Gail P. Jarvik

List of Publications by Year
in descending order

442 papers	34,790 citations	3731 89 h-index	5120 166 g-index
459 all docs	459 docs citations	459 times ranked	41332 citing authors

#	Article	IF	Citations
1	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
2	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	21.4	1,676
3	VTE, Thrombophilia, Antithrombotic Therapy, and Pregnancy. Chest, 2012, 141, e691S-e736S.	0.8	1,418
4	Evidence-Based Management of Anticoagulant Therapy. Chest, 2012, 141, e152S-e184S.	0.8	1,105
5	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
6	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	17.5	846
7	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
8	The eMERGE Network: A consortium of biorepositories linked to electronic medical records data for conducting genomic studies. BMC Medical Genomics, 2011, 4, 13.	1.5	618
9	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
10	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
11	Presence of Intraplaque Hemorrhage Stimulates Progression of Carotid Atherosclerotic Plaques. Circulation, 2005, 111, 2768-2775.	1.6	518
12	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
13	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.	6.2	432
14	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
15	Actionable, Pathogenic Incidental Findings in 1,000 Participantsâ€™ Exomes. American Journal of Human Genetics, 2013, 93, 631-640.	6.2	342
16	Return of Genomic Results to Research Participants: The Floor, the Ceiling, and the Choices In Between. American Journal of Human Genetics, 2014, 94, 818-826.	6.2	342
17	Effects of 5â€² Regulatory-Region Polymorphisms on Paraoxonase-Gene (PON1) Expression. American Journal of Human Genetics, 2001, 68, 1428-1436.	6.2	338
18	Ethical and Practical Guidelines for Reporting Genetic Research Results to Study Participants. Circulation: Cardiovascular Genetics, 2010, 3, 574-580.	5.1	328

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19	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	5.5	313
20	Periventricular leukomalacia is common after neonatal cardiac surgery. Journal of Thoracic and Cardiovascular Surgery, 2004, 127, 692-704.	0.8	305
21	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, 2441-2447.	2.4	294
22	Evidence for a Rare Prostate Cancerâ€“Susceptibility Locus at Chromosome 1p36. American Journal of Human Genetics, 1999, 64, 776-787.	6.2	292
23	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
24	Recommendations for returning genomic incidental findings? We need to talk!. Genetics in Medicine, 2013, 15, 854-859.	2.4	272
25	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, 212-218.	4.4	270
26	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	12.6	269
27	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
28	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
29	Toll-like Receptor 1 Polymorphisms Affect Innate Immune Responses and Outcomes in Sepsis. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 710-720.	5.6	258
30	Functional Genomics of the Paraoxonase (PON1) Polymorphisms: Effects on Pesticide Sensitivity, Cardiovascular Disease, and Drug Metabolism. Annual Review of Medicine, 2003, 54, 371-392.	12.2	244
31	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
32	Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. American Journal of Human Genetics, 2011, 89, 529-542.	6.2	232
33	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
34	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, 1344-1353.e3.	0.8	225
35	Consideration of Cosegregation in the Pathogenicity Classification of Genomic Variants. American Journal of Human Genetics, 2016, 98, 1077-1081.	6.2	205
36	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193

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37	Apolipoprotein E genotype and neurodevelopmental sequelae of infant cardiac surgery. Journal of Thoracic and Cardiovascular Surgery, 2003, 126, 1736-1745.	0.8	190
38	Neurodevelopmental Outcomes After Staged Palliation for Hypoplastic Left Heart Syndrome. Pediatrics, 2008, 121, 476-483.	2.1	179
39	ColoSeq Provides Comprehensive Lynch and Polyposis Syndrome Mutational Analysis Using Massively Parallel Sequencing. Journal of Molecular Diagnostics, 2012, 14, 357-366.	2.8	179
40	WNT1 Mutations in Families Affected by Moderately Severe and Progressive Recessive Osteogenesis Imperfecta. American Journal of Human Genetics, 2013, 92, 590-597.	6.2	179
41	Polymorphisms in the human paraoxonase (PON1) promoter. Pharmacogenetics and Genomics, 2001, 11, 77-84.	5.7	174
42	Vitamin C and E Intake Is Associated With Increased Paraoxonase Activity. Arteriosclerosis, Thrombosis, and Vascular Biology, 2002, 22, 1329-1333.	2.4	174
43	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	3.1	174
44	Genomic research and wide data sharing: Views of prospective participants. Genetics in Medicine, 2010, 12, 486-495.	2.4	172
45	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.	6.2	172
46	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
47	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	9.0	166
48	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.8	166
49	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, 388-399.	2.4	163
50	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
51	Lower Cognitive Performance in Normal Older Adult Male Twins Carrying the Apolipoprotein E Â4 Allele. Archives of Neurology, 1994, 51, 1189-1192.	4.5	156
52	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
53	Paraoxonases-1, -2 and -3: What are their functions?. Chemico-Biological Interactions, 2016, 259, 51-62.	4.0	145
54	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.1	144

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55	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
56	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
57	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, 1278-1286.	0.8	139
58	A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancerâ€“Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229.	6.2	138
59	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
60	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.	3.8	135
61	The Clinical and Economic Consequences of Nosocomial Central Venous Catheter-Related Infection: Are Antimicrobial Catheters Useful?. Infection Control and Hospital Epidemiology, 2000, 21, 375-380.	1.8	134
62	Assessing the cost-effectiveness of pharmacogenomics. AAPS PharmSci, 2000, 2, 80-90.	1.3	133
63	Apolipoprotein E Genotype Modifies the Risk of Behavior Problems After Infant Cardiac Surgery. Pediatrics, 2009, 124, 241-250.	2.1	130
64	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	2.3	130
65	Recommendations for the integration of genomics into clinical practice. Genetics in Medicine, 2016, 18, 1075-1084.	2.4	125
66	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
67	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
68	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.	6.2	122
69	Paraoxonase Activity, But Not Haplotype Utilizing the Linkage Disequilibrium Structure, Predicts Vascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2003, 23, 1465-1471.	2.4	118
70	Predictors of impaired neurodevelopmental outcomes at one year of age after infant cardiac surgeryâ˜†â˜†â˜†. European Journal of Cardio-thoracic Surgery, 2009, 36, 40-48.	1.4	118
71	Next-Generation Sequencing Panels for the Diagnosis of Colorectal Cancer and Polyposis Syndromes: A Cost-Effectiveness Analysis. Journal of Clinical Oncology, 2015, 33, 2084-2091.	1.6	118
72	Technical desiderata for the integration of genomic data into Electronic Health Records. Journal of Biomedical Informatics, 2012, 45, 419-422.	4.3	117

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73	Glad You Asked: Participants' Opinions of Re-Consent for DbGap Data Submission. Journal of Empirical Research on Human Research Ethics, 2010, 5, 9-16.	1.3	116
74	Perioperative Stroke in Infants Undergoing Open Heart Operations for Congenital Heart Disease. Annals of Thoracic Surgery, 2009, 88, 823-829.	1.3	115
75	Follow-up of carriers of BRCA1 and BRCA2 variants of unknown significance: Variant reclassification and surgical decisions. Genetics in Medicine, 2011, 13, 998-1005.	2.4	115
76	Linkage Analysis of 49 High-Risk Families Does Not Support a Common Familial Prostate Cancerâ€"Susceptibility Gene at 1q24-25. American Journal of Human Genetics, 1997, 61, 347-353.	6.2	114
77	Paraoxonase 1 (PON1) status and substrate hydrolysis. Toxicology and Applied Pharmacology, 2009, 235, 1-9.	2.8	114
78	Predictors of carotid atherosclerotic plaque progression as measured by noninvasive magnetic resonance imaging. Atherosclerosis, 2007, 194, e34-e42.	0.8	113
79	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
80	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.	2.4	111
81	Desiderata for computable representations of electronic health records-driven phenotype algorithms. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1220-1230.	4.4	110
82	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.	5.5	110
83	National Institutes of Health State-of-the-Science Conference Statement: Family History and Improving Health. Annals of Internal Medicine, 2009, 151, 872-7.	3.9	108
84	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. Human Genetics, 2012, 131, 639-652.	3.8	103
85	The cost-effectiveness of returning incidental findings from next-generation genomic sequencing. Genetics in Medicine, 2015, 17, 587-595.	2.4	101
86	Determination of Paraoxonase 1 Status Without the Use of Toxic Organophosphate Substrates. Circulation: Cardiovascular Genetics, 2008, 1, 147-152.	5.1	99
87	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, 860-867.	2.4	99
88	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
89	Human PON1, a biomarker of risk of disease and exposure. Chemico-Biological Interactions, 2010, 187, 355-361.	4.0	98
90	haplotype structure in European American warfarin patients and association with clinical outcomes. Clinical Pharmacology and Therapeutics, 2005, 77, 353-364.	4.7	94

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91	Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records and Genomics (eMERGE) Network. Genetics in Medicine, 2012, 14, 424-431.	2.4	94
92	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.	6.2	93
93	Heritability of Longitudinal Measures of Body Mass Index and Lipid and Lipoprotein Levels in Aging Twins. Twin Research and Human Genetics, 2007, 10, 703-711.	0.6	92
94	Return of results: Ethical and legal distinctions between research and clinical care. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 105-111.	1.6	92
95	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.	5.6	91
96	The Responsibility to Recontact Research Participants after Reinterpretation of Genetic and Genomic Research Results. American Journal of Human Genetics, 2019, 104, 578-595.	6.2	91
97	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, 181-189.	0.8	89
98	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
99	A Genomic Scan of Families with Prostate Cancer Identifies Multiple Regions of Interest. American Journal of Human Genetics, 2000, 67, 100-109.	6.2	88
100	Genome-wide association study of plasma lipoprotein(a) levels identifies multiple genes on chromosome 6q. Journal of Lipid Research, 2009, 50, 798-806.	4.2	86
101	Research Practice and Participant Preferences: The Growing Gulf. Science, 2011, 331, 287-288.	12.6	86
102	A formal risk-benefit framework for genomic tests: Facilitating the appropriate translation of genomics into clinical practice. Genetics in Medicine, 2010, 12, 686-693.	2.4	83
103	Is cardiac diagnosis a predictor of neurodevelopmental outcome after cardiac surgery in infancy?. Journal of Thoracic and Cardiovascular Surgery, 2010, 140, 1230-1237.	0.8	81
104	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	2.3	79
105	Complex Segregation Analyses: Uses and Limitations. American Journal of Human Genetics, 1998, 63, 942-946.	6.2	78
106	Role of Paraoxonase (PON1) Status in Pesticide Sensitivity: Genetic and Temporal Determinants. NeuroToxicology, 2005, 26, 651-659.	3.0	78
107	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
108	Arterial Remodeling in the Subclinical Carotid Artery Disease. JACC: Cardiovascular Imaging, 2009, 2, 1381-1389.	5.3	76

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109	Identifying Patients at High Risk of a Cardiovascular Event in the Near Future. Circulation, 2010, 121, 1447-1454.	1.6	76
110	Quantification of HDL Particle Concentration by Calibrated Ion Mobility Analysis. Clinical Chemistry, 2014, 60, 1393-1401.	3.2	76
111	The FDA and Genomic Tests â€" Getting Regulation Right. New England Journal of Medicine, 2015, 372, 2258-2264.	27.0	76
112	Societal preferences for the return of incidental findings from clinical genomic sequencing: a discrete-choice experiment. Cmaj, 2015, 187, E190-E197.	2.0	76
113	Novel paraoxonase (PON1) nonsense and missense mutations predicted by functional genomic assay of PON1 status. Pharmacogenetics and Genomics, 2003, 13, 291-295.	5.7	73
114	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, 1231-1242.	4.4	73
115	Return of incidental findings in genomic medicine: measuring what patients valueâ€"development of an instrument to measure preferences for information from next-generation testing (IMPRINT). Genetics in Medicine, 2013, 15, 873-881.	2.4	72
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, 887-898.	1.3	71
117	Analysis of Chromosome 1q42.2-43 in 152 Families with High Risk of Prostate Cancer. American Journal of Human Genetics, 1999, 64, 1087-1095.	6.2	70
118	Variant Interpretation for Dilated Cardiomyopathy. Circulation Genomic and Precision Medicine, 2020, 13, e002480.	3.6	70
119	Polymorphisms of the IL1-Receptor Antagonist Gene (IL1RN) Are Associated With Multiple Markers of Systemic Inflammation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1407-1412.	2.4	68
120	A survey of current practices for genomic sequencing test interpretation and reporting processes in US laboratories. Genetics in Medicine, 2017, 19, 575-582.	2.4	68
121	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.	2.3	66
122	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
123	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
124	A survey of informatics approaches to whole-exome and whole-genome clinical reporting in the electronic health record. Genetics in Medicine, 2013, 15, 824-832.	2.4	62
125	Frequency of genomic secondaryÂfindings among 21,915 eMERGE network participants. Genetics in Medicine, 2020, 22, 1470-1477.	2.4	61
126	Paraoxonase 1 Status as a Risk Factor for Disease or Exposure. Advances in Experimental Medicine and Biology, 2010, 660, 29-35.	1.6	61

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127	Cost-Effectiveness of Recombinant Tissue-Type Plasminogen Activator Within 3 Hours of Acute Ischemic Stroke. Stroke, 2014, 45, 3032-3039.	2.0	60
128	Genomic scan of 254 hereditary prostate cancer families. Prostate, 2003, 57, 309-319.	2.3	59
129	ClinGen Pathogenicity Calculator: a configurable system for assessing pathogenicity of genetic variants. Genome Medicine, 2017, 9, 3.	8.2	59
130	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, 171-181.	6.2	57
131	Genetic factors are important determinants of neurodevelopmental outcome after repair of tetralogy of Fallot. Journal of Thoracic and Cardiovascular Surgery, 2008, 135, 91-97.	0.8	56
132	Exome Sequencing Reveals Novel Rare Variants in the Ryanodine Receptor and Calcium Channel Genes in Malignant Hyperthermia Families. Anesthesiology, 2013, 119, 1054-1065.	2.5	56
133	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	2.9	56
134	Complement Receptor 1 Gene Variants Are Associated with Erythrocyte Sedimentation Rate. American Journal of Human Genetics, 2011, 89, 131-138.	6.2	55
135	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, 1147-1151.e4.	0.8	55
136	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, 375-384.	1.3	54
137	Validation of association of the apolipoprotein E Îµ2 allele with neurodevelopmental dysfunction after cardiac surgery in neonates and infants. Journal of Thoracic and Cardiovascular Surgery, 2014, 148, 2560-2568.	0.8	53
138	Analysis of paraoxonase (PON1) L55M status requires both genotype and phenotype. Pharmacogenetics and Genomics, 2000, 10, 453-460.	5.7	52
139	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.	6.2	51
140	Characterizing genetic variants for clinical action. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 93-104.	1.6	50
141	Modifiable risk factors for chronic back pain: insights using the co-twin control design. Spine Journal, 2017, 17, 4-14.	1.3	50
142	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. JAMA Neurology, 2015, 72, 781.	9.0	49
143	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.	1.3	49
144	Informed Consent in Genome-Scale Research: What Do Prospective Participants Think?. American Journal of Bioethics Primary Research, 2012, 3, 3-11.	1.5	48

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145	An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. Cell Host and Microbe, 2018, 24, 308-323.e6.	11.0	48
146	Development and validation of a trans-ancestry polygenic risk score for type 2 diabetes in diverse populations. Genome Medicine, 2022, 14, .	8.2	48
147	Pharmacogenomic considerations of the paraoxonase polymorphisms. Pharmacogenomics, 2002, 3, 341-348.	1.3	47
148	The correlation of paraoxonase (PON1) activity with lipid and lipoprotein levels differs with vascular disease status. Journal of Lipid Research, 2005, 46, 1888-1895.	4.2	47
149	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, 512-520.	6.2	47
150	Genetic Linkage Analysis of Prostate Cancer Families to Xq27â€“28. Human Heredity, 2001, 51, 107-113.	0.8	46
151	Genetic Variation in LPAL2 , LPA , and PLG Predicts Plasma Lipoprotein(a) Level and Carotid Artery Disease Risk. Stroke, 2011, 42, 2-9.	2.0	46
152	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.	2.4	46
153	Leveraging the electronic health record to implement genomic medicine. Genetics in Medicine, 2013, 15, 270-271.	2.4	46
154	Feasibility of incorporating genomic knowledge into electronic medical records for pharmacogenomic clinical decision support. BMC Bioinformatics, 2010, 11, S10.	2.6	45
155	Multiple genome-wide analyses of smoking behavior in the Framingham Heart Study. BMC Genetics, 2003, 4, S102.	2.7	44
156	Interaction between Fibrinogen and ILâ€6 Genetic Variants and Associations with Cardiovascular Disease Risk in the Cardiovascular Health Study. Annals of Human Genetics, 2010, 74, 1-10.	0.8	44
157	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, 475-483.	2.4	44
158	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, 939-947.	0.9	44
159	Sequencing of sporadic Attentionâ€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.	1.7	44
160	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. Journal of Personalized Medicine, 2018, 8, 2.	2.5	44
161	Cost-effectiveness of Population-Wide Genomic Screening for Hereditary Breast and Ovarian Cancer in the United States. JAMA Network Open, 2020, 3, e2022874.	5.9	44
162	Linkage analysis of 150 high-risk prostate cancer families at 1q24-25. , 2000, 18, 251-275.		43

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163	Genetic Loci Implicated in Erythroid Differentiation and Cell Cycle Regulation Are Associated With Red Blood Cell Traits. Mayo Clinic Proceedings, 2012, 87, 461-474.	3.0	43
164	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, 132-139.	0.8	43
165	Linkage of Low-Density Lipoprotein Size to the Lipoprotein Lipase Gene in Heterozygous Lipoprotein Lipase Deficiency. American Journal of Human Genetics, 1999, 64, 608-618.	6.2	42
166	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.	2.4	42
167	Cost Effectiveness of Entecavir versus Lamivudine with Adefovir Salvage in HBeAg-Positive Chronic Hepatitis B. Pharmacoeconomics, 2007, 25, 963-977.	3.3	42
168	High Density GWAS for LDL Cholesterol in African Americans Using Electronic Medical Records Reveals a Strong Protective Variant in APOE. Clinical and Translational Science, 2012, 5, 394-399.	3.1	42
169	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
170	Evidence Against Linkage of Familial Combined Hyperlipidemia to the Apolipoprotein AI-CIII-AIV Gene Complex. Arteriosclerosis, Thrombosis, and Vascular Biology, 1998, 18, 215-226.	2.4	41
171	Fondaparinux for Isolated Superficial Vein Thrombosis of the Legs. Chest, 2012, 141, 321-329.	0.8	41
172	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	9.0	41
173	Diabetes Impairs Cellular Cholesterol Efflux From ABCA1 to Small HDL Particles. Circulation Research, 2020, 127, 1198-1210.	4.5	41
174	Evidence for genetic influences on smoking in adult women twins. Clinical Genetics, 1995, 47, 236-244.	2.0	40
175	Return of results in the genomic medicine projects of the eMERGE network. Frontiers in Genetics, 2014, 5, 50.	2.3	40
176	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.	2.3	40
177	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
178	Deep Hypothermic circulatory arrest does not impair neurodevelopmental outcome in school-age children after infant cardiac surgery. Annals of Thoracic Surgery, 2010, 90, 1985-1995.	1.3	39
179	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.	6.2	39
180	The Feelings About genomiC Testing Results (FACToR) Questionnaire: Development and Preliminary Validation. Journal of Genetic Counseling, 2019, 28, 477-490.	1.6	39

#	Article	IF	Citations
181	Returning Results in the Genomic Era: Initial Experiences of the eMERGE Network. Journal of Personalized Medicine, 2020, 10, 30.	2.5	39
182	Medical records-based chronic kidney disease phenotype for clinical care and â€œbig dataâ€•observational and genetic studies. Npj Digital Medicine, 2021, 4, 70.	10.9	39
183	Familial combined hyperlipidemia in children: Clinical expression, metabolic defects, and management. Journal of Pediatrics, 1993, 123, 177-184.	1.8	37
184	Low-Density Lipoprotein Particle Size Loci in Familial Combined Hyperlipidemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 1942-1950.	2.4	37
185	Dietary cholesterol increases paraoxonase 1 enzyme activity. Journal of Lipid Research, 2012, 53, 2450-2458.	4.2	37
186	Refining the structure and content of clinical genomic reports. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 85-92.	1.6	37
187	De novo EIF2AK1 and EIF2AK2 Variants Are Associated with Developmental Delay, Leukoencephalopathy, and Neurologic Decompensation. American Journal of Human Genetics, 2020, 106, 570-583.	6.2	37
188	Inflammatory Response After Influenza Vaccination in Men With and Without Carotid Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 2738-2744.	2.4	36
189	Prediction of periventricular leukomalacia. Part I: Selection of hemodynamic features using logistic regression and decision tree algorithms. Artificial Intelligence in Medicine, 2009, 46, 201-215.	6.5	36
190	Joint Linkage and Association Analysis with Exome Sequence Data Implicates SLC25A40 in Hypertriglyceridemia. American Journal of Human Genetics, 2013, 93, 1035-1045.	6.2	36
191	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
192	Risk of Alzheimer Disease with the Â±4 Allele for Apolipoprotein E in a Population-Based Study of Men Aged 62â€“73 Years. Alzheimer Disease and Associated Disorders, 1998, 12, 40-44.	1.3	35
193	Modeling the Cost and Outcomes of Pharmacist-Prescribed Emergency Contraception. American Journal of Public Health, 2001, 91, 1443-1445.	2.7	35
194	Pharmacogenetics of paraoxonase activity: elucidating the role of high-density lipoprotein in disease. Pharmacogenomics, 2013, 14, 1495-1515.	1.3	35
195	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, 463-471.	2.4	35
196	HDLâ€ƀ is a Superior Predictor of Carotid Artery Disease in a Caseâ€€control Cohort of 1725 Participants. Journal of the American Heart Association, 2014, 3, e000902.	3.7	35
197	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	2.5	35
198	Illustrative case studies in the return of exome and genome sequencing results. Personalized Medicine, 2015, 12, 283-295.	1.5	35

#	Article	IF	Citations
199	Preconception Carrier Screening by Genome Sequencing: Results from the Clinical Laboratory. American Journal of Human Genetics, 2018, 102, 1078-1089.	6.2	35
200	The Genomic Medicine Integrative Research Framework: A Conceptual Framework for Conducting Genomic Medicine Research. American Journal of Human Genetics, 2019, 104, 1088-1096.	6.2	35
201	Oligogenic segregation analysis of hereditary prostate cancer pedigrees: Evidence for multiple loci affecting age at onset. International Journal of Cancer, 2003, 105, 630-635.	5.1	34
202	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.	2.5	34
203	Concentration of Smaller Highâ€Density Lipoprotein Particle (HDLâ€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, .	3.7	34
204	Is â€œincidental findingâ€•the best term?: a study of patientsâ€™ preferences. Genetics in Medicine, 2017, 19, 176-181.	2.4	34
205	Navigating the researchâ€“clinical interface in genomic medicine: analysis from the CSER Consortium. Genetics in Medicine, 2018, 20, 545-553.	2.4	34
206	Novel gene-by-environment interactions: APOB and NPC1L1 variants affect the relationship between dietary and total plasma cholesterol. Journal of Lipid Research, 2013, 54, 1512-1520.	4.2	33
207	Complex segregation analysis of LDL peak particle diameter. Genetic Epidemiology, 1993, 10, 599-604.	1.3	32
208	Genetic predictors of common disease: Apolipoprotein E genotype as a paradigm. Annals of Epidemiology, 1997, 7, 357-362.	1.9	32
209	Association of Genetic Variation in Serum Amyloid-A with Cardiovascular Disease and Interactions withIL6, IL1RN, IL1.BETA. and TNF Genes in the Cardiovascular Health Study. Journal of Atherosclerosis and Thrombosis, 2009, 16, 419-430.	2.0	32
210	Additional Common Polymorphisms in thePONGene Cluster Predict PON1 Activity but Not Vascular Disease. Journal of Lipids, 2012, 2012, 1-11.	4.8	32
211	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.	3.0	31
212	Generalizability of Polygenic Risk Scores for Breast Cancer Among Women With European, African, and Latinx Ancestry. JAMA Network Open, 2021, 4, e2119084.	5.9	31
213	Patient Genotypes Impact Survival After Surgery for Isolated Congenital Heart Disease. Annals of Thoracic Surgery, 2014, 98, 104-111.	1.3	30
214	Germline mutations in the p73 gene do not predispose to familial prostate-brain cancer. Prostate, 2001, 48, 292-296.	2.3	29
215	Neurodevelopmental outcome after early repair of a ventricular septal defect with or without aortic arch obstruction. Journal of Thoracic and Cardiovascular Surgery, 2006, 131, 792-798.	0.8	29
216	Trends in expenditures for Medicare liver transplant recipients. Liver Transplantation, 2001, 7, 858-862.	2.4	28

#	Article	IF	Citations
217	Genomics of the NF-ÎºB signaling pathway: hypothesized role in ovarian cancer. Cancer Causes and Control, 2011, 22, 785-801.	1.8	28
218	The Cost-Effectiveness of Primary Stroke Centers for Acute Stroke Care. Stroke, 2012, 43, 1617-1623.	2.0	28
219	Regulatory changes raise troubling questions for genomic testing. Genetics in Medicine, 2014, 16, 799-803.	2.4	28
220	Initiation of universal tumor screening for <scp>L</scp>ynch syndrome in colorectal cancer patients as a model for the implementation of genetic information into clinical oncology practice. Cancer, 2016, 122, 393-401.	4.1	28
221	TagSNP analyses of the PON gene cluster: effects on PON1 activity, LDL oxidative susceptibility, and vascular disease. Journal of Lipid Research, 2006, 47, 1014-1024.	4.2	27
222	Mastering genomic terminology. Genetics in Medicine, 2017, 19, 491-492.	2.4	27
223	Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. Molecular Vision, 2014, 20, 1281-95.	1.1	27
224	Evidence of linkage of HDL level variation to APOC3 in two samples with different ascertainment. Human Genetics, 2003, 113, 522-533.	3.8	26
225	Genetic and nongenetic sources of variation in phospholipid transfer protein activity. Journal of Lipid Research, 2010, 51, 983-990.	4.2	26
226	Confirmation of the Reported Association of Clonal Chromosomal Mosaicism with an Increased Risk of Incident Hematologic Cancer. PLoS ONE, 2013, 8, e59823.	2.5	26
227	Design of a randomized controlled trial for genomic carrier screening in healthy patients seeking preconception genetic testing. Contemporary Clinical Trials, 2017, 53, 100-105.	1.8	26
228	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
229	Development of clinical decision support alerts for pharmacogenomic incidental findings from exome sequencing. Genetics in Medicine, 2015, 17, 939-942.	2.4	25
230	Generating a taxonomy for genetic conditions relevant to reproductive planning. American Journal of Medical Genetics, Part A, 2016, 170, 565-573.	1.2	25
231	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, 641-651.	2.4	25
232	Parentsâ€™ attitudes toward consent and data sharing in biobanks: A multisite experimental survey. AJOB Empirical Bioethics, 2018, 9, 128-142.	1.6	25
233	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases. JAMA Oncology, 2022, 8, 835.	7.1	25
234	A common VLDLR polymorphism interacts with APOE genotype in the prediction of carotid artery disease risk. Journal of Lipid Research, 2008, 49, 588-596.	4.2	24

#	Article	IF	Citations
235	Prediction of periventricular leukomalacia. Part II: Selection of hemodynamic features using computational intelligence. Artificial Intelligence in Medicine, 2009, 46, 217-231.	6.5	24
236	Genome sequencing and carrier testing: decisions on categorization and whether to disclose results of carrier testing. Genetics in Medicine, 2017, 19, 803-808.	2.4	24
237	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
238	Genotype at a major locus with large effects on apolipoprotein B levels predicts familial combined hyperlipidemia. Genetic Epidemiology, 1993, 10, 257-270.	1.3	23
239	Apolipoprotein E genotype and the risk of gallbladder disease in pregnancy. Hepatology, 2000, 31, 18-23.	7.3	23
240	Identification of a prostate cancer susceptibility locus on chromosome 7q11â€"21 in Jewish families. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1939-1944.	7.1	23
241	Linkage and association of phospholipid transfer protein activity to LASS4. Journal of Lipid Research, 2011, 52, 1837-1846.	4.2	23
242	Enhancing the Power of Genetic Association Studies through the Use of Silver Standard Cases Derived from Electronic Medical Records. PLoS ONE, 2013, 8, e63481.	2.5	23
243	Rare coding variation in paraoxonase-1 is associated with ischemic stroke in the NHLBI Exome Sequencing Project. Journal of Lipid Research, 2014, 55, 1173-1178.	4.2	23
244	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. Genome Medicine, 2015, 7, 67.	8.2	23
245	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. JAMA Cardiology, 2019, 4, 136.	6.1	23
246	Demand for Precision Medicine: A Discrete-Choice Experiment and External Validation Study. Pharmacoeconomics, 2020, 38, 57-68.	3.3	22
247	Genome scan for quantitative trait loci influencing HDL levels: evidence for multilocus inheritance in familial combined hyperlipidemia. Human Genetics, 2005, 117, 494-505.	3.8	21
248	Ex vivo measures of LDL oxidative susceptibility predict carotid artery disease. Atherosclerosis, 2005, 179, 147-153.	0.8	21
249	CLIA-tested genetic variants on commercial SNP arrays: Potential for incidental findings in genome-wide association studies. Genetics in Medicine, 2010, 12, 355-363.	2.4	21
250	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. Genetics in Medicine, 2014, 16, 529-534.	2.4	21
251	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	3.3	21
252	Biallelic MADD variants cause a phenotypic spectrum ranging from developmental delay to a multisystem disorder. Brain, 2020, 143, 2437-2453.	7.6	21

#	Article	IF	Citations
253	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.	3.6	21
254	The Use of Meta-Analysis in Cost-Effectiveness Analysis. Pharmacoeconomics, 1999, 15, 1-8.	3.3	20
255	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, 19, Unit4.12.	1.1	20
256	Practical Barriers and Ethical Challenges in Genetic Data Sharing. International Journal of Environmental Research and Public Health, 2014, 11, 8383-8398.	2.6	20
257	Biologyâ€Driven Geneâ€Gene Interaction Analysis of Ageâ€Related Cataract in the eMERGE Network. Genetic Epidemiology, 2015, 39, 376-384.	1.3	20
258	Patients' ratings 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, 574-582.	1.2	20
259	Genetic variation in the SIM1 locus is associated with erectile dysfunction. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11018-11023.	7.1	20
260	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.	2.4	20
261	PON1 Polymorphisms. , 2002, , 53-77.		20
262	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	2.4	19
263	Evaluation of the MC4R gene across eMERGE network identifies many unreported obesity-associated variants. International Journal of Obesity, 2021, 45, 155-169.	3.4	19
264	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.	1.8	19
265	Artificial intelligence in breast cancer screening: primary care provider preferences. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1117-1124.	4.4	19
266	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, 514-520.	0.4	18
267	A GWAS Study on Liver Function Test Using eMERGE Network Participants. PLoS ONE, 2015, 10, e0138677.	2.5	18
268	Impact of Body Mass Index and Genetics on Warfarin Major Bleeding Outcomes in a Community Setting. American Journal of Medicine, 2017, 130, 222-228.	1.5	18
269	Harmonizing Outcomes for Genomic Medicine: Comparison of eMERGE Outcomes to ClinGen Outcome/Intervention Pairs. Healthcare (Switzerland), 2018, 6, 83.	2.0	18
270	Clinical sites of the Undiagnosed Diseases Network: unique contributions to genomic medicine and science. Genetics in Medicine, 2021, 23, 259-271.	2.4	18

#	Article	IF	Citations
271	â€œGetting off the Bus Closer to Your Destinationâ€• Patientsâ€™ Views about Pharmacogenetic Testing. , 2015, 19, 21-27.		18
272	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
273	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.	3.8	17
274	Novel common and rare genetic determinants of paraoxonase activity: FTO, SERPINA12, and ITGAL. Journal of Lipid Research, 2013, 54, 552-560.	4.2	17
275	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.	1.8	17
276	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Mining, 2015, 8, 41.	4.0	17
277	Impact of HIPAAâ€™s minimum necessary standard on genomic data sharing. Genetics in Medicine, 2018, 20, 531-535.	2.4	17
278	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.	3.5	17
279	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.	4.2	17
280	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
281	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.	2.2	17
282	Effects of dietary components on high-density lipoprotein measures in a cohort of 1,566 participants. Nutrition and Metabolism, 2014, 11, 44.	3.0	16
283	Effect of congenital heart disease on 4-year neurodevelopment within multiple-gestation births. Journal of Thoracic and Cardiovascular Surgery, 2017, 154, 273-281.e2.	0.8	16
284	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.	5.9	16
285	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.	3.0	15
286	PLTP activity inversely correlates with CAAD: effects of PON1 enzyme activity and genetic variants on PLTP activity. Journal of Lipid Research, 2015, 56, 1351-1362.	4.2	15
287	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.	0.8	15
288	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.	1.2	15

#	Article	IF	Citations
289	VKORC 1 and Novel CYP 2C9 Variation Predict Warfarin Response in Alaska Native and American Indian People. Clinical and Translational Science, 2019, 12, 312-320.	3.1	15
290	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, 38.	2.5	15
291	Early infantile epileptic encephalopathy due to biallelic pathogenic variants in <scp>PIGQ</scp>: Report of seven new subjects and review of the literature. Journal of Inherited Metabolic Disease, 2020, 43, 1321-1332.	3.6	15
292	Genomic considerations for FHIRÂ®; eMERGE implementation lessons. Journal of Biomedical Informatics, 2021, 118, 103795.	4.3	15
293	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using GWAS Data. PLoS ONE, 2013, 8, e81503.	2.5	15
294	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.	2.3	14
295	Cost-Effectiveness Analysis of Patiromer and Spironolactone Therapy in Heart Failure Patients with Hyperkalemia. Pharmacoeconomics, 2018, 36, 1463-1473.	3.3	14
296	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.	2.8	14
297	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.	1.6	14
298	Penetrance of Breast Cancer Susceptibility Genes from the eMERGE III Network. JNCI Cancer Spectrum, 2021, 5, pkab044.	2.9	14
299	Linkage and association analyses identify a candidate region for apoB level on chromosome 4q32.3 in FCHL families. Human Genetics, 2010, 127, 705-719.	3.8	13
300	Results of Genome-Wide Analyses on Neurodevelopmental Phenotypes at Four-Year Follow-Up following Cardiac Surgery in Infancy. PLoS ONE, 2012, 7, e45936.	2.5	13
301	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
302	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. Scientific Reports, 2020, 10, 7561.	3.3	13
303	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.	5.2	13
304	Cost-effectiveness of population-wide genomic screening for Lynch syndrome in the United States. Genetics in Medicine, 2022, 24, 1017-1026.	2.4	13
305	Effect of congenital heart disease on neurodevelopmental outcomes within multiple-gestation births. Journal of Thoracic and Cardiovascular Surgery, 2005, 130, 1511-1516.	0.8	12
306	Assessment and implications of linkage disequilibrium in genome-wide single-nucleotide polymorphism and microsatellite panels. Genetic Epidemiology, 2005, 29, S72-S76.	1.3	12

#	Article	IF	Citations
307	A Framework for Prioritizing Research Investments in Precision Medicine. Medical Decision Making, 2016, 36, 567-580.	2.4	12
308	Copy number variation analysis in the context of electronic medical records and large-scale genomics consortium efforts. Frontiers in Genetics, 2014, 5, 51.	2.3	11
309	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. Genetic Epidemiology, 2016, 40, 470-474.	1.3	11
310	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	3.8	11
311	Anticipated responses of early adopter genetic specialists and nongenetic specialists to unsolicited genomic secondary findings. Genetics in Medicine, 2018, 20, 1186-1195.	2.4	11
312	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.	2.2	11
313	Detection of a mosaic CDKL5 deletion and inversion by optical genome mapping ends an exhaustive diagnostic odyssey. Molecular Genetics & Genomic Medicine, 2021, 9, e1665.	1.2	11
314	Use of real-world evidence in economic assessments of pharmaceuticals in the United States. Journal of Managed Care & Specialty Pharmacy, 2021, 27, 5-14.	0.9	11
315	Conceptualization of utility in translational clinical genomics research. American Journal of Human Genetics, 2021, 108, 2027-2036.	6.2	11
316	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC Genetics, 2005, 6, S1.	2.7	10
317	Bias of allele-sharing linkage statistics in the presence of intermarker linkage disequilibrium. BMC Genetics, 2005, 6, S82.	2.7	10
318	Frequent Detection of Familial Hypercholesterolemia Mutations in Familial Combined Hyperlipidemia. Journal of the American College of Cardiology, 2008, 52, 1554-1556.	2.8	10
319	Beneficence, Clinical Urgency, and the Return of Individual Research Results to Relatives. American Journal of Bioethics, 2012, 12, 9-10.	0.9	10
320	Rare loss of function variants in candidate genes and risk of colorectal cancer. Human Genetics, 2018, 137, 795-806.	3.8	10
321	Lessons Learned From A Study Of Genomics-Based Carrier Screening For Reproductive Decision Making. Health Affairs, 2018, 37, 809-816.	5.2	10
322	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.	0.3	10
323	Genomic Medicine Year in Review: 2019. American Journal of Human Genetics, 2019, 105, 1072-1075.	6.2	10
324	Development of FamilyTalk: an Intervention to Support Communication and Educate Families About Colorectal Cancer Risk. Journal of Cancer Education, 2020, 35, 470-478.	1.3	10

#	Article	IF	Citations
325	Payer Preferences and Willingness to Pay for Genomic Precision Medicine: A Discrete Choice Experiment. Journal of Managed Care & Specialty Pharmacy, 2020, 26, 529-537.	0.9	10
326	Pleiotropy in the Genetic Predisposition to Rheumatoid Arthritis: A Phenomeâ€Wide Association Study and Inverse Varianceâ€“Weighted Metaâ€Analysis. Arthritis and Rheumatology, 2020, 72, 1483-1492.	5.6	10
327	Confirmation of Prostate Cancer Susceptibility Genes Using High-Risk Families. Journal of the National Cancer Institute Monographs, 1999, 1999, 81-87.	2.1	9
328	Allocation of Resources to Communication of Research Result Summaries. Journal of Empirical Research on Human Research Ethics, 2016, 11, 364-369.	1.3	9
329	Conducting a large, multi-site survey about patientsâ€™ views on broad consent: challenges and solutions. BMC Medical Research Methodology, 2016, 16, 162.	3.1	9
330	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.	0.8	9
331	Post-traumatic Stress Disorder Symptoms are Associated With Incident Chronic Back Pain. Spine, 2019, 44, 1220-1227.	2.0	9
332	A Template for Authoring and Adapting Genomic Medicine Content in the eMERGE Infobutton Project. AMIA ... Annual Symposium proceedings, 2014, 2014, 944-53.	0.2	9
333	An examination of the genotyping error detection function of SIMWALK2. BMC Genetics, 2003, 4, S40.	2.7	8
334	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
335	â€œIt would be so much easierâ€¦ health system-led genetic risk notificationâ€”feasibility and acceptability of cascade screening in an integrated system. Journal of Community Genetics, 2019, 10, 461-470.	1.2	8
336	DYRK1A pathogenic variants in two patients with syndromic intellectual disability and a review of the literature. Molecular Genetics & Genomic Medicine, 2020, 8, e1544.	1.2	8
337	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.	1.9	8
338	Host and environmental effects on plasma apolipoprotein B. International Journal of Clinical and Laboratory Research, 1993, 23, 215-220.	1.0	7
339	Analysis of quantitative risk factors for a common oligogenic disease. Genetic Epidemiology, 1995, 12, 759-764.	1.3	7
340	Impact of family structure on the power of linkage tests using sib-pair methods. Genetic Epidemiology, 1999, 17, S575-S579.	1.3	7
341	Defining a Contemporary Ischemic Heart Disease Genetic Risk Profile Using Historical Data. Circulation: Cardiovascular Genetics, 2016, 9, 521-530.	5.1	7
342	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	4.0	7

#	Article	IF	Citations
343	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.	0.8	7
344	CNV Association of Diverse Clinical Phenotypes from eMERGE reveals novel disease biology underlying cardiovascular disease. International Journal of Cardiology, 2020, 298, 107-113.	1.7	7
345	Cost-Effectiveness of Cannabidiol Adjunct Therapy versus Usual Care for the Treatment of Seizures in Lennox-Gastaut Syndrome. Pharmacoeconomics, 2020, 38, 1237-1245.	3.3	7
346	Differences in atheroma between Caucasian and Asian subjects with anterior stroke: A vessel wall MRI study. Stroke and Vascular Neurology, 2021, 6, 25-32.	3.3	7
347	Harmonizing variant classification for return of results in the All of Us Research Program. Human Mutation, 2022, 43, 1114-1121.	2.5	7
348	Challenges in evaluating next-generation sequence data for clinical decisions. Nursing Outlook, 2015, 63, 48-50.	2.6	6
349	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.	1.2	6
350	Riskâ€“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.	1.3	6
351	Cost-effectiveness of population genomic screening. Genetics in Medicine, 2019, 21, 2840-2841.	2.4	6
352	Clinical exome sequencing vs. usual care for hereditary colorectal cancer diagnosis: A pilot comparative effectiveness study. Contemporary Clinical Trials, 2019, 84, 105820.	1.8	6
353	A Novel LCâ€MS/MS Assay for Quantification of Desâ€carboxy Prothrombin and Characterization of Warfarinâ€Induced Changes. Clinical and Translational Science, 2020, 13, 718-726.	3.1	6
354	Loci identified by a genomeâ€wide association study of carotid artery stenosis in the eMERGE network. Genetic Epidemiology, 2021, 45, 4-15.	1.3	6
355	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
356	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.	0.7	6
357	Reanalysis of eMERGE phase III sequence variants in 10,500 participants and infrastructure to support the automated return of knowledge updates. Genetics in Medicine, 2022, 24, 454-462.	2.4	6
358	Laboratory-related outcomes from integrating an accessible delivery model for hereditary cancer risk assessment and genetic testing in populations with barriers to access. Genetics in Medicine, 2022, 24, 1196-1205.	2.4	6
359	Large-scale genomic analyses reveal insights into pleiotropy across circulatory system diseases and nervous system disorders. Nature Communications, 2022, 13, .	12.8	6
360	Familial combined hyperlipidemia in children: Clinical expression, metabolic defects, and management. Current Problems in Pediatrics, 1994, 24, 295-305.	1.1	5

#	Article	IF	Citations
361	Summary report: Missing data and pedigree and genotyping errors. Genetic Epidemiology, 2003, 25, S36-S42.	1.3	5
362	Responseâ€”The Risks and Benefits of Re-Consent. Science, 2011, 332, 306-306.	12.6	5
363	Next-generation gene discovery for variants of large impact on lipid traits. Current Opinion in Lipidology, 2015, 26, 114-119.	2.7	5
364	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, 515-519.	1.6	5
365	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.	5.9	5
366	Considerations in initiating genomic screening programs in health care systems. Nursing Outlook, 2018, 66, 570-575.	2.6	5
367	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.	1.3	5
368	Genomic Medicine Year in Review: 2020. American Journal of Human Genetics, 2020, 107, 1007-1010.	6.2	5
369	Returning negative results from <scp>largeâ€scale</scp> genomic screening: Experiences from the <scp>eMERGE III</scp> network. American Journal of Medical Genetics, Part A, 2021, 185, 508-516.	1.2	5
370	Genetic Variant Reinterpretation: Economic and Population Health Management Challenges. Population Health Management, 2021, 24, 310-313.	1.7	5
371	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	6.2	5
372	Modeling the Ex Post Real Option Value in Metastatic Melanoma Using Real-World Data. Value in Health, 2021, 24, 1746-1753.	0.3	5
373	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.	1.4	5
374	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, .	0.1	5
375	Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. Genetic Epidemiology, 1997, 14, 999-1004.	1.3	4
376	The role of parametric linkage methods in complex trait analyses using microsatellites. BMC Genetics, 2005, 6, S48.	2.7	4
377	Building a family network from genetic testing. Molecular Genetics & Genomic Medicine, 2017, 5, 122-129.	1.2	4
378	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.	2.1	4

#	Article	IF	Citations
379	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.	6.2	4
380	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.	4.4	4
381	Unfolding of hidden white blood cell count phenotypes for gene discovery using latent class mixed modeling. Genes and Immunity, 2019, 20, 555-565.	4.1	4
382	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
383	Family genetic result communication in rare and undiagnosed disease communities: Understanding the practice. Journal of Genetic Counseling, 2021, 30, 439-447.	1.6	4
384	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	1.5	4
385	ShareDNA: a smartphone app to facilitate family communication of genetic results. BMC Medical Genomics, 2021, 14, 10.	1.5	4
386	Preferences of biobank participants for receiving actionable genomic test results: results of a recontacting study. Genetics in Medicine, 2021, 23, 1163-1166.	2.4	4
387	The genetic architecture of plasma kynurenine includes cardiometabolic disease mechanisms associated with the SH2B3 gene. Scientific Reports, 2021, 11, 15652.	3.3	4
388	Genomic medicine year in review: 2021. American Journal of Human Genetics, 2021, 108, 2210-2214.	6.2	4
389	Uterine fibroid polygenic risk score (PRS) associates and predicts risk for uterine fibroid. Human Genetics, 2022, 141, 1739-1748.	3.8	4
390	A research agenda to support the development and implementation of genomics-based clinical informatics tools and resources. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1342-1349.	4.4	4
391	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis. Human Genetics and Genomics Advances, 2020, 1, 100010.	1.7	3
392	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.	2.5	3
393	Neptune: an environment for the delivery of genomic medicine. Genetics in Medicine, 2021, 23, 1838-1846.	2.4	3
394	Barriers to family history knowledge and family communication among LGBTQ+ individuals in the context of hereditary cancer risk assessment. Journal of Genetic Counseling, 2021, , .	1.6	3
395	Reimbursement for genetic variant reinterpretation: five questions payers should ask. American Journal of Managed Care, 2021, 27, e336-e338.	1.1	3
396	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3

#	Article	IF	Citations
397	Modeling the Ex Ante Clinical Real Option Value in an Innovative Therapeutic Area: ALK-Positive Non-Small-Cell Lung Cancer. Pharmacoeconomics, 2022, 40, 623-631.	3.3	3
398	Developing the Value Proposition for Personalized Medicine. , 2017, , 327-342.		2
399	Arno G. Motulsky (1923â€“2018): A Founder of Medical Genetics, Creator of Pharmacogenetics, and Former ASHG President. American Journal of Human Genetics, 2018, 102, 335-339.	6.2	2
400	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.	0.3	2
401	How can clinical researchers quantify the value of their proposed comparative research?. American Heart Journal, 2019, 209, 116-125.	2.7	2
402	The FamilyTalk randomized controlled trial: patient-reported outcomes in clinical genetic sequencing for colorectal cancer. Cancer Causes and Control, 2021, 32, 483-492.	1.8	2
403	Genetic association of primary nonresponse to anti-TNFÎ± therapy in patients with inflammatory bowel disease. Pharmacogenetics and Genomics, 2022, 32, 1-9.	1.5	2
404	Replication of SCN5A Associations with Electrocardiographic Traits in African Americans from Clinical and Epidemiologic Studies. Lecture Notes in Computer Science, 2014, 2014, 939-951.	1.3	2
405	Comment on â€œMultidimensional Results Reporting to Participants in Genomic Studies: Getting It Rightâ€• Science Translational Medicine, 2011, 3, 70le1.	12.4	1
406	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 3394-3395.	2.9	1
407	Can Next Generation Sequencing Save Lives and Provide a Good Economic Value in Colon Cancer Prevention?. Value in Health, 2014, 17, A86-A87.	0.3	1
408	2016 Victor A. McKusick Leadership Award Introduction: Stanley Gartler 1. American Journal of Human Genetics, 2017, 100, 401-402.	6.2	1
409	Clinical verification of genetic results returned to research participants: findings from a Colon Cancer Family Registry. Molecular Genetics & Genomic Medicine, 2017, 5, 700-708.	1.2	1
410	Arno G. Motulsky, MD (1923â€“2018): Holocaust survivor who cofounded the field of medical genetics. Genetics in Medicine, 2018, 20, 477-479.	2.4	1
411	The use of real-world evidence in ICERâ€™s scoping process and clinical evidence assessments. Journal of Managed Care & Specialty Pharmacy, 2020, 26, 1590-1595.	0.9	1
412	Economic value of exome sequencing for suspected monogenic disorders. Genetics in Medicine, 2020, 22, 1909.	2.4	1
413	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.	2.4	1
414	Authorsâ€™ Reply to Comment on â€œCost-Effectiveness of Cannabidiol Adjunct Therapy Versus Usual Care for the Treatment of Seizures in Lennox-Gastaut Syndromeâ€• Pharmacoeconomics, 2021, 39, 477-478.	3.3	1

#	Article	IF	Citations
415	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.	1.2	1
416	Practice Patterns After Return of Rare Variants Associated With Cardiomyopathy in the Electronic Medical Records and Genomics Network. Circulation: Heart Failure, 2021, 14, e008155.	3.9	1
417	Real-world evidence for option value in metastatic melanoma. Journal of Managed Care & Specialty Pharmacy, 2021, 27, 1-10.	0.9	1
418	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.	0.9	1
419	The annual ASHG dinner. American Journal of Human Genetics, 2022, 109, 377-378.	6.2	1
420	Health care utilization and expenditures of parents of children with and without hemophilia A. Journal of Managed Care & Specialty Pharmacy, 2022, 28, 529-537.	0.9	1
421	ORCA, a values-based decision aid for selecting additional findings from genomic sequencing in adults: Efficacy results from a randomized trial. Genetics in Medicine, 2022, 24, 1664-1674.	2.4	1
422	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.	2.5	1
423	1.P.295 Paraoxonase activity is independent of HDL-related phenotypes. Atherosclerosis, 1997, 134, 79.	0.8	0
424	Paraoxonase 1 (PON1) Status in Risk Assessment for Organophosphate Exposure and Pharmacokinetics. ACS Symposium Series, 2012, , 133-147.	0.5	0
425	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	6.2	0
426	Potential Association of a Single Nucleotide Polymorphism in the CDNK1B Gene and Carotid Plaque Fibrous Cap Status by MRI. Journal of Vascular Surgery, 2013, 58, 561.	1.1	0
427	Response to Phillips et al.. Genetics in Medicine, 2015, 17, 315-315.	2.4	0
428	A case for expanding carrier testing to include actionable Xâ€linked disorders. Clinical Case Reports (discontinued), 2018, 6, 2092-2095.	0.5	0
429	Reply to Liu et al.: Tissue specificity of SIM1 gene expression and erectile dysfunction. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3349-3350.	7.1	0
430	Influence of Modeling Choices on Value of Information Analysis: An Empirical Analysis from a Real-World Experiment. Pharmacoeconomics, 2020, 38, 171-179.	3.3	0
431	Barriers to knowledge of family history and family communication among LGBTQ+ individuals in the context of hereditary cancer risk assessment. Molecular Genetics and Metabolism, 2021, 132, S200.	1.1	0
432	Genetic Predisposition to Prostate Cancer. , 2002, , 279-285.		0

#	Article	IF	Citations
433	TCIRG1 Associated Congenital Neutropenia. Blood, 2013, 122, 440-440.	1.4	0
434	A Value-of-Information Framework for Personalizing the Timing of Surveillance Testing. Medical Decision Making, 2021, , 0272989X2110492.	2.4	0
435	2021 ASHG presidential addressâ€"Imagination and daring: Past, present, and future. American Journal of Human Genetics, 2022, 109, 381-383.	6.2	0
436	Title is missing!. , 2020, 16, e1008684.		0
437	Title is missing!. , 2020, 16, e1008684.		0
438	Title is missing!. , 2020, 16, e1008684.		0
439	Title is missing!. , 2020, 16, e1008684.		0
440	Title is missing!. , 2020, 16, e1008684.		0
441	Title is missing!. , 2020, 16, e1008684.		0
442	Implementation matters: How patient experiences differ when genetic counseling accompanies the return of genetic variants of uncertain significance.. AMIA ... Annual Symposium proceedings, 2021, 2021, 950-958.	0.2	0