

Marc Jan Bonder

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6429990/publications.pdf>

Version: 2024-02-01

65
papers

15,765
citations

53751

45
h-index

95218

68
g-index

90
all docs

90
docs citations

90
times ranked

26375
citing authors

#	ARTICLE	IF	CITATIONS
1	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
2	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
3	Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , 2016, 65, 740-748.	6.1	885
4	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	13.5	806
5	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
6	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
7	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016, 48, 1407-1412.	9.4	672
8	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
9	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	9.4	590
10	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
11	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017, 49, 131-138.	9.4	390
12	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017, 49, 139-145.	9.4	363
13	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	6.0	358
14	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	351
15	Multi-tissue DNA methylation age predictor in mouse. <i>Genome Biology</i> , 2017, 18, 68.	3.8	341
16	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> , 2011, 7, e1002197.	1.5	324
17	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	9.4	294
18	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284

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19	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020, 11, 810.	5.8	235
20	The influence of a short-term gluten-free diet on the human gut microbiome. <i>Genome Medicine</i> , 2016, 8, 45.	3.6	198
21	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , 2018, 6, 379-388.	5.2	170
22	Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. <i>Nature Communications</i> , 2019, 10, 4361.	5.8	157
23	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016, 17, 138.	3.8	154
24	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
25	The single-cell eQTLGen consortium. <i>ELife</i> , 2020, 9, .	2.8	150
26	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , 2021, 53, 304-312.	9.4	146
27	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019, 124, 1808-1820.	2.0	137
28	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. <i>Gut Microbes</i> , 2017, 8, 351-358.	4.3	136
29	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. <i>BMC Genomics</i> , 2014, 15, 860.	1.2	124
30	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. <i>BMC Research Notes</i> , 2014, 7, 901.	0.6	122
31	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016, 17, 191.	3.8	120
32	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019, 10, 358-366.	4.3	118
33	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	2.6	116
34	A linear mixed-model approach to study multivariate gene-environment interactions. <i>Nature Genetics</i> , 2019, 51, 180-186.	9.4	112
35	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	109
36	DNA methylation markers associated with type 2 diabetes, fasting glucose and HbA1c levels: a systematic review and replication in a case-control sample of the Lifelines study. <i>Diabetologia</i> , 2018, 61, 354-368.	2.9	105

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37	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	9.4	97
38	Gut microbiota composition associated with stool consistency. <i>Gut</i> , 2016, 65, 540-542.	6.1	95
39	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. <i>Genome Medicine</i> , 2015, 7, 30.	3.6	91
40	Comparing clustering and pre-processing in taxonomy analysis. <i>Bioinformatics</i> , 2012, 28, 2891-2897.	1.8	76
41	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , 2017, 22, 1680-1690.	4.1	70
42	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. <i>Nature Communications</i> , 2020, 11, 2927.	5.8	67
43	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. <i>Genome Biology</i> , 2019, 20, 146.	3.8	66
44	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016, 68, 62-74.	3.0	64
45	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. <i>Genome Biology</i> , 2019, 20, 30.	3.8	61
46	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , 2017, 18, 25.	1.2	49
47	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020, 17, 414-421.	9.0	48
48	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	48
49	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	0.7	47
50	Tobacco smoking is associated with DNA methylation of diabetes susceptibility genes. <i>Diabetologia</i> , 2016, 59, 998-1006.	2.9	43
51	DNA methylation signatures of educational attainment. <i>Npj Science of Learning</i> , 2018, 3, 7.	1.5	42
52	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. <i>Nature Genetics</i> , 2021, 53, 313-321.	9.4	42
53	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	2.8	40
54	Optimizing expression quantitative trait locus mapping workflows for single-cell studies. <i>Genome Biology</i> , 2021, 22, 188.	3.8	36

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55	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020, 21, 220.	3.8	27
56	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. <i>Nature Communications</i> , 2022, 13, 1779.	5.8	25
57	Genetic, parental and lifestyle factors influence telomere length. <i>Communications Biology</i> , 2022, 5, .	2.0	23
58	A locus at 7p14.3 predisposes to refractory celiac disease progression from celiac disease. <i>European Journal of Gastroenterology and Hepatology</i> , 2018, 30, 828-837.	0.8	22
59	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. <i>Nature Communications</i> , 2020, 11, 2928.	5.8	22
60	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021, 26, 2148-2162.	4.1	21
61	A GWAS meta-analysis suggests roles for xenobiotic metabolism and ion channel activity in the biology of stool frequency. <i>Gut</i> , 2017, 66, 756-758.	6.1	14
62	DNA methylation in peripheral tissues and left-handedness. <i>Scientific Reports</i> , 2022, 12, 5606.	1.6	12
63	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	1.1	10
64	Breast Cancer Subtype Specific Classifiers of Response to Neoadjuvant Chemotherapy Do Not Outperform Classifiers Trained on All Subtypes. <i>PLoS ONE</i> , 2014, 9, e88551.	1.1	8
65	Evidence for mitochondrial genetic control of autosomal gene expression. <i>Human Molecular Genetics</i> , 2016, 25, ddw347.	1.4	6