Hugues Aschard

List of Publications by Year
in descending order

80 papers	5,797 citations	126907 33 h-index	91884 69 g-index
102 all docs	102 docs citations	102 times ranked	12478 citing authors

#	Article	IF	Citations
1	Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. American Journal of Human Genetics, 2022, 109, 12-23.	6.2	136
2	Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739.	2.8	11
3	Statin Use in Relation to Intraocular Pressure, Glaucoma, and Ocular Coherence Tomography Parameters in the UK Biobank. , 2022, 63, 31.		7
4	Fitting Gaussian mixture models on incomplete data. BMC Bioinformatics, 2022, 23, .	2.6	2
5	Intraocular Pressure, Glaucoma, and Dietary Caffeine Consumption. Ophthalmology, 2021, 128, 866-876.	5.2	35
6	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
7	Estimating the effective sample size in association studies of quantitative traits. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	12
8	Genetic meta-analysis of cancer diagnosis following statin use identifies new associations and implicates human leukocyte antigen (HLA) in women. Pharmacogenomics Journal, 2021, 21, 446-457.	2.0	4
9	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
10	Multitrait GWAS to connect disease variants and biological mechanisms. PLoS Genetics, 2021, 17, e1009713.	3.5	16
11	Powerful gene-based testing by integrating long-range chromatin interactions and knockoff genotypes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
12	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
13	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. European Journal of Human Genetics, 2020, 28, 656-668.	2.8	7
14	Ultrarare heterozygous pathogenic variants of genes causing dominant forms of early-onset deafness underlie severe presbycusis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31278-31289.	7.1	29
15	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
16	Deriving stratified effects from joint models investigating gene-environment interactions. BMC Bioinformatics, 2020, 21, 251.	2.6	2
17	JASS: command line and web interface for the joint analysis of GWAS results. NAR Genomics and Bioinformatics, 2020, 2, lqaa003.	3.2	11
18	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62

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19	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. Nature Communications, 2019, 10, 4788.	12.8	59
20	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
21	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
22	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	3.3	12
23	RAISS: robust and accurate imputation from summary statistics. Bioinformatics, 2019, 35, 4837-4839.	4.1	14
24	Efficient Implementation of Penalized Regression for Genetic Risk Prediction. Genetics, 2019, 212, 65-74.	2.9	51
25	Genetic effects on the commensal microbiota in inflammatory bowel disease patients. PLoS Genetics, 2019, 15, e1008018.	3.5	35
26	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
27	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
28	Adjusting for Principal Components of Molecular Phenotypes Induces Replicating False Positives. Genetics, 2019, 211, 1179-1189.	2.9	17
29	Making the Most of Clumping and Thresholding for Polygenic Scores. American Journal of Human Genetics, 2019, 105, 1213-1221.	6.2	123
30	Joint Analysis of Multiple Interaction Parameters in Genetic Association Studies. Genetics, 2019, 211, 483-494.	2.9	12
31	A test for geneâ€“environment interaction in the presence of measurement error in the environmental variable. Genetic Epidemiology, 2018, 42, 250-264.	1.3	5
32	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
33	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
34	lme4qtl: linear mixed models with flexible covariance structure for genetic studies of related individuals. BMC Bioinformatics, 2018, 19, 68.	2.6	123
35	VarExp: estimating variance explained by genome-wide GxE summary statistics. Bioinformatics, 2018, 34, 3412-3414.	4.1	13
36	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. Bioinformatics, 2018, 34, 2781-2787.	4.1	217

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37	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
38	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. Genome Biology, 2018, 19, 222.	8.8	101
39	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
40	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
41	Fungal microbiota dysbiosis in IBD. Gut, 2017, 66, 1039-1048.	12.1	939
42	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
43	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	21.4	27
44	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	3.4	23
45	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
46	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 762-770.	3.4	79
47	Age at natural menopause genetic risk score in relation to age at natural menopause and primary open-angle glaucoma in a US-based sample. Menopause, 2017, 24, 150-156.	2.0	6
48	Sex-Based Genetic Association Study Identifies CELSR1 as a Possible Chronic Obstructive Pulmonary Disease Risk Locus among Women. American Journal of Respiratory Cell and Molecular Biology, 2017, 56, 332-341.	2.9	28
49	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	3.4	150
50	Screening for interaction effects in gene expression data. PLoS ONE, 2017, 12, e0173847.	2.5	4
51	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. PLoS ONE, 2017, 12, e0173997.	2.5	52
52	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
53	A perspective on interaction effects in genetic association studies. Genetic Epidemiology, 2016, 40, 678-688.	1.3	77
54	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83

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55	Genomics, Telomere Length, Epigenetics, and Metabolomics in the Nursesâ€™ Health Studies. American Journal of Public Health, 2016, 106, 1663-1668.	2.7	32
56	Pancreatic Cancer Risk Associated with Prediagnostic Plasma Levels of Leptin and Leptin Receptor Genetic Polymorphisms. Cancer Research, 2016, 76, 7160-7167.	0.9	46
57	Emergence of Antimicrobial-ResistantEscherichia coliof Animal Origin Spreading in Humans. Molecular Biology and Evolution, 2016, 33, 898-914.	8.9	65
58	Response to Day etÂal.. American Journal of Human Genetics, 2016, 98, 394-395.	6.2	1
59	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
60	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. BMC Genetics, 2015, 16, 124.	2.7	14
61	Finding the missing geneâ€“environment interactions. European Journal of Epidemiology, 2015, 30, 353-355.	5.7	33
62	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. American Journal of Human Genetics, 2015, 96, 329-339.	6.2	230
63	Fitness cost of antibiotic susceptibility during bacterial infection. Science Translational Medicine, 2015, 7, 297ra114.	12.4	122
64	Variation in Predictive Ability of Common Genetic Variants by Established Strata. Epidemiology, 2015, 26, 51-58.	2.7	11
65	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	6.2	149
66	Enhanced in vivo fitness of carbapenem-resistant oprD mutants of Pseudomonas aeruginosa revealed through high-throughput sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20747-20752.	7.1	128
67	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	3.1	26
68	A Comprehensive Analysis of In Vitro and In Vivo Genetic Fitness of Pseudomonas aeruginosa Using High-Throughput Sequencing of Transposon Libraries. PLoS Pathogens, 2013, 9, e1003582.	4.7	178
69	A Nonparametric Test to Detect Quantitative Trait Loci Where the Phenotypic Distribution Differs by Genotypes. Genetic Epidemiology, 2013, 37, 323-333.	1.3	26
70	Exploring genome-wide â€“ dietary heme iron intake interactions and the risk of type 2 diabetes. Frontiers in Genetics, 2013, 4, 7.	2.3	12
71	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
72	Challenges and opportunities in genome-wide environmental interaction (GWEI) studies. Human Genetics, 2012, 131, 1591-1613.	3.8	128

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73	Inclusion of Gene-Gene and Gene-Environment Interactions Unlikely to Dramatically Improve Risk Prediction for Complex Diseases. American Journal of Human Genetics, 2012, 90, 962-972.	6.2	96
74	Inclusion of Gene-Gene and Gene-Environment Interactions Unlikely to Dramatically Improve Risk Prediction for Complex Diseases. American Journal of Human Genetics, 2012, 90, 1116.	6.2	1
75	Combining effects from rare and common genetic variants in an exome-wide association study of sequence data. BMC Proceedings, 2011, 5, S44.	1.6	5
76	Inflated type I error rates when using aggregation methods to analyze rare variants in the 1000 Genomes Project exon sequencing data in unrelated individuals: summary results from Group 7 at Genetic Analysis Workshop 17. Genetic Epidemiology, 2011, 35, S56-60.	1.3	23
77	Genome-Wide Meta-Analysis of Joint Tests for Genetic and Gene-Environment Interaction Effects. Human Heredity, 2010, 70, 292-300.	0.8	71
78	Effect of 17q21 Variants and Smoking Exposure in Early-Onset Asthma. New England Journal of Medicine, 2008, 359, 1985-1994.	27.0	351
79	A two-step multiple-marker strategy for genome-wide association studies. BMC Proceedings, 2007, 1, S134.	1.6	5
80	Multistage designs in the genomic era: Providing balance in complex disease studies. Genetic Epidemiology, 2007, 31, S118-S123.	1.3	6