Dana C Crawford

List of Publications by Year
in descending order

217 papers	18,864 citations	26567 56 h-index	15218 126 g-index
227 all docs	227 docs citations	227 times ranked	27617 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
4	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover geneâ€“disease associations. Bioinformatics, 2010, 26, 1205-1210.	1.8	966
5	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	9.4	846
6	FMR1 and the fragile X syndrome: Human genome epidemiology review. Genetics in Medicine, 2001, 3, 359-371.	1.1	556
7	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. Blood, 2010, 115, 3827-3834.	0.6	331
8	Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record. American Journal of Human Genetics, 2010, 86, 560-572.	2.6	302
9	Definition and Clinical Importance of Haplotypes. Annual Review of Medicine, 2005, 56, 303-320.	5.0	283
10	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
11	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
12	Evidence for substantial fine-scale variation in recombination rates across the human genome. Nature Genetics, 2004, 36, 700-706.	9.4	256
13	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. Lancet, The, 2013, 382, 790-796.	6.3	237
14	Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. PLoS Biology, 2013, 11, e1001661.	2.6	235
15	Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. American Journal of Human Genetics, 2011, 89, 529-542.	2.6	232
16	Unravelling the human genomeâ€“phenome relationship using phenome-wide association studies. Nature Reviews Genetics, 2016, 17, 129-145.	7.7	222
17	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
18	Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. PLoS Genetics, 2013, 9, e1003087.	1.5	171

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19	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
20	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	2.0	166
21	Haplotype Diversity across 100 Candidate Genes for Inflammation, Lipid Metabolism, and Blood Pressure Regulation in Two Populations. American Journal of Human Genetics, 2004, 74, 610-622.	2.6	163
22	The Next PAGE in Understanding Complex Traits: Design for the Analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. American Journal of Epidemiology, 2011, 174, 849-859.	1.6	161
23	Pattern of Sequence Variation Across 213 Environmental Response Genes. Genome Research, 2004, 14, 1821-1831.	2.4	157
24	A Large Candidate Gene Survey Identifies the KCNE1 D85N Polymorphism as a Possible Modulator of Drug-Induced Torsades de Pointes. Circulation: Cardiovascular Genetics, 2012, 5, 91-99.	5.1	150
25	Genetic Determinants of Lipid Traits in Diverse Populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2011, 7, e1002138.	1.5	146
26	Genetic Variation Is Associated With C-Reactive Protein Levels in the Third National Health and Nutrition Examination Survey. Circulation, 2006, 114, 2458-2465.	1.6	136
27	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	1.1	130
28	Prevalence of the fragile X syndrome in African-Americans. American Journal of Medical Genetics Part A, 2002, 110, 226-233.	2.4	127
29	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	13.5	121
30	Prevalence and Phenotype Consequence of FRAXA and FRAXE Alleles in a Large, Ethnically Diverse, Special Educationâ€“Needs Population. American Journal of Human Genetics, 1999, 64, 495-507.	2.6	119
31	Identification of Genomic Predictors of Atrioventricular Conduction. Circulation, 2010, 122, 2016-2021.	1.6	117
32	THE PATTERNS OF NATURAL VARIATION IN HUMAN GENES. Annual Review of Genomics and Human Genetics, 2005, 6, 287-312.	2.5	113
33	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. PLoS Genetics, 2013, 9, e1003379.	1.5	112
34	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. Human Genetics, 2012, 131, 639-652.	1.8	103
35	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
36	Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. Genetics in Medicine, 2010, 12, 648-650.	1.1	94

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37	Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records and Genomics (eMERGE) Network. Genetics in Medicine, 2012, 14, 424-431.	1.1	94
38	Predicting warfarin dosage in Europeanâ€“Americans and Africanâ€“Americans using DNA samples linked to an electronic health record. Pharmacogenomics, 2012, 13, 407-418.	0.6	90
39	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	1.1	79
40	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	2.6	77
41	Facilitating pharmacogenetic studies using electronic health records and natural-language processing: a case study of warfarin. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 387-391.	2.2	74
42	Association of Functional Polymorphism rs2231142 (Q141K) in the ABCG2 Gene With Serum Uric Acid and Gout in 4 US Populations. American Journal of Epidemiology, 2013, 177, 923-932.	1.6	74
43	Using Electronic Health Records To Generate Phenotypes For Research. Current Protocols in Human Genetics, 2019, 100, e80.	3.5	74
44	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. Genetic Epidemiology, 2011, 35, 887-898.	0.6	71
45	Evaluation of the Metabochip Genotyping Array in African Americans and Implications for Fine Mapping of GWAS-Identified Loci: The PAGE Study. PLoS ONE, 2012, 7, e35651.	1.1	71
46	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
47	Genetic risk factors for BMI and obesity in an ethnically diverse population: Results from the population architecture using genomics and epidemiology (PAGE) study. Obesity, 2013, 21, 835-846.	1.5	68
48	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	1.1	66
49	Paternally Transmitted FMR1 Alleles Are Less Stable than Maternally Transmitted Alleles in the Common and Intermediate Size Range. American Journal of Human Genetics, 2002, 70, 1532-1544.	2.6	64
50	Detection of Pleiotropy through a Phenome-Wide Association Study (PheWAS) of Epidemiologic Data as Part of the Environmental Architecture for Genes Linked to Environment (EAGLE) Study. PLoS Genetics, 2014, 10, e1004678.	1.5	64
51	A Systematic Mapping Approach of 16q12.2/FTO and BMI in More Than 20,000 African Americans Narrows in on the Underlying Functional Variation: Results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2013, 9, e1003171.	1.5	63
52	Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. PLoS ONE, 2011, 6, e19586.	1.1	60
53	Characterization of mitochondrial haplogroups in a large population-based sample from the United States. Human Genetics, 2014, 133, 861-868.	1.8	60
54	Association of the FTO Obesity Risk Variant rs8050136 With Percentage of Energy Intake From Fat in Multiple Racial/Ethnic Populations. American Journal of Epidemiology, 2013, 178, 780-790.	1.6	59

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55	Genetic Determinants of Age-Related Macular Degeneration in Diverse Populations From the PAGE Study. Investigative Ophthalmology and Visual Science, 2014, 55, 6839-6850.	3.3	59
56	Genotype Imputation of <scp>M</scp>etabochip<scp>SNPs</scp> Using a Studyâ€Specific Reference Panel of â¼4,000 Haplotypes in <scp>A</scp>frican <scp>A</scp>mericans From the Women's Health Initiative. Genetic Epidemiology, 2012, 36, 107-117.	0.6	57
57	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
58	Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes. PLoS ONE, 2013, 8, e78511.	1.1	57
59	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	1.4	56
60	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
61	Consistent Directions of Effect for Established Type 2 Diabetes Risk Variants Across Populations. Diabetes, 2012, 61, 1642-1647.	0.3	49
62	Survey of the Fragile X Syndrome CGG Repeat and the Short-Tandem-Repeat and Single-Nucleotide-Polymorphism Haplotypes in an African American Population. American Journal of Human Genetics, 2000, 66, 480-493.	2.6	45
63	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45
64	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nature Reviews Nephrology, 2020, 16, 686-696.	4.1	45
65	The detection and characterization of pleiotropy: discovery, progress, and promise. Briefings in Bioinformatics, 2016, 17, 13-22.	3.2	43
66	Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. BioData Mining, 2010, 3, 10.	2.2	42
67	High Density GWAS for LDL Cholesterol in African Americans Using Electronic Medical Records Reveals a Strong Protective Variant in APOE. Clinical and Translational Science, 2012, 5, 394-399.	1.5	42
68	Visually integrating and exploring high throughput Phenome-Wide Association Study (PheWAS) results using PheWAS-View. BioData Mining, 2012, 5, 5.	2.2	42
69	Genetic Variation and Reproductive Timing: African American Women from the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2013, 8, e55258.	1.1	39
70	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. Journal of Thoracic Oncology, 2018, 13, 1464-1473.	0.5	38
71	Characterization of Genome-Wide Association-Identified Variants for Atrial Fibrillation in African Americans. PLoS ONE, 2012, 7, e32338.	1.1	37
72	Generalization of Variants Identified by Genomeâ€Wide Association Studies for Electrocardiographic Traits in African Americans. Annals of Human Genetics, 2013, 77, 321-332.	0.3	37

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73	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	1.8	36
74	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	1.1	36
75	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. Gut, 2014, 63, 800-807.	6.1	35
76	Pleiotropic Associations of Risk Variants Identified for Other Cancers With Lung Cancer Risk: The PAGE and TRICL Consortia. Journal of the National Cancer Institute, 2014, 106, dju061.	3.0	35
77	Variation in LPA Is Associated with Lp(a) Levels in Three Populations from the Third National Health and Nutrition Examination Survey. PLoS ONE, 2011, 6, e16604.	1.1	34
78	Genetic Variants Associated with Serum Thyroid Stimulating Hormone (TSH) Levels in European Americans and African Americans from the eMERGE Network. PLoS ONE, 2014, 9, e111301.	1.1	34
79	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. Human Heredity, 2015, 79, 137-146.	0.4	34
80	Lack of associations of ten candidate coronary heart disease risk genetic variants and subclinical atherosclerosis in four U.S. populations: The Population Architecture using Genomics and Epidemiology (PAGE) study. Atherosclerosis, 2013, 228, 390-399.	0.4	33
81	Genetic Variants That Confer Resistance to Malaria Are Associated with Red Blood Cell Traits in African-Americans: An Electronic Medical Record-based Genome-Wide Association Study. G3: Genes, Genomes, Genetics, 2013, 3, 1061-1068.	0.8	32
82	SecureMA: protecting participant privacy in genetic association meta-analysis. Bioinformatics, 2014, 30, 3334-3341.	1.8	32
83	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. European Urology, 2020, 78, 316-320.	0.9	32
84	Rare VariantAPOC3R19X Is Associated With Cardio-Protective Profiles in a Diverse Population-Based Survey as Part of the Epidemiologic Architecture for Genes Linked to Environment Study. Circulation: Cardiovascular Genetics, 2014, 7, 848-853.	5.1	31
85	Multiancestral Analysis of Inflammation-Related Genetic Variants and C-Reactive Protein in the Population Architecture Using Genomics and Epidemiology Study. Circulation: Cardiovascular Genetics, 2014, 7, 178-188.	5.1	31
86	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	1.8	31
87	Identifying Host Genetic Risk Factors in the Context of Public Health Surveillance for Invasive Pneumococcal Disease. PLoS ONE, 2011, 6, e23413.	1.1	31
88	Accuracy of Administratively-Assigned Ancestry for Diverse Populations in an Electronic Medical Record-Linked Biobank. PLoS ONE, 2014, 9, e99161.	1.1	31
89	<i>LPA</i> and <i>PLG</i> Sequence Variation and Kringle IV-2 Copy Number in Two Populations. Human Heredity, 2008, 66, 199-209.	0.4	30
90	Gene-carbohydrate and gene-fiber interactions and type 2 diabetes in diverse populations from the National Health and Nutrition Examination Surveys (NHANES) as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. BMC Genetics, 2014, 15, 69.	2.7	30

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91	Identifying the genotype behind the phenotype: a role model found inVKORC1and its association with warfarin dosing. Pharmacogenomics, 2007, 8, 487-496.	0.6	29
92	The Influence of Obesity-Related Single Nucleotide Polymorphisms on BMI Across the Life Course: The PAGE Study. Diabetes, 2013, 62, 1763-1767.	0.3	29
93	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. Human Molecular Genetics, 2016, 25, 5500-5512.	1.4	29
94	Evidence for Age As a Modifier of Genetic Associations for Lipid Levels. Annals of Human Genetics, 2011, 75, 589-597.	0.3	28
95	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. BMC Medical Genomics, 2016, 9, 32.	0.7	26
96	Genetic variation in recipient B-cell activating factor modulates phenotype of GVHD. Blood, 2011, 118, 1140-1144.	0.6	25
97	Genetic determinants of the ankle-brachial index: A meta-analysis of a cardiovascular candidate gene 50K SNP panel in the candidate gene association resource (CARe) consortium. Atherosclerosis, 2012, 222, 138-147.	0.4	25
98	ENVIRONMENT-WIDE ASSOCIATION STUDY (EWAS) FOR TYPE 2 DIABETES IN THE MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT BIOBANK. , 2013, , .		25
99	Extraction of echocardiographic data from the electronic medical record is a rapid and efficient method for study of cardiac structure and function. Journal of Clinical Bioinformatics, 2014, 4, 12.	1.2	25
100	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. PLoS ONE, 2018, 13, e0200486.	1.1	25
101	Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 200-11.	0.7	25
102	A common VLDLR polymorphism interacts with APOE genotype in the prediction of carotid artery disease risk. Journal of Lipid Research, 2008, 49, 588-596.	2.0	24
103	Investigation of gene-by-sex interactions for lipid traits in diverse populations from the population architecture using genomics and epidemiology study. BMC Genetics, 2013, 14, 33.	2.7	24
104	Genetic variants associated with fasting glucose and insulin concentrations in an ethnically diverse population: results from the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Medical Genetics, 2013, 14, 98.	2.1	24
105	Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. Pharmacogenomics, 2013, 14, 735-744.	0.6	24
106	Africanâ€specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. International Journal of Cancer, 2021, 148, 99-105.	2.3	24
107	Surveillance for Anthrax Cases Associated with Contaminated Letters, New Jersey, Delaware, and Pennsylvania, 2001. Emerging Infectious Diseases, 2002, 8, 1073-1077.	2.0	23
108	Population Differences in Genetic Risk for Age-Related Macular Degeneration and Implications for Genetic Testing. JAMA Ophthalmology, 2012, 130, 116.	2.6	23

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109	Association of Cancer Susceptibility Variants with Risk of Multiple Primary Cancers: The Population Architecture using Genomics and Epidemiology Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2568-2578.	1.1	23
110	SCN5A Variation Is Associated With Electrocardiographic Traits in the Jackson Heart Study. Circulation: Cardiovascular Genetics, 2011, 4, 139-144.	5.1	22
111	A Rare Germline HOXB13 Variant Contributes to Risk of Prostate Cancer in Men of African Ancestry. European Urology, 2022, 81, 458-462.	0.9	22
112	CRP Polymorphisms and Progression of Chronic Kidney Disease in African Americans. Clinical Journal of the American Society of Nephrology: CJASN, 2010, 5, 24-33.	2.2	21
113	Effects of smoking on the genetic risk of obesity: the population architecture using genomics and epidemiology study. BMC Medical Genetics, 2013, 14, 6.	2.1	21
114	Replication of Associations between GWAS SNPs and Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Journal of Investigative Dermatology, 2014, 134, 2049-2052.	0.3	21
115	DEVELOPMENT AND PERFORMANCE OF TEXT-MINING ALGORITHMS TO EXTRACT SOCIOECONOMIC STATUS FROM DE-IDENTIFIED ELECTRONIC HEALTH RECORDS. , 2017, 22, 230-241.		21
116	Allelic spectrum of the natural variation in CRP. Human Genetics, 2006, 119, 496-504.	1.8	20
117	Biologyâ€Driven Geneâ€Gene Interaction Analysis of Ageâ€Related Cataract in the eMERGE Network. Genetic Epidemiology, 2015, 39, 376-384.	0.6	20
118	Phenome-Wide Association Studies: Embracing Complexity for Discovery. Human Heredity, 2015, 79, 111-123.	0.4	20
119	Pleiotropic and Sex-Specific Effects of Cancer GWAS SNPs on Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2015, 10, e0120491.	1.1	19
120	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. Heart Rhythm, 2017, 14, 572-580.	0.3	19
121	Genome-Wide Association Study of Serum Creatinine Levels during Vancomycin Therapy. PLoS ONE, 2015, 10, e0127791.	1.1	19
122	Genetic Variation in Donor CTLA-4 Regulatory Region is a Strong Predictor of Outcome after Allogeneic Hematopoietic Cell Transplantation for Hematologic Malignancies. Biology of Blood and Marrow Transplantation, 2012, 18, 1069-1075.	2.0	18
123	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. Carcinogenesis, 2014, 35, 2068-2073.	1.3	18
124	Global variation in sequencing impedes SARS-CoV-2 surveillance. PLoS Genetics, 2021, 17, e1009620.	1.5	18
125	Investigating the relationship between mitochondrial genetic variation and cardiovascular-related traits to develop a framework for mitochondrial phenome-wide association studies. BioData Mining, 2014, 7, 6.	2.2	16
126	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Molecular Genetics, 2018, 27, 2940-2953.	1.4	16

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127	Genome-wide association analysis of common genetic variants of resistant hypertension. Pharmacogenomics Journal, 2019, 19, 295-304.	0.9	16
128	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010113.	1.5	16
129	Admixture Mapping and Subsequent Fine-Mapping Suggests a Biologically Relevant and Novel Association on Chromosome 11 for Type 2 Diabetes in African Americans. PLoS ONE, 2014, 9, e86931.	1.1	15
130	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. PLoS ONE, 2019, 14, e0226771.	1.1	15
131	VKORC1 Common Variation and Bone Mineral Density in the Third National Health and Nutrition Examination Survey. PLoS ONE, 2010, 5, e15088.	1.1	15
132	DETECTING AND CHARACTERIZING PLEIOTROPY: NEW METHODS FOR UNCOVERING THE CONNECTION BETWEEN THE COMPLEXITY OF GENOMIC ARCHITECTURE AND MULTIPLE PHENOTYPES- SESSION INTRODUCTION. , 2013, , 183-187.		14
133	Controlling for population structure and genotyping platform bias in the eMERGE multi-institutional biobank linked to electronic health records. Frontiers in Genetics, 2014, 5, 352.	1.1	14
134	Shared Genetic Etiology of Autoimmune Diseases in Patients from a Biorepository Linked to De-identified Electronic Health Records. Frontiers in Genetics, 2016, 7, 185.	1.1	14
135	VISUAL INTEGRATION OF RESULTS FROM A LARGE DNA BIOBANK (BIOVU) USING SYNTHESIS-VIEW. , 2010, , 265-275.		14
136	Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. Prostate Cancer and Prostatic Diseases, 2022, 25, 755-761.	2.0	14
137	Characterization of Î²-globin haplotypes using blood spots from a population-based cohort of newborns with homozygous HbS. Genetics in Medicine, 2002, 4, 328-335.	1.1	13
138	Willingness to Participate in a National Precision Medicine Cohort: Attitudes of Chronic Kidney Disease Patients at a Cleveland Public Hospital. Journal of Personalized Medicine, 2018, 8, 21.	1.1	13
139	Reducing Clinical Noise for Body Mass Index Measures Due to Unit and Transcription Errors in the Electronic Health Record. AMIA Summits on Translational Science Proceedings, 2017, 2017, 102-111.	0.4	13
140	Serum vitamins A and E as modifiers of lipid trait genetics in the National Health and Nutrition Examination Surveys as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Genetics, 2012, 131, 1699-1708.	1.8	12
141	Lipid trait-associated genetic variation is associated with gallstone disease in the diverse Third National Health and Nutrition Examination Survey (NHANES III). BMC Medical Genetics, 2013, 14, 120.	2.1	12
142	Genetic variation in the Î²1-adrenergic receptor is associated with the risk of atrial fibrillation after cardiac surgery. American Heart Journal, 2014, 167, 101-108.e1.	1.2	12
143	Population Stratification in the Context of Diverse Epidemiologic Surveys Sans Genome-Wide Data. Frontiers in Genetics, 2016, 7, 76.	1.1	12
144	Optimizing identification of resistant hypertension: Computable phenotype development and validation. Pharmacoepidemiology and Drug Safety, 2020, 29, 1393-1401.	0.9	12

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145	Enabling high-throughput genotype-phenotype associations in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 373-84.	0.7	12
146	Atopy history and the genomics of wheezing after influenza vaccination in children 6â€“59 months of age. Vaccine, 2011, 29, 3431-3437.	1.7	11
147	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. BioData Mining, 2015, 8, 35.	2.2	11
148	Extracting Primary Open-Angle Glaucoma from Electronic Medical Records for Genetic Association Studies. PLoS ONE, 2015, 10, e0127817.	1.1	11
149	CRP polymorphisms and chronic kidney disease in the third national health and nutrition examination survey. BMC Medical Genetics, 2011, 12, 65.	2.1	10
150	Replication and characterisation of genetic variants in the fibrinogen gene cluster with plasma fibrinogen levels and haematological traits in the Third National Health and Nutrition Examination Survey. Thrombosis and Haemostasis, 2012, 107, 458-467.	1.8	10
151	The effects of electronic medical record phenotyping details on genetic association studies: HDL-C as a case study. BioData Mining, 2015, 8, 15.	2.2	10
152	Evidence for extensive pleiotropy among pharmacogenes. Pharmacogenomics, 2016, 17, 853-866.	0.6	10
153	Local genetic ancestry in CDKN2B-AS1 is associated with primary open-angle glaucoma in an African American cohort extracted from de-identified electronic health records. BMC Medical Genomics, 2018, 11, 70.	0.7	10
154	Mind the gap: resources required to receive, process and interpret research-returned whole genome data. Human Genetics, 2019, 138, 691-701.	1.8	10
155	Methods for optimizing statistical analyses in pharmacogenomics research. Expert Review of Clinical Pharmacology, 2009, 2, 559-570.	1.3	9
156	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. Pharmacogenomics, 2009, 10, 1043-1053.	0.6	9
157	UTILIZATION OF AN EMR-BIOREPOSITORY TO IDENTIFY THE GENETIC PREDICTORS OF CALCINEURIN-INHIBITOR TOXICITY IN HEART TRANSPLANT RECIPIENTS. , 2013, , .		9
158	Bridging the Gaps in Personalized Medicine Value Assessment: A Review of the Need for Outcome Metrics across Stakeholders and Scientific Disciplines. Public Health Genomics, 2019, 22, 16-24.	0.6	9
159	Performance of African-ancestry-specific polygenic hazard score varies according to local ancestry in 8q24. Prostate Cancer and Prostatic Diseases, 2022, 25, 229-237.	2.0	9
160	Hi-MC: a novel method for high-throughput mitochondrial haplogroup classification. PeerJ, 2018, 6, e5149.	0.9	9
161	Maturation and application of phenome-wide association studies. Trends in Genetics, 2022, 38, 353-363.	2.9	9
162	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program. Frontiers in Genetics, 2021, 12, 777076.	1.1	9

#	Article	IF	Citations
163	Integrating Host Genomics with Surveillance for Invasive Bacterial Diseases. Emerging Infectious Diseases, 2008, 14, 1138-1140.	2.0	8
164	MITOCHONDRIAL VARIATION AND THE RISK OF AGE-RELATED MACULAR DEGENERATION ACROSS DIVERSE POPULATIONS. , 2014, , .		8
165	Editorial: The Importance of Diversity in Precision Medicine Research. Frontiers in Genetics, 2020, 11, 875.	1.1	8
166	Utilization of an EMR-biorepository to identify the genetic predictors of calcineurin-inhibitor toxicity in heart transplant recipients. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 253-64.	0.7	8
167	ENABLING HIGH-THROUGHPUT GENOTYPE-PHENOTYPE ASSOCIATIONS IN THE EPIDEMIOLOGIC ARCHITECTURE FOR GENES LINKED TO ENVIRONMENT (EAGLE) PROJECT AS PART OF THE POPULATION ARCHITECTURE USING GENOMICS AND EPIDEMIOLOGY (PAGE) STUDY. , 2012, , .		7
168	No evidence of interaction between known lipid-associated genetic variants and smoking in the multi-ethnic PAGE population. Human Genetics, 2013, 132, 1427-1431.	1.8	7
169	Cryptic relatedness in epidemiologic collections accessed for genetic association studies: experiences from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study and the National Health and Nutrition Examination Surveys (NHANES). Frontiers in Genetics, 2015, 6, 317.	1.1	7
170	Germline Genetic Variants and Lung Cancer Survival in African Americans. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1288-1295.	1.1	7
171	A Social Determinant of Health May Modify Genetic Associations for Blood Pressure: Evidence From a SNP by Education Interaction in an African American Population. Frontiers in Genetics, 2019, 10, 428.	1.1	7
172	Characterization of the Metabochip in diverse populations from the International HapMap Project in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 188-99.	0.7	7
173	THE CHALLENGES IN USING ELECTRONIC HEALTH RECORDS FOR PHARMACOGENOMICS AND PRECISION MEDICINE RESEARCH. , 2016, , .		6
174	Genetic Risk Factors for BMI and Obesity in an Ethnically Diverse Population: Results From the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Obesity, 0, , .	1.5	6
175	Mitochondrial variation and the risk of age-related macular degeneration across diverse populations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 243-54.	0.7	6
176	Local ancestry transitions modify snp-trait associations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 424-435.	0.7	6
177	Single nucleotide polymorphism discovery in TBX1 in individuals with and without 22q11.2 deletion syndrome. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 54-63.	1.6	5
178	Post-Genome-Wide Association Study Challenges for Lipid Traits: Describing Age as a Modifier of Gene-Lipid Associations in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Annals of Human Genetics, 2013, 77, 416-425.	0.3	5
179	Local ancestry transitions modify snp-trait associations. , 2018, , .		5
180	Frequency and phenotype consequence of APOC3 rare variants in patients with very low triglyceride levels. BMC Medical Genomics, 2018, 11, 66.	0.7	5

#	Article	IF	Citations
181	CHARACTERIZATION OF THE METABOCHIP IN DIVERSE POPULATIONS FROM THE INTERNATIONAL HAPMAP PROJECT IN THE EPIDEMIOLOGIC ARCHITECTURE FOR GENES LINKED TO ENVIRONMENT (EAGLE) PROJECT. , 2012, , .		5
182	THE CHALLENGES IN USING ELECTRONIC HEALTH RECORDS FOR PHARMACOGENOMICS AND PRECISION MEDICINE RESEARCH. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 369-80.	0.7	5
183	An association test of the spatial distribution of rare missense variants within protein structures identifies Alzheimer's diseaseâ€“related patterns. Genome Research, 2022, 32, 778-790.	2.4	5
184	Peptide tyrosine tyrosine levels are increased in patients with urea cycle disorders. Molecular Genetics and Metabolism, 2012, 106, 39-42.	0.5	4
185	Identification of gene-gene and gene-environment interactions within the fibrinogen gene cluster for fibrinogen levels in three ethnically diverse populations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 219-30.	0.7	4
186	Somatic T-cell Receptor Diversity in a Chronic Kidney Disease PatientPopulation Linked to Electronic Health Records. AMIA Summits on Translational Science Proceedings, 2018, 2017, 63-71.	0.4	4
187	Development and Evaluation of a Rules-based Algorithm for Primary Open-Angle Glaucoma in the VA Million Veteran Program. Ophthalmic Epidemiology, 2022, 29, 640-648.	0.8	4
188	Replication of European hypertension associations in a case-control study of 9,534 African Americans. PLoS ONE, 2021, 16, e0259962.	1.1	4
189	Strategies for Genotyping. Current Protocols in Human Genetics, 2011, 68, Unit1.3.	3.5	3
190	INTEGRATING COMMUNITY-LEVEL DATA RESOURCES FOR PRECISION MEDICINE RESEARCH. , 2018, , .		3
191	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
192	IDENTIFICATION OF GENE-GENE AND GENE-ENVIRONMENT INTERACTIONS WITHIN THE FIBRINOGEN GENE CLUSTER FOR FIBRINOGEN LEVELS IN THREE ETHNICALLY DIVERSE POPULATIONS. , 2014, , .		3
193	TESTING POPULATION-SPECIFIC QUANTITATIVE TRAIT ASSOCIATIONS FOR CLINICAL OUTCOME RELEVANCE IN A BIOREPOSITORY LINKED TO ELECTRONIC HEALTH RECORDS: LPA AND MYOCARDIAL INFARCTION IN AFRICAN AMERICANS. , 2016, , .		3
194	Development of a data-mining algorithm to identify ages at reproductive milestones in electronic medical records. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 376-87.	0.7	3
195	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 285-96.	0.7	3
196	Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record. American Journal of Human Genetics, 2010, 87, 310.	2.6	2
197	DEVELOPMENT OF A DATA-MINING ALGORITHM TO IDENTIFY AGES AT REPRODUCTIVE MILESTONES IN ELECTRONIC MEDICAL RECORDS. , 2013, , .		2
198	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE. , 2016, , .		2

#	Article	IF	Citations
199	Replication of SCN5A Associations with Electrocardiographic Traits in African Americans from Clinical and Epidemiologic Studies. Lecture Notes in Computer Science, 2014, 2014, 939-951.	1.0	2
200	MEASURES OF EXPOSURE IMPACT GENETIC ASSOCIATION STUDIES: AN EXAMPLE IN VITAMIN K LEVELS AND VKORC1. , 2014, , .		2
201	Measures of exposure impact genetic association studies: an example in vitamin K levels and VKORC1. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 161-70.	0.7	2
202	TESTING POPULATION-SPECIFIC QUANTITATIVE TRAIT ASSOCIATIONS FOR CLINICAL OUTCOME RELEVANCE IN A BIOREPOSITORY LINKED TO ELECTRONIC HEALTH RECORDS: LPA AND MYOCARDIAL INFARCTION IN AFRICAN AMERICANS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 96-107.	0.7	2
203	DRUG-DRUG INTERACTION PROFILES OF MEDICATION REGIMENS EXTRACTED FROM A DE-IDENTIFIED ELECTRONIC MEDICAL RECORDS SYSTEM. AMIA Summits on Translational Science Proceedings, 2016, 2016, 33-40.	0.4	2
204	Searching in the Dark: Phenotyping Diabetic Retinopathy in a De-Identified Electronic Medical Record Sample of African Americans. AMIA Summits on Translational Science Proceedings, 2016, 2016, 221-30.	0.4	2
205	Extracting Country-of-Origin from Electronic Health Records for Gene- Environment Studies as Part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Study. AMIA Summits on Translational Science Proceedings, 2017, 2017, 50-57.	0.4	2
206	Predicting Incident Coronary Heart Disease Many Markers at a Time. Circulation: Cardiovascular Genetics, 2016, 9, 472-473.	5.1	1
207	Biobanks Linked to Electronic Health Records Accelerate Genomic Discovery. Journal of the American Society of Nephrology: JASN, 2021, 32, 1828-1829.	3.0	1
208	Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital. , 2019, , .		1
209	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 389-399.	0.7	1
210	Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 575-586.	0.7	1
211	A Primer in Statistical Methods in Genetics. , 0, , 20-32.		0
212	Computational Challenges and Artificial Intelligence in Precision Medicine. , 2020, , .		0
213	Genetic Variation In Recipient BAFF Modulates Phenotype of Chronic GvHD After HCT. Blood, 2010, 116, 215-215.	0.6	0
214	Precision Medicine: Improving health through high-resolution analysis of personal data. , 2018, , .		0
215	Abstract 3517: A germline variant at 8q24 contributes to familial clustering of prostate cancer in men of African ancestry. , 2020, , .		0
216	Genetically-guided algorithm development and sample size optimization for age-related macular degeneration cases and controls in electronic health records from the VA Million Veteran Program. AMIA Summits on Translational Science Proceedings, 2019, 2019, 153-162.	0.4	0

#	Article	IF	Citations
217	Precision Medicine: Using Artificial Intelligence to Improve Diagnostics and Healthcare. , 2021, , .		0