Jeroen R Huyghe

List of Publications by Year
in descending order

67 papers	5,551 citations	117625 34 h-index	98798 67 g-index
71 all docs	71 docs citations	71 times ranked	11955 citing authors

#	Article	IF	Citations
1	Large-scale Integrated Analysis of Genetics and Metabolomic Data Reveals Potential Links Between Lipids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1216-1226.	2.5	3
2	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	2.5	6
3	Genetic Regulation of DNA Methylation Yields Novel Discoveries in GWAS of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1068-1076.	2.5	1
4	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	6.3	0
5	Association between germline variants and somatic mutations in colorectal cancer. Scientific Reports, 2022, 12, .	3.3	1
6	A Statistical Method for Association Analysis of Cell Type Compositions. Statistics in Biosciences, 2021, 13, 373-385.	1.2	0
7	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	1.3	36
8	Genetic Predictors of Severe Skin Toxicity in Patients with Stage III Colon Cancer Treated with Cetuximab: NCCTG N0147 (Alliance). Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 404-411.	2.5	1
9	Ethanol exposure drives colon location specific cell composition changes in a normal colon crypt 3D organoid model. Scientific Reports, 2021, 11, 432.	3.3	14
10	Genetic Effects on Transcriptome Profiles in Colon Epithelium Provide Functional Insights for Genetic Risk Loci. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 181-197.	4.5	18
11	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	12.1	44
12	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	6.2	5
13	Assessment of a Polygenic Risk Score for Colorectal Cancer to Predict Risk of Lynch Syndrome Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkab022.	2.9	15
14	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.7	6
15	DNA repair and cancer in colon and rectum: Novel players in genetic susceptibility. International Journal of Cancer, 2020, 146, 363-372.	5.1	40
16	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
17	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. Gastroenterology, 2020, 158, 1300-1312.e20.	1.3	90
18	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	2.5	25

#	Article	IF	Citations
19	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	12.8	55
20	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
21	Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. BMC Medicine, 2020, 18, 229.	5.5	28
22	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. PLoS Genetics, 2020, 16, e1008947.	3.5	6
23	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396.	5.5	76
24	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	12.8	193
25	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
26	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
27	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	3.8	44
28	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
29	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	9.4	367
30	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. Human Molecular Genetics, 2018, 27, 1664-1674.	2.9	30
31	Determining Risk of Colorectal Cancer and Starting Age of Screening Based on Lifestyle, Environmental, and Genetic Factors. Gastroenterology, 2018, 154, 2152-2164.e19.	1.3	226
32	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	6.2	47
33	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomics. American Journal of Human Genetics, 2018, 102, 904-919.	6.2	30
34	One-carbon metabolism biomarkers and genetic variants in relation to colorectal cancer risk by KRAS and BRAF mutation status. PLoS ONE, 2018, 13, e0196233.	2.5	9
35	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
36	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	2.5	48

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37	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
38	Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data. PLoS ONE, 2017, 12, e0186518.	2.5	8
39	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	3.5	49
40	Heterozygous Loss-of-Function SEC61A1 Mutations Cause Autosomal-Dominant Tubulo-Interstitial and Glomerulocystic Kidney Disease with Anemia. American Journal of Human Genetics, 2016, 99, 174-187.	6.2	124
41	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
42	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114
43	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
44	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
45	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	6.2	49
46	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
47	A Common Functional Regulatory Variant at a Type 2 Diabetes Locus Upregulates ARAP1 Expression in the Pancreatic Beta Cell. American Journal of Human Genetics, 2014, 94, 186-197.	6.2	67
48	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
49	Congenital cataracts: de novo gene conversion event in CRYBB2. Molecular Vision, 2014, 20, 1579-93.	1.1	10
50	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nature Genetics, 2013, 45, 197-201.	21.4	247
51	Familial Aggregation of Pure Tone Hearing Thresholds in an Aging European Population. Otology and Neurotology, 2013, 34, 838-844.	1.3	15
52	Autosomal Dominant Diabetes Arising From a Wolfram Syndrome 1 Mutation. Diabetes, 2013, 62, 3943-3950.	0.6	100
53	Possible implication of NFKB1A and NKG2D genes in susceptibility to HTLVâ€1â€associated myelopathy/tropical spastic paraparesis in Peruvian patients infected with HTLVâ€1. Journal of Medical Virology, 2012, 84, 319-326.	5.0	10
54	Genetic signature of population fragmentation varies with mobility in seven bird species of a fragmented Kenyan cloud forest. Molecular Ecology, 2011, 20, 1829-1844.	3.9	88

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55	A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies. European Journal of Human Genetics, 2011, 19, 347-352.	2.8	19
56	Evaluation of host genetic and viral factors as surrogate markers for HTLVâ€1â€associated myelopathy/tropical spastic paraparesis in Peruvian HTLVâ€1â€infected patients. Journal of Medical Virology, 2010, 82, 460-466.	5.0	16
57	A genome-wide association study for age-related hearing impairment in the Saami. European Journal of Human Genetics, 2010, 18, 685-693.	2.8	88
58	Heritability of audiometric shape parameters and familial aggregation of presbycusis in an elderly Flemish population. Hearing Research, 2010, 265, 1-10.	2.0	18
59	Role of killer cell immunoglobulin-like receptor gene content and human leukocyte antigenâ€“C group in susceptibility to human T-lymphotropic virus 1â€“associated myelopathy/tropical spastic paraparesis in Peru. Human Immunology, 2010, 71, 804-808.	2.4	4
60	Genome-wide SNP analysis reveals no gain in power for association studies of common variants in the Finnish Saami. European Journal of Human Genetics, 2010, 18, 569-574.	2.8	3
61	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	2.9	174
62	Variations in HSP70 genes associated with noise-induced hearing loss in two independent populations. European Journal of Human Genetics, 2009, 17, 329-335.	2.8	78
63	Association of Bone Morphogenetic Proteins With Otosclerosis. Journal of Bone and Mineral Research, 2008, 23, 507-516.	2.8	58
64	Occupational Noise, Smoking, and a High Body Mass Index are Risk Factors for Age-related Hearing Impairment and Moderate Alcohol Consumption is Protective: A European Population-based Multicenter Study. JARO - Journal of the Association for Research in Otolaryngology, 2008, 9, 264-276.	1.8	214
65	Genome-wide SNP-Based Linkage Scan Identifies a Locus on 8q24 for an Age-Related Hearing Impairment Trait. American Journal of Human Genetics, 2008, 83, 401-407.	6.2	54
66	The grainyhead like 2 gene (GRHL2), alias TFCP2L3, is associated with age-related hearing impairment. Human Molecular Genetics, 2008, 17, 159-169.	2.9	121
67	Association between variations in CAT and noise-induced hearing loss in two independent noise-exposed populations. Human Molecular Genetics, 2007, 16, 1872-1883.	2.9	85