Alan R Shuldiner

List of Publications by Year
in descending order

468 papers	68,374 citations	1368 108 h-index	849 244 g-index
491 all docs	491 docs citations	491 times ranked	60809 citing authors

#	Article	IF	Citations
1	A missense variant Arg611Cys in LIPE which encodes hormone sensitive lipase decreases lipolysis and increases risk of type 2 diabetes in American Indians. Diabetes/Metabolism Research and Reviews, 2022, 38, e3504.	1.7	3
2	Clinical Pharmacogenetics Implementation Consortium Guideline for CYP2C19 Genotype and Clopidogrel Therapy: 2022 Update. Clinical Pharmacology and Therapeutics, 2022, 112, 959-967.	2.3	166
3	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	9.4	68
4	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. Nature Genetics, 2022, 54, 382-392.	9.4	97
5	Clinical characterization of familial hypercholesterolemia due to an amish founder mutation in Apolipoprotein B. BMC Cardiovascular Disorders, 2022, 22, 109.	0.7	2
6	Mucus sialylation determines intestinal host-commensal homeostasis. Cell, 2022, 185, 1172-1188.e28.	13.5	66
7	An Amish founder population reveals rare-population genetic determinants of the human lipidome. Communications Biology, 2022, 5, 334.	2.0	7
8	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
9	Impact of parental relatedness on reproductive outcomes among the Old Order Amish of Lancaster County. American Journal of Medical Genetics, Part A, 2022, , .	0.7	0
10	Pharmacogenomics: the low-hanging fruit in the personalized medicine tree. Human Genetics, 2022, , .	1.8	1
11	Pharmacogenomic Study of Statin-Associated Muscle Symptoms in the ODYSSEY OUTCOMES Trial. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003503.	1.6	3
12	Impact of natural selection on global patterns of genetic variation and association with clinical phenotypes at genes involved in SARS-CoV-2 infection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123000119.	3.3	7
13	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. Nature Genetics, 2022, 54, 772-782.	9.4	29
14	Population-scale analysis of common and rare genetic variation associated with hearing loss in adults. Communications Biology, 2022, 5, .	2.0	12
15	Model for Integration of Monogenic Diabetes Diagnosis Into Routine Care: The Personalized Diabetes Medicine Program. Diabetes Care, 2022, 45, 1799-1806.	4.3	6
16	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. Biological Psychiatry, 2021, 89, 236-245.	0.7	26
17	When phenotype does not match genotype: importance of â€œreal-timeâ€•refining of phenotypic information for exome data interpretation. Genetics in Medicine, 2021, 23, 215-221.	1.1	10
18	Effect of serum zinc and copper levels on insulin secretion, insulin resistance and pancreatic Î² cell dysfunction in US adults: Findings from the National Health and Nutrition Examination Survey (NHANES) 2011â€“2012. Diabetes Research and Clinical Practice, 2021, 172, 108627.	1.1	13

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19	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	2.6	42
20	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	1.8	77
21	The role of phenotype-based search approaches using public online databases in diagnostics of Mendelian disorders. Genetics in Medicine, 2021, 23, 1095-1100.	1.1	5
22	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	2.7	14
23	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
24	Two intronic cisâ€acting variants in both alleles of the POLR3A gene cause progressive spastic ataxia with hypodontia. Clinical Genetics, 2021, 99, 713-718.	1.0	2
25	Heterozygosity for a Pathogenic Variant in SLC12A3 That Causes Autosomal Recessive Gitelman Syndrome Is Associated with Lower Serum Potassium. Journal of the American Society of Nephrology: JASN, 2021, 32, 756-765.	3.0	11
26	Mutation spectrum of NOD2 reveals recessive inheritance as a main driver of Early Onset Crohnâ€™s Disease. Scientific Reports, 2021, 11, 5595.	1.6	29
27	Genetic versus stress and mood determinants of sleep in the Amish. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 113-121.	1.1	2
28	The diagnostic efficacy of exome data analysis using fixed neurodevelopmental gene lists: Implications for prenatal setting. Prenatal Diagnosis, 2021, 41, 701-707.	1.1	3
29	Impact of genetic relatedness of parents on reproductive outcomes. Molecular Genetics and Metabolism, 2021, 132, S214-S215.	0.5	0
30	Multiple dimensions of stress vs. genetic effects on depression. Translational Psychiatry, 2021, 11, 254.	2.4	4
31	Genome-wide survey of parent-of-origin-specific associations across clinical traits derived from electronic health records. Human Genetics and Genomics Advances, 2021, 2, 100039.	1.0	3
32	Genomeâ€wide association analysis of serum alanine and aspartate aminotransferase, and the modifying effects of BMI in 388kÂEuropean individuals. Genetic Epidemiology, 2021, 45, 664-681.	0.6	9
33	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	5.8	29
34	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
35	Next generation sequencing for HLA loci in full heritage Pima Indians of Arizona, Part II: HLA-A, -B, and -C with selected non-classical loci at 4-field resolution from whole genome sequences. Human Immunology, 2021, 82, 385-403.	1.2	0
36	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	2.6	72

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37	Sequencing of 640,000 exomes identifies GPR75 variants associated with protection from obesity. Science, 2021, 373, .	6.0	130
38	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms. Nature Communications, 2021, 12, 4571.	5.8	26
39	The burden of pathogenic variants in clinically actionable genes in a founder population. American Journal of Medical Genetics, Part A, 2021, 185, 3476-3484.	0.7	4
40	Rare genetic coding variants associated with human longevity and protection against age-related diseases. Nature Aging, 2021, 1, 783-794.	5.3	22
41	Exome sequencing and analysis of 454,787 UK Biobank participants. Nature, 2021, 599, 628-634.	13.7	377
42	Genome-wide association analyses highlight etiological differences underlying newly defined subtypes of diabetes. Nature Genetics, 2021, 53, 1534-1542.	9.4	81
43	Genetic and functional evidence links a missense variant in B4GALT1 to lower LDL and fibrinogen. Science, 2021, 374, 1221-1227.	6.0	14
44	Homozygosity for CHEK2 p.Gly167Arg leads to a unique cancer syndrome with multiple complex chromosomal translocations in peripheral blood karyotype. Journal of Medical Genetics, 2020, 57, 500-504.	1.5	12
45	Pharmacogenomic polygenic response score predicts ischaemic events and cardiovascular mortality in clopidogrel-treated patients. European Heart Journal - Cardiovascular Pharmacotherapy, 2020, 6, 203-210.	1.4	69
46	Global Pharmacogenomics Within Precision Medicine: Challenges and Opportunities. Clinical Pharmacology and Therapeutics, 2020, 107, 57-61.	2.3	42
47	Clinical and Molecular Prevalence of Lipodystrophy in an Unascertained Large Clinical Care Cohort. Diabetes, 2020, 69, 249-258.	0.3	51
48	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	13.7	369
49	Parkinsonâ€™s Disease-Related Motor and Nonmotor Symptoms in the Lancaster Amish. Neuroepidemiology, 2020, 54, 392-397.	1.1	1
50	Prevalence, control, and treatment of diabetes, hypertension, and high cholesterol in the Amish. BMJ Open Diabetes Research and Care, 2020, 8, e000912.	1.2	12
51	Exome Sequencing Identifies A Nonsense Variant in DAO Associated With Reduced Energy Expenditure in American Indians. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e3989-e4000.	1.8	6
52	Similar burden of pathogenic coding variants in exceptionally longâ€lived individuals and individuals without exceptional longevity. Aging Cell, 2020, 19, e13216.	3.0	7
53	Assessment of the potential role of natural selection in type 2 diabetes and related traits across human continental ancestry groups: comparison of phenotypic with genotypic divergence. Diabetologia, 2020, 63, 2616-2627.	2.9	2
54	KCNQ1 and Long QT Syndrome in 1/45 Amish. Circulation Genomic and Precision Medicine, 2020, 13, e003133.	1.6	7

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55	Genomewide Association Study of Platelet Reactivity and Cardiovascular Response in Patients Treated With Clopidogrel: A Study by the International Clopidogrel Pharmacogenomics Consortium. Clinical Pharmacology and Therapeutics, 2020, 108, 1067-1077.	2.3	32
56	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
57	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.	9.4	445
58	Genetic Variation in PEAR1, Cardiovascular Outcomes and Effects of Aspirin in a Healthy Elderly Population. Clinical Pharmacology and Therapeutics, 2020, 108, 1289-1298.	2.3	13
59	Paediatric systemic lupus erythematosus as a manifestation of constitutional mismatch repair deficiency. Journal of Medical Genetics, 2020, 57, 505-508.	1.5	7
60	Characterization of Exome Variants and Their Metabolic Impact in 6,716 American Indians from the Southwest US. American Journal of Human Genetics, 2020, 107, 251-264.	2.6	12
61	Next generation sequencing and the classical HLA loci in full heritage Pima Indians of Arizona: Defining the core HLA variation for North American Paleo-Indians. Human Immunology, 2019, 80, 955-965.	1.2	13
62	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
63	Clinical and genetic validity of quantitative bipolarity. Translational Psychiatry, 2019, 9, 228.	2.4	4
64	A Unique Presentation of Infantile-Onset Colitis and Eosinophilic Disease without Recurrent Infections Resulting from a Novel Homozygous CARMIL2 Variant. Journal of Clinical Immunology, 2019, 39, 430-439.	2.0	21
65	A novel TUFM homozygous variant in a child with mitochondrial cardiomyopathy expands the phenotype of combined oxidative phosphorylation deficiency 4. Journal of Human Genetics, 2019, 64, 589-595.	1.1	14
66	Self-Reported Sleep Duration and Pattern in Old Order Amish and Non-Amish Adults. Journal of Clinical Sleep Medicine, 2019, 15, 1321-1328.	1.4	6
67	Cardiovascular risks impact human brain N -acetylaspartate in regionally specific patterns. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25243-25249.	3.3	6
68	Increased usual physical activity is associated with a blunting of the triglyceride response to a high-fat meal. Journal of Clinical Lipidology, 2019, 13, 109-114.	0.6	9
69	Polyherbal dietary supplementation for prediabetic adults: study protocol for a randomized controlled trial. Trials, 2019, 20, 24.	0.7	11
70	Genome-wide association analysis of common genetic variants of resistant hypertension. Pharmacogenomics Journal, 2019, 19, 295-304.	0.9	16
71	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	1.1	15
72	Abstract 37: Secondary Stroke Prevention With Aspirin and Clopidogrel in CYP2C19 *17 Carriers Increases Risk of Major Non-CNS Bleeding. Stroke, 2019, 50, .	1.0	0

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73	Alcohol Consumption and Risk of Coronary Artery Disease (from the Million Veteran Program). American Journal of Cardiology, 2018, 121, 1162-1168.	0.7	23
74	Genome-wide and candidate gene approaches of clopidogrel efficacy using pharmacodynamic and clinical end pointsâ€"Rationale and design of the International Clopidogrel Pharmacogenomics Consortium (ICPC). American Heart Journal, 2018, 198, 152-159.	1.2	24
75	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. American Journal of Human Genetics, 2018, 102, 874-889.	2.6	58
76	An APOO Pseudogene on Chromosome 5q Is Associated With Low-Density Lipoprotein Cholesterol Levels. Circulation, 2018, 138, 1343-1355.	1.6	10
77	A Protein-TruncatingHSD17B13Variant and Protection from Chronic Liver Disease. New England Journal of Medicine, 2018, 378, 1096-1106.	13.9	556
78	Genomic diagnostics within a medically underserved population: efficacy and implications. Genetics in Medicine, 2018, 20, 31-41.	1.1	47
79	Monogenic diabetes in overweight and obese youth diagnosed with type 2 diabetes: the TODAY clinical trial. Genetics in Medicine, 2018, 20, 583-590.	1.1	68
80	Multisite Investigation of Outcomes WithÂImplementation of CYP2C19 Genotype-Guided Antiplatelet Therapy After Percutaneous Coronary Intervention. JACC: Cardiovascular Interventions, 2018, 11, 181-191.	1.1	213
81	Loss-of-Function ABCC8 Mutations in Pulmonary Arterial Hypertension. Circulation Genomic and Precision Medicine, 2018, 11, e002087.	1.6	62
82	KCNJ11 Mutation in One Family is Associated with Adult-Onset Rather than Neonatal-Onset Diabetes Mellitus. AACE Clinical Case Reports, 2018, 4, e411-e414.	0.4	2
83	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	1.6	17
84	Evaluation of WISP1 as a candidate gene for bone mineral density in the Old Order Amish. Scientific Reports, 2018, 8, 7141.	1.6	3
85	Establishing the role of PLVAP in protein-losing enteropathy: a homozygous missense variant leads to an attenuated phenotype. Journal of Medical Genetics, 2018, 55, 779-784.	1.5	14
86	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
87	Body Image and Life Satisfaction in Amish, Catholic, and Non-Religious Women. Journal of Amish and Plain Anabaptist Studies, 2018, 6, 174-191.	0.5	2
88	Genetic Variants of PEAR1 are Associated with Platelet Function and Antiplatelet Drug Efficacy: A Systematic Review and Meta-Analysis. Current Pharmaceutical Design, 2018, 23, 6815-6827.	0.9	10
89	Familial Hypercholesterolemia and Type 2 Diabetes in the Old Order Amish. Diabetes, 2017, 66, 2054-2058.	0.3	28
90	Genome-wide analysis of clopidogrel active metabolite levels identifies novel variants that influence antiplatelet response. Pharmacogenetics and Genomics, 2017, 27, 159-163.	0.7	22

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91	Variation in Maturity-Onset Diabetes of the Young Genes Influence Response to Interventions for Diabetes Prevention. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2678-2689.	1.8	16
92	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	9.4	116
93	CPT1A methylation is associated with plasma adiponectin. Nutrition, Metabolism and Cardiovascular Diseases, 2017, 27, 225-233.	1.1	21
94	The GH receptor exon 3 deletion is a marker of male-specific exceptional longevity associated with increased GH sensitivity and taller stature. Science Advances, 2017, 3, e1602025.	4.7	47
95	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	13.9	633
96	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	3.0	24
97	Heritability of plasma neopterin levels in the Old Order Amish. Journal of Neuroimmunology, 2017, 307, 37-41.	1.1	5
98	Sex-specific effects of serum sulfate level and SLC13A1 nonsense variants on DHEA homeostasis. Molecular Genetics and Metabolism Reports, 2017, 10, 84-91.	0.4	1
99	Pharmacogenetic Associations of Î²1-Adrenergic Receptor Polymorphisms With Cardiovascular Outcomes in the SPS3 Trial (Secondary Prevention of Small Subcortical Strokes). Stroke, 2017, 48, 1337-1343.	1.0	24
100	TM6SF2 rs58542926 impacts lipid processing in liver and small intestine. Hepatology, 2017, 65, 1526-1542.	3.6	62
101	Lipid Metabolism, Abdominal Adiposity, and Cerebral Health in the Amish. Obesity, 2017, 25, 1876-1880.	1.5	8
102	556. Adiponectin Gene Polymorphism and Seasonality in the Old Order Amish. Biological Psychiatry, 2017, 81, S225.	0.7	1
103	203. Environmental Risk Factors for Toxoplasma Gondii Seropositivity in the Old Order Amish. Biological Psychiatry, 2017, 81, S84.	0.7	1
104	A population-specific reference panel empowers genetic studies of Anabaptist populations. Scientific Reports, 2017, 7, 6079.	1.6	16
105	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
106	Identifying clinically relevant sources of variability: The clopidogrel challenge. Clinical Pharmacology and Therapeutics, 2017, 101, 264-273.	2.3	14
107	Clopidogrel pharmacogenetics: Beyond candidate genes and genomeâ€wide association studies. Clinical Pharmacology and Therapeutics, 2017, 101, 323-325.	2.3	8
108	Gender differences in first and secondhand smoke exposure, spirometric lung function and cardiometabolic health in the old order Amish: A novel population without female smoking. PLoS ONE, 2017, 12, e0174354.	1.1	19

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109	Epigenetic Signature of Impaired Fasting Glucose in the Old Order Amish. Journal of Clinical Epigenetics, 2017, 03, .	0.3	0
110	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
111	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. , 2017, , 1-24.		0
112	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. , 2017, , 191-214.		0
113	A Common Variant in the SETD7 Gene Predicts Serum Lycopene Concentrations. Nutrients, 2016, 8, 82.	1.7	45
114	Cognitive profiles and heritability estimates in the Old Order Amish. Psychiatric Genetics, 2016, 26, 178-183.	0.6	3
115	Heritability of complex white matter diffusion traits assessed in a population isolate. Human Brain Mapping, 2016, 37, 525-535.	1.9	19
116	Clopidogrel Improves Skin Microcirculatory Endothelial Function in Persons With Heightened Platelet Aggregation. Journal of the American Heart Association, 2016, 5, .	1.6	6
117	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	6.0	464
118	Genetic identification of familial hypercholesterolemia within a single U.S. health care system. Science, 2016, 354, .	6.0	349
119	Variants inANGPTL4and the Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 375, 2303-2306.	13.9	18
120	The <i>CAPN2/CAPN8</i> Locus on Chromosome 1q Is Associated with Variation in Serum Alpha-Carotene Concentrations. Journal of Nutrigenetics and Nutrigenomics, 2016, 9, 254-264.	1.8	9
121	Assignment of Functional Relevance to Genes at Type 2 Diabetes-Associated Loci Through Investigation of Î²-Cell Mass Deficits. Molecular Endocrinology, 2016, 30, 429-445.	3.7	17
122	User-centered design of multi-gene sequencing panel reports for clinicians. Journal of Biomedical Informatics, 2016, 63, 1-10.	2.5	18
123	From Genotype to Phenotype: Nonsense Variants in SLC13A1 Are Associated with Decreased Serum Sulfate and Increased Serum Aminotransferases. G3: Genes, Genomes, Genetics, 2016, 6, 2909-2918.	0.8	10
124	Historical Overview of Gene Discovery Methodologies in Type 2 Diabetes. , 2016, , 3-12.		1
125	Educational innovations in clinical pharmacogenomics. Clinical Pharmacology and Therapeutics, 2016, 99, 582-584.	2.3	27
126	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217

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127	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
128	Development of a physiology-directed population pharmacokinetic and pharmacodynamic model for characterizing the impact of genetic and demographic factors on clopidogrel response in healthy adults. European Journal of Pharmaceutical Sciences, 2016, 82, 64-78.	1.9	26
129	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 1123-1133.	13.9	411
130	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
131	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
132	Gene Expression Differences Between Offspring of Long-Lived Individuals and Controls in Candidate Longevity Regions: Evidence forPAPSS2as a Longevity Gene. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 1295-1299.	1.7	10
133	The common genetic influence over processing speed and white matter microstructure: Evidence from the Old Order Amish and Human Connectome Projects. NeuroImage, 2016, 125, 189-197.	2.1	29
134	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. , 2016, , 1-24.		0
135	Elabela-Apelin Receptor Signaling Pathway is Functional in Mammalian Systems. Scientific Reports, 2015, 5, 8170.	1.6	156
136	The IGNITE network: a model for genomic medicine implementation and research. BMC Medical Genomics, 2015, 9, 1.	0.7	189
137	The Pharmacogenomics of Anti-Platelet Intervention (PAPI) Study: Variation in Platelet Response to Clopidogrel and Aspirin. Current Vascular Pharmacology, 2015, 14, 116-124.	0.8	10
138	Prioritizing Approaches to Engage Community Members and Build Trust in Biobanks: A Survey of Attitudes and Opinions of Adults within Outpatient Practices at the University of Maryland. Journal of Personalized Medicine, 2015, 5, 264-279.	1.1	14
139	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
140	Global implementation of genomic medicine: We are not alone. Science Translational Medicine, 2015, 7, 290ps13.	5.8	146
141	CYP2C19 Metabolizer Status and Clopidogrel Efficacy in the Secondary Prevention of Small Subcortical Strokes (SPS3) Study. Journal of the American Heart Association, 2015, 4, e001652.	1.6	44
142	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
143	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
144	Evidence for several independent genetic variants affecting lipoprotein (a) cholesterol levels. Human Molecular Genetics, 2015, 24, 2390-2400.	1.4	47

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145	Vitamin and Supplement Use among Old Order Amish: Sex-Specific Prevalence and Associations with Use. Journal of the Academy of Nutrition and Dietetics, 2015, 115, 397-405.e3.	0.4	11
146	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
147	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.	1.5	33
148	Oxylipid Profile of Lowâ€Ðose Aspirin Exposure: A Pharmacometabolomics Study. Journal of the American Heart Association, 2015, 4, e002203.	1.6	24
149	Chronotype and seasonality: Morningness is associated with lower seasonal mood and behavior changes in the Old Order Amish. Journal of Affective Disorders, 2015, 174, 209-214.	2.0	28
150	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	2.6	113
151	Identification of a Variant in KDR Associated with Serum VEGFR2 and Pharmacodynamics of Pazopanib. Clinical Cancer Research, 2015, 21, 365-372.	3.2	29
152	Effect of zinc supplementation on insulin secretion: interaction between zinc and SLC30A8 genotype in Old Order Amish. Diabetologia, 2015, 58, 295-303.	2.9	34
153	Mapping Genes in Isolated Populations: Lessons from the Old Order Amish. , 2015, , 141-153.		4
154	Seasonality Shows Evidence for Polygenic Architecture and Genetic Correlation With Schizophrenia and Bipolar Disorder. Journal of Clinical Psychiatry, 2015, 76, 128-134.	1.1	25
155	Abstract 15465: Precision Medicine Approach to Resistant Hypertension: Genetic Markers of Resistant Hypertension Through a Genome-wide Association Study (GWAS) in the Secondary Prevention of Subcortical Strokes (SPS3). Circulation, 2015, 132, .	1.6	0
156	Using Workflow Modeling to Identify Areas to Improve Genetic Test Processes in the University of Maryland Translational Pharmacogenomics Project. AMIA ... Annual Symposium proceedings, 2015, 2015, 466-74.	0.2	4
157	Thrombin-induced platelet-fibrin clot strength: Relation to high on-clopidogrel platelet reactivity, genotype, and post-percutaneous coronary intervention outcomes. Thrombosis and Haemostasis, 2014, 111, 713-724.	1.8	22
158	Calcified Granulomatous Disease: Occupational Associations and Lack of Familial Aggregation. Lung, 2014, 192, 841-847.	1.4	2
159	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
160	Extension of GWAS results for lipid-related phenotypes to extreme obesity using electronic health record (EHR) data and the Metabochip. Frontiers in Genetics, 2014, 5, 222.	1.1	6
161	Implementation of pharmacogenetics: The University of Maryland personalized antiâ€platelet pharmacogenetics program. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 76-84.	0.7	82
162	Familial Aggregation of Tobacco Use Behaviors Among Amish Men. Nicotine and Tobacco Research, 2014, 16, 923-930.	1.4	11

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163	Genome-wide association studies identified novel loci for non-high-density lipoprotein cholesterol and its postprandial lipemic response. Human Genetics, 2014, 133, 919-930.	1.8	10
164	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	1.4	28
165	Analysis of the bereavement effect after the death of a spouse in the Amish: a population-based retrospective cohort study. BMJ Open, 2014, 4, e003670.	0.8	12
166	The Influence of Rare Genetic Variation in SLC30A8 on Diabetes Incidence and Î²-Cell Function. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E926-E930.	1.8	20
167	Metformin Pharmacogenomics: Current Status and Future Directions. Diabetes, 2014, 63, 2590-2599.	0.3	112
168	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
169	Effectiveness of clopidogrel dose escalation to normalize active metabolite exposure and antiplatelet effects in CYP2C19 poor metabolizers. Journal of Clinical Pharmacology, 2014, 54, 865-873.	1.0	31
170	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
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172	Null Mutation in Hormone-Sensitive Lipase Gene and Risk of Type 2 Diabetes. New England Journal of Medicine, 2014, 370, 2307-2315.	13.9	163
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