

Harm-Jan Westra

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/975562/harm-jan-westra-publications-by-year.pdf>
Version: 2024-04-10

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.

83 papers	18,799 citations	49 h-index	96 g-index
96 ext. papers	24,179 ext. citations	20.5 avg, IF	4.87 L-index

#	Paper	IF	Citations
83	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. <i>Nature Communications</i> , 2022 , 13,	17.4	2
82	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021 , 53, 1636-1648	36.3	19
81	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
80	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021 , 596, E1-E3	50.4	1
79	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	36.3	60
78	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. <i>Biological Psychiatry</i> , 2020 , 88, 470-479	7.9	6
77	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020 , 2, 1135-1148	14.6	61
76	An epigenome-wide association study identifies multiple DNA methylation markers of exposure to endocrine disruptors. <i>Environment International</i> , 2020 , 144, 106016	12.9	6
75	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <i>Nature Communications</i> , 2020 , 11, 4930	17.4	8
74	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response. <i>PLoS Pathogens</i> , 2020 , 16, e1008408	7.6	11
73	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
72	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
71	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
70	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
69	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
68	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , 2019 , 104, 879-895	11	21
67	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39

66	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. <i>Nature Genetics</i> , 2018 , 50, 1180-1188	36.3	14
65	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018 , 10, 96	14.4	19
64	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , 2018 , 19, 168	18.3	19
63	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. <i>Nature Genetics</i> , 2018 , 50, 1366-1374	36.3	82
62	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
61	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , 2017 , 13, e1006643	6	75
60	reGenotyper: Detecting mislabeled samples in genetic data. <i>PLoS ONE</i> , 2017 , 12, e0171324	3.7	13
59	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
58	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
57	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5	90
56	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016 , 48, 510-8	36.3	404
55	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
54	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
53	Gene expression analysis identifies global gene dosage sensitivity in cancer. <i>Nature Genetics</i> , 2015 , 47, 115-25	36.3	219
52	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015 , 6, 5890	17.4	489
51	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
50	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015 , 47, 979-986	36.3	1278
49	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229

48	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
47	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. <i>Human Molecular Genetics</i> , 2015 , 24, 397-409	5.6	43
46	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
45	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. <i>American Journal of Human Genetics</i> , 2015 , 97, 139-52	11	94
44	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. <i>Genome Medicine</i> , 2015 , 7, 105	14.4	26
43	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
42	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015 , 6, 7208	17.4	126
41	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 556-8	11.5	3
40	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
39	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
38	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 1486-93.e8	11.5	19
37	Detection and replication of epistasis influencing transcription in humans. <i>Nature</i> , 2014 , 508, 249-53	50.4	149
36	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014 , 506, 376-81	50.4	1426
35	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014 , 5, 4926	17.4	121
34	Correlation of genetic risk and messenger RNA expression in a Th17/IL23 pathway analysis in inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2014 , 20, 777-82	4.5	16
33	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
32	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014 , 46, 901-4	36.3	75
31	From genome to function by studying eQTLs. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014 , 1842, 1896-1902	6.9	95

30	Improved imputation quality of low-frequency and rare variants in European samples using the Genome of The NetherlandsV <i>European Journal of Human Genetics</i> , 2014 , 22, 1321-6	5.3	74
29	Mediation analysis demonstrates that trans-eQTLs are often explained by cis-mediation: a genome-wide analysis among 1,800 South Asians. <i>PLoS Genetics</i> , 2014 , 10, e1004818	6	56
28	Hemani et al. reply. <i>Nature</i> , 2014 , 514, E5-6	50.4	8
27	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. <i>BMC Research Notes</i> , 2014 , 7, 901	2.3	74
26	Copper metabolism domain-containing 1 represses genes that promote inflammation and protects mice from colitis and colitis-associated cancer. <i>Gastroenterology</i> , 2014 , 147, 184-195.e3	13.3	24
25	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. <i>Human Molecular Genetics</i> , 2014 , 23, 2481-9	5.6	23
24	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013 , 45, 1238-1243	36.3	1244
23	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013 , 45, 542-545	36.3	77
22	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
21	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563
20	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003201	6	209
19	DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. <i>PLoS Genetics</i> , 2013 , 9, e1003594	6	32
18	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. <i>Nature Genetics</i> , 2012 , 44, 1336-40	36.3	436
17	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257
16	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. <i>American Journal of Human Genetics</i> , 2012 , 91, 744-53	11	58
15	Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression. <i>PLoS Genetics</i> , 2012 , 8, e1002431	6	163
14	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. <i>Nature Genetics</i> , 2011 , 43, 246-52	36.3	1028
13	Blood pressure loci identified with a gene-centric array. <i>American Journal of Human Genetics</i> , 2011 , 89, 688-700	11	137

12	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL, and CARD9. <i>Hepatology</i> , 2011 , 53, 1977-85	11.2	96
11	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. <i>Human Molecular Genetics</i> , 2011 , 20, 4748-57	5.6	13
10	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. <i>Bioinformatics</i> , 2011 , 27, 2104-11	7.2	60
9	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. <i>PLoS Genetics</i> , 2011 , 7, e1002004	6	260
8	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	6	261
7	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors		1
6	Discovering in vivo cytokine eQTL interactions from a lupus clinical trial		3
5	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
4	Genomic evaluation of circulating proteins for drug target characterisation and precision medicine		5
3	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
2	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
1	Brain expression quantitative trait locus and network analysis reveals downstream effects and putative drivers for brain-related diseases		4