

Harm-Jan Westra

List of Publications by Citations

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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	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
82	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014 , 506, 376-81	50.4	1426
81	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
80	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
79	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013 , 45, 1238-1243	36.3	1244
78	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
77	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
76	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
75	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
74	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563
73	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015 , 6, 5890	17.4	489
72	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. <i>Nature Genetics</i> , 2012 , 44, 1336-40	36.3	436
71	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
70	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
69	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
68	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
67	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257

66	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
65	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
64	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
63	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
62	Gene expression analysis identifies global gene dosage sensitivity in cancer. <i>Nature Genetics</i> , 2015 , 47, 115-25	36.3	219
61	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
60	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003201	6	209
59	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
58	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
57	Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression. <i>PLoS Genetics</i> , 2012 , 8, e1002431	6	163
56	Detection and replication of epistasis influencing transcription in humans. <i>Nature</i> , 2014 , 508, 249-53	50.4	149
55	Blood pressure loci identified with a gene-centric array. <i>American Journal of Human Genetics</i> , 2011 , 89, 688-700	11	137
54	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
53	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014 , 5, 4926	17.4	121
52	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
51	From genome to function by studying eQTLs. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014 , 1842, 1896-1902	6.9	95
50	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
49	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

48	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
47	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
46	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
45	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013 , 45, 542-545	36.3	77
44	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
43	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
42	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014 , 46, 901-4	36.3	75
41	Improved imputation quality of low-frequency and rare variants in European samples using the Genome of The Netherlands. <i>European Journal of Human Genetics</i> , 2014 , 22, 1321-6	5.3	74
40	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. <i>BMC Research Notes</i> , 2014 , 7, 901	2.3	74
39	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020 , 2, 1135-1148	14.6	61
38	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
37	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
36	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
35	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
34	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
33	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
32	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
31	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. <i>Genome Medicine</i> , 2015 , 7, 105	14.4	26

30	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
29	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
28	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
27	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
26	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
25	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018 , 10, 96	14.4	19
24	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , 2018 , 19, 168	18.3	19
23	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
22	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. <i>Nature Genetics</i> , 2018 , 50, 1180-1188	36.3	14
21	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
20	reGenotyper: Detecting mislabeled samples in genetic data. <i>PLoS ONE</i> , 2017 , 12, e0171324	3.7	13
19	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
18	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
17	Hemani et al. reply. <i>Nature</i> , 2014 , 514, E5-6	50.4	8
16	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
15	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
14	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
13	Genomic evaluation of circulating proteins for drug target characterisation and precision medicine		5

12	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
11	Brain expression quantitative trait locus and network analysis reveals downstream effects and putative drivers for brain-related diseases		4
10	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
9	Discovering in vivo cytokine eQTL interactions from a lupus clinical trial		3
8	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
7	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors		1
6	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021 , 596, E1-E3	50.4	1
5	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
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2	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		
1	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response 2020 , 16, e1008408		