Elizabeth R Hauser

List of Publications by Year
in descending order

144 papers	6,199 citations	66343 42 h-index	85541 71 g-index
154 all docs	154 docs citations	154 times ranked	9264 citing authors

#	Article	IF	Citations
1	Drebrin attenuates atherosclerosis by limiting smooth muscle cell transdifferentiation. Cardiovascular Research, 2022, 118, 772-784.	3.8	8
2	Ten or More Cumulative Lifetime Adenomas Are Associated with Increased Risk for Advanced Neoplasia and Colorectal Cancer. Digestive Diseases and Sciences, 2022, 67, 2526-2534.	2.3	2
3	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	1.3	114
4	Associations between neighborhood socioeconomic cluster and hypertension, diabetes, myocardial infarction, and coronary artery disease within a cohort of cardiac catheterization patients. American Heart Journal, 2022, 243, 201-209.	2.7	7
5	Screening Colonoscopy Findings Are Associated With Noncolorectal Cancer Mortality. Clinical and Translational Gastroenterology, 2022, 13, e00479.	2.5	2
6	Health-Related Quality of Life by Gulf War Illness Case Status. International Journal of Environmental Research and Public Health, 2022, 19, 4425.	2.6	3
7	Rheumatoid arthritis T cell and muscle oxidative metabolism associate with exercise-induced changes in cardiorespiratory fitness. Scientific Reports, 2022, 12, 7450.	3.3	9
8	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	3.5	12
9	Sex-dimorphic gene effects on survival outcomes in people with coronary artery disease. American Heart Journal Plus, 2022, 17, 100152.	0.6	1
10	Exposures to low-levels of fine particulate matter are associated with acute changes in heart rate variability, cardiac repolarization, and circulating blood lipids in coronary artery disease patients. Environmental Research, 2022, 214, 113768.	7.5	3
11	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
12	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
13	Th17 Immunity in the Colon Is Controlled by Two Novel Subsets of Colon-Specific Mononuclear Phagocytes. Frontiers in Immunology, 2021, 12, 661290.	4.8	3
14	Characterizing chronological accumulation of comorbidities in healthy veterans: a computational approach. Scientific Reports, 2021, 11, 8104.	3.3	2
15	Association between short-term exposure to ambient fine particulate matter and myocardial injury in the CATHGEN cohort. Environmental Pollution, 2021, 275, 116663.	7.5	15
16	An atlas connecting shared genetic architecture of human diseases and molecular phenotypes provides insight into COVID-19 susceptibility. Genome Medicine, 2021, 13, 83.	8.2	40
17	Genomics of Gulf War Illness in U.S. Veterans Who Served during the 1990â€“1991 Persian Gulf War: Methods and Rationale for Veterans Affairs Cooperative Study #2006. Brain Sciences, 2021, 11, 845.	2.3	7
18	Genome-Wide Variants Associated With Longitudinal Survival Outcomes Among Individuals With Coronary Artery Disease. Frontiers in Genetics, 2021, 12, 661497.	2.3	3

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19	Gulf War illness in the Gulf War Era Cohort and Biorepository: The Kansas and Centers for Disease Control definitions. Life Sciences, 2021, 278, 119454.	4.3	14
20	Research tool for classifying Gulf War illness using survey responses: Lessons for writing replicable algorithms for symptom-based conditions. Life Sciences, 2021, 282, 119808.	4.3	5
21	Geneâ€"Toxicant Interactions in Gulf War Illness: Differential Effects of the PON1 Genotype. Brain Sciences, 2021, 11, 1558.	2.3	5
22	Baseline Colonoscopy Findings Associated With 10-Year Outcomes in a Screening Cohort Undergoing Colonoscopy Surveillance. Gastroenterology, 2020, 158, 862-874.e8.	1.3	51
23	High-Risk Adenomas at Screening Colonoscopy Remain Predictive of Future High-Risk Adenomas Despite an Intervening Negative Colonoscopy. American Journal of Gastroenterology, 2020, 115, 1275-1282.	0.4	4
24	Evaluating the precision of EBF1 SNP x stress interaction association: sex, race, and age differences in a big harmonized data set of 28,026 participants. Translational Psychiatry, 2020, 10, 351.	4.8	1
25	Genetic Colorectal Cancer and Adenoma Risk Variants Are Associated with Increasing Cumulative Adenoma Counts. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2269-2276.	2.5	7
26	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. Nature Genetics, 2020, 52, 680-691.	21.4	445
27	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	6.2	118
28	Accelerated epigenetic age as a biomarker of cardiovascular sensitivity to traffic-related air pollution. Aging, 2020, 12, 24141-24155.	3.1	18
29	Systolic Blood Pressure and Socioeconomic Status in a large multi-study population. SSM - Population Health, 2019, 9, 100498.	2.7	6
30	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. American Journal of Human Genetics, 2019, 105, 763-772.	6.2	169
31	Evaluating DNA methylation age on the Illumina MethylationEPIC Bead Chip. PLoS ONE, 2019, 14, e0207834.	2.5	44
32	Neighborhood Sociodemographic Effects on the Associations Between Long-term PM2.5 Exposure and Cardiovascular Outcomes and Diabetes Mellitus. Environmental Epidemiology, 2019, 3, e038.	3.0	20
33	Association of long-term PM2.5 exposure with traditional and novel lipid measures related to cardiovascular disease risk. Environment International, 2019, 122, 193-200.	10.0	83
34	Validation of the NCI Colorectal Cancer Risk Assessment Tool for baseline advanced neoplasia in a veterans cohort.. Journal of Clinical Oncology, 2019, 37, 521-521.	1.6	0
35	Characterization of temporal relationships of comorbidities developed following cancer diagnoses in veterans.. Journal of Clinical Oncology, 2019, 37, e18049-e18049.	1.6	0
36	Associations Between Residential Proximity to Traffic and Vascular Disease in a Cardiac Catheterization Cohort. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 275-282.	2.4	15

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37	Lack of Association of a Functional Polymorphism in the Serotonin Receptor Gene With Body Mass Index and Depressive Symptoms in a Large Meta-Analysis of Population Based Studies. Frontiers in Genetics, 2018, 9, 423.	2.3	5
38	Short-term effects of fine particulate matter and ozone on the cardiac conduction system in patients undergoing cardiac catheterization. Particle and Fibre Toxicology, 2018, 15, 38.	6.2	26
39	Genetic Variation in Acid Ceramidase Predicts Non-completion of an Exercise Intervention. Frontiers in Physiology, 2018, 9, 781.	2.8	8
40	The Gulf War Era Cohort and Biorepository: A Longitudinal Research Resource of Veterans of the 1990â€“1991 Gulf War Era. American Journal of Epidemiology, 2018, 187, 2279-2291.	3.4	17
41	Developing a synthetic psychosocial stress measure and harmonizing CVD-risk data: a way forward to GxE meta- and mega-analyses. BMC Research Notes, 2018, 11, 504.	1.4	3
42	Brain-derived neurotrophic factor rs6265 (Val66Met) polymorphism is associated with disease severity and incidence of cardiovascular events in a patient cohort. American Heart Journal, 2017, 190, 40-45.	2.7	25
43	Colorectal Cancer Risk Factors in Veterans with and Without Adenoma Multiplicity in a Screening Cohort. Gastroenterology, 2017, 152, S543-S544.	1.3	0
44	Fine particulate matter and cardiovascular disease: Comparison of assessment methods for long-term exposure. Environmental Research, 2017, 159, 16-23.	7.5	63
45	Apolipoprotein L1 Genetic Variants Are Associated with Chronic Kidney Disease but Not with Cardiovascular Disease in a Population Referred for Cardiac Catheterization. CardioRenal Medicine, 2017, 7, 96-103.	1.9	8
46	Impact of Genetic Testing and Family Health History Based Risk Counseling on Behavior Change and Cognitive Precursors for Type 2 Diabetes. Journal of Genetic Counseling, 2017, 26, 133-140.	1.6	21
47	A novel approach for measuring residential socioeconomic factors associated with cardiovascular and metabolic health. Journal of Exposure Science and Environmental Epidemiology, 2017, 27, 281-289.	3.9	17
48	Recommendations for Improving Identification and Quantification in Non-Targeted, GC-MS-Based Metabolomic Profiling of Human Plasma. Metabolites, 2017, 7, 45.	2.9	14
49	Ozone exposure is associated with acute changes in inflammation, fibrinolysis, and endothelial cell function in coronary artery disease patients. Environmental Health, 2017, 16, 126.	4.0	67
50	A genome-wide trans-ethnic interaction study links the PIGR-FCAMR locus to coronary atherosclerosis via interactions between genetic variants and residential exposure to traffic. PLoS ONE, 2017, 12, e0173880.	2.5	21
51	APOL1 risk alleles among individuals with CKD in Northern Tanzania: A pilot study. PLoS ONE, 2017, 12, e0181811.	2.5	7
52	Validation of the NCI colorectal cancer risk assessment tool in the CSP 380 veterans cohort.. Journal of Clinical Oncology, 2017, 35, e15135-e15135.	1.6	0
53	Genetic Variants in the Bone Morphogenic Protein Gene Family Modify the Association between Residential Exposure to Traffic and Peripheral Arterial Disease. PLoS ONE, 2016, 11, e0152670.	2.5	23
54	Case-Only Survival Analysis Reveals Unique Effects of Genotype, Sex, and Coronary Disease Severity on Survivorship. PLoS ONE, 2016, 11, e0154856.	2.5	6

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55	Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243.	3.3	145
56	Mo1724 Risk Factors Associated With the Development of Adenoma Multiplicity in a Screening Cohort. Gastroenterology, 2016, 150, S763.	1.3	0
57	Short-term effects of air temperature on plasma metabolite concentrations in patients undergoing cardiac catheterization. Environmental Research, 2016, 151, 224-232.	7.5	5
58	Associations among plasma metabolite levels and short-term exposure to PM2.5 and ozone in a cardiac catheterization cohort. Environment International, 2016, 97, 76-84.	10.0	51
59	858 Clinical Risk Group at Baseline Is Associated With 10 Year Outcomes in a Screening Cohort-Longitudinal Analysis of the CSP 380 Cohort. Gastroenterology, 2016, 150, S184.	1.3	4
60	Association between satellite-based estimates of long-term PM2.5 exposure and coronary artery disease. Environmental Research, 2016, 145, 9-17.	7.5	69
61	Association of standard clinical and laboratory variables with red blood cell distribution width. American Heart Journal, 2016, 174, 22-28.	2.7	10
62	Clinical utility of a Web-enabled risk-assessment and clinical decision support program. Genetics in Medicine, 2016, 18, 1020-1028.	2.4	34
63	Interaction Between the FOXO1A-209 Genotype and Tea Drinking Is Significantly Associated with Reduced Mortality at Advanced Ages. Rejuvenation Research, 2016, 19, 195-203.	1.8	14
64	Computing a Synthetic Chronic Psychosocial Stress Measurement in Multiple Datasets and its Application in the Replication of G Ã— E Interactions of the EBF1 Gene. Genetic Epidemiology, 2015, 39, 489-497.	1.3	8
65	Association of Roadway Proximity with Fasting Plasma Glucose and Metabolic Risk Factors for Cardiovascular Disease in a Cross-Sectional Study of Cardiac Catheterization Patients. Environmental Health Perspectives, 2015, 123, 1007-1014.	6.0	27
66	Simultaneous Consideration of Multiple Candidate Protein Biomarkers for Long-Term Risk for Cardiovascular Events. Circulation: Cardiovascular Genetics, 2015, 8, 168-177.	5.1	17
67	A Guide for a Cardiovascular Genomics Biorepository: the CATHGEN Experience. Journal of Cardiovascular Translational Research, 2015, 8, 449-457.	2.4	64
68	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
69	Gene by stress genome-wide interaction analysis and path analysis identify EBF1 as a cardiovascular and metabolic risk gene. European Journal of Human Genetics, 2015, 23, 854-862.	2.8	42
70	GxE Interactions between FOXO Genotypes and Tea Drinking Are Significantly Associated with Cognitive Disability at Advanced Ages in China. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 426-433.	3.6	34
71	Metabolomic Quantitative Trait Loci (mQTL) Mapping Implicates the Ubiquitin Proteasome System in Cardiovascular Disease Pathogenesis. PLoS Genetics, 2015, 11, e1005553.	3.5	81
72	Genetic Variants Associated with Vein Graft Stenosis after Coronary Artery Bypass Grafting. Heart Surgery Forum, 2015, 18, 001.	0.5	4

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73	Epigenetic Profiling Identifies Novel Genes for Ascending Aortic Aneurysm Formation with Bicuspid Aortic Valves. Heart Surgery Forum, 2015, 18, 134.	0.5	17
74	Risk factors for interval advanced colorectal neoplasia after screening colonoscopy.. Journal of Clinical Oncology, 2015, 33, 3539-3539.	1.6	0
75	Abstract 18660: CVSN Best Abstract Award: Genome-wide Candidates Unique to Females With Coronary Artery Disease Significantly Predict Mortality Risk. Circulation, 2015, 132, .	1.6	0
76	Validation of the association between a branched chain amino acid metabolite profile and extremes of coronary artery disease in patients referred for cardiac catheterization. Atherosclerosis, 2014, 232, 191-196.	0.8	109
77	Geneâ€“smoking interactions in multiple Rho-GTPase pathway genes in an early-onset coronary artery disease cohort. Human Genetics, 2013, 132, 1371-1382.	3.8	10
78	Phenotyping clinical disorders: lessons learned from pelvic organ prolapse. American Journal of Obstetrics and Gynecology, 2013, 208, 360-365.	1.3	10
79	The genomic medicine model: an integrated approach to implementation of family health history in primary care. Personalized Medicine, 2013, 10, 295-306.	1.5	22
80	Genome-Wide Linkage Analysis of Cardiovascular Disease Biomarkers in a Large, Multigenerational Family. PLoS ONE, 2013, 8, e71779.	2.5	12
81	A Functional Polymorphism in the 5HTR2C Gene Associated with Stress Responses Also Predicts Incident Cardiovascular Events. PLoS ONE, 2013, 8, e82781.	2.5	21
82	The genetic basis for survivorship in coronary artery disease. Frontiers in Genetics, 2013, 4, 191.	2.3	6
83	Baseline metabolomic profiles predict cardiovascular events in patients at risk for coronary artery disease. American Heart Journal, 2012, 163, 844-850.e1.	2.7	271
84	Metabolic profiles predict adverse events after coronary artery bypass grafting. Journal of Thoracic and Cardiovascular Surgery, 2012, 143, 873-878.	0.8	45
85	Fine mapping of a linkage peak with integration of lipid traits identifies novel coronary artery disease genes on chromosome 5. BMC Genetics, 2012, 13, 12.	2.7	21
86	Polymorphic variants in tenascin-C (TNC) are associated with atherosclerosis and coronary artery disease. Human Genetics, 2011, 129, 641-654.	3.8	25
87	Cigarette smoking status has a modifying effect on the association between polymorphisms in KALRN and measures of cardiovascular risk in the diabetes heart study. Genes and Genomics, 2011, 33, 483-490.	1.4	2
88	A common variant in the CDKN2B gene on chromosome 9p21 protects against coronary artery disease in Americans of African ancestry. Journal of Human Genetics, 2011, 56, 224-229.	2.3	43
89	Ordered subset analysis for caseâ€control studies. Genetic Epidemiology, 2010, 34, 407-417.	1.3	8
90	Genomeâ€wide linkage analysis of quantitative biomarker traits of osteoarthritis in a large, multigenerational extended family. Arthritis and Rheumatism, 2010, 62, 781-790.	6.7	20

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91	Assessment of LD Matrix Measures for the Analysis of Biological Pathway Association. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article35.	0.6	3
92	Association of a Peripheral Blood Metabolic Profile With Coronary Artery Disease and Risk of Subsequent Cardiovascular Events. Circulation: Cardiovascular Genetics, 2010, 3, 207-214.	5.1	390
93	Aging-related atherosclerosis is exacerbated by arterial expression of tumor necrosis factor receptor-1: evidence from mouse models and human association studies. Human Molecular Genetics, 2010, 19, 2754-2766.	2.9	32
94	Reclassification of cardiovascular risk using integrated clinical and molecular biosignatures: Design of and rationale for the Measurement to Understand the Reclassification of Disease of Cabarrus and Kannapolis (MURDOCK) Horizon 1 Cardiovascular Disease Study. American Heart Journal, 2010, 160, 371-379.e2.	2.7	33
95	High heritability of metabolomic profiles in families burdened with premature cardiovascular disease. Molecular Systems Biology, 2009, 5, 258.	7.2	140
96	Neuropeptide Y Gene Polymorphisms Confer Risk of Early-Onset Atherosclerosis. PLoS Genetics, 2009, 5, e1000318.	3.5	87
97	Genetic effects in the leukotriene biosynthesis pathway and association with atherosclerosis. Human Genetics, 2009, 125, 217-229.	3.8	51
98	Validation Study of Genetic Associations with Coronary Artery Disease on Chromosome 3q13â€21 and Potential Effect Modification by Smoking. Annals of Human Genetics, 2009, 73, 551-558.	0.8	27
99	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. Human Genomics, 2009, 3, 221.	2.9	7
100	Genetic and functional association of FAM5C with myocardial infarction. BMC Medical Genetics, 2008, 9, 33.	2.1	31
101	Orderedâ€subset analysis (OSA) for familyâ€based association mapping of complex traits. Genetic Epidemiology, 2008, 32, 627-637.	1.3	10
102	ALOX5AP variants are associated with in-stent restenosis after percutaneous coronary intervention. Atherosclerosis, 2008, 201, 148-154.	0.8	22
103	Comprehensive genetic analysis of the platelet activating factor acetylhydrolase (PLA2G7) gene and cardiovascular disease in caseâ€“control and family datasets. Human Molecular Genetics, 2008, 17, 1318-1328.	2.9	66
104	Increased Efficiency of Case-Control Association Analysis by Using Allele-Sharing and Covariate Information. Human Heredity, 2008, 65, 154-165.	0.8	5
105	Peakwide Mapping on Chromosome 3q13 Identifies the Kalirin Gene as a Novel Candidate Gene for Coronary Artery Disease. American Journal of Human Genetics, 2007, 80, 650-663.	6.2	110
106	Visualizing genotype Ã— phenotype relationships in the GAW15 simulated data. BMC Proceedings, 2007, 1, S132.	1.6	3
107	Two-stage study designs for analyzing disease-associated covariates: linkage thresholds and case-selection strategies. BMC Proceedings, 2007, 1, S138.	1.6	2
108	Comparison of GIST and LAMP on the GAW15 simulated data. BMC Proceedings, 2007, 1, S41.	1.6	3

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109	Interpretation of simultaneous linkage and familyâ€based association tests in genome screens. Genetic Epidemiology, 2007, 31, 134-142.	1.3	14
110	Interpreting analyses of continuous covariates in affected sibling pair linkage studies. Genetic Epidemiology, 2007, 31, 541-552.	1.3	6
111	Multistage designs in the genomic era: Providing balance in complex disease studies. Genetic Epidemiology, 2007, 31, S118-S123.	1.3	6
112	Association of maternal IL-1 receptor antagonist intron 2Âgene polymorphism and preterm birth. American Journal of Obstetrics and Gynecology, 2006, 195, 1249-1253.	1.3	57
113	Linkage analysis with gene-environment interaction: model illustration and performance of ordered subset analysis. Genetic Epidemiology, 2006, 30, 409-422.	1.3	7
114	The APL Test: Extension to General Nuclear Families and Haplotypes and Examination of Its Robustness. Human Heredity, 2006, 61, 189-199.	0.8	48
115	GATA2 Is Associated with Familial Early-Onset Coronary Artery Disease. PLoS Genetics, 2006, 2, e139.	3.5	82
116	Searching for epistatic interactions in nuclear families using conditional linkage analysis. BMC Genetics, 2005, 6, S148.	2.7	5
117	Early Adult-Onset POAG Linked to 15q11-13 Using Ordered Subset Analysis. , 2005, 46, 2002.		86
118	Extension of the SIMLA Package for Generating Pedigrees with Complex Inheritance Patterns: Environmental Covariates, Gene-Gene and Gene-Environment Interaction. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article15.	0.6	47
119	Linkage Disequilibrium Inflates Type I Error Rates in Multipoint Linkage Analysis when Parental Genotypes Are Missing. Human Heredity, 2005, 59, 220-227.	0.8	74
120	Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. BMC Genetics, 2004, 5, 18.	2.7	48
121	Ordered subset analysis in genetic linkage mapping of complex traits. Genetic Epidemiology, 2004, 27, 53-63.	1.3	154
122	A Genomewide Scan for Early-Onset Coronary Artery Disease in 438 Families: The GENECARD Study. American Journal of Human Genetics, 2004, 75, 436-447.	6.2	152
123	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. Diabetes, 2004, 53, 821-829.	0.6	73
124	Effects of covariates: A summary of Group 5 contributions. Genetic Epidemiology, 2003, 25, S43-S49.	1.3	9
125	Adjusting for covariates on a slippery slope: linkage analysis of change over time. BMC Genetics, 2003, 4, S50.	2.7	3
126	Design of the Genetics of Early Onset Cardiovascular Disease (GENECARD) study. American Heart Journal, 2003, 145, 602-613.	2.7	55

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127	Accounting for Linkage in Family-Based Tests of Association with Missing Parental Genotypes. American Journal of Human Genetics, 2003, 73, 1016-1026.	6.2	89
128	Ordered-Subsets Linkage Analysis Detects Novel Alzheimer Disease Loci on Chromosomes 2q34 and 15q22. American Journal of Human Genetics, 2003, 73, 1041-1051.	6.2	99
129	Genomic convergence: identifying candidate genes for Parkinson's disease by combining serial analysis of gene expression and genetic linkage. Human Molecular Genetics, 2003, 12, 671-7.	2.9	44
130	Angiotensin-converting enzyme gene insertion/deletion polymorphism and cardiovascular disease: Identifying the guideposts for navigating the genetics landscape. American Heart Journal, 2002, 144, 747-749.	2.7	5
131	Pedigree Selection and Information Content. Current Protocols in Human Genetics, 2001, 29, Unit 1.2.	3.5	1
132	Life After the Screen: Making Sense of Many Pâ€Values. Genetic Epidemiology, 2001, 21, S546-51.	1.3	5
133	The Finlandâ€“United States Investigation of Nonâ€“Insulin-Dependent Diabetes Mellitus Genetics (FUSION) Study. I. An Autosomal Genome Scan for Genes That Predispose to Type 2 Diabetes. American Journal of Human Genetics, 2000, 67, 1174-1185.	6.2	71
134	The Finlandâ€“United States Investigation of Nonâ€“Insulin-Dependent Diabetes Mellitus Genetics (FUSION) Study. II. An Autosomal Genome Scan for Diabetes-Related Quantitative-Trait Loci. American Journal of Human Genetics, 2000, 67, 1186-1200.	6.2	121
135	Genetic analysis for common complex disease. American Heart Journal, 2000, 140, S36-S44.	2.7	21
136	The Finlandâ€“United States Investigation of Nonâ€“Insulinâ€Dependent Diabetes Mellitus Genetics (FUSION) Study. I. An Autosomal Genome Scan for Genes That Predispose to Type 2 Diabetes. American Journal of Human Genetics, 2000, 67, 1174-1185.	6.2	186
137	The Finlandâ€“United States Investigation of Nonâ€“Insulinâ€Dependent Diabetes Mellitus Genetics (FUSION) Study. II. An Autosomal Genome Scan for Diabetesâ€Related Quantitativeâ€Trait Loci. American Journal of Human Genetics, 2000, 67, 1186-1200.	6.2	28
138	Familiality of Quantitative Metabolic Traits in Finnish Families with Non-Insulin-Dependent Diabetes mellitus. Human Heredity, 1999, 49, 159-168.	0.8	115
139	Genetic Linkage Analysis of Complex Genetic Traits by Using Affected Sibling Pairs. Biometrics, 1998, 54, 1238.	1.4	55
140	Affected-sib-pair interval mapping and exclusion for complex genetic traits: Sampling considerations. , 1996, 13, 117-137.		198
141	Increased hypothalamic [3H]flunitrazepam binding in hypothalamic-pituitary-adrenal axis hyporesponsive Lewis rats. Brain Research, 1992, 569, 295-299.	2.2	29
142	Prospective treatment of urea cycle disorders. Journal of Pediatrics, 1991, 119, 923-928.	1.8	143
143	Simple method of measurement of orotic acid and orotidine in urine. Biomedical Applications, 1989, 493, 388-391.	1.7	40
144	Nonparametric Linkage Analysis. , 0, , 283-328.		0