Michael A Province

List of Publications by Year
in descending order

113	8,054	76326	62596
papers	citations	40 h-index	80 g-index

118	118	118	14730
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic Pleiotropy Between Pulmonary Function and Age-Related Traits: The Long Life Family Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2024, 79, .	3.6	3
2	NIA Long Life Family Study: Objectives, Design, and Heritability of Cross-Sectional and Longitudinal Phenotypes. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 717-727.	3.6	20
3	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. Diabetes Care, 2022, 45, 232-240.	8.6	10
4	Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739.	2.8	11
5	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
6	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 372-387.	3.6	12
7	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
8	Allele-specific variation atAPOEincreases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimerâ€™s disease and myocardial infarction. Human Molecular Genetics, 2021, 30, 1443-1456.	2.9	20
9	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
10	Heterogeneity of the Predictive Polygenic Risk Scores for Coronary Heart Disease Age-at-Onset in Three Different Coronary Heart Disease Family-Based Ascertainments. Circulation Genomic and Precision Medicine, 2021, 14, e003201.	3.6	3
11	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
12	Pleiotropic Genes for Pulmonary Function and Aging-Related Traits: The Long Life Family Study (LLFS). Innovation in Aging, 2021, 5, 138-138.	0.1	0
13	Metabolomic Profile Differences Between Demented and Non-Demented APOE4 Carriers in the Long Life Family Study. Innovation in Aging, 2021, 5, 581-581.	0.1	0
14	Linkage Guided Sequence Analysis Revealed a Novel Gene PKD1L2 for Adiponectin: The Long Life Family Study (LLFS). Innovation in Aging, 2021, 5, 580-580.	0.1	0
15	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
16	Mechanisms underlying familial aggregation of exceptional health and survival: A threeâ€generation cohort study. Aging Cell, 2020, 19, e13228.	6.7	12
17	Carbohydrate and fat intake associated with risk of metabolic diseases through epigenetics of CPT1A. American Journal of Clinical Nutrition, 2020, 112, 1200-1211.	4.7	48
18	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26

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19	Genetics and geography of leukocyte telomere length in sub-Saharan Africans. Human Molecular Genetics, 2020, 29, 3014-3020.	2.9	5
20	Leukocyte Telomere Length Is Unrelated to Cognitive Performance Among Non-Demented and Demented Persons: An Examination of Long Life Family Study Participants. Journal of the International Neuropsychological Society, 2020, 26, 906-917.	1.8	6
21	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
22	Gene discovery for high-density lipoprotein cholesterol level change over time in prospective family studies. Atherosclerosis, 2020, 297, 102-110.	0.8	9
23	Salivary AMY1 Copy Number Variation Modifies Age-Related Type 2 Diabetes Risk. Clinical Chemistry, 2020, 66, 718-726.	3.2	7
24	Whole Genome Linkage Scan Identifies a Novel Locus on 3q28 for TG/HDL-C Ratio Change Over Time. Innovation in Aging, 2020, 4, 492-492.	0.1	0
25	Long Life Family Study Shows Reduced Coronary Artery Disease Despite High Polygenic Hazard Scores. Innovation in Aging, 2020, 4, 212-212.	0.1	0
26	The Long Life Family Study: Sequencing Exceptional Pedigrees for Rare Protective Variants. Innovation in Aging, 2020, 4, 851-852.	0.1	0
27	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
28	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
29	Insulin Resistance Exacerbates Genetic Predisposition to Nonalcoholic Fatty Liver Disease in Individuals Without Diabetes. Hepatology Communications, 2019, 3, 894-907.	4.3	41
30	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
31	Genome-wide linkage analysis of carotid artery traits in exceptionally long-lived families. Atherosclerosis, 2019, 291, 19-26.	0.8	5
32	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
33	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
34	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
35	Dairy Intake and Body Composition and Cardiometabolic Traits among Adults: Mendelian Randomization Analysis of 182041 Individuals from 18 Studies. Clinical Chemistry, 2019, 65, 751-760.	3.2	20
36	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549

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37	An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. Frontiers in Genetics, 2019, 10, 158.	2.3	2
38	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
39	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
40	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
41	The NIEHS TaRGET II Consortium and environmental epigenomics. Nature Biotechnology, 2018, 36, 225-227.	17.5	79
42	An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians from the GOLDN cohort. Journal of Lipid Research, 2018, 59, 722-729.	4.2	10
43	Genetics of Human Longevity From Incomplete Data: New Findings From the Long Life Family Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 1472-1481.	3.6	24
44	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
45	Clinical Pharmacogenetics Implementation Consortium (CPIC) Guideline for CYP2D6 and Tamoxifen Therapy. Clinical Pharmacology and Therapeutics, 2018, 103, 770-777.	4.7	244
46	VarExp: estimating variance explained by genome-wide GxE summary statistics. Bioinformatics, 2018, 34, 3412-3414.	4.1	13
47	Genomeâ€Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. Molecular Nutrition and Food Research, 2018, 62, 1700347.	3.3	9
48	Dairy Consumption and Body Mass Index Among Adults: Mendelian Randomization Analysis of 184802 Individuals from 25 Studies. Clinical Chemistry, 2018, 64, 183-191.	3.2	34
49	Methods for detecting methylation by SNP interaction in GAW20 simulation. BMC Proceedings, 2018, 12, 37.	1.6	2
50	How Well Does the Family Longevity Selection Score Work: A Validation Test Using the Utah Population Database. Frontiers in Public Health, 2018, 6, 277.	2.7	5
51	Simulation of a medication and methylation effects on triglycerides in the Genetic Analysis Workshop 20. BMC Proceedings, 2018, 12, 25.	1.6	5
52	A high throughput, functional screen of human Body Mass Index GWAS loci using tissue-specific RNAi Drosophila melanogaster crosses. PLoS Genetics, 2018, 14, e1007222.	3.5	22
53	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
54	Epigenomics and metabolomics reveal the mechanism of the APOA2-saturated fat intake interaction affecting obesity. American Journal of Clinical Nutrition, 2018, 108, 188-200.	4.7	54

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55	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
56	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
57	Genome- and CD4 + T-cell methylome-wide association study of circulating trimethylamine-N-oxide in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). Journal of Nutrition & Intermediary Metabolism, 2017, 8, 1-7.	1.7	11
58	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
59	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
60	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
61	Assessment of postprandial triglycerides in clinical practice: Validation in a general population and coronary heart disease patients. Journal of Clinical Lipidology, 2016, 10, 1163-1171.	1.5	22
62	General Framework for Metaâ€Analysis of Haplotype Association Tests. Genetic Epidemiology, 2016, 40, 244-252.	1.3	0
63	Epigenome-wide association study of triglyceride postprandial responses to a high-fat dietary challenge. Journal of Lipid Research, 2016, 57, 2200-2207.	4.2	40
64	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
65	Candidate gene resequencing to identify rare, pedigree-specific variants influencing healthy aging phenotypes in the long life family study. BMC Geriatrics, 2016, 16, 80.	2.7	17
66	A Framework for Interpreting Type I Error Rates from a Productâ€Term Model of Interaction Applied to Quantitative Traits. Genetic Epidemiology, 2016, 40, 144-153.	1.3	13
67	Admixture mapping of coronary artery calcification in African Americans from the NHLBI family heart study. BMC Genetics, 2015, 16, 42.	2.7	10
68	Heritability of telomere length in a study of long-lived families. Neurobiology of Aging, 2015, 36, 2785-2790.	3.1	61
69	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
70	Selection of models for the analysis of risk-factor trees: leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. Bioinformatics, 2015, 31, 1607-1613.	4.1	12
71	Genome-wide association study of triglyceride response to a high-fat meal among participants of the NHLBI Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). Metabolism: Clinical and Experimental, 2015, 64, 1359-1371.	3.4	33
72	Age, Gender, and Cancer but Not Neurodegenerative and Cardiovascular Diseases Strongly Modulate Systemic Effect of the Apolipoprotein E4 Allele on Lifespan. PLoS Genetics, 2014, 10, e1004141.	3.5	49

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73	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
74	Common Genetic Variants on 6q24 Associated With Exceptional Episodic Memory Performance in the Elderly. JAMA Neurology, 2014, 71, 1514.	9.0	14
75	Re: CYP2D6 Genotyping and the Use of Tamoxifen in Breast Cancer. Journal of the National Cancer Institute, 2014, 106, djt379-djt379.	6.3	1
76	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
77	Cytochrome P450 Gene Variants, Race, and Mortality Among Clopidogrel-Treated Patients After Acute Myocardial Infarction. Circulation: Cardiovascular Genetics, 2014, 7, 277-286.	5.1	50
78	Genome-wide association study identifies common loci influencing circulating glycated hemoglobin (HbA1c) levels in non-diabetic subjects: The Long Life Family Study (LLFS). Metabolism: Clinical and Experimental, 2014, 63, 461-468.	3.4	22
79	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
80	A correlated meta-analysis strategy for data mining "OMIC" scans. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 236-46.	0.7	17
81	A CORRELATED META-ANALYSIS STRATEGY FOR DATA MINING â€œOMICâ€•SCANS. , 2012, , .		7
82	Genetics of Hypertension and Cardiovascular Disease and Their Interconnected Pathways: Lessons from Large Studies. Current Hypertension Reports, 2011, 13, 46-54.	3.5	33
83	Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP Ã— environment regression coefficients. Genetic Epidemiology, 2011, 35, 11-18.	1.3	158
84	The SCARB1 gene is associated with lipid response to dietary and pharmacological interventions. Journal of Human Genetics, 2008, 53, 709-717.	2.3	32
85	Gathering the gold dust: methods for assessing the aggregate impact of small effect genes in genomic scans. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 190-200.	0.7	9
86	Identification of Polymorphisms Associated with Susceptibility to Therapy-Related MDS and AML.. Blood, 2007, 110, 15-15.	1.4	5
87	Relationship between Red Blood Cell Thiopurine Methyltransferase Activity and Myelotoxicity in Dogs Receiving Azathioprine. Journal of Veterinary Internal Medicine, 2004, 18, 339-345.	1.6	15
88	A meta-analysis of genome-wide linkage scans for hypertension:The National Heart, Lung and BloodInstitute Family Blood Pressure Program. American Journal of Hypertension, 2003, 16, 144-147.	2.0	100
89	Searching for the mountains of the moon: Genome scans for atherosclerosis. Current Atherosclerosis Reports, 2002, 4, 169-175.	4.8	0
90	Treeâ€based recursive partitioning methods for subdividing sibpairs into relatively more homogeneous subgroups. Genetic Epidemiology, 2001, 20, 293-306.	1.3	45

#	Article	IF	Citations
91	International Genetic Epidemiology Society: Commentary onDarkness in El Dorado by Patrick Tierney. Genetic Epidemiology, 2001, 21, 81-104.	1.3	6
92	Family risk score of coronary heart disease (CHD) as a predictor of CHD: the atherosclerosis risk in communities (ARIC) study and The NHLBI Family Heart Study. , 2000, 18, 236-250.		53
93	A single, sequential, genome-wide test to identify simultaneously all promising areas in a linkage scan. Genetic Epidemiology, 2000, 19, 301-322.	1.3	21
94	Familial Aggregation of Amount and Distribution of Subcutaneous Fat and Their Responses to Exercise Training in the HERITAGE Family Study. Obesity, 2000, 8, 140-150.	4.0	41
95	Evidence of Pleiotropic Loci for Fasting Insulin, Total Fat Mass, and Abdominal Visceral Fat in a Sedentary Population: The HERITAGE Family Study. Obesity, 2000, 8, 151-159.	4.0	5
96	Inheritance of the Waistâ€toâ€Hip Ratio in the National Heart, Lung, and Blood Institute Family Heart Study. Obesity, 2000, 8, 294-301.	4.0	15
97	Genomic scan for maximal oxygen uptake and its response to training in the HERITAGE Family Study[*]. Journal of Applied Physiology, 2000, 88, 551-559.	2.5	177
98	The impact of marker allele frequency misspecification in variance components quantitative trait locus analysis using sibship data. Genetic Epidemiology, 1999, 17, S73-S77.	1.3	3
99	A frailty approach for modelling diseases with variable age of onset in families: the NHLBI family heart study. , 1999, 18, 1517-1528.		7
100	Meta-analysis methodology for combining non-parametric sibpair linkage results: Genetic homogeneity and identical markers. Genetic Epidemiology, 1998, 15, 609-626.	1.3	52
101	Evidence for Multiple Determinants of the Body Mass Index: The National Heart, Lung, and Blood Institute Family Heart Study. Obesity, 1998, 6, 107-114.	4.0	64
102	Metaâ€analysis methodology for combining nonâ€parametric sibpair linkage results: Genetic homogeneity and identical markers. Genetic Epidemiology, 1998, 15, 609-626.	1.3	1
103	Familial Resemblance of Plasma Lipids, Lipoproteins and Postheparin Lipoprotein and Hepatic Lipases in the HERITAGE Family Study. Arteriosclerosis, Thrombosis, and Vascular Biology, 1997, 17, 3263-3269.	2.4	147
104	Race differences in reproducibilities: The HERITAGE family study. , 1997, 9, 415-424.		5
105	Family History of Coronary Heart Disease and Hemostatic Variables in Middle-Aged Adults. Thrombosis and Haemostasis, 1997, 77, 087-093.	3.4	29
106	Proliferative rate by S-phase measurement may affect cure of breast carcinoma. Cancer, 1995, 76, 1009-1018.	4.1	26
107	General purpose model and a computer program for combined segregation and path analysis (SEGPATH): Automatically creating computer programs from symbolic language model specifications. Genetic Epidemiology, 1995, 12, 203-219.	1.3	100
108	S-phase fraction and nuclear size in long term prognosis of patients with breast cancer. Cancer, 1994, 74, 2287-2299.	4.1	42

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109	Frailty and Injuries in Later Life: The FICSIT Trials. Journal of the American Geriatrics Society, 1993, 41, 283-296.	2.6	164
110	Family study of Î±₁â€antitrypsin deficiency: Effects of cigarette smoking, measured genotype, and their interaction on pulmonary function and biochemical traits. Genetic Epidemiology, 1992, 9, 317-331.	1.3	49
111	Heterogeneity among populations for familial aggregation of blood pressure. American Journal of Human Biology, 1991, 3, 515-523.	1.6	3
112	Heterogeneity in the familial aggregation of fasting serum uric acid level in five North American populations: The lipid research clinics family study. American Journal of Medical Genetics Part A, 1990, 36, 219-225.	2.4	22
113	Clinical investigation in duchenne muscular dystrophy: IV. Double. Blind controlled trial of leucine. Muscle and Nerve, 1984, 7, 535-541.	2.2	42