

Dana B Hancock

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8253777/publications.pdf>

Version: 2024-02-01

71
papers

5,618
citations

147726

31
h-index

88593

70
g-index

87
all docs

87
docs citations

87
times ranked

10316
citing authors

#	ARTICLE	IF	CITATIONS
1	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. <i>Nature Genetics</i> , 2011, 43, 887-892.	9.4	736
2	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. <i>Nature Genetics</i> , 2010, 42, 45-52.	9.4	549
3	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	7.1	490
4	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132.	9.4	472
5	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
6	Pesticide exposure and risk of Parkinson's disease: A family-based case-control study. <i>BMC Neurology</i> , 2008, 8, 6.	0.8	221
7	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	3.7	200
8	Genome-Wide Association Studies Identify <i>CHRNA5</i> and <i>HTR4</i> in the Development of Airflow Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 622-632.	2.5	164
9	Genome-Wide Association Study Implicates Chromosome 9q21.31 as a Susceptibility Locus for Asthma in Mexican Children. <i>PLoS Genetics</i> , 2009, 5, e1000623.	1.5	139
10	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
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.	1.5	130
12	Smoking, Caffeine, and Nonsteroidal Anti-inflammatory Drugs in Families With Parkinson Disease. <i>Archives of Neurology</i> , 2007, 64, 576.	4.9	107
13	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. <i>Neuron</i> , 2021, 109, 3088-3103.e5.	3.8	95
14	Genome-wide association study of lung function decline in adults with and without asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1218-1228.	1.5	94
15	Nitric oxide synthase genes and their interactions with environmental factors in Parkinson's disease. <i>Neurogenetics</i> , 2008, 9, 249-262.	0.7	91
16	Human Genetics of Addiction: New Insights and Future Directions. <i>Current Psychiatry Reports</i> , 2018, 20, 8.	2.1	90
17	Evaluation of candidate genes in a genome-wide association study of childhood asthma in Mexicans. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 125, 321-327.e13.	1.5	88
18	Genome-wide meta-analysis reveals common splice site acceptor variant in <i>CHRNA4</i> associated with nicotine dependence. <i>Translational Psychiatry</i> , 2015, 5, e651-e651.	2.4	86

#	ARTICLE	IF	CITATIONS
19	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. <i>Molecular Psychiatry</i> , 2020, 25, 1673-1687.	4.1	82
20	Genome-wide association study across European and African American ancestries identifies a SNP in DNMT3B contributing to nicotine dependence. <i>Molecular Psychiatry</i> , 2018, 23, 1911-1919.	4.1	80
21	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. <i>Nature Communications</i> , 2020, 11, 5562.	5.8	80
22	Genome-Wide Meta-Analysis of Joint Tests for Genetic and Gene-Environment Interaction Effects. <i>Human Heredity</i> , 2010, 70, 292-300.	0.4	71
23	Genetic correlation between smoking behaviors and schizophrenia. <i>Schizophrenia Research</i> , 2018, 194, 86-90.	1.1	71
24	Cis-Expression Quantitative Trait Loci Mapping Reveals Replicable Associations with Heroin Addiction in OPRM1. <i>Biological Psychiatry</i> , 2015, 78, 474-484.	0.7	64
25	Association Between Substance Use Disorder and Polygenic Liability to Schizophrenia. <i>Biological Psychiatry</i> , 2017, 82, 709-715.	0.7	62
26	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. <i>PLoS ONE</i> , 2014, 9, e100776.	1.1	52
27	Assessment of Genotype Imputation Performance Using 1000 Genomes in African American Studies. <i>PLoS ONE</i> , 2012, 7, e50610.	1.1	50
28	Imputation across genotyping arrays for genome-wide association studies: assessment of bias and a correction strategy. <i>Human Genetics</i> , 2013, 132, 509-522.	1.8	44
29	NOS2A and the modulating effect of cigarette smoking in Parkinson's disease. <i>Annals of Neurology</i> , 2006, 60, 366-373.	2.8	38
30	DSM-5 cannabis use disorder: A phenotypic and genomic perspective. <i>Drug and Alcohol Dependence</i> , 2014, 134, 362-369.	1.6	38
31	Methods for interaction analyses using family-based case-control data: conditional logistic regression versus generalized estimating equations. <i>Genetic Epidemiology</i> , 2007, 31, 883-893.	0.6	36
32	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	0.9	36
33	Data compatibility in the addiction sciences: An examination of measure commonality. <i>Drug and Alcohol Dependence</i> , 2014, 141, 153-158.	1.6	34
34	A multi-ancestry study identifies novel genetic associations with <i>CHRNA5</i> methylation in human brain and risk of nicotine dependence. <i>Human Molecular Genetics</i> , 2015, 24, 5940-5954.	1.4	31
35	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , 2015, 24, 6836-6848.	1.4	28
36	When Does Choice of Accuracy Measure Alter Imputation Accuracy Assessments?. <i>PLoS ONE</i> , 2015, 10, e0137601.	1.1	25

#	ARTICLE	IF	CITATIONS
37	A genome-wide association study of asthma symptoms in Latin American children. <i>BMC Genetics</i> , 2015, 16, 141.	2.7	24
38	Novel Genetic Locus Implicated for HIV-1 Acquisition with Putative Regulatory Links to HIV Replication and Infectivity: A Genome-Wide Association Study. <i>PLoS ONE</i> , 2015, 10, e0118149.	1.1	23
39	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Nicotine and Tobacco Research</i> , 2018, 20, 448-457.	1.4	21
40	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. <i>Neuropsychopharmacology</i> , 2021, 46, 554-560.	2.8	19
41	Cis-Regulatory Variants Affect CHRNA5 mRNA Expression in Populations of African and European Ancestry. <i>PLoS ONE</i> , 2013, 8, e80204.	1.1	19
42	<i>KAT2B</i> polymorphism identified for drug abuse in African Americans with regulatory links to drug abuse pathways in human prefrontal cortex. <i>Addiction Biology</i> , 2016, 21, 1217-1232.	1.4	18
43	STAT6 and LRP1 polymorphisms are associated with food allergen sensitization in Mexican children. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1673-1676.	1.5	17
44	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. <i>Nicotine and Tobacco Research</i> , 2020, 22, 900-909.	1.4	17
45	Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 173-182.	1.1	17
46	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. <i>Molecular Psychiatry</i> , 2020, 25, 3267-3277.	4.1	16
47	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal <i>DPP10</i> Pulmonary Function Association. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 631-642.	2.5	14
48	DNA methylation mediates the effect of cocaine use on HIV severity. <i>Clinical Epigenetics</i> , 2020, 12, 140.	1.8	14
49	Genetic architecture of four smoking behaviors using partitioned SNP heritability. <i>Addiction</i> , 2021, 116, 2498-2508.	1.7	14
50	Chromatin architecture in addiction circuitry identifies risk genes and potential biological mechanisms underlying cigarette smoking and alcohol use traits. <i>Molecular Psychiatry</i> , 2022, 27, 3085-3094.	4.1	13
51	Associations of common variants in the <i>BST2</i> region with HIV-1 acquisition in African American and European American people who inject drugs. <i>Aids</i> , 2015, 29, 767-777.	1.0	12
52	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	1.1	12
53	Alcohol and cigarette smoking consumption as genetic proxies for alcohol misuse and nicotine dependence. <i>Drug and Alcohol Dependence</i> , 2021, 221, 108612.	1.6	11
54	Comprehensive evaluation of disease- and trait-specific enrichment for eight functional elements among GWAS-identified variants. <i>Human Genetics</i> , 2017, 136, 911-919.	1.8	10

#	ARTICLE	IF	CITATIONS
55	Population-Based Case-Control Association Studies. Current Protocols in Human Genetics, 2012, 74, Unit 1.17.	3.5	9
56	Replication of <i>ZNF804A</i> gene variant associations with risk of heroin addiction. Genes, Brain and Behavior, 2015, 14, 635-640.	1.1	9
57	Meta-analysis across Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium provides evidence for an association of serum vitamin D with pulmonary function. British Journal of Nutrition, 2018, 120, 1159-1170.	1.2	9
58	DNA methylation biomarker selected by an ensemble machine learning approach predicts mortality risk in an HIV-positive veteran population. Epigenetics, 2021, 16, 741-753.	1.3	9
59	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. Molecular Psychiatry, 2022, 27, 2158-2170.	4.1	9
60	<i>ADAM19</i> and <i>HTR4</i> Variants and Pulmonary Function. Circulation: Cardiovascular Genetics, 2014, 7, 350-358.	5.1	8
61	Oral contraceptive pill use before pregnancy and respiratory outcomes in early childhood. Pediatric Allergy and Immunology, 2011, 22, 528-536.	1.1	7
62	Dissecting the genetic overlap of smoking behaviors, lung cancer, and chronic obstructive pulmonary disease: A focus on nicotinic receptors and nicotine metabolizing enzyme. Genetic Epidemiology, 2020, 44, 748-758.	0.6	7
63	Population-Based Case-Control Association Studies. Current Protocols in Human Genetics, 2007, 52, Unit 1.17.	3.5	6
64	Studying the Utility of Using Genetics to Predict Smoking-Related Outcomes in a Population-Based Study and a Selected Cohort. Nicotine and Tobacco Research, 2021, 23, 2110-2116.	1.4	6
65	Strategies for cellular deconvolution in human brain RNA sequencing data. F1000Research, 0, 10, 750.	0.8	4
66	Determinants of Lung Function, COPD, and Asthma. New England Journal of Medicine, 2011, 364, 86-87.	13.9	3
67	Is the Fagerstr�m test for nicotine dependence invariant across secular trends in smoking? A question for cross-birth cohort analysis of nicotine dependence. Drug and Alcohol Dependence, 2018, 185, 127-132.	1.6	3
68	Using Imputed Genotypes for Relative Risk Estimation in Case-Parent Studies. American Journal of Epidemiology, 2011, 173, 553-559.	1.6	2
69	Two Adjustment Strategies for Imputation across Genotyping Arrays. Human Heredity, 2014, 78, 73-80.	0.4	1
70	Change in plasma α -tocopherol associations with attenuated pulmonary function decline and with CYP4F2 missense variation. American Journal of Clinical Nutrition, 2022, 115, 1205-1216.	2.2	1
71	Compelling Interaction of Cigarette Smoking and Polygenetic Risk Emerges for Lung Function and COPD. JAMA Network Open, 2021, 4, e2140347.	2.8	1