  
L-index

#	Paper	IF	Citations
78	Population-level analysis of gut microbiome variation. <i>Science</i> , <b>2016</b> , 352, 560-4	33.3	1120
77	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , <b>2016</b> , 352, 565-9	33.3	929
76	Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , <b>2016</b> , 65, 740-8	19.2	575
75	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , <b>2017</b> , 541, 81-86	50.4	511
74	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , <b>2016</b> , 167, 1125-1136	36.3	434
73	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , <b>2016</b> , 48, 1407-1412	36.3	434
72	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. <i>Circulation Research</i> , <b>2015</b> , 117, 817-24	15.7	368
71	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , <b>2018</b> , 67, 108-119	19.2	368
70	Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002197	6	261
69	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , <b>2017</b> , 49, 131-138	36.3	252
68	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , <b>2017</b> , 49, 139-145	36.3	240
67	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , <b>2015</b> , 47, 1282-1293	36.3	223
66	Multi-tissue DNA methylation age predictor in mouse. <i>Genome Biology</i> , <b>2017</b> , 18, 68	18.3	220
65	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , <b>2016</b> , 48, 1462-1472	36.3	198
64	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
63	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	159
62	The influence of a short-term gluten-free diet on the human gut microbiome. <i>Genome Medicine</i> , <b>2016</b> , 8, 45	14.4	135

61	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , <b>2018</b> , 6, 379-388	35.1	119
60	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , <b>2016</b> , 17, 138	18.3	118
59	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , <b>2021</b> , 372,	33.3	100
58	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. <i>BMC Genomics</i> , <b>2014</b> , 15, 860	4.5	90
57	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. <i>Gut Microbes</i> , <b>2017</b> , 8, 351-358	8.8	87
56	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 75-85	11	85
55	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 888-902	11	83
54	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , <b>2016</b> , 17, 191	18.3	80
53	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , <b>2021</b> , 53, 156-165	36.3	80
52	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , <b>2019</b> , 124, 1808-1820	15.7	77
51	Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. <i>Nature Communications</i> , <b>2019</b> , 10, 4361	17.4	76
50	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , <b>2020</b> , 11, 810	17.4	76
49	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. <i>BMC Research Notes</i> , <b>2014</b> , 7, 901	2.3	74
48	Gut microbiota composition associated with stool consistency. <i>Gut</i> , <b>2016</b> , 65, 540-2	19.2	72
47	The single-cell eQTLGen consortium. <i>ELife</i> , <b>2020</b> , 9,	8.9	68
46	Comparing clustering and pre-processing in taxonomy analysis. <i>Bioinformatics</i> , <b>2012</b> , 28, 2891-7	7.2	65
45	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , <b>2019</b> , 10, 358-366	8.8	65
44	DNA methylation markers associated with type 2 diabetes, fasting glucose and HbA levels: a systematic review and replication in a case-control sample of the Lifelines study. <i>Diabetologia</i> , <b>2018</b> , 61, 354-368	10.3	64

43	A linear mixed-model approach to study multivariate gene-environment interactions. <i>Nature Genetics</i> , <b>2019</b> , 51, 180-186	36.3	63
42	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , <b>2021</b> , 53, 1300-1310	36.3	60
41	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , <b>2018</b> , 50, 1524-1532	36.3	54
40	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , <b>2018</b> , 6, 101	16.6	53
39	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , <b>2017</b> , 22, 1680-1690	15.1	46
38	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. <i>Genome Medicine</i> , <b>2015</b> , 7, 30	14.4	45
37	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , <b>2016</b> , 68, 62-74	15.5	44
36	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , <b>2021</b> , 53, 304-312	36.3	37
35	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. <i>Genome Biology</i> , <b>2019</b> , 20, 30	18.3	36
34	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. <i>Genome Biology</i> , <b>2019</b> , 20, 146	18.3	36
33	Tobacco smoking is associated with DNA methylation of diabetes susceptibility genes. <i>Diabetologia</i> , <b>2016</b> , 59, 998-1006	10.3	33
32	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , <b>2017</b> , 18, 25	4.5	32
31	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , <b>2018</b> , 6, e4303	3.1	28
30	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , <b>2019</b> , 86, 599-607	7.9	24
29	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. <i>Nature Communications</i> , <b>2020</b> , 11, 2927	17.4	22
28	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , <b>2020</b> , 17, 414-421	21.6	17
27	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , <b>2020</b> , 9,	8.9	16
26	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. <i>Nature Genetics</i> , <b>2021</b> , 53, 313-321	36.3	16

25	A locus at 7p14.3 predisposes to refractory celiac disease progression from celiac disease. <i>European Journal of Gastroenterology and Hepatology</i> , <b>2018</b> , 30, 828-837	2.2	16
24	DNA methylation signatures of educational attainment. <i>Npj Science of Learning</i> , <b>2018</b> , 3, 7	6	14
23	A GWAS meta-analysis suggests roles for xenobiotic metabolism and ion channel activity in the biology of stool frequency. <i>Gut</i> , <b>2017</b> , 66, 756-758	19.2	12
22	Cardelino: Integrating whole exomes and single-cell transcriptomes to reveal phenotypic impact of somatic variants		12
21	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression		12
20	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. <i>Nature Communications</i> , <b>2020</b> , 11, 2928	17.4	11
19	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , <b>2020</b> , 21, 220	18.3	10
18	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation		9
17	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
16	Systematic assessment of regulatory effects of human disease variants in pluripotent cells		9
15	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , <b>2017</b> , 12, e0182472	3.7	8
14	A linear mixed model approach to study multivariate gene-environment interactions		8
13	Hypothesis-free identification of modulators of genetic risk factors		7
12	Optimizing expression quantitative trait locus mapping workflows for single-cell studies. <i>Genome Biology</i> , <b>2021</b> , 22, 188	18.3	7
11	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2148-2162	15.1	7
10	Disease variants alter transcription factor levels and methylation of their binding sites		6
9	Breast cancer subtype specific classifiers of response to neoadjuvant chemotherapy do not outperform classifiers trained on all subtypes. <i>PLoS ONE</i> , <b>2014</b> , 9, e88551	3.7	5
8	Evidence for mitochondrial genetic control of autosomal gene expression. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 5332-5338	5.6	4

7	Genomic properties of structural variants and short tandem repeats that impact gene expression and complex traits in humans	3
6	De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation	3
5	Optimising expression quantitative trait locus mapping workflows for single-cell studies	3
4	Discovery and Quality Analysis of a Comprehensive Set of Structural Variants and Short Tandem Repeats	2
3	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses.. <i>Nature Communications</i> , <b>2022</b> , 13, 1779	17.4 2
2	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity	
1	DNA methylation in peripheral tissues and left-handedness.. <i>Scientific Reports</i> , <b>2022</b> , 12, 5606	4.9 0