Dana C Crawford

List of Publications by Citations

197 papers	14,027 citations	50 h-index	116 g-index
227 ext. papers	17,026 ext. citations	6.7 avg, IF	5.51 L-index

#	Paper	IF	Citations
197	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
196	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
195	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
194	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations. *Bioinformatics*, **2010**, 26, 1205-10	7.2	668
193	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. *Nature Biotechnology*, **2013**, 31, 1102-10	44.5	555
192	FMR1 and the fragile X syndrome: human genome epidemiology review. *Genetics in Medicine*, **2001**, 3, 359-71	8.1	474
191	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. *Blood*, **2010**, 115, 3827-34	2.2	289
190	Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. *American Journal of Human Genetics*, **2010**, 86, 560-72	11	264
189	Definition and clinical importance of haplotypes. *Annual Review of Medicine*, **2005**, 56, 303-20	17.4	243
188	Evidence for substantial fine-scale variation in recombination rates across the human genome. *Nature Genetics*, **2004**, 36, 700-6	36.3	233
187	Quality control procedures for genome-wide association studies. *Current Protocols in Human Genetics*, **2011**, Chapter 1, Unit1.19	3.2	199
186	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, 529-42	11	199
185	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. *Lancet, The*, **2013**, 382, 790-6	40	191
184	Unravelling the human genome-phenome relationship using phenome-wide association studies. *Nature Reviews Genetics*, **2016**, 17, 129-45	30.1	167
183	Generalization and dilution of association results from European GWAS in populations of non-European ancestry: the PAGE study. *PLoS Biology*, **2013**, 11, e1001661	9.7	155
182	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	6	151
181	Pattern of sequence variation across 213 environmental response genes. *Genome Research*, **2004**, 14, 1821-31	9.7	147

180	Haplotype diversity across 100 candidate genes for inflammation, lipid metabolism, and blood pressure regulation in two populations. *American Journal of Human Genetics*, **2004**, 74, 610-22	11	146
179	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, 849-59	3.8	141
178	Genome- and phenome-wide analyses of cardiac conduction identifies markers of arrhythmia risk. *Circulation*, **2013**, 127, 1377-85	16.7	133
177	Genetic determinants of lipid traits in diverse populations from the population architecture using genomics and epidemiology (PAGE) study. *PLoS Genetics*, **2011**, 7, e1002138	6	128
176	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, 91-9		127
175	Phenome-wide association study (PheWAS) for detection of pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. *PLoS Genetics*, **2013**, 9, e1003087	6	126
174	Genetic variation is associated with C-reactive protein levels in the Third National Health and Nutrition Examination Survey. *Circulation*, **2006**, 114, 2458-65	16.7	126
173	Prevalence of the fragile X syndrome in African-Americans. *American Journal of Medical Genetics Part A*, **2002**, 110, 226-33		118
172	Prevalence and phenotype consequence of FRAXA and FRAXE alleles in a large, ethnically diverse, special education-needs population. *American Journal of Human Genetics*, **1999**, 64, 495-507	11	110
171	Identification of genomic predictors of atrioventricular conduction: using electronic medical records as a tool for genome science. *Circulation*, **2010**, 122, 2016-21	16.7	107
170	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circulation Research*, **2017**, 120, 341-353	15.7	97
169	The patterns of natural variation in human genes. *Annual Review of Genomics and Human Genetics*, **2005**, 6, 287-312	9.7	96
168	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. *Cell*, **2017**, 170, 199-212.e20	56.2	94
167	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	6	94
166	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. *Human Genetics*, **2012**, 131, 639-52	6.3	92
165	Imputation and quality control steps for combining multiple genome-wide datasets. *Frontiers in Genetics*, **2014**, 5, 370	4.5	90
164	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, 424-31	8.1	85
163	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, 100-12		84

162	Predicting warfarin dosage in European-Americans and African-Americans using DNA samples linked to an electronic health record. *Pharmacogenomics*, **2012**, 13, 407-18	2.6	83
161	Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. *Genetics in Medicine*, **2010**, 12, 648-50	8.1	72
160	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, 387-91	8.6	66
159	eMERGEing progress in genomics-the first seven years. *Frontiers in Genetics*, **2014**, 5, 184	4.5	65
158	Fine Mapping and Identification of BMI Loci in African Americans. *American Journal of Human Genetics*, **2013**, 93, 661-71	11	63
157	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	36.3	62
156	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, 835-46	8	60
155	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	3.7	59
154	Association of functional polymorphism rs2231142 (Q141K) in the ABCG2 gene with serum uric acid and gout in 4 US populations: the PAGE Study. *American Journal of Epidemiology*, **2013**, 177, 923-32	3.8	59
153	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	6	56
152	Knowledge-driven multi-locus analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent EMR-linked biobanks. *PLoS ONE*, **2011**, 6, e19586	3.7	55
151	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. *Genetic Epidemiology*, **2011**, 35, 887-98	2.6	55
150	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, 1532-44	11	54
149	Association of the FTO obesity risk variant rs8050136 with percentage of energy intake from fat in multiple racial/ethnic populations: the PAGE study. *American Journal of Epidemiology*, **2013**, 178, 780-90	3.8	53
148	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	4.5	53
147	Genetic determinants of age-related macular degeneration in diverse populations from the PAGE study. *Investigative Ophthalmology and Visual Science*, **2014**, 55, 6839-50		50
146	Genotype imputation of Metabochip SNPs using a study-specific reference panel of ~4,000 haplotypes in African Americans from the Women's Health Initiative. *Genetic Epidemiology*, **2012**, 36, 107-17	2.6	49
145	Characterization of mitochondrial haplogroups in a large population-based sample from the United States. *Human Genetics*, **2014**, 133, 861-8	6.3	48

144	Genome wide analysis of drug-induced torsades de pointes: lack of common variants with large effect sizes. *PLoS ONE*, **2013**, 8, e78511	3.7	48
143	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	6	47
142	Genetic variation associated with circulating monocyte count in the eMERGE Network. *Human Molecular Genetics*, **2013**, 22, 2119-27	5.6	46
141	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, 480-93	11	44
140	Consistent directions of effect for established type 2 diabetes risk variants across populations: the population architecture using Genomics and Epidemiology (PAGE) Consortium. *Diabetes*, **2012**, 61, 1642-7	9.9	42
139	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American Journal of Human Genetics*, **2016**, 99, 56-75	11	41
138	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
137	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
136	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, 394-9	4.9	38
135	Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. *BioData Mining*, **2010**, 3, 10	4.3	36
134	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
133	Visually integrating and exploring high throughput Phenome-Wide Association Study (PheWAS) results using PheWAS-View. *BioData Mining*, **2012**, 5, 5	4.3	33
132	Characterization of genome-wide association-identified variants for atrial fibrillation in African Americans. *PLoS ONE*, **2012**, 7, e32338	3.7	33
131	Genetic variation and reproductive timing: African American women from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *PLoS ONE*, **2013**, 8, e55258	3.7	32
130	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. *Bioinformatics*, **2013**, 29, 2744-9	7.2	30
129	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	3.7	29
128	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	3.7	28
127	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	9.7	28

126	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. *Human Heredity*, **2015**, 79, 137-46	1.1	27
125	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. *Gut*, **2014**, 63, 800-7	19.2	27
124	SecureMA: protecting participant privacy in genetic association meta-analysis. *Bioinformatics*, **2014**, 30, 3334-41	7.2	26
123	Generalization of variants identified by genome-wide association studies for electrocardiographic traits in African Americans. *Annals of Human Genetics*, **2013**, 77, 321-32	2.2	26
122	LPA and PLG sequence variation and kringle IV-2 copy number in two populations. *Human Heredity*, **2008**, 66, 199-209	1.1	26
121	Accuracy of administratively-assigned ancestry for diverse populations in an electronic medical record-linked biobank. *PLoS ONE*, **2014**, 9, e99161	3.7	26
120	The detection and characterization of pleiotropy: discovery, progress, and promise. *Briefings in Bioinformatics*, **2016**, 17, 13-22	13.4	25
119	The influence of obesity-related single nucleotide polymorphisms on BMI across the life course: the PAGE study. *Diabetes*, **2013**, 62, 1763-7	0.9	25
118	Identifying the genotype behind the phenotype: a role model found in VKORC1 and its association with warfarin dosing. *Pharmacogenomics*, **2007**, 8, 487-96	2.6	25
117	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, 1061-8	3.2	24
116	A common VLDLR polymorphism interacts with APOE genotype in the prediction of carotid artery disease risk. *Journal of Lipid Research*, **2008**, 49, 588-96	6.3	24
115	Identifying host genetic risk factors in the context of public health surveillance for invasive pneumococcal disease. *PLoS ONE*, **2011**, 6, e23413	3.7	24
114	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	1.3	24
113	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	6.3	23
112	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. *BMC Medical Genomics*, **2016**, 9 Suppl 1, 32	3.7	23
111	Lack of associations of ten candidate coronary heart disease risk genetic variants and subclinical atherosclerosis in four US populations: the Population Architecture using Genomics and Epidemiology (PAGE) study. *Atherosclerosis*, **2013**, 228, 390-9	3.1	23
110	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	2.6	23
109	Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. *Pharmacogenomics*, **2013**, 14, 735-44	2.6	23

108	Genome-wide study of resistant hypertension identified from electronic health records. *PLoS ONE*, **2017**, 12, e0171745	3.7	23
107	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	5.6	22
106	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	22
105	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, 178-88		22
104	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, 2568-78	4	21
103	Genetic variation in recipient B-cell activating factor modulates phenotype of GVHD. *Blood*, **2011**, 118, 1140-4	2.2	21
102	Evidence for age as a modifier of genetic associations for lipid levels. *Annals of Human Genetics*, **2011**, 75, 589-97	2.2	21
101	Using Electronic Health Records To Generate Phenotypes For Research. *Current Protocols in Human Genetics*, **2019**, 100, e80	3.2	21
100	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	2.6	20
99	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	20
98	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		20
97	Rare variant APOC3 R19X 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, 848-53		20
96	Surveillance for anthrax cases associated with contaminated letters, New Jersey, Delaware, and Pennsylvania, 2001. *Emerging Infectious Diseases*, **2002**, 8, 1073-7	10.2	20
95	Population differences in genetic risk for age-related macular degeneration and implications for genetic testing. *JAMA Ophthalmology*, **2012**, 130, 116-7		19
94	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, 138-47	3.1	18
93	SCN5A variation is associated with electrocardiographic traits in the Jackson Heart Study. *Circulation: Cardiovascular Genetics*, **2011**, 4, 139-44		18
92	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17
91	CRP polymorphisms and progression of chronic kidney disease in African Americans. *Clinical Journal of the American Society of Nephrology: CJASN*, **2010**, 5, 24-33	6.9	17

90	Allelic spectrum of the natural variation in CRP. *Human Genetics*, **2006**, 119, 496-504	6.3	17
89	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. *Nature Reviews Nephrology*, **2020**, 16, 686-696	14.9	17
88	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. *Journal of Thoracic Oncology*, **2018**, 13, 1464-1473	8.9	16
87	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	4.3	16
86	Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. *Genetic Epidemiology*, **2015**, 39, 376-84	2.6	16
85	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	4.3	16
84	Genome-Wide Association Study of Serum Creatinine Levels during Vancomycin Therapy. *PLoS ONE*, **2015**, 10, e0127791	3.7	16
83	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	6.7	15
82	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	3.7	14
81	DEVELOPMENT AND PERFORMANCE OF TEXT-MINING ALGORITHMS TO EXTRACT SOCIOECONOMIC STATUS FROM DE-IDENTIFIED ELECTRONIC HEALTH RECORDS. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 230-241	1.3	14
80	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	3.7	14
79	Phenome-Wide Association Studies: Embracing Complexity for Discovery. *Human Heredity*, **2015**, 79, 111-23	1.1	13
78	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. *European Urology*, **2020**, 78, 316-320	10.2	13
77	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, 1069-75	4.7	13
76	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	4.5	12
75	Characterization of beta-globin haplotypes using blood spots from a population-based cohort of newborns with homozygous HbS. *Genetics in Medicine*, **2002**, 4, 328-35	8.1	12
74	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	1.3	12
73	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	3.7	11

72	VKORC1 common variation and bone mineral density in the Third National Health and Nutrition Examination Survey. *PLoS ONE*, **2010**, 5, e15088	3.7	11
71	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	1.1	11
70	Global variation in sequencing impedes SARS-CoV-2 surveillance. *PLoS Genetics*, **2021**, 17, e1009620	6	11
69	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	10
68	Genetic variation in the 1-adrenergic receptor is associated with the risk of atrial fibrillation after cardiac surgery. *American Heart Journal*, **2014**, 167, 101-108.e1	4.9	10
67	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, 1699-708	6.3	10
66	Visual integration of results from a large DNA biobank (BioVU) using synthesis-view. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2011**, 265-75	1.3	10
65	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. *BioData Mining*, **2015**, 8, 35	4.3	9
64	CRP polymorphisms and chronic kidney disease in the third national health and nutrition examination survey. *BMC Medical Genetics*, **2011**, 12, 65	2.1	9
63	Extracting Primary Open-Angle Glaucoma from Electronic Medical Records for Genetic Association Studies. *PLoS ONE*, **2015**, 10, e0127817	3.7	9
62	Evidence for extensive pleiotropy among pharmacogenes. *Pharmacogenomics*, **2016**, 17, 853-66	2.6	8
61	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	5.6	8
60	Atopy history and the genomics of wheezing after influenza vaccination in children 6-59 months of age. *Vaccine*, **2011**, 29, 3431-7	4.1	8
59	Methods for optimizing statistical analyses in pharmacogenomics research. *Expert Review of Clinical Pharmacology*, **2009**, 2, 559-570	3.8	8
58	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics*, **2009**, 10, 1043-53	2.6	8
57	Population Stratification in the Context of Diverse Epidemiologic Surveys Sans Genome-Wide Data. *Frontiers in Genetics*, **2016**, 7, 76	4.5	8
56	Shared Genetic Etiology of Autoimmune Diseases in Patients from a Biorepository Linked to De-identified Electronic Health Records. *Frontiers in Genetics*, **2016**, 7, 185	4.5	8
55	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	3.7	8

54	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	3.7	8
53	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	1.9	7
52	The effects of electronic medical record phenotyping details on genetic association studies: HDL-C as a case study. *BioData Mining*, **2015**, 8, 15	4.3	7
51	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, 458-67	7	7
50	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	1.3	7
49	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	1.3	7
48	Genome-wide association analysis of common genetic variants of resistant hypertension. *Pharmacogenomics Journal*, **2019**, 19, 295-304	3.5	7
47	African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. *International Journal of Cancer*, **2021**, 148, 99-105	7.5	7
46	Mind the gap: resources required to receive, process and interpret research-returned whole genome data. *Human Genetics*, **2019**, 138, 691-701	6.3	6
45	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,	3.6	6
44	No evidence of interaction between known lipid-associated genetic variants and smoking in the multi-ethnic PAGE population. *Human Genetics*, **2013**, 132, 1427-31	6.3	6
43	Mitochondrial variation and the risk of age-related macular degeneration across diverse populations. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2015**, 243-54	1.3	6
42	Hi-MC: a novel method for high-throughput mitochondrial haplogroup classification. *PeerJ*, **2018**, 6, e5149	3.1	6
41	Genetic Risk Factors for BMI and Obesity in an Ethnically Diverse Population: Results From the Population Architecture Using Genomics and Epidemiology (PAGE) Study. *Obesity*,	8	6
40	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		5
39	Integrating host genomics with surveillance for invasive bacterial diseases. *Emerging Infectious Diseases*, **2008**, 14, 1138-40	10.2	5
38	Germline Genetic Variants and Lung Cancer Survival in African Americans. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1288-1295	4	4
37	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	4.5	4

36	MITOCHONDRIAL VARIATION AND THE RISK OF AGE-RELATED MACULAR DEGENERATION ACROSS DIVERSE POPULATIONS **2014**,		4
35	Peptide tyrosine tyrosine levels are increased in patients with urea cycle disorders. *Molecular Genetics and Metabolism*, **2012**, 106, 39-42	3.7	4
34	Detecting and Characterizing Pleiotropy: New Methods for Uncovering the Connection Between the Complexity of Genomic Architecture and Multiple phenotypes. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2014**, 183-187	1.3	4
33	ENVIRONMENT-WIDE ASSOCIATION STUDY (EWAS) FOR TYPE 2 DIABETES IN THE MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT BIOBANK **2013**,		4
32	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, 416-25	2.2	4
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