Harm-Jan Westra

List of Publications by Year
in descending order

76	27,683	36303 51	74163 75
papers	citations	h-index	g-index

96	96	96	39322
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
3	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	21.4	1,965
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
5	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
6	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
7	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
8	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	21.4	1,201
9	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
10	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
11	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
12	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
13	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
14	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
15	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	21.4	558
16	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
17	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
18	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362

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19	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
20	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	11.9	327
21	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	3.5	324
22	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
23	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	21.4	313
24	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
25	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	3.5	307
26	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
27	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	3.5	247
28	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
29	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
30	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	3.5	194
31	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
32	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
33	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
34	From genome to function by studying eQTLs. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1896-1902.	3.8	137
35	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	1.4	122
36	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	6.2	122

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37	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. Nature Genetics, 2018, 50, 1366-1374.	21.4	122
38	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115
39	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
40	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL , and CARD9. Hepatology, 2011, 53, 1977-1985.	7.3	110
41	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
42	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. PLoS Genetics, 2017, 13, e1006643.	3.5	110
43	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	21.4	104
44	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	21.4	96
45	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
46	Mediation Analysis Demonstrates That Trans-eQTLs Are Often Explained by Cis-Mediation: A Genome-Wide Analysis among 1,800 South Asians. PLoS Genetics, 2014, 10, e1004818.	3.5	88
47	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	4.1	81
48	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
49	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
50	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. Human Molecular Genetics, 2015, 24, 397-409.	2.9	54
51	An integrative approach for building personalized gene regulatory networks for precision medicine. Genome Medicine, 2018, 10, 96.	8.2	49
52	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. American Journal of Human Genetics, 2019, 104, 879-895.	6.2	49
53	DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. PLoS Genetics, 2013, 9, e1003594.	3.5	45
54	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. Nature Communications, 2022, 13, .	12.8	39

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55	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. Genome Biology, 2018, 19, 168.	8.8	36
56	Copper Metabolism Domain-Containing 1 Represses Genes That Promote Inflammation and Protects Mice From Colitis and Colitis-Associated Cancer. Gastroenterology, 2014, 147, 184-195.e3.	1.3	33
57	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
58	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. Nature Genetics, 2018, 50, 1180-1188.	21.4	31
59	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. Genome Medicine, 2015, 7, 105.	8.2	30
60	reGenotyper: Detecting mislabeled samples in genetic data. PLoS ONE, 2017, 12, e0171324.	2.5	25
61	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. Journal of Allergy and Clinical Immunology, 2015, 135, 1486-1493.e8.	2.9	24
62	An epigenome-wide association study identifies multiple DNA methylation markers of exposure to endocrine disruptors. Environment International, 2020, 144, 106016.	10.0	21
63	Correlation of Genetic Risk and Messenger RNA Expression in a Th17/IL23 Pathway Analysis in Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2014, 20, 777-782.	1.9	20
64	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. Nature Communications, 2020, 11, 4930.	12.8	20
65	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response. PLoS Pathogens, 2020, 16, e1008408.	4.7	18
66	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	27.8	16
67	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. Biological Psychiatry, 2020, 88, 470-479.	1.3	14
68	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. Human Molecular Genetics, 2011, 20, 4748-4757.	2.9	13
69	Hemani et al. reply. Nature, 2014, 514, E5-E6.	27.8	12
70	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. Journal of Allergy and Clinical Immunology, 2015, 135, 556-558.e13.	2.9	4
71	FC 011KIDNEYNETWORK: USING KIDNEY DERIVED GENE EXPRESSION DATA TO PREDICT AND PRIORITIZE NOVEL GENES INVOLVED IN KIDNEY DISEASE. Nephrology Dialysis Transplantation, 2021, 36, .	0.7	0
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73	Title is missing!. , 2020, 16, e1008408.		0
74	Title is missing!. , 2020, 16, e1008408.		0
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