Dana C Crawford

List of Publications by Year in Descending Order

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	An association test of the spatial distribution of rare missense variants within protein structures identify Alzheimer's disease-related patterns.. *Genome Research*, **2022**,	9.7	1
196	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	6	0
195	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	4.5	1
194	Study Design for Genetic Studies **2021**, 58-78		
193	Development and Evaluation of a Rules-based Algorithm for Primary Open-Angle Glaucoma in the VA Million Veteran Program. *Ophthalmic Epidemiology*, **2021**, 1-9	1.9	0
192	Replication of European hypertension associations in a case-control study of 9,534 African Americans. *PLoS ONE*, **2021**, 16, e0259962	3.7	1
191	Global variation in sequencing impedes SARS-CoV-2 surveillance. *PLoS Genetics*, **2021**, 17, e1009620	6	11
190	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
189	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
188	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
187	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	1.3	1
186	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. *Nature Reviews Nephrology*, **2020**, 16, 686-696	14.9	17
185	Optimizing identification of resistant hypertension: Computable phenotype development and validation. *Pharmacoepidemiology and Drug Safety*, **2020**, 29, 1393-1401	2.6	3
184	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
183	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	4.5	3
182	Mind the gap: resources required to receive, process and interpret research-returned whole genome data. *Human Genetics*, **2019**, 138, 691-701	6.3	6
181	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	1.1	

180	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
179	Genome-wide association analysis of common genetic variants of resistant hypertension. *Pharmacogenomics Journal*, **2019**, 19, 295-304	3.5	7
178	Using Electronic Health Records To Generate Phenotypes For Research. *Current Protocols in Human Genetics*, **2019**, 100, e80	3.2	21
177	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES **2018**,		2
176	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
175	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
174	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
173	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. *Journal of Thoracic Oncology*, **2018**, 13, 1464-1473	8.9	16
172	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
171	Local ancestry transitions modify snp-trait associations. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 424-435	1.3	4
170	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	1.1	4
169	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 389-399	1.3	
168	Hi-MC: a novel method for high-throughput mitochondrial haplogroup classification. *PeerJ*, **2018**, 6, e5149	3.1	6
167	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
166	Frequency and phenotype consequence of APOC3 rare variants in patients with very low triglyceride levels. *BMC Medical Genomics*, **2018**, 11, 66	3.7	2
165	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
164	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
163	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

162	Germline Genetic Variants and Lung Cancer Survival in African Americans. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1288-1295	4	4
161	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. *Cell*, **2017**, 170, 199-212.e20	56.2	94
160	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
159	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
158	Genome-wide study of resistant hypertension identified from electronic health records. *PLoS ONE*, **2017**, 12, e0171745	3.7	23
157	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	1.1	2
156	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
155	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE **2016**,		1
154	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
153	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
152	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
151	Evidence for extensive pleiotropy among pharmacogenes. *Pharmacogenomics*, **2016**, 17, 853-66	2.6	8
150	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
149	The detection and characterization of pleiotropy: discovery, progress, and promise. *Briefings in Bioinformatics*, **2016**, 17, 13-22	13.4	25
148	Unravelling the human genome-phenome relationship using phenome-wide association studies. *Nature Reviews Genetics*, **2016**, 17, 129-45	30.1	167
147	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*	1.3	2
146	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	1.3	4
145	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2016**, 21, 285-96	1.3	3

144	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	1.1	2
143	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	1.1	2
142	Population Stratification in the Context of Diverse Epidemiologic Surveys Sans Genome-Wide Data. *Frontiers in Genetics*, **2016**, 7, 76	4.5	8
141	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
140	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. *Human Heredity*, **2015**, 79, 137-46	1.1	27
139	Phenome-Wide Association Studies: Embracing Complexity for Discovery. *Human Heredity*, **2015**, 79, 111-23	1.1	13
138	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
137	Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. *Genetic Epidemiology*, **2015**, 39, 376-84	2.6	16
136	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. *BioData Mining*, **2015**, 8, 35	4.3	9
135	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
134	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
133	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
132	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
131	Genome-Wide Association Study of Serum Creatinine Levels during Vancomycin Therapy. *PLoS ONE*, **2015**, 10, e0127791	3.7	16
130	Extracting Primary Open-Angle Glaucoma from Electronic Medical Records for Genetic Association Studies. *PLoS ONE*, **2015**, 10, e0127817	3.7	9
129	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
128	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	1.3	2
127	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	1.3	4

126	Characterization of mitochondrial haplogroups in a large population-based sample from the United States. *Human Genetics*, **2014**, 133, 861-8	6.3	48
125	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17
124	Genetic determinants of age-related macular degeneration in diverse populations from the PAGE study. *Investigative Ophthalmology and Visual Science*, **2014**, 55, 6839-50		50
123	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
122	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
121	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
120	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
119	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
118	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
117	eMERGEing progress in genomics-the first seven years. *Frontiers in Genetics*, **2014**, 5, 184	4.5	65
116	Imputation and quality control steps for combining multiple genome-wide datasets. *Frontiers in Genetics*, **2014**, 5, 370	4.5	90
115	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
114	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
113	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
112	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
111	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
110	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
109	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

108	SecureMA: protecting participant privacy in genetic association meta-analysis. *Bioinformatics*, **2014**, 30, 3334-41	7.2	26
107	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
106	MITOCHONDRIAL VARIATION AND THE RISK OF AGE-RELATED MACULAR DEGENERATION ACROSS DIVERSE POPULATIONS **2014**,		4
105	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
104	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
103	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
102	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
101	Accuracy of administratively-assigned ancestry for diverse populations in an electronic medical record-linked biobank. *PLoS ONE*, **2014**, 9, e99161	3.7	26
100	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	1.3	3
99	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
98	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
97	Replication of Associations with Electrocardio-graphic Traits in African Americans from Clinical and Epidemiologic Studies. *Lecture Notes in Computer Science*, **2014**, 2014, 939-951	0.9	2
96	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
95	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
94	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
93	Fine Mapping and Identification of BMI Loci in African Americans. *American Journal of Human Genetics*, **2013**, 93, 661-71	11	63
92	UTILIZATION OF AN EMR-BIOREPOSITORY TO IDENTIFY THE GENETIC PREDICTORS OF CALCINEURIN-INHIBITOR TOXICITY IN HEART TRANSPLANT RECIPIENTS **2013**,		2
91	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

90	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
89	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
88	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
87	Genome- and phenome-wide analyses of cardiac conduction identifies markers of arrhythmia risk. *Circulation*, **2013**, 127, 1377-85	16.7	133
86	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
85	Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. *Pharmacogenomics*, **2013**, 14, 735-44	2.6	23
84	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. *Lancet, The*, **2013**, 382, 790-6	40	191
83	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
82	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
81	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
80	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
79	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. *Bioinformatics*, **2013**, 29, 2744-9	7.2	30
78	Genetic variation associated with circulating monocyte count in the eMERGE Network. *Human Molecular Genetics*, **2013**, 22, 2119-27	5.6	46
77	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
76	ENVIRONMENT-WIDE ASSOCIATION STUDY (EWAS) FOR TYPE 2 DIABETES IN THE MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT BIOBANK **2013**,		4
75	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
74	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
73	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

72	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
71	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
70	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
69	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
68	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
67	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
66	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
65	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
64	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
63	Peptide tyrosine tyrosine levels are increased in patients with urea cycle disorders. *Molecular Genetics and Metabolism*, **2012**, 106, 39-42	3.7	4
62	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
61	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
60	Visually integrating and exploring high throughput Phenome-Wide Association Study (PheWAS) results using PheWAS-View. *BioData Mining*, **2012**, 5, 5	4.3	33
59	Characterization of genome-wide association-identified variants for atrial fibrillation in African Americans. *PLoS ONE*, **2012**, 7, e32338	3.7	33
58	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
57	Population differences in genetic risk for age-related macular degeneration and implications for genetic testing. *JAMA Ophthalmology*, **2012**, 130, 116-7		19
56	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
55	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

54	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
53	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
52	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
51	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
50	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
49	Strategies for genotyping. *Current Protocols in Human Genetics*, **2011**, Chapter 1, Unit1.3	3.2	3
48	Quality control procedures for genome-wide association studies. *Current Protocols in Human Genetics*, **2011**, Chapter 1, Unit1.19	3.2	199
47	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
46	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
45	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
44	Genetic variation in recipient B-cell activating factor modulates phenotype of GVHD. *Blood*, **2011**, 118, 1140-4	2.2	21
43	Evidence for age as a modifier of genetic associations for lipid levels. *Annals of Human Genetics*, **2011**, 75, 589-97	2.2	21
42	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
41	CRP polymorphisms and chronic kidney disease in the third national health and nutrition examination survey. *BMC Medical Genetics*, **2011**, 12, 65	2.1	9
40	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
39	SCN5A variation is associated with electrocardiographic traits in the Jackson Heart Study. *Circulation: Cardiovascular Genetics*, **2011**, 4, 139-44		18
38	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
37	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

36	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
35	Identifying host genetic risk factors in the context of public health surveillance for invasive pneumococcal disease. *PLoS ONE*, **2011**, 6, e23413	3.7	24
34	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
33	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
32	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
31	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
30	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations. *Bioinformatics*, **2010**, 26, 1205-10	7.2	668
29	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
28	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. *Blood*, **2010**, 115, 3827-34	2.2	289
27	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
26	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
25	VKORC1 common variation and bone mineral density in the Third National Health and Nutrition Examination Survey. *PLoS ONE*, **2010**, 5, e15088	3.7	11
24	Genetic Variation In Recipient BAFF Modulates Phenotype of Chronic GvHD After HCT. *Blood*, **2010**, 116, 215-215	2.2	
23	Methods for optimizing statistical analyses in pharmacogenomics research. *Expert Review of Clinical Pharmacology*, **2009**, 2, 559-570	3.8	8
22	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics*, **2009**, 10, 1043-53	2.6	8
21	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
20	LPA and PLG sequence variation and kringle IV-2 copy number in two populations. *Human Heredity*, **2008**, 66, 199-209	1.1	26
19	Integrating host genomics with surveillance for invasive bacterial diseases. *Emerging Infectious Diseases*, **2008**, 14, 1138-40	10.2	5

18	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
17	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
16	Allelic spectrum of the natural variation in CRP. *Human Genetics*, **2006**, 119, 496-504	6.3	17
15	The patterns of natural variation in human genes. *Annual Review of Genomics and Human Genetics*, **2005**, 6, 287-312	9.7	96
14	Definition and clinical importance of haplotypes. *Annual Review of Medicine*, **2005**, 56, 303-20	17.4	243
13	Fragile X **2005**, 495-513		
12	Pattern of sequence variation across 213 environmental response genes. *Genome Research*, **2004**, 14, 1821-31	9.7	147
11	Evidence for substantial fine-scale variation in recombination rates across the human genome. *Nature Genetics*, **2004**, 36, 700-6	36.3	233
10	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
9	Surveillance for anthrax cases associated with contaminated letters, New Jersey, Delaware, and Pennsylvania, 2001. *Emerging Infectious Diseases*, **2002**, 8, 1073-7	10.2	20
8	Prevalence of the fragile X syndrome in African-Americans. *American Journal of Medical Genetics Part A*, **2002**, 110, 226-33		118
7	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
6	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
5	FMR1 and the fragile X syndrome: human genome epidemiology review. *Genetics in Medicine*, **2001**, 3, 359-71	8.1	474
4	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
3	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
2	A Primer in Statistical Methods in Genetics20-32		
1	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