Gail P. Jarvik

List of Publications by Year in Descending Order

428 papers	25,846 citations	80 h-index	150 g-index
459 ext. papers	30,936 ext. citations	7.1 avg, IF	6.31 L-index

#	Paper	IF	Citations
428	Genetic association of primary nonresponse to anti-TNF□therapy in patients with inflammatory bowel disease. *Pharmacogenetics and Genomics*, **2022**, 32, 1-9	1.9	0
427	Uterine fibroid polygenic risk score (PRS) associates and predicts risk for uterine fibroid.. *Human Genetics*, **2022**, 1	6.3	
426	2021 ASHG presidential address-Imagination and daring: Past, present, and future.. *American Journal of Human Genetics*, **2022**, 109, 381-383	11	
425	The annual ASHG dinner.. *American Journal of Human Genetics*, **2022**, 109, 377-378	11	1
424	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases.. *JAMA Oncology*, **2022**,	13.4	2
423	Health care utilization and expenditures of parents of children with and without hemophilia A.. *Journal of Managed Care & Specialty Pharmacy*, **2022**, 28, 529-537	1.9	
422	Modeling the Ex Ante Clinical Real Option Value in an Innovative Therapeutic Area: ALK-Positive Non-Small-Cell Lung Cancer.. *Pharmacoeconomics*, **2022**, 1	4.4	0
421	Mendelian randomization analysis of plasma levels of CD209 and MICB proteins and the risk of varicose veins of lower extremities.. *PLoS ONE*, **2022**, 17, e0268725	3.7	
420	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
419	A Value-of-Information Framework for Personalizing the Timing of Surveillance Testing. *Medical Decision Making*, **2021**, 272989X211049213	2.5	
418	Conceptualization of utility in translational clinical genomics research. *American Journal of Human Genetics*, **2021**, 108, 2027-2036	11	0
417	Reanalysis of eMERGE phase III sequence variants in 10,500 participants and infrastructure to support the automated return of knowledge updates.. *Genetics in Medicine*, **2021**,	8.1	1
416	Genomic medicine year in review: 2021. *American Journal of Human Genetics*, **2021**, 108, 2210-2214	11	1
415	Reimbursement for genetic variant reinterpretation: five questions payers should ask. *American Journal of Managed Care*, **2021**, 27, e336-e338	2.1	0
414	Artificial intelligence in breast cancer screening: primary care provider preferences. *Journal of the American Medical Informatics Association: JAMIA*, **2021**, 28, 1117-1124	8.6	5
413	Response to Li and Hopper. *American Journal of Human Genetics*, **2021**, 108, 527-529	11	1
412	Medical records-based chronic kidney disease phenotype for clinical care and "big data" observational and genetic studies. *Npj Digital Medicine*, **2021**, 4, 70	15.7	7

411	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
410	What improves the likelihood of people receiving genetic test results communicating to their families about genetic risk?. *Patient Education and Counseling*, **2021**, 104, 726-731	3.1	3
409	Penetrance of Breast Cancer Susceptibility Genes From the eMERGE III Network. *JNCI Cancer Spectrum*, **2021**, 5, pkab044	4.6	4
408	Progressive cerebellar atrophy in a patient with complex II and III deficiency and a novel deleterious variant in SDHA: A Counseling Conundrum. *Molecular Genetics & Genomic Medicine*, **2021**, 9, e1692	2.3	
407	Practice Patterns After Return of Rare Variants Associated With Cardiomyopathy in the Electronic Medical Records and Genomics Network. *Circulation: Heart Failure*, **2021**, 14, e008155	7.6	
406	Development and early implementation of an Accessible, Relational, Inclusive and Actionable approach to genetic counseling: The ARIA model. *Patient Education and Counseling*, **2021**, 104, 969-978	3.1	4
405	Detection of a mosaic CDKL5 deletion and inversion by optical genome mapping ends an exhaustive diagnostic odyssey. *Molecular Genetics & Genomic Medicine*, **2021**, 9, e1665	2.3	1
404	Genomic considerations for FHIR ; eMERGE implementation lessons. *Journal of Biomedical Informatics*, **2021**, 118, 103795	10.2	5
403	A Mendelian Randomization Approach Using 3-HMG-Coenzyme-A Reductase Gene Variation to Evaluate the Association of Statin-Induced Low-Density Lipoprotein Cholesterol Lowering With Noncardiovascular Disease Phenotypes. *JAMA Network Open*, **2021**, 4, e2112820	10.4	5
402	Usefulness of mobile apps for communication of genetic test results to at-risk family members in a U.S. integrated health system: a qualitative approach from user-testing. *Health Policy and Technology*, **2021**, 10, 100511-100511	4.8	0
401	A genome-wide association study suggests correlations of common genetic variants with peritoneal solute transfer rates in patients with kidney failure receiving peritoneal dialysis. *Kidney International*, **2021**, 100, 1101-1111	9.9	4
400	Neptune: an environment for the delivery of genomic medicine. *Genetics in Medicine*, **2021**, 23, 1838-1848	8.1	1
399	Barriers to family history knowledge and family communication among LGBTQ+ individuals in the context of hereditary cancer risk assessment. *Journal of Genetic Counseling*, **2021**,	2.5	1
398	Relationship between genetic knowledge and familial communication of CRC risk and intent to communicate CRCP genetic information: insights from FamilyTalk eMERGE III. *Translational Behavioral Medicine*, **2021**, 11, 563-572	3.2	0
397	Returning negative results from large-scale genomic screening: Experiences from the eMERGE III network. *American Journal of Medical Genetics, Part A*, **2021**, 185, 508-516	2.5	2
396	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel: A Meta-analysis. *JAMA Neurology*, **2021**, 78, 102-113	17.2	32
395	Family genetic result communication in rare and undiagnosed disease communities: Understanding the practice. *Journal of Genetic Counseling*, **2021**, 30, 439-447	2.5	1
394	Clinical sites of the Undiagnosed Diseases Network: unique contributions to genomic medicine and science. *Genetics in Medicine*, **2021**, 23, 259-271	8.1	6

393	Differences in atheroma between Caucasian and Asian subjects with anterior stroke: A vessel wall MRI study. *Stroke and Vascular Neurology*, **2021**, 6, 25-32	9.1	2
392	Evaluation of the MC4R gene across eMERGE network identifies many unreported obesity-associated variants. *International Journal of Obesity*, **2021**, 45, 155-169	5.5	5
391	Loci identified by a genome-wide association study of carotid artery stenosis in the eMERGE network. *Genetic Epidemiology*, **2021**, 45, 4-15	2.6	5
390	Genetic Variant Reinterpretation: Economic and Population Health Management Challenges. *Population Health Management*, **2021**, 24, 310-313	1.8	2
389	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. *BMC Medical Genomics*, **2021**, 14, 11	3.7	2
388	ShareDNA: a smartphone app to facilitate family communication of genetic results. *BMC Medical Genomics*, **2021**, 14, 10	3.7	2
387	Genome-wide association studies of low back pain and lumbar spinal disorders using electronic health record data identify a locus associated with lumbar spinal stenosis. *Pain*, **2021**, 162, 2263-2272	8	2
386	The FamilyTalk randomized controlled trial: patient-reported outcomes in clinical genetic sequencing for colorectal cancer. *Cancer Causes and Control*, **2021**, 32, 483-492	2.8	0
385	Preferences of biobank participants for receiving actionable genomic test results: results of a recontacting study. *Genetics in Medicine*, **2021**, 23, 1163-1166	8.1	2
384	AuthorsOReply to Comment on "Cost-Effectiveness of Cannabidiol Adjunct Therapy Versus Usual Care for the Treatment of Seizures in Lennox-Gastaut Syndrome". *Pharmacoeconomics*, **2021**, 39, 477-478	4.4	
383	Cancer Health Assessments Reaching Many (CHARM): A clinical trial assessing a multimodal cancer genetics services delivery program and its impact on diverse populations. *Contemporary Clinical Trials*, **2021**, 106, 106432	2.3	1
382	Generalizability of Polygenic Risk Scores for Breast Cancer Among Women With European, African, and Latinx Ancestry. *JAMA Network Open*, **2021**, 4, e2119084	10.4	5
381	Real-world evidence for option value in metastatic melanoma. *Journal of Managed Care & Specialty Pharmacy*, **2021**, 27, 1546-1555	1.9	1
380	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003354	5.2	5
379	The genetic architecture of plasma kynurenine includes cardiometabolic disease mechanisms associated with the SH2B3 gene. *Scientific Reports*, **2021**, 11, 15652	4.9	1
378	Modeling the Ex Post Real Option Value in Metastatic Melanoma Using Real-World Data. *Value in Health*, **2021**, 24, 1746-1753	3.3	1
377	Online tools to synthesize real-world evidence of comparative effectiveness research to enhance formulary decision making. *Journal of Managed Care & Specialty Pharmacy*, **2021**, 27, 95-104	1.9	0
376	Use of real-world evidence in economic assessments of pharmaceuticals in the United States. *Journal of Managed Care & Specialty Pharmacy*, **2021**, 27, 5-14	1.9	4

375	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study.. *Circulation*, **2021**,	16.7	2
374	Implementation matters: How patient experiences differ when genetic counseling accompanies the return of genetic variants of uncertain significance. **2021**, 2021, 950-958	0.7	
373	DYRK1A pathogenic variants in two patients with syndromic intellectual disability and a review of the literature. *Molecular Genetics & Genomic Medicine*, **2020**, 8, e1544	2.3	1
372	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis.. *Human Genetics and Genomics Advances*, **2020**, 1, 100010	0.8	1
371	Cost-effectiveness of Population-Wide Genomic Screening for Hereditary Breast and Ovarian Cancer in the United States. *JAMA Network Open*, **2020**, 3, e2022874	10.4	11
370	Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies. *American Journal of Human Genetics*, **2020**, 107, 932-941	11	17
369	Medication persistence of targeted immunomodulators for plaque psoriasis: A retrospective analysis using a U.S. claims database. *Pharmacoepidemiology and Drug Safety*, **2020**, 29, 675-683	2.6	5
368	Understanding the Return of Genomic Sequencing Results Process: Content Review of Participant Summary Letters in the eMERGE Research Network. *Journal of Personalized Medicine*, **2020**, 10,	3.6	4
367	Returning Results in the Genomic Era: Initial Experiences of the eMERGE Network. *Journal of Personalized Medicine*, **2020**, 10,	3.6	19
366	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. *Scientific Reports*, **2020**, 10, 7561	4.9	3
365	Payer Preferences and Willingness to Pay for Genomic Precision Medicine: A Discrete Choice Experiment. *Journal of Managed Care & Specialty Pharmacy*, **2020**, 26, 529-537	1.9	3
364	Frequency of genomic secondary findings among 21,915 eMERGE network participants. *Genetics in Medicine*, **2020**, 22, 1470-1477	8.1	23
363	Predictive Utility of Polygenic Risk Scores for Coronary Heart Disease in Three Major Racial and Ethnic Groups. *American Journal of Human Genetics*, **2020**, 106, 707-716	11	37
362	De novo EIF2AK1 and EIF2AK2 Variants Are Associated with Developmental Delay, Leukoencephalopathy, and Neurologic Decompensation. *American Journal of Human Genetics*, **2020** , 106, 570-583	11	21
361	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. *PLoS Genetics*, **2020**, 16, e1008684	6	5
360	Variant Interpretation for Dilated Cardiomyopathy: Refinement of the American College of Medical Genetics and Genomics/ClinGen Guidelines for the DCM Precision Medicine Study. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002480	5.2	27
359	Early infantile epileptic encephalopathy due to biallelic pathogenic variants in PIGQ: Report of seven new subjects and review of the literature. *Journal of Inherited Metabolic Disease*, **2020**, 43, 1321-1332	5.4	6
358	Economic value of exome sequencing for suspected monogenic disorders. *Genetics in Medicine*, **2020**, 22, 1909	8.1	1

357	Pleiotropy in the Genetic Predisposition to Rheumatoid Arthritis: A Phenome-Wide Association Study and Inverse Variance-Weighted Meta-Analysis. *Arthritis and Rheumatology*, **2020**, 72, 1483-1492	9.5	4
356	Influence of Modeling Choices on Value of Information Analysis: An Empirical Analysis from a Real-World Experiment. *Pharmacoeconomics*, **2020**, 38, 171-179	4.4	
355	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	17
354	Points to consider: is there evidence to support BRCA1/2 and other inherited breast cancer genetic testing for all breast cancer patients? A statement of the American College of Medical Genetics and Genomics (ACMG). *Genetics in Medicine*, **2020**, 22, 681-685	8.1	14
353	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation*, **2020**, 142, 1633-1646	16.7	24
352	A Novel LC-MS/MS Assay for Quantification of Des-carboxy Prothrombin and Characterization of Warfarin-Induced Changes. *Clinical and Translational Science*, **2020**, 13, 718-726	4.9	0
351	Genomic Medicine Year in Review: 2020. *American Journal of Human Genetics*, **2020**, 107, 1007-1010	11	2
350	The use of real-world evidence in ICER© scoping process and clinical evidence assessments. *Journal of Managed Care & Specialty Pharmacy*, **2020**, 26, 1590-1595	1.9	1
349	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 432-444	11	31
348	Cost-Effectiveness of Cannabidiol Adjunct Therapy versus Usual Care for the Treatment of Seizures in Lennox-Gastaut Syndrome. *Pharmacoeconomics*, **2020**, 38, 1237-1245	4.4	3
347	Biallelic MADD variants cause a phenotypic spectrum ranging from developmental delay to a multisystem disorder. *Brain*, **2020**, 143, 2437-2453	11.2	7
346	Diabetes Impairs Cellular Cholesterol Efflux From ABCA1 to Small HDL Particles. *Circulation Research*, **2020**, 127, 1198-1210	15.7	11
345	Development of FamilyTalk: an Intervention to Support Communication and Educate Families About Colorectal Cancer Risk. *Journal of Cancer Education*, **2020**, 35, 470-478	1.8	6
344	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. *World Journal of Surgery*, **2020**, 44, 84-94	3.3	1
343	CNV Association of Diverse Clinical Phenotypes from eMERGE reveals novel disease biology underlying cardiovascular disease. *International Journal of Cardiology*, **2020**, 298, 107-113	3.2	2
342	Demand for Precision Medicine: A Discrete-Choice Experiment and External Validation Study. *Pharmacoeconomics*, **2020**, 38, 57-68	4.4	11
341	A genome-wide association study of polycystic ovary syndrome identified from electronic health records. *American Journal of Obstetrics and Gynecology*, **2020**, 223, 559.e1-559.e21	6.4	20
340	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		

339	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		
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335	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		
334	Clinical exome sequencing vs. usual care for hereditary colorectal cancer diagnosis: A pilot comparative effectiveness study. *Contemporary Clinical Trials*, **2019**, 84, 105820	2.3	4
333	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. *American Journal of Human Genetics*, **2019**, 105, 588-605	11	63
332	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation: A Phenome-Wide Association Study and Inverse-Variance Weighted Average Meta-analysis. *JAMA Cardiology*, **2019**, 4, 136-143	16.2	20
331	Failure to validate association of mannose-binding lectin deficiency with adverse neurodevelopmental outcomes after cardiac surgery in infants. *Journal of Thoracic and Cardiovascular Surgery*, **2019**, 157, e397-e398	1.5	3
330	The Genomic Medicine Integrative Research Framework: A Conceptual Framework for Conducting Genomic Medicine Research. *American Journal of Human Genetics*, **2019**, 104, 1088-1096	11	24
329	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. *Scientific Reports*, **2019**, 9, 6077	4.9	11
328	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. *Genetics in Medicine*, **2019**, 21, 2135-2144	8.1	13
327	Lynch Syndrome: From Screening to Diagnosis to Treatment in the Era of Modern Molecular Oncology. *Annual Review of Genomics and Human Genetics*, **2019**, 20, 293-307	9.7	19
326	VKORC1 and Novel CYP2C9 Variation Predict Warfarin Response in Alaska Native and American Indian People. *Clinical and Translational Science*, **2019**, 12, 312-320	4.9	8
325	"It would be so much easier": health system-led genetic risk notification-feasibility and acceptability of cascade screening in an integrated system. *Journal of Community Genetics*, **2019**, 10, 461-470	2.5	1
324	The Responsibility to Recontact Research Participants after Reinterpretation of Genetic and Genomic Research Results. *American Journal of Human Genetics*, **2019**, 104, 578-595	11	50
323	Rates of Actionable Genetic Findings in Individuals with Colorectal Cancer or Polyps Ascertained from a Community Medical Setting. *American Journal of Human Genetics*, **2019**, 105, 526-533	11	2
322	Insurance coverage does not predict outcomes of genetic testing: The search for meaning in payer decisions for germline cancer tests. *Journal of Genetic Counseling*, **2019**, 28, 1208-1213	2.5	5

321	GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. *BMC Medicine*, **2019**, 17, 135	11.4	53
320	Cost-effectiveness of population genomic screening. *Genetics in Medicine*, **2019**, 21, 2840-2841	8.1	2
319	Projected Cost-Effectiveness for 2 Gene-Drug Pairs Using a Multigene Panel for Patients Undergoing Percutaneous Coronary Intervention. *Value in Health*, **2019**, 22, 1231-1239	3.3	4
318	Genomic Information for Clinicians in the Electronic Health Record: Lessons Learned From the Clinical Genome Resource Project and the Electronic Medical Records and Genomics Network. *Frontiers in Genetics*, **2019**, 10, 1059	4.5	21
317	Are There Different Evidence Thresholds for Genomic Versus Clinical Precision Medicine? A Value of Information-Based Framework Applied to Antiplatelet Drug Therapy. *Value in Health*, **2019**, 22, 988-994	3.3	2
316	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2019**, 24, 272-283	1.3	6
315	Post-traumatic Stress Disorder Symptoms are Associated With Incident Chronic Back Pain: A Longitudinal Twin Study of Older Male Veterans. *Spine*, **2019**, 44, 1220-1227	3.3	4
314	Genetic meta-analysis of diagnosed Alzheimer disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
313	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
312	A phenome-wide association study to discover pleiotropic effects of , , and. *Npj Genomic Medicine*, **2019**, 4, 3	6.2	14
311	Reply to Liu et al.: Tissue specificity of gene expression and erectile dysfunction. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 3349-3350	11.5	
310	Genomic Medicine Year in Review: 2019. *American Journal of Human Genetics*, **2019**, 105, 1072-1075	11	7
309	The Feelings About genomiC Testing Results (FACToR) Questionnaire: Development and Preliminary Validation. *Journal of Genetic Counseling*, **2019**, 28, 477-490	2.5	24
308	Enrichment sampling for a multi-site patient survey using electronic health records and census data. *Journal of the American Medical Informatics Association: JAMIA*, **2019**, 26, 219-227	8.6	2
307	Unfolding of hidden white blood cell count phenotypes for gene discovery using latent class mixed modeling. *Genes and Immunity*, **2019**, 20, 555-565	4.4	2
306	Obinutuzumab plus chemotherapy followed by obinutuzumab monotherapy is cost-effective vs. rituximab plus chemotherapy followed by rituximab monotherapy for previously untreated follicular lymphoma patients in the United States. *Leukemia and Lymphoma*, **2019**, 60, 1668-1676	1.9	5
305	How can clinical researchers quantify the value of their proposed comparative research?. *American Heart Journal*, **2019**, 209, 116-125	4.9	1
304	Secondary findings from clinical genomic sequencing: prevalence, patient perspectives, family history assessment, and health-care costs from a multisite study. *Genetics in Medicine*, **2019**, 21, 1100-1110	8.1	61

303	The eMERGE genotype set of 83,717 subjects imputed to ~40 million variants genome wide and association with the herpes zoster medical record phenotype. *Genetic Epidemiology*, **2019**, 43, 63-81	2.6	32
302	Anticipated responses of early adopter genetic specialists and nongenetic specialists to unsolicited genomic secondary findings. *Genetics in Medicine*, **2018**, 20, 1186-1195	8.1	9
301	Autosomal dominant mannose-binding lectin deficiency is associated with worse neurodevelopmental outcomes after cardiac surgery in infants. *Journal of Thoracic and Cardiovascular Surgery*, **2018**, 155, 1139-1147.e2	1.5	7
300	Arno G. Motulsky, MD (1923-2018): Holocaust survivor who cofounded the field of medical genetics. *Genetics in Medicine*, **2018**, 20, 477-479	8.1	1
299	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. *Circulation*, **2018**, 138, 1839-1849	16.7	40
298	Navigating the research-clinical interface in genomic medicine: analysis from the CSER Consortium. *Genetics in Medicine*, **2018**, 20, 545-553	8.1	24
297	Impact of HIPAA's minimum necessary standard on genomic data sharing. *Genetics in Medicine*, **2018**, 20, 531-535	8.1	9
296	Lessons Learned From A Study Of Genomics-Based Carrier Screening For Reproductive Decision Making. *Health Affairs*, **2018**, 37, 809-816	7	8
295	Considerations in initiating genomic screening programs in health care systems. *Nursing Outlook*, **2018**, 66, 570-575	2.7	3
294	Preconception Carrier Screening by Genome Sequencing: Results from the Clinical Laboratory. *American Journal of Human Genetics*, **2018**, 102, 1078-1089	11	18
293	Arno G. Motulsky (1923–2018): A Founder of Medical Genetics, Creator of Pharmacogenetics, and Former ASHG President. *American Journal of Human Genetics*, **2018**, 102, 335-339	11	2
292	An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. *Cell Host and Microbe*, **2018**, 24, 308-323.e6	23.4	25
291	Patient preferences for massively parallel sequencing genetic testing of colorectal cancer risk: a discrete choice experiment. *European Journal of Human Genetics*, **2018**, 26, 1257-1265	5.3	9
290	Cost-effectiveness of obinutuzumab plus bendamustine followed by obinutuzumab monotherapy for the treatment of follicular lymphoma patients who relapse after or are refractory to a rituximab-containing regimen in the US. *Journal of Medical Economics*, **2018**, 21, 960-967	2.4	3
289	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
288	A vascular endothelial growth factor A genetic variant is associated with improved ventricular function and transplant-free survival after surgery for non-syndromic CHD. *Cardiology in the Young*, **2018**, 28, 39-45	1	6
287	A case for expanding carrier testing to include actionable X-linked disorders. *Clinical Case Reports (discontinued)*, **2018**, 6, 2092-2095	0.7	
286	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. *PLoS Genetics*, **2018**, 14, e1007601	6	60

285	Parents' attitudes toward consent and data sharing in biobanks: A multisite experimental survey. *AJOB Empirical Bioethics*, **2018**, 9, 128-142	3	13
284	Rare loss of function variants in candidate genes and risk of colorectal cancer. *Human Genetics*, **2018**, 137, 795-806	6.3	6
283	Genetic variation in the locus is associated with erectile dysfunction. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11018-11023	11.5	14
282	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. *Circulation*, **2018**, 138, 2469-2481	16.7	23
281	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. *Journal of Personalized Medicine*, **2018**, 8,	3.6	32
280	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. *Nature Communications*, **2018**, 9, 3522	17.4	7
279	The Clinical Sequencing Evidence-Generating Research Consortium: Integrating Genomic Sequencing in Diverse and Medically Underserved Populations. *American Journal of Human Genetics* , **2018**, 103, 319-327	11	64
278	Harmonizing Outcomes for Genomic Medicine: Comparison of eMERGE Outcomes to ClinGen Outcome/Intervention Pairs. *Healthcare (Switzerland)*, **2018**, 6,	3.4	9
277	Approaches to carrier testing and results disclosure in translational genomics research: The clinical sequencing exploratory research consortium experience. *Molecular Genetics & Genomic Medicine*, **2018**, 6, 898-909	2.3	10
276	Cost-Effectiveness Analysis of Patiromer and Spironolactone Therapy in Heart Failure Patients with Hyperkalemia. *Pharmacoeconomics*, **2018**, 36, 1463-1473	4.4	11
275	ClinGen Pathogenicity Calculator: a configurable system for assessing pathogenicity of genetic variants. *Genome Medicine*, **2017**, 9, 3	14.4	47
274	Genome sequencing and carrier testing: decisions on categorization and whether to disclose results of carrier testing. *Genetics in Medicine*, **2017**, 19, 803-808	8.1	20
273	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
272	Effect of congenital heart disease on 4-year neurodevelopment within multiple-gestation births. *Journal of Thoracic and Cardiovascular Surgery*, **2017**, 154, 273-281.e2	1.5	8
271	Public Attitudes toward Consent and Data Sharing in Biobank Research: A Large Multi-site Experimental Survey in the US. *American Journal of Human Genetics*, **2017**, 100, 414-427	11	114
270	Transethnic genome-wide scan identifies novel Alzheimer's disease loci. *Alzheimer's and Dementia*, **2017**, 13, 727-738	1.2	106
269	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. *Circulation: Cardiovascular Genetics*, **2017**, 10,		7
268	Developing the Value Proposition for Personalized Medicine **2017**, 327-342		1

267	2016 Victor A. McKusick Leadership Award Introduction: Stanley Gartler. *American Journal of Human Genetics*, **2017**, 100, 401-402	11	1
266	Sequencing of sporadic Attention-Deficit Hyperactivity Disorder (ADHD) identifies novel and potentially pathogenic de novo variants and excludes overlap with genes associated with autism spectrum disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 381-389	3.5	22
265	What is the value of conducting a trial of r-tPA for the treatment of mild stroke patients?. *International Journal of Stroke*, **2017**, 12, 137-144	6.3	3
264	Design of a randomized controlled trial for genomic carrier screening in healthy patients seeking preconception genetic testing. *Contemporary Clinical Trials*, **2017**, 53, 100-105	2.3	22
263	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25	4.3	5
262	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
261	Building a family network from genetic testing. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 122-129	2.3	1
260	Discordance in selected designee for return of genomic findings in the event of participant death and estate executor. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 172-176	2.3	6
259	Clinical verification of genetic results returned to research participants: findings from a Colon Cancer Family Registry. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 700-708	2.3	1
258	Modifiable risk factors for chronic back pain: insights using the co-twin control design. *Spine Journal* , **2017**, 17, 4-14	4	35
257	A survey of current practices for genomic sequencing test interpretation and reporting processes in US laboratories. *Genetics in Medicine*, **2017**, 19, 575-582	8.1	52
256	Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Human Genetics*, **2017**, 136, 165-178	6.3	8
255	Risk-Benefit Analysis of Pediatric-Inspired Versus Hyperfractionated Cyclophosphamide, Vincristine, Doxorubicin, and Dexamethasone Protocols for Acute Lymphoblastic Leukemia in Adolescents and Young Adults. *Journal of Adolescent and Young Adult Oncology*, **2017**, 6, 53-61	2.2	5
254	Is "incidental finding" the best term?: a study of patients preferences. *Genetics in Medicine*, **2017**, 19, 176-181	8.1	27
253	Identification of Four Novel Loci in Asthma in European American and African American Populations. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 195, 456-463	10.2	59
252	Impact of Body Mass Index and Genetics on Warfarin Major Bleeding Outcomes in a Community Setting. *American Journal of Medicine*, **2017**, 130, 222-228	2.4	13
251	Genome-wide study of resistant hypertension identified from electronic health records. *PLoS ONE*, **2017**, 12, e0171745	3.7	23
250	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175

249	Defining a Contemporary Ischemic Heart Disease Genetic Risk Profile Using Historical Data. *Circulation: Cardiovascular Genetics*, **2016**, 9, 521-530		6
248	Conducting a large, multi-site survey about patients' views on broad consent: challenges and solutions. *BMC Medical Research Methodology*, **2016**, 16, 162	4.7	7
247	Consideration of Cosegregation in the Pathogenicity Classification of Genomic Variants. *American Journal of Human Genetics*, **2016**, 98, 1077-1081	11	127
246	Paraoxonases-1, -2 and -3: What are their functions?. *Chemico-Biological Interactions*, **2016**, 259, 51-62	5	108
245	Burden of potentially pathologic copy number variants is higher in children with isolated congenital heart disease and significantly impairs covariate-adjusted transplant-free survival. *Journal of Thoracic and Cardiovascular Surgery*, **2016**, 151, 1147-51.e4	1.5	35
244	Next Generation Sequencing in the Clinic: a Patterns of Care Study in a Retrospective Cohort of Subjects Referred to a Genetic Medicine Clinic for Suspected Lynch Syndrome. *Journal of Genetic Counseling*, **2016**, 25, 515-9	2.5	3
243	Development and Evaluation of an Approach to Using Value of Information Analyses for Real-Time Prioritization Decisions Within SWOG, a Large Cancer Clinical Trials Cooperative Group. *Medical Decision Making*, **2016**, 36, 641-51	2.5	20
242	The phenotypic legacy of admixture between modern humans and Neandertals. *Science*, **2016**, 351, 737-41	33.3	172
241	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. *JAMA - Journal of the American Medical Association*, **2016**, 315, 47-57	27.4	115
240	A Framework for Prioritizing Research Investments in Precision Medicine. *Medical Decision Making*, **2016**, 36, 567-80	2.5	10
239	What Is the Cost-Effectiveness of Obinutuzumab Plus Bendamustine Followed By Obinutuzumab Monotherapy for the Treatment of Follicular Lymphoma Patients Who Relapse after or Are Refractory to a Rituximab-Containing Regimen in the US?. *Blood*, **2016**, 128, 3605-3605	2.2	5
238	Clopidogrel-Proton Pump Inhibitor Drug-Drug Interaction and Risk of Adverse Clinical Outcomes Among PCI-Treated ACS Patients: A Meta-analysis. *Journal of Managed Care & Specialty Pharmacy*, **2016**, 22, 939-47	1.9	30
237	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. *Genetic Epidemiology*, **2016**, 40, 470-4	2.6	8
236	Initiation of universal tumor screening for Lynch syndrome in colorectal cancer patients as a model for the implementation of genetic information into clinical oncology practice. *Cancer*, **2016**, 122, 393-401	6.4	23
235	Generating a taxonomy for genetic conditions relevant to reproductive planning. *American Journal of Medical Genetics, Part A*, **2016**, 170, 565-73	2.5	19
234	Allocation of Resources to Communication of Research Result Summaries. *Journal of Empirical Research on Human Research Ethics*, **2016**, 11, 364-369	1.6	4
233	Concentration of Smaller High-Density Lipoprotein Particle (HDL-P) Is Inversely Correlated With Carotid Intima Media Thickening After Confounder Adjustment: The Multi Ethnic Study of Atherosclerosis (MESA). *Journal of the American Heart Association*, **2016**, 5,	6	21
232	Assessment of the genetic variance of late-onset Alzheimer's disease. *Neurobiology of Aging*, **2016**, 41, 200.e13-200.e20	5.6	119

231	Performance of ACMG-AMP Variant-Interpretation Guidelines among Nine Laboratories in the Clinical Sequencing Exploratory Research Consortium. *American Journal of Human Genetics*, **2016**, 98, 1067-1076	11	271
230	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. *American Journal of Human Genetics*, **2016**, 98, 1051-1066	11	107
229	Recommendations for the integration of genomics into clinical practice. *Genetics in Medicine*, **2016**, 18, 1075-1084	8.1	92
228	PatientsÕratings of genetic conditions validate a taxonomy to simplify decisions about preconception carrier screening via genome sequencing. *American Journal of Medical Genetics, Part A*, **2016**, 170, 574-82	2.5	18
227	Development of clinical decision support alerts for pharmacogenomic incidental findings from exome sequencing. *Genetics in Medicine*, **2015**, 17, 939-42	8.1	20
226	A Robust e-Epidemiology Tool in Phenotyping Heart Failure with Differentiation for Preserved and Reduced Ejection Fraction: the Electronic Medical Records and Genomics (eMERGE) Network. *Journal of Cardiovascular Translational Research*, **2015**, 8, 475-83	3.3	25
225	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke: The NHLBI Exome Sequence Project. *JAMA Neurology*, **2015**, 72, 781-8	17.2	37
224	Next-Generation Sequencing Panels for the Diagnosis of Colorectal Cancer and Polyposis Syndromes: A Cost-Effectiveness Analysis. *Journal of Clinical Oncology*, **2015**, 33, 2084-91	2.2	93
223	Next-generation gene discovery for variants of large impact on lipid traits. *Current Opinion in Lipidology*, **2015**, 26, 114-9	4.4	3
222	Penetrance of Hemochromatosis in HFE Genotypes Resulting in p.Cys282Tyr and p.[Cys282Tyr];[His63Asp] in the eMERGE Network. *American Journal of Human Genetics*, **2015**, 97, 512-20	11	33
221	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. *Genome Medicine*, **2015**, 7, 67	14.4	11
220	Illustrative case studies in the return of exome and genome sequencing results. *Personalized Medicine*, **2015**, 12, 283-295	2.2	33
219	Societal preferences for the return of incidental findings from clinical genomic sequencing: a discrete-choice experiment. *Cmaj*, **2015**, 187, E190-E197	3.5	64
218	Response to Phillips et al. *Genetics in Medicine*, **2015**, 17, 315	8.1	
217	Desiderata for computable representations of electronic health records-driven phenotype algorithms. *Journal of the American Medical Informatics Association: JAMIA*, **2015**, 22, 1220-30	8.6	75
216	CSER and eMERGE: current and potential state of the display of genetic information in the electronic health record. *Journal of the American Medical Informatics Association: JAMIA*, **2015**, 22, 1231-42	8.6	63
215	PLTP activity inversely correlates with CAAD: effects of PON1 enzyme activity and genetic variants on PLTP activity. *Journal of Lipid Research*, **2015**, 56, 1351-62	6.3	13
214	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. *Genome Research*, **2015**, 25, 305-15	9.7	252

213	Parallel reaction monitoring (PRM) and selected reaction monitoring (SRM) exhibit comparable linearity, dynamic range and precision for targeted quantitative HDL proteomics. *Journal of Proteomics*, **2015**, 113, 388-99	3.9	132
212	The cost-effectiveness of returning incidental findings from next-generation genomic sequencing. *Genetics in Medicine*, **2015**, 17, 587-95	8.1	78
211	Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. *Genetic Epidemiology*, **2015**, 39, 376-84	2.6	16
210	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). *BioData Mining*, **2015**, 8, 41	4.3	12
209	A GWAS Study on Liver Function Test Using eMERGE Network Participants. *PLoS ONE*, **2015**, 10, e0138677	3.7	17
208	Rarity of the Alzheimer disease-protective APP A673T variant in the United States. *JAMA Neurology* , **2015**, 72, 209-16	17.2	31
207	The FDA and genomic tests--getting regulation right. *New England Journal of Medicine*, **2015**, 372, 2258-64	59.2	62
206	Challenges in evaluating next-generation sequence data for clinical decisions. *Nursing Outlook*, **2015**, 63, 48-50	2.7	6
205	ePhenotyping for Abdominal Aortic Aneurysm in the Electronic Medical Records and Genomics (eMERGE) Network: Algorithm Development and Konstanz Information Miner Workflow. *International Journal of Biomedical Data Mining*, **2015**, 4,		5
204	"Getting off the Bus Closer to Your Destination": PatientsÕViews about Pharmacogenetic Testing **2015**, 19, 21-7		11
203	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
202	Return of genomic results to research participants: the floor, the ceiling, and the choices in between. *American Journal of Human Genetics*, **2014**, 94, 818-26	11	283
201	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. *Genetics in Medicine*, **2014**, 16, 529-34	8.1	16
200	A genome- and phenome-wide association study to identify genetic variants influencing platelet count and volume and their pleiotropic effects. *Human Genetics*, **2014**, 133, 95-109	6.3	104
199	Comparative effectiveness of next generation genomic sequencing for disease diagnosis: design of a randomized controlled trial in patients with colorectal cancer/polyposis syndromes. *Contemporary Clinical Trials*, **2014**, 39, 1-8	2.3	16
198	Refining the structure and content of clinical genomic reports. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2014**, 166C, 85-92	3.1	30
197	Characterizing genetic variants for clinical action. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2014**, 166C, 93-104	3.1	41
196	Return of results: ethical and legal distinctions between research and clinical care. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2014**, 166C, 105-11	3.1	80

195	Validation of association of the apolipoprotein E ε2 allele with neurodevelopmental dysfunction after cardiac surgery in neonates and infants. *Journal of Thoracic and Cardiovascular Surgery*, **2014**, 148, 2560-6	1.5	40
194	Rare coding variation in paraoxonase-1 is associated with ischemic stroke in the NHLBI Exome Sequencing Project. *Journal of Lipid Research*, **2014**, 55, 1173-8	6.3	19
193	Patient genotypes impact survival after surgery for isolated congenital heart disease. *Annals of Thoracic Surgery*, **2014**, 98, 104-10; discussion 110-1	2.7	22
192	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
191	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
190	Return of results in the genomic medicine projects of the eMERGE network. *Frontiers in Genetics*, **2014**, 5, 50	4.5	32
189	Copy number variation analysis in the context of electronic medical records and large-scale genomics consortium efforts. *Frontiers in Genetics*, **2014**, 5, 51	4.5	9
188	Practical barriers and ethical challenges in genetic data sharing. *International Journal of Environmental Research and Public Health*, **2014**, 11, 8383-98	4.6	16
187	HDL-3 is a superior predictor of carotid artery disease in a case-control cohort of 1725 participants. *Journal of the American Heart Association*, **2014**, 3, e000902	6	31
186	eMERGEing progress in genomics-the first seven years. *Frontiers in Genetics*, **2014**, 5, 184	4.5	65
185	Imputation and quality control steps for combining multiple genome-wide datasets. *Frontiers in Genetics*, **2014**, 5, 370	4.5	90
184	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
183	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
182	Regulatory changes raise troubling questions for genomic testing. *Genetics in Medicine*, **2014**, 16, 799-808	8.1	24
181	TCIRG1-associated congenital neutropenia. *Human Mutation*, **2014**, 35, 824-7	4.7	30
180	Effects of dietary components on high-density lipoprotein measures in a cohort of 1,566 participants. *Nutrition and Metabolism*, **2014**, 11, 44	4.6	12
179	Cost-effectiveness of recombinant tissue-type plasminogen activator within 3 hours of acute ischemic stroke: current evidence. *Stroke*, **2014**, 45, 3032-9	6.7	43
178	Effects of multiple genetic loci on age at onset in late-onset Alzheimer disease: a genome-wide association study. *JAMA Neurology*, **2014**, 71, 1394-404	17.2	129

177	Quantification of HDL particle concentration by calibrated ion mobility analysis. *Clinical Chemistry*, **2014**, 60, 1393-401	5.5	56
176	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
175	Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. *Molecular Vision*, **2014**, 20, 1281-95	2.3	26
174	A Template for Authoring and Adapting Genomic Medicine Content in the eMERGE Infobutton Project **2014**, 2014, 944-53	0.7	7
173	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
172	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. *Genetics in Medicine*, **2013**, 15, 761-71	8.1	484
171	Recommendations for returning genomic incidental findings? We need to talk!. *Genetics in Medicine* , **2013**, 15, 854-9	8.1	246
170	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
169	Joint linkage and association analysis with exome sequence data implicates SLC25A40 in hypertriglyceridemia. *American Journal of Human Genetics*, **2013**, 93, 1035-45	11	35
168	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
167	Dietary fatty acid intake is associated with paraoxonase 1 activity in a cohort-based analysis of 1,548 subjects. *Lipids in Health and Disease*, **2013**, 12, 183	4.4	12
166	Actionable, pathogenic incidental findings in 1,000 participantsŒexomes. *American Journal of Human Genetics*, **2013**, 93, 631-40	11	302
165	A survey of informatics approaches to whole-exome and whole-genome clinical reporting in the electronic health record. *Genetics in Medicine*, **2013**, 15, 824-32	8.1	56
164	Genome- and phenome-wide analyses of cardiac conduction identifies markers of arrhythmia risk. *Circulation*, **2013**, 127, 1377-85	16.7	133
163	Postoperative electroencephalographic seizures are associated with deficits in executive function and social behaviors at 4 years of age following cardiac surgery in infancy. *Journal of Thoracic and Cardiovascular Surgery*, **2013**, 146, 132-7	1.5	31
162	WNT1 mutations in families affected by moderately severe and progressive recessive osteogenesis imperfecta. *American Journal of Human Genetics*, **2013**, 92, 590-7	11	156
161	Pharmacogenetics of paraoxonase activity: elucidating the role of high-density lipoprotein in disease. *Pharmacogenomics*, **2013**, 14, 1495-515	2.6	33
160	Improving the efficiency and relevance of evidence-based recommendations in the era of whole-genome sequencing: an EGAPP methods update. *Genetics in Medicine*, **2013**, 15, 14-24	8.1	43

159	Leveraging the electronic health record to implement genomic medicine. *Genetics in Medicine*, **2013**, 15, 270-1	8.1	40
158	Return of incidental findings in genomic medicine: measuring what patients value--development of an instrument to measure preferences for information from next-generation testing (IMPRINT). *Genetics in Medicine*, **2013**, 15, 873-81	8.1	64
157	Exome sequencing reveals novel rare variants in the ryanodine receptor and calcium channel genes in malignant hyperthermia families. *Anesthesiology*, **2013**, 119, 1054-65	4.3	45
156	Genetic variation associated with circulating monocyte count in the eMERGE Network. *Human Molecular Genetics*, **2013**, 22, 2119-27	5.6	46
155	Value-of-information analysis within a stakeholder-driven research prioritization process in a US setting: an application in cancer genomics. *Medical Decision Making*, **2013**, 33, 463-71	2.5	30
154	Novel gene-by-environment interactions: APOB and NPC1L1 variants affect the relationship between dietary and total plasma cholesterol. *Journal of Lipid Research*, **2013**, 54, 1512-20	6.3	30
153	Processes and preliminary outputs for identification of actionable genes as incidental findings in genomic sequence data in the Clinical Sequencing Exploratory Research Consortium. *Genetics in Medicine*, **2013**, 15, 860-7	8.1	95
152	Novel common and rare genetic determinants of paraoxonase activity: FTO, SERPINA12, and ITGAL. *Journal of Lipid Research*, **2013**, 54, 552-60	6.3	15
151	Confirmation of the reported association of clonal chromosomal mosaicism with an increased risk of incident hematologic cancer. *PLoS ONE*, **2013**, 8, e59823	3.7	20
150	Enhancing the power of genetic association studies through the use of silver standard cases derived from electronic medical records. *PLoS ONE*, **2013**, 8, e63481	3.7	15
149	Mechanistic phenotypes: an aggregative phenotyping strategy to identify disease mechanisms using GWAS data. *PLoS ONE*, **2013**, 8, e81503	3.7	11
148	TCIRG1 Associated Congenital Neutropenia. *Blood*, **2013**, 122, 440-440	2.2	
147	Technical desiderata for the integration of genomic data into Electronic Health Records. *Journal of Biomedical Informatics*, **2012**, 45, 419-22	10.2	96
146	ColoSeq provides comprehensive lynch and polyposis syndrome mutational analysis using massively parallel sequencing. *Journal of Molecular Diagnostics*, **2012**, 14, 357-66	5.1	163
145	Beneficence, clinical urgency, and the return of individual research results to relatives. *American Journal of Bioethics*, **2012**, 12, 9-10	1.1	8
144	The cost-effectiveness of primary stroke centers for acute stroke care. *Stroke*, **2012**, 43, 1617-23	6.7	22
143	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. *Neurology*, **2012**, 79, 221-8	6.5	124
142	Use of diverse electronic medical record systems to identify genetic risk for type 2 diabetes within a genome-wide association study. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, 212-8	8.6	216

141	VTE, thrombophilia, antithrombotic therapy, and pregnancy: Antithrombotic Therapy and Prevention of Thrombosis, 9th ed: American College of Chest Physicians Evidence-Based Clinical Practice Guidelines. *Chest*, **2012**, 141, e691S-e736S	5.3	977
140	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
139	Pilot genome-wide association search identifies potential loci for risk of erectile dysfunction in type 1 diabetes using the DCCT/EDIC study cohort. *Journal of Urology*, **2012**, 188, 514-20	2.5	14
138	Genetic Loci implicated in erythroid differentiation and cell cycle regulation are associated with red blood cell traits. *Mayo Clinic Proceedings*, **2012**, 87, 461-74	6.4	33
137	Results of genome-wide analyses on neurodevelopmental phenotypes at four-year follow-up following cardiac surgery in infancy. *PLoS ONE*, **2012**, 7, e45936	3.7	11
136	Detectable clonal mosaicism from birth to old age and its relationship to cancer. *Nature Genetics*, **2012**, 44, 642-50	36.3	409
135	Paraoxonase 1 (PON1) Status in Risk Assessment for Organophosphate Exposure and Pharmacokinetics. *ACS Symposium Series*, **2012**, 133-147	0.4	
134	Evidence-based management of anticoagulant therapy: Antithrombotic Therapy and Prevention of Thrombosis, 9th ed: American College of Chest Physicians Evidence-Based Clinical Practice Guidelines. *Chest*, **2012**, 141, e152S-e184S	5.3	920
133	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
132	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
131	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
130	Informed Consent in Genome-Scale Research: What Do Prospective Participants Think?. *American Journal of Bioethics Primary Research*, **2012**, 3, 3-11		39
129	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
128	Additional Common Polymorphisms in the PON Gene Cluster Predict PON1 Activity but Not Vascular Disease. *Journal of Lipids*, **2012**, 2012, 476316	2.7	25
127	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
126	Dietary cholesterol increases paraoxonase 1 enzyme activity. *Journal of Lipid Research*, **2012**, 53, 2450-8	6.3	33
125	Fondaparinux for isolated superficial vein thrombosis of the legs: a cost-effectiveness analysis. *Chest*, **2012**, 141, 321-329	5.3	35
124	Quality control procedures for genome-wide association studies. *Current Protocols in Human Genetics*, **2011**, Chapter 1, Unit1.19	3.2	199

123	Follow-up of carriers of BRCA1 and BRCA2 variants of unknown significance: variant reclassification and surgical decisions. *Genetics in Medicine*, **2011**, 13, 998-1005	8.1	94
122	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer disease. *Nature Genetics*, **2011**, 43, 436-41	36.3	1367
121	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
120	Complement receptor 1 gene variants are associated with erythrocyte sedimentation rate. *American Journal of Human Genetics*, **2011**, 89, 131-8	11	51
119	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
118	Genomics of the NF-B signaling pathway: hypothesized role in ovarian cancer. *Cancer Causes and Control*, **2011**, 22, 785-801	2.8	22
117	The eMERGE Network: a consortium of biorepositories linked to electronic medical records data for conducting genomic studies. *BMC Medical Genomics*, **2011**, 4, 13	3.7	505
116	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
115	Genetic variation in LPAL2, LPA, and PLG predicts plasma lipoprotein(a) level and carotid artery disease risk. *Stroke*, **2011**, 42, 2-9	6.7	31
114	Comment on "Multidimensional results reporting to participants in genomic studies: getting it right". *Science Translational Medicine*, **2011**, 3, 70le1	17.5	1
113	Response--The Risks and Benefits of Re-Consent. *Science*, **2011**, 332, 306-306	33.3	5
112	Linkage and association of phospholipid transfer protein activity to LASS4. *Journal of Lipid Research* , **2011**, 52, 1837-46	6.3	17
111	Research ethics. Research practice and participant preferences: the growing gulf. *Science*, **2011**, 331, 287-8	33.3	79
110	Interaction between fibrinogen and IL-6 genetic variants and associations with cardiovascular disease risk in the Cardiovascular Health Study. *Annals of Human Genetics*, **2010**, 74, 1-10	2.2	36
109	Glad you asked: participantsOpinions of re-consent for dbGap data submission. *Journal of Empirical Research on Human Research Ethics*, **2010**, 5, 9-16	1.6	101
108	Genetic and nongenetic sources of variation in phospholipid transfer protein activity. *Journal of Lipid Research*, **2010**, 51, 983-90	6.3	25
107	Identifying patients at high risk of a cardiovascular event in the near future: current status and future directions: report of a national heart, lung, and blood institute working group. *Circulation*, **2010**, 121, 1447-54	16.7	63
106	Genomic research and wide data sharing: views of prospective participants. *Genetics in Medicine*, **2010**, 12, 486-95	8.1	142

105	CLIA-tested genetic variants on commercial SNP arrays: potential for incidental findings in genome-wide association studies. *Genetics in Medicine*, **2010**, 12, 355-63	8.1	18
104	A formal risk-benefit framework for genomic tests: facilitating the appropriate translation of genomics into clinical practice. *Genetics in Medicine*, **2010**, 12, 686-93	8.1	72
103	Feasibility of incorporating genomic knowledge into electronic medical records for pharmacogenomic clinical decision support. *BMC Bioinformatics*, **2010**, 11 Suppl 9, S10	3.6	38
102	Ethical and practical guidelines for reporting genetic research results to study participants: updated guidelines from a National Heart, Lung, and Blood Institute working group. *Circulation: Cardiovascular Genetics*, **2010**, 3, 574-80		297
101	Linkage and association analyses identify a candidate region for apoB level on chromosome 4q32.3 in FCHL families. *Human Genetics*, **2010**, 127, 705-19	6.3	11
100	Is cardiac diagnosis a predictor of neurodevelopmental outcome after cardiac surgery in infancy?. *Journal of Thoracic and Cardiovascular Surgery*, **2010**, 140, 1230-7	1.5	68
99	J. Maxwell Chamberlain Memorial Paper for congenital heart surgery. Deep hypothermic circulatory arrest does not impair neurodevelopmental outcome in school-age children after infant cardiac surgery. *Annals of Thoracic Surgery*, **2010**, 90, 1985-94; discussion 1994-5	2.7	36
98	Human PON1, a biomarker of risk of disease and exposure. *Chemico-Biological Interactions*, **2010**, 187, 355-61	5	82
97	Paraoxonase 1 status as a risk factor for disease or exposure. *Advances in Experimental Medicine and Biology*, **2010**, 660, 29-35	3.6	51
96	Predictors of impaired neurodevelopmental outcomes at one year of age after infant cardiac surgery. *European Journal of Cardio-thoracic Surgery*, **2009**, 36, 40-7	3	93
95	Genome-wide association study of plasma lipoprotein(a) levels identifies multiple genes on chromosome 6q. *Journal of Lipid Research*, **2009**, 50, 798-806	6.3	78
94	Paraoxonase 1 (PON1) status and substrate hydrolysis. *Toxicology and Applied Pharmacology*, **2009**, 235, 1-9	4.6	99
93	Prediction of periventricular leukomalacia. Part II: Selection of hemodynamic features using computational intelligence. *Artificial Intelligence in Medicine*, **2009**, 46, 217-31	7.4	20
92	Prediction of periventricular leukomalacia. Part I: Selection of hemodynamic features using logistic regression and decision tree algorithms. *Artificial Intelligence in Medicine*, **2009**, 46, 201-15	7.4	32
91	Apolipoprotein E genotype modifies the risk of behavior problems after infant cardiac surgery. *Pediatrics*, **2009**, 124, 241-50	7.4	113
90	Arterial remodeling in [corrected] subclinical carotid artery disease. *JACC: Cardiovascular Imaging*, **2009**, 2, 1381-9	8.4	66
89	Analysis of recently identified dyslipidemia alleles reveals two loci that contribute to risk for carotid artery disease. *Lipids in Health and Disease*, **2009**, 8, 52	4.4	27
88	Perioperative stroke in infants undergoing open heart operations for congenital heart disease. *Annals of Thoracic Surgery*, **2009**, 88, 823-9	2.7	86

87	Association of genetic variation in serum amyloid-A with cardiovascular disease and interactions with IL6, IL1RN, IL1beta and TNF genes in the Cardiovascular Health Study. *Journal of Atherosclerosis and Thrombosis*, **2009**, 16, 419-30	4	26
86	National Institutes of Health State-of-the-Science Conference Statement: Family History and Improving Health. *Annals of Internal Medicine*, **2009**, 151, 872-7	8	79
85	Genetic factors are important determinants of neurodevelopmental outcome after repair of tetralogy of Fallot. *Journal of Thoracic and Cardiovascular Surgery*, **2008**, 135, 91-7	1.5	44
84	Frequent detection of familial hypercholesterolemia mutations in familial combined hyperlipidemia. *Journal of the American College of Cardiology*, **2008**, 52, 1554-6	15.1	8
83	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
82	Polymorphisms of the IL1-receptor antagonist gene (IL1RN) are associated with multiple markers of systemic inflammation. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 1407-12	9.4	64
81	Toll-like receptor 1 polymorphisms affect innate immune responses and outcomes in sepsis. *American Journal of Respiratory and Critical Care Medicine*, **2008**, 178, 710-20	10.2	226
80	Determination of paraoxonase 1 status without the use of toxic organophosphate substrates. *Circulation: Cardiovascular Genetics*, **2008**, 1, 147-52		89
79	Neurodevelopmental outcomes after staged palliation for hypoplastic left heart syndrome. *Pediatrics*, **2008**, 121, 476-83	7.4	139
78	Patient characteristics are important determinants of neurodevelopmental outcome at one year of age after neonatal and infant cardiac surgery. *Journal of Thoracic and Cardiovascular Surgery*, **2007**, 133, 1344-53, 1353.e1-3	1.5	189
77	TagSNP evaluation for the association of 42 inflammation loci and vascular disease: evidence of IL6, FGB, ALOX5, NFKBIA, and IL4R loci effects. *Human Genetics*, **2007**, 121, 65-75	6.3	15
76	Heritability of longitudinal measures of body mass index and lipid and lipoprotein levels in aging twins. *Twin Research and Human Genetics*, **2007**, 10, 703-11	2.2	56
75	Pharmacogenomic testing to prevent aminoglycoside-induced hearing loss in cystic fibrosis patients: potential impact on clinical, patient, and economic outcomes. *Genetics in Medicine*, **2007**, 9, 695-704	8.1	39
74	Predictors of carotid atherosclerotic plaque progression as measured by noninvasive magnetic resonance imaging. *Atherosclerosis*, **2007**, 194, e34-42	3.1	99
73	Cost effectiveness of entecavir versus lamivudine with adefovir salvage in HBeAg-positive chronic hepatitis B. *Pharmacoeconomics*, **2007**, 25, 963-77	4.4	34
72	The relationship of postoperative electrographic seizures to neurodevelopmental outcome at 1 year of age after neonatal and infant cardiac surgery. *Journal of Thoracic and Cardiovascular Surgery* , **2006**, 131, 181-9	1.5	75
71	Neurodevelopmental outcome after early repair of a ventricular septal defect with or without aortic arch obstruction. *Journal of Thoracic and Cardiovascular Surgery*, **2006**, 131, 792-8	1.5	27
70	TagSNP analyses of the PON gene cluster: effects on PON1 activity, LDL oxidative susceptibility, and vascular disease. *Journal of Lipid Research*, **2006**, 47, 1014-24	6.3	26

69	Inflammatory response after influenza vaccination in men with and without carotid artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2006**, 26, 2738-44	9.4	29
68	Ex vivo measures of LDL oxidative susceptibility predict carotid artery disease. *Atherosclerosis*, **2005** , 179, 147-53	3.1	19
67	A combined genomewide linkage scan of 1,233 families for prostate cancer-susceptibility genes conducted by the international consortium for prostate cancer genetics. *American Journal of Human Genetics*, **2005**, 77, 219-29	11	129
66	Presence of intraplaque hemorrhage stimulates progression of carotid atherosclerotic plaques: a high-resolution magnetic resonance imaging study. *Circulation*, **2005**, 111, 2768-75	16.7	450
65	Role of paraoxonase (PON1) status in pesticide sensitivity: genetic and temporal determinants. *NeuroToxicology*, **2005**, 26, 651-9	4.4	69
64	CYP2C9 haplotype structure in European American warfarin patients and association with clinical outcomes. *Clinical Pharmacology and Therapeutics*, **2005**, 77, 353-64	6.1	76
63	Increasing duration of deep hypothermic circulatory arrest is associated with an increased incidence of postoperative electroencephalographic seizures. *Journal of Thoracic and Cardiovascular Surgery*, **2005**, 130, 1278-86	1.5	117
62	Effect of congenital heart disease on neurodevelopmental outcomes within multiple-gestation births. *Journal of Thoracic and Cardiovascular Surgery*, **2005**, 130, 1511-6	1.5	10
61	Assessment and implications of linkage disequilibrium in genome-wide single-nucleotide polymorphism and microsatellite panels. *Genetic Epidemiology*, **2005**, 29 Suppl 1, S72-6	2.6	12
60	Genome scan for quantitative trait loci influencing HDL levels: evidence for multilocus inheritance in familial combined hyperlipidemia. *Human Genetics*, **2005**, 117, 494-505	6.3	21
59	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. *BMC Genetics*, **2005**, 6 Suppl 1, S1	2.6	6
58	The role of parametric linkage methods in complex trait analyses using microsatellites. *BMC Genetics*, **2005**, 6 Suppl 1, S48	2.6	4
57	Bias of allele-sharing linkage statistics in the presence of intermarker linkage disequilibrium. *BMC Genetics*, **2005**, 6 Suppl 1, S82	2.6	10
56	The correlation of paraoxonase (PON1) activity with lipid and lipoprotein levels differs with vascular disease status. *Journal of Lipid Research*, **2005**, 46, 1888-95	6.3	41
55	Identification of a prostate cancer susceptibility locus on chromosome 7q11-21 in Jewish families. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 1939-44	11.5	20
54	Low-density lipoprotein particle size loci in familial combined hyperlipidemia: evidence for multiple loci from a genome scan. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2004**, 24, 1942-50	9.4	35
53	Periventricular leukomalacia is common after neonatal cardiac surgery. *Journal of Thoracic and Cardiovascular Surgery*, **2004**, 127, 692-704	1.5	266
52	Determination of paraoxonase 1 status and genotypes at specific polymorphic sites. *Current Protocols in Toxicology / Editorial Board, Mahin D Maines (editor-in-chief) [et Al]*, **2004**, Chapter 4, Unit4.12	1	16

51	Novel paraoxonase (PON1) nonsense and missense mutations predicted by functional genomic assay of PON1 status. *Pharmacogenetics and Genomics*, **2003**, 13, 291-5		69
50	Functional genomic of the paraoxonase (PON1) polymorphisms: effects on pesticide sensitivity, cardiovascular disease, and drug metabolism. *Annual Review of Medicine*, **2003**, 54, 371-92	17.4	214
49	Evidence of linkage of HDL level variation to APOC3 in two samples with different ascertainment. *Human Genetics*, **2003**, 113, 522-33	6.3	25
48	Apolipoprotein E genotype and neurodevelopmental sequelae of infant cardiac surgery. *Journal of Thoracic and Cardiovascular Surgery*, **2003**, 126, 1736-45	1.5	169
47	Summary report: Missing data and pedigree and genotyping errors. *Genetic Epidemiology*, **2003**, 25 Suppl 1, S36-42	2.6	4
46	Oligogenic segregation analysis of hereditary prostate cancer pedigrees: evidence for multiple loci affecting age at onset. *International Journal of Cancer*, **2003**, 105, 630-5	7.5	30
45	Multiple genome-wide analyses of smoking behavior in the Framingham Heart Study. *BMC Genetics*, **2003**, 4 Suppl 1, S102	2.6	40
44	An examination of the genotyping error detection function of SIMWALK2. *BMC Genetics*, **2003**, 4 Suppl 1, S40	2.6	8
43	Genomic scan of 254 hereditary prostate cancer families. *Prostate*, **2003**, 57, 309-19	4.2	57
42	Paraoxonase activity, but not haplotype utilizing the linkage disequilibrium structure, predicts vascular disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2003**, 23, 1465-71	9.4	110
41	Vitamin C and E intake is associated with increased paraoxonase activity. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2002**, 22, 1329-33	9.4	153
40	Pharmacogenomic considerations of the paraoxonase polymorphisms. *Pharmacogenomics*, **2002**, 3, 341-8	2.6	40
39	Genetic Predisposition to Prostate Cancer **2002**, 279-285		
38	PON1 Polymorphisms **2002**, 53-77		19
37	Polymorphisms in the human paraoxonase (PON1) promoter. *Pharmacogenetics and Genomics*, **2001** , 11, 77-84		161
36	Modeling the cost and outcomes of pharmacist-prescribed emergency contraception. *American Journal of Public Health*, **2001**, 91, 1443-5	5.1	30
35	Germline mutations in the p73 gene do not predispose to familial prostate-brain cancer. *Prostate*, **2001**, 48, 292-6	4.2	27
34	Trends in expenditures for Medicare liver transplant recipients. *Liver Transplantation*, **2001**, 7, 858-62	4.5	23

33	Effects of 5Oregulatory-region polymorphisms on paraoxonase-gene (PON1) expression. *American Journal of Human Genetics*, **2001**, 68, 1428-36	11	307
32	Genetic linkage analysis of prostate cancer families to Xq27-28. *Human Heredity*, **2001**, 51, 107-13	1.1	45
31	Analysis of paraoxonase (PON1) L55M status requires both genotype and phenotype. *Pharmacogenetics and Genomics*, **2000**, 10, 453-60		49
30	Linkage analysis of 150 high-risk prostate cancer families at 1q24-25. *Genetic Epidemiology*, **2000**, 18, 251-75	2.6	35
29	Apolipoprotein E genotype and the risk of gallbladder disease in pregnancy. *Hepatology*, **2000**, 31, 18-23	11.2	21
28	Assessing the cost-effectiveness of pharmacogenomics. *AAPS PharmSci*, **2000**, 2, E29		108
27	A genomic scan of families with prostate cancer identifies multiple regions of interest. *American Journal of Human Genetics*, **2000**, 67, 100-9	11	77
26	The clinical and economic consequences of nosocomial central venous catheter-related infection: are antimicrobial catheters useful?. *Infection Control and Hospital Epidemiology*, **2000**, 21, 375-80	2	117
25	Paraoxonase (PON1) phenotype is a better predictor of vascular disease than is PON1(192) or PON1(55) genotype. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2000**, 20, 2441-7	9.4	276
24	Confirmation of prostate cancer susceptibility genes using high-risk families. *Journal of the National Cancer Institute Monographs*, **1999**, 81-7	4.8	7
23	Linkage of low-density lipoprotein size to the lipoprotein lipase gene in heterozygous lipoprotein lipase deficiency. *American Journal of Human Genetics*, **1999**, 64, 608-18	11	35
22	Evidence for a rare prostate cancer-susceptibility locus at chromosome 1p36. *American Journal of Human Genetics*, **1999**, 64, 776-87	11	272
21	Analysis of chromosome 1q42.2-43 in 152 families with high risk of prostate cancer. *American Journal of Human Genetics*, **1999**, 64, 1087-95	11	64
20	The use of meta-analysis in cost-effectiveness analysis. Issues and recommendations. *Pharmacoeconomics*, **1999**, 15, 1-8	4.4	14
19	Impact of family structure on the power of linkage tests using sib-pair methods. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S575-9	2.6	7
18	Complex segregation analyses: uses and limitations. *American Journal of Human Genetics*, **1998**, 63, 942-61	11	71
17	Evidence against linkage of familial combined hyperlipidemia to the apolipoprotein AI-CIII-AIV gene complex. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **1998**, 18, 215-26	9.4	40
16	Risk of Alzheimer disease with the epsilon4 allele for apolipoprotein E in a population-based study of men aged 62-73 years. *Alzheimer Disease and Associated Disorders*, **1998**, 12, 40-4	2.5	27

15	Genetic predictors of common disease: apolipoprotein E genotype as a paradigm. *Annals of Epidemiology*, **1997**, 7, 357-62	6.4	28
14	Evidence that the apolipoprotein E-genotype effects on lipid levels can change with age in males: a longitudinal analysis. *American Journal of Human Genetics*, **1997**, 61, 171-81	11	49
13	Linkage analysis of 49 high-risk families does not support a common familial prostate cancer-susceptibility gene at 1q24-25. *American Journal of Human Genetics*, **1997**, 61, 347-53	11	107
12	Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. *Genetic Epidemiology*, **1997**, 14, 999-1004	2.6	4
11	Evidence for genetic influences on smoking in adult women twins. *Clinical Genetics*, **1995**, 47, 236-44	4	32
10	Analysis of quantitative risk factors for a common oligogenic disease. *Genetic Epidemiology*, **1995**, 12, 759-64	2.6	6
9	Lower cognitive performance in normal older adult male twins carrying the apolipoprotein E epsilon 4 allele. *Archives of Neurology*, **1994**, 51, 1189-92		144
8	Genetic influences on age-related change in total cholesterol, low density lipoprotein-cholesterol, and triglyceride levels: longitudinal apolipoprotein E genotype effects. *Genetic Epidemiology*, **1994**, 11, 375-84	2.6	48
7	Familial combined hyperlipidemia in children: clinical expression, metabolic defects, and management. *Current Problems in Pediatrics*, **1994**, 24, 295-305		4
6	Familial combined hyperlipidemia in children: clinical expression, metabolic defects, and management. *Journal of Pediatrics*, **1993**, 123, 177-84	3.6	32
5	Genotype at a major locus with large effects on apolipoprotein B levels predicts familial combined hyperlipidemia. *Genetic Epidemiology*, **1993**, 10, 257-70	2.6	22
4	Complex segregation analysis of LDL peak particle diameter. *Genetic Epidemiology*, **1993**, 10, 599-604	2.6	25
3	Host and environmental effects on plasma apolipoprotein B. *International Journal of Clinical and Laboratory Research*, **1993**, 23, 215-20		7
2	Genome-wide association study of susceptibility to hospitalised respiratory infections. *Wellcome Open Research*,6, 290	4.8	0
1	Rare coding variants in 35 genes associate with circulating lipid levels a multi-ancestry analysis of 170,000 exomes		2