

Hugues Aschard

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6010687/publications.pdf>

Version: 2024-02-01

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	Fungal microbiota dysbiosis in IBD. <i>Gut</i> , 2017, 66, 1039-1048.	12.1	939
2	Effect of 17q21 Variants and Smoking Exposure in Early-Onset Asthma. <i>New England Journal of Medicine</i> , 2008, 359, 1985-1994.	27.0	351
3	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	12.8	295
4	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 329-339.	6.2	230
5	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. <i>Bioinformatics</i> , 2018, 34, 2781-2787.	4.1	217
6	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. <i>Nature Genetics</i> , 2016, 48, 189-194.	21.4	211
7	A Comprehensive Analysis of In Vitro and In Vivo Genetic Fitness of <i>Pseudomonas aeruginosa</i> Using High-Throughput Sequencing of Transposon Libraries. <i>PLoS Pathogens</i> , 2013, 9, e1003582.	4.7	178
8	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , 2017, 186, 753-761.	3.4	150
9	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2014, 94, 662-676.	6.2	149
10	Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. <i>American Journal of Human Genetics</i> , 2022, 109, 12-23.	6.2	136
11	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. <i>PLoS Genetics</i> , 2012, 8, e1003098.	3.5	130
12	Challenges and opportunities in genome-wide environmental interaction (GWEI) studies. <i>Human Genetics</i> , 2012, 131, 1591-1613.	3.8	128
13	Enhanced in vivo fitness of carbapenem-resistant <i>oprD</i> mutants of <i>Pseudomonas aeruginosa</i> revealed through high-throughput sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20747-20752.	7.1	128
14	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
15	lme4qtl: linear mixed models with flexible covariance structure for genetic studies of related individuals. <i>BMC Bioinformatics</i> , 2018, 19, 68.	2.6	123
16	Making the Most of Clumping and Thresholding for Polygenic Scores. <i>American Journal of Human Genetics</i> , 2019, 105, 1213-1221.	6.2	123
17	Fitness cost of antibiotic susceptibility during bacterial infection. <i>Science Translational Medicine</i> , 2015, 7, 297ra114.	12.4	122
18	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120

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19	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
20	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. <i>Genome Biology</i> , 2018, 19, 222.	8.8	101
21	Inclusion of Gene-Gene and Gene-Environment Interactions Unlikely to Dramatically Improve Risk Prediction for Complex Diseases. <i>American Journal of Human Genetics</i> , 2012, 90, 962-972.	6.2	96
22	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
23	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
24	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	6.7	83
25	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. <i>American Journal of Epidemiology</i> , 2017, 186, 762-770.	3.4	79
26	A perspective on interaction effects in genetic association studies. <i>Genetic Epidemiology</i> , 2016, 40, 678-688.	1.3	77
27	Genome-Wide Meta-Analysis of Joint Tests for Genetic and Gene-Environment Interaction Effects. <i>Human Heredity</i> , 2010, 70, 292-300.	0.8	71
28	Emergence of Antimicrobial-Resistant <i>Escherichia coli</i> of Animal Origin Spreading in Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 898-914.	8.9	65
29	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
30	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	12.8	62
31	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. <i>Nature Communications</i> , 2019, 10, 4788.	12.8	59
32	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. <i>PLoS ONE</i> , 2017, 12, e0173997.	2.5	52
33	Efficient Implementation of Penalized Regression for Genetic Risk Prediction. <i>Genetics</i> , 2019, 212, 65-74.	2.9	51
34	Pancreatic Cancer Risk Associated with Prediagnostic Plasma Levels of Leptin and Leptin Receptor Genetic Polymorphisms. <i>Cancer Research</i> , 2016, 76, 7160-7167.	0.9	46
35	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	1.9	36
36	Genetic effects on the commensal microbiota in inflammatory bowel disease patients. <i>PLoS Genetics</i> , 2019, 15, e1008018.	3.5	35

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37	Intraocular Pressure, Glaucoma, and Dietary Caffeine Consumption. <i>Ophthalmology</i> , 2021, 128, 866-876.	5.2	35
38	Finding the missing gene-environment interactions. <i>European Journal of Epidemiology</i> , 2015, 30, 353-355.	5.7	33
39	Genomics, Telomere Length, Epigenetics, and Metabolomics in the Nurses' Health Studies. <i>American Journal of Public Health</i> , 2016, 106, 1663-1668.	2.7	32
40	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	2.9	31
41	Ultrarare heterozygous pathogenic variants of genes causing dominant forms of early-onset deafness underlie severe presbycusis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31278-31289.	7.1	29
42	Sex-Based Genetic Association Study Identifies <i>CELSR1</i> as a Possible Chronic Obstructive Pulmonary Disease Risk Locus among Women. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 56, 332-341.	2.9	28
43	Covariate selection for association screening in multiphenotype genetic studies. <i>Nature Genetics</i> , 2017, 49, 1789-1795.	21.4	27
44	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. <i>Endocrine-Related Cancer</i> , 2013, 20, 875-887.	3.1	26
45	A Nonparametric Test to Detect Quantitative Trait Loci Where the Phenotypic Distribution Differs by Genotypes. <i>Genetic Epidemiology</i> , 2013, 37, 323-333.	1.3	26
46	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. <i>Genetic Epidemiology</i> , 2011, 35, S56-60.	1.3	23
47	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. <i>American Journal of Epidemiology</i> , 2017, 186, 771-777.	3.4	23
48	An Empirical Comparison of Joint and Stratified Frameworks for Studying G x E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016, 40, 404-415.	1.3	18
49	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. <i>European Journal of Human Genetics</i> , 2017, 25, 1261-1267.	2.8	18
50	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	1.3	17
51	Adjusting for Principal Components of Molecular Phenotypes Induces Replicating False Positives. <i>Genetics</i> , 2019, 211, 1179-1189.	2.9	17
52	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
53	Multitrait GWAS to connect disease variants and biological mechanisms. <i>PLoS Genetics</i> , 2021, 17, e1009713.	3.5	16
54	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. <i>BMC Genetics</i> , 2015, 16, 124.	2.7	14

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55	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
56	RAISS: robust and accurate imputation from summary statistics. <i>Bioinformatics</i> , 2019, 35, 4837-4839.	4.1	14
57	VarExp: estimating variance explained by genome-wide GxE summary statistics. <i>Bioinformatics</i> , 2018, 34, 3412-3414.	4.1	13
58	Multi-ancestry genome-wide gene-environment interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	7.9	13
59	Exploring genome-wide gene-environment dietary heme iron intake interactions and the risk of type 2 diabetes. <i>Frontiers in Genetics</i> , 2013, 4, 7.	2.3	12
60	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. <i>American Journal of Ophthalmology</i> , 2019, 206, 245-255.	3.3	12
61	Joint Analysis of Multiple Interaction Parameters in Genetic Association Studies. <i>Genetics</i> , 2019, 211, 483-494.	2.9	12
62	Estimating the effective sample size in association studies of quantitative traits. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	12
63	Variation in Predictive Ability of Common Genetic Variants by Established Strata. <i>Epidemiology</i> , 2015, 26, 51-58.	2.7	11
64	JASS: command line and web interface for the joint analysis of GWAS results. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa003.	3.2	11
65	Gene-lifestyle interactions in the genomics of human complex traits. <i>European Journal of Human Genetics</i> , 2022, 30, 730-739.	2.8	11
66	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. <i>European Journal of Human Genetics</i> , 2020, 28, 656-668.	2.8	7
67	Statin Use in Relation to Intraocular Pressure, Glaucoma, and Ocular Coherence Tomography Parameters in the UK Biobank. , 2022, 63, 31.		7
68	Multistage designs in the genomic era: Providing balance in complex disease studies. <i>Genetic Epidemiology</i> , 2007, 31, S118-S123.	1.3	6
69	Age at natural menopause genetic risk score in relation to age at natural menopause and primary open-angle glaucoma in a US-based sample. <i>Menopause</i> , 2017, 24, 150-156.	2.0	6
70	A two-step multiple-marker strategy for genome-wide association studies. <i>BMC Proceedings</i> , 2007, 1, S134.	1.6	5
71	Combining effects from rare and common genetic variants in an exome-wide association study of sequence data. <i>BMC Proceedings</i> , 2011, 5, S44.	1.6	5
72	A test for gene-environment interaction in the presence of measurement error in the environmental variable. <i>Genetic Epidemiology</i> , 2018, 42, 250-264.	1.3	5

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73	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
74	Screening for interaction effects in gene expression data. PLoS ONE, 2017, 12, e0173847.	2.5	4
75	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
76	Deriving stratified effects from joint models investigating gene-environment interactions. BMC Bioinformatics, 2020, 21, 251.	2.6	2
77	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
78	Fitting Gaussian mixture models on incomplete data. BMC Bioinformatics, 2022, 23, .	2.6	2
79	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
80	Response to Day etÂal.. American Journal of Human Genetics, 2016, 98, 394-395.	6.2	1