

Dana B Hancock

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

5,618
citations

147801
31
h-index

88630
70
g-index

87
all docs

87
docs citations

87
times ranked

10316
citing authors

#	ARTICLE	IF	CITATIONS
1	Change in plasma α -tocopherol associations with attenuated pulmonary function decline and with CYP4F2 missense variation. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 1205-1216.	4.7	1
2	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. <i>Molecular Psychiatry</i> , 2022, 27, 2158-2170.	7.9	9
3	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.	7.9	13
4	DNA methylation biomarker selected by an ensemble machine learning approach predicts mortality risk in an HIV-positive veteran population. <i>Epigenetics</i> , 2021, 16, 741-753.	2.7	9
5	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. <i>Neuropsychopharmacology</i> , 2021, 46, 554-560.	5.4	19
6	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.	1.7	17
7	Genetic architecture of four smoking behaviors using partitioned SNP heritability. <i>Addiction</i> , 2021, 116, 2498-2508.	3.3	14
8	Alcohol and cigarette smoking consumption as genetic proxies for alcohol misuse and nicotine dependence. <i>Drug and Alcohol Dependence</i> , 2021, 221, 108612.	3.2	11
9	Studying the Utility of Using Genetics to Predict Smoking-Related Outcomes in a Population-Based Study and a Selected Cohort. <i>Nicotine and Tobacco Research</i> , 2021, 23, 2110-2116.	2.6	6
10	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	2.2	12
11	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.	8.1	95
12	Compelling Interaction of Cigarette Smoking and Polygenetic Risk Emerges for Lung Function and COPD. <i>JAMA Network Open</i> , 2021, 4, e2140347.	5.9	1
13	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. <i>Molecular Psychiatry</i> , 2020, 25, 3267-3277.	7.9	16
14	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. <i>Nicotine and Tobacco Research</i> , 2020, 22, 900-909.	2.6	17
15	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	7.4	200
16	DNA methylation mediates the effect of cocaine use on HIV severity. <i>Clinical Epigenetics</i> , 2020, 12, 140.	4.1	14
17	Dissecting the genetic overlap of smoking behaviors, lung cancer, and chronic obstructive pulmonary disease: A focus on nicotinic receptors and nicotine metabolizing enzyme. <i>Genetic Epidemiology</i> , 2020, 44, 748-758.	1.3	7
18	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. <i>Nature Communications</i> , 2020, 11, 5562.	12.8	80

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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.	7.9	82
20	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.	5.6	14
21	Human Genetics of Addiction: New Insights and Future Directions. <i>Current Psychiatry Reports</i> , 2018, 20, 8.	4.5	90
22	Is the Fagerstr�m test for nicotine dependence invariant across secular trends in smoking? A question for cross-birth cohort analysis of nicotine dependence. <i>Drug and Alcohol Dependence</i> , 2018, 185, 127-132.	3.2	3
23	Genetic correlation between smoking behaviors and schizophrenia. <i>Schizophrenia Research</i> , 2018, 194, 86-90.	2.0	71
24	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.	2.6	21
25	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.	7.9	80
26	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	14.8	490
27	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. <i>British Journal of Nutrition</i> , 2018, 120, 1159-1170.	2.3	9
28	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	1.9	36
29	Association Between Substance Use Disorder and Polygenic Liability to Schizophrenia. <i>Biological Psychiatry</i> , 2017, 82, 709-715.	1.3	62
30	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.	21.4	472
31	Comprehensive evaluation of disease- and trait-specific enrichment for eight functional elements among GWAS-identified variants. <i>Human Genetics</i> , 2017, 136, 911-919.	3.8	10
32	<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.	2.6	18
33	A genome-wide association study of asthma symptoms in Latin American children. <i>BMC Genetics</i> , 2015, 16, 141.	2.7	24
34	Replication of <i>ZNF804A</i> gene variant associations with risk of heroin addiction. <i>Genes, Brain and Behavior</i> , 2015, 14, 635-640.	2.2	9
35	Associations of common variants in the BST2 region with HIV-1 acquisition in African American and European American people who inject drugs. <i>Aids</i> , 2015, 29, 767-777.	2.2	12
36	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.	2.5	23

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37	When Does Choice of Accuracy Measure Alter Imputation Accuracy Assessments?. PLoS ONE, 2015, 10, e0137601.	2.5	25
38	Genome-wide meta-analysis reveals common splice site acceptor variant in CHRNA4 associated with nicotine dependence. Translational Psychiatry, 2015, 5, e651-e651.	4.8	86
39	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
40	A multiethnic study identifies novel genetic associations with CHRNA5 methylation in human brain and risk of nicotine dependence. Human Molecular Genetics, 2015, 24, 5940-5954.	2.9	31
41	Cis-Expression Quantitative Trait Loci Mapping Reveals Replicable Associations with Heroin Addiction in OPRM1. Biological Psychiatry, 2015, 78, 474-484.	1.3	64
42	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
43	ADAM19 and HTR4 Variants and Pulmonary Function. Circulation: Cardiovascular Genetics, 2014, 7, 350-358.	5.1	8
44	Two Adjustment Strategies for Imputation across Genotyping Arrays. Human Heredity, 2014, 78, 73-80.	0.8	1
45	DSM-5 cannabis use disorder: A phenotypic and genomic perspective. Drug and Alcohol Dependence, 2014, 134, 362-369.	3.2	38
46	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
47	Data compatibility in the addiction sciences: An examination of measure commonality. Drug and Alcohol Dependence, 2014, 141, 153-158.	3.2	34
48	Imputation across genotyping arrays for genome-wide association studies: assessment of bias and a correction strategy. Human Genetics, 2013, 132, 509-522.	3.8	44
49	Cis-Regulatory Variants Affect CHRNA5 mRNA Expression in Populations of African and European Ancestry. PLoS ONE, 2013, 8, e80204.	2.5	19
50	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
51	Genome-Wide Association Studies Identify CHRNA5/3 and HTR4 in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	5.6	164
52	Population-Based Case-Control Association Studies. Current Protocols in Human Genetics, 2012, 74, Unit1.17.	3.5	9
53	Genome-wide association study of lung function decline in adults with and without asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1218-1228.	2.9	94
54	STAT6 and LRP1 polymorphisms are associated with food allergen sensitization in Mexican children. Journal of Allergy and Clinical Immunology, 2012, 129, 1673-1676.	2.9	17

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55	Assessment of Genotype Imputation Performance Using 1000 Genomes in African American Studies. PLoS ONE, 2012, 7, e50610.	2.5	50
56	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
57	Oral contraceptive pill use before pregnancy and respiratory outcomes in early childhood. Pediatric Allergy and Immunology, 2011, 22, 528-536.	2.6	7
58	Using Imputed Genotypes for Relative Risk Estimation in Case-Parent Studies. American Journal of Epidemiology, 2011, 173, 553-559.	3.4	2
59	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
60	Determinants of Lung Function, COPD, and Asthma. New England Journal of Medicine, 2011, 364, 86-87.	27.0	3
61	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. Nature Genetics, 2010, 42, 45-52.	21.4	549
62	Genome-Wide Meta-Analysis of Joint Tests for Genetic and Gene-Environment Interaction Effects. Human Heredity, 2010, 70, 292-300.	0.8	71
63	Evaluation of candidate genes in a genome-wide association study of childhood asthma in Mexicans. Journal of Allergy and Clinical Immunology, 2010, 125, 321-327.e13.	2.9	88
64	Genome-Wide Association Study Implicates Chromosome 9q21.31 as a Susceptibility Locus for Asthma in Mexican Children. PLoS Genetics, 2009, 5, e1000623.	3.5	139
65	Nitric oxide synthase genes and their interactions with environmental factors in Parkinson's disease. Neurogenetics, 2008, 9, 249-262.	1.4	91
66	Pesticide exposure and risk of Parkinson's disease: A family-based case-control study. BMC Neurology, 2008, 8, 6.	1.8	221
67	Smoking, Caffeine, and Nonsteroidal Anti-inflammatory Drugs in Families With Parkinson Disease. Archives of Neurology, 2007, 64, 576.	4.5	107
68	Population-Based Case-Control Association Studies. Current Protocols in Human Genetics, 2007, 52, Unit 1.17.	3.5	6
69	Methods for interaction analyses using family-based case-control data: conditional logistic regression versus generalized estimating equations. Genetic Epidemiology, 2007, 31, 883-893.	1.3	36
70	NOS2A and the modulating effect of cigarette smoking in Parkinson's disease. Annals of Neurology, 2006, 60, 366-373.	5.3	38
71	Strategies for cellular deconvolution in human brain RNA sequencing data. F1000Research, 0, 10, 750.	1.6	4