Yurii Aulchenko

List of Publications by Citations

253 papers	34,397 citations	81 h-index	184 g-index
272 ext. papers	38,836 ext. citations	9.3 avg, IF	5.85 L-index

#	Paper	IF	Citations
253	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
252	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
251	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
250	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
249	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
248	GenABEL: an R library for genome-wide association analysis. *Bioinformatics*, **2007**, 23, 1294-6	7.2	1397
247	Genome-wide association study of blood pressure and hypertension. *Nature Genetics*, **2009**, 41, 677-87	36.3	1065
246	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
245	Genome-wide analysis of genetic loci associated with Alzheimer disease. *JAMA - Journal of the American Medical Association*, **2010**, 303, 1832-40	27.4	888
244	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. *Nature Genetics*, **2012**, 44, 491-501	36.3	866
243	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708
242	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
241	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
240	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
239	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010** , 42, 448-53	36.3	582
238	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. *Nature Genetics*, **2009**, 41, 1199-206	36.3	566
237	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527

236	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genetics*, **2009**, 5, e1000504	6	495
235	Multiple loci associated with indices of renal function and chronic kidney disease. *Nature Genetics*, **2009**, 41, 712-7	36.3	469
234	Parental origin of sequence variants associated with complex diseases. *Nature*, **2009**, 462, 868-74	50.4	459
233	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
232	Genomewide association studies of stroke. *New England Journal of Medicine*, **2009**, 360, 1718-28	59.2	376
231	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
230	Genomewide rapid association using mixed model and regression: a fast and simple method for genomewide pedigree-based quantitative trait loci association analysis. *Genetics*, **2007**, 177, 577-85	4	338
229	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
228	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 2264-76	9.4	318
227	ProbABEL package for genome-wide association analysis of imputed data. *BMC Bioinformatics*, **2010**, 11, 134	3.6	310
226	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
225	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34	0.9	285
224	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. *Nature Genetics*, **2010**, 42, 869-73	36.3	277
223	Meta-analysis of genome-wide association studies for personality. *Molecular Psychiatry*, **2012**, 17, 337-49	15.1	274
222	Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. *PLoS Genetics*, **2013**, 9, e1003225	6	242
221	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
220	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 7119-24	11.5	218
219	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. *Annals of Internal Medicine*, **2009**, 151, 528-37	8	215

218	NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. *PLoS Genetics*, **2009**, 5, e1000539	6	203
217	Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies. *Nature Genetics*, **2006**, 38, 556-60	36.3	202
216	Glycans are a novel biomarker of chronological and biological ages. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2014**, 69, 779-89	6.4	192
215	A genomic background based method for association analysis in related individuals. *PLoS ONE*, **2007**, 2, e1274	3.7	191
214	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
213	Three genome-wide association studies and a linkage analysis identify HERC2 as a human iris color gene. *American Journal of Human Genetics*, **2008**, 82, 411-23	11	183
212	A genome-wide association study identifies a susceptibility locus for refractive errors and myopia at 15q14. *Nature Genetics*, **2010**, 42, 897-901	36.3	181
211	Predictive testing for complex diseases using multiple genes: fact or fiction?. *Genetics in Medicine*, **2006**, 8, 395-400	8.1	181
210	PredictABEL: an R package for the assessment of risk prediction models. *European Journal of Epidemiology*, **2011**, 26, 261-4	12.1	175
209	Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA - Journal of the American Medical Association*, **2009**, 302, 168-78	27.4	164
208	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
207	A genome-wide association study of optic disc parameters. *PLoS Genetics*, **2010**, 6, e1000978	6	157
206	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	6	151
205	Genetic determinants of circulating sphingolipid concentrations in European populations. *PLoS Genetics*, **2009**, 5, e1000672	6	150
204	Genetic variation in the KIF1B locus influences susceptibility to multiple sclerosis. *Nature Genetics*, **2008**, 40, 1402-3	36.3	150
203	Association of genome-wide variation with the risk of incident heart failure in adults of European and African ancestry: a prospective meta-analysis from the cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 256-66		147
202	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
201	Rapid variance components-based method for whole-genome association analysis. *Nature Genetics*, **2012**, 44, 1166-70	36.3	145

200	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27	11	145
199	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
198	Genome-wide association and functional follow-up reveals new loci for kidney function. *PLoS Genetics*, **2012**, 8, e1002584	6	143
197	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
196	Common genetic determinants of intraocular pressure and primary open-angle glaucoma. *PLoS Genetics*, **2012**, 8, e1002611	6	131
195	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
194	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: results of genome-wide association analyses including 4659 European individuals. *Atherosclerosis*, **2010**, 208, 412-20	3.1	128
193	A genomewide screen for late-onset Alzheimer disease in a genetically isolated Dutch population. *American Journal of Human Genetics*, **2007**, 81, 17-31	11	124
192	Identification of novel genetic Loci associated with thyroid peroxidase antibodies and clinical thyroid disease. *PLoS Genetics*, **2014**, 10, e1004123	6	122
191	Comparative performance of four methods for high-throughput glycosylation analysis of immunoglobulin G in genetic and epidemiological research. *Molecular and Cellular Proteomics*, **2014**, 13, 1598-610	7.6	120
190	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. *Molecular Psychiatry*, **2011**, 16, 773-83	15.1	116
189	Genome-wide association study of smoking initiation and current smoking. *American Journal of Human Genetics*, **2009**, 84, 367-79	11	116
188	Inflammatory bowel disease associates with proinflammatory potential of the immunoglobulin G glycome. *Inflammatory Bowel Diseases*, **2015**, 21, 1237-47	4.5	108
187	A meta-analysis of four genome-wide association studies of survival to age 90 years or older: the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2010**, 65, 478-87	6.4	107
186	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
185	The Effect of Genetic Drift in a Young Genetically Isolated Population. *Annals of Human Genetics*, **2005**, 69, 288-295	2.2	105
184	Sex-specific genetic effects influence variation in body composition. *Diabetologia*, **2008**, 51, 2233-41	10.3	97
183	Linkage disequilibrium in young genetically isolated Dutch population. *European Journal of Human Genetics*, **2004**, 12, 527-34	5.3	95

182	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. *Molecular Psychiatry*, **2012**, 17, 1116-29	15.1	93
181	Genetic contributions to glaucoma: heritability of intraocular pressure, retinal nerve fiber layer thickness, and optic disc morphology. *Investigative Ophthalmology and Visual Science*, **2007**, 48, 3669-76		92
180	Heritability of the function and structure of the arterial wall: findings of the Erasmus Rucphen Family (ERF) study. *Stroke*, **2005**, 36, 2351-6	6.7	92
179	Predicting human height by Victorian and genomic methods. *European Journal of Human Genetics*, **2009**, 17, 1070-5	5.3	91
178	The empirical power of rare variant association methods: results from sanger sequencing in 1,998 individuals. *PLoS Genetics*, **2012**, 8, e1002496	6	89
177	A major SNP haplotype of the arginine vasopressin 1B receptor protects against recurrent major depression. *Molecular Psychiatry*, **2004**, 9, 287-92	15.1	88
176	IgG Glycome in Colorectal Cancer. *Clinical Cancer Research*, **2016**, 22, 3078-86	12.9	85
175	Association between chromosome 9p21 variants and the ankle-brachial index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics*, **2012**, 5, 100-12		84
174	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. *Translational Psychiatry*, **2011**, 1, e50	8.6	83
173	Glycosylation of Immunoglobulin G Associates With Clinical Features of Inflammatory Bowel Diseases. *Gastroenterology*, **2018**, 154, 1320-1333.e10	13.3	82
172	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. *Human Molecular Genetics*, **2009**, 18, 373-80	5.6	81
171	Association of novel genetic Loci with circulating fibrinogen levels: a genome-wide association study in 6 population-based cohorts. *Circulation: Cardiovascular Genetics*, **2009**, 2, 125-33		77
170	Shared genetic factors in migraine and depression: evidence from a genetic isolate. *Neurology*, **2010**, 74, 288-94	6.5	75
169	Eight genetic loci associated with variation in lipoprotein-associated phospholipase A2 mass and activity and coronary heart disease: meta-analysis of genome-wide association studies from five community-based studies. *European Heart Journal*, **2012**, 33, 238-51	9.5	75
168	Genome-wide association studies of MRI-defined brain infarcts: meta-analysis from the CHARGE Consortium. *Stroke*, **2010**, 41, 210-7	6.7	74
167	Prevalence and heritability of the metabolic syndrome and its individual components in a Dutch isolate: the Erasmus Rucphen Family study. *Journal of Medical Genetics*, **2008**, 45, 572-7	5.8	73
166	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. *European Journal of Human Genetics*, **2011**, 19, 901-7	5.3	70
165	A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. *Human Molecular Genetics*, **2009**, 18, 3516-24	5.6	70

164	Heritability of blood pressure traits and the genetic contribution to blood pressure variance explained by four blood-pressure-related genes. *Journal of Hypertension*, **2007**, 25, 565-70	1.9	69
163	The Association Between Glycosylation of Immunoglobulin G and Hypertension: A Multiple Ethnic Cross-Sectional Study. *Medicine (United States)*, **2016**, 95, e3379	1.8	69
162	The effect of genetic drift in a young genetically isolated population. *Annals of Human Genetics*, **2005**, 69, 288-95	2.2	67
161	Genomic variation associated with mortality among adults of European and African ancestry with heart failure: the cohorts for heart and aging research in genomic epidemiology consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 248-55		66
160	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
159	Variance heterogeneity analysis for detection of potentially interacting genetic loci: method and its limitations. *BMC Genetics*, **2010**, 11, 92	2.6	64
158	EVI5 is a risk gene for multiple sclerosis. *Genes and Immunity*, **2008**, 9, 334-7	4.4	64
157	Evidence of inbreeding depression on human height. *PLoS Genetics*, **2012**, 8, e1002655	6	62
156	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. *PLoS Genetics*, **2018**, 14, e1007601	6	60
155	A genome-wide association scan of RR and QT interval duration in 3 European genetically isolated populations: the EUROSPAN project. *Circulation: Cardiovascular Genetics*, **2009**, 2, 322-8		58
154	Genome-wide linkage analysis of serum creatinine in three isolated European populations. *Kidney International*, **2009**, 76, 297-306	9.9	57
153	Replication of CD58 and CLEC16A as genome-wide significant risk genes for multiple sclerosis. *Journal of Human Genetics*, **2009**, 54, 676-80	4.3	57
152	Genetic architecture of plasma adiponectin overlaps with the genetics of metabolic syndrome-related traits. *Diabetes Care*, **2010**, 33, 908-13	14.6	54
151	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. *Human Molecular Genetics*, **2012**, 21, 5329-43	5.6	54
150	Insulin-resistance and metabolic syndrome are related to executive function in women in a large family-based study. *European Journal of Epidemiology*, **2010**, 25, 561-8	12.1	54
149	Familial clustering and genetic risk for dementia in a genetically isolated Dutch population. *Brain*, **2004**, 127, 1641-9	11.2	52
148	The apolipoprotein E gene and its age-specific effects on cognitive function. *Neurobiology of Aging*, **2010**, 31, 1831-3	5.6	51
147	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. *American Journal of Clinical Nutrition*, **2011**, 93, 851-60	7	50

146	Genetic and clinical analysis of a large Dutch Gilles de la Tourette family. *Molecular Psychiatry*, **2006**, 11, 954-64	15.1	50
145	Identification of 12 genetic loci associated with human healthspan. *Communications Biology*, **2019**, 2, 41	6.7	49
144	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. *Nature Communications*, **2017**, 8, 447	17.4	48
143	An approach for cutting large and complex pedigrees for linkage analysis. *European Journal of Human Genetics*, **2008**, 16, 854-60	5.3	48
142	Maternal transmission of multiple sclerosis in a dutch population. *Archives of Neurology*, **2008**, 65, 345-8		48
141	Plasma N-Glycan Signatures Are Associated With Features of Inflammatory Bowel Diseases. *Gastroenterology*, **2018**, 155, 829-843	13.3	47
140	Migraine is not associated with enhanced atherosclerosis. *Cephalalgia*, **2013**, 33, 228-35	6.1	47
139	The Menkes and Wilson disease genes counteract in copper toxicosis in Labrador retrievers: a new canine model for copper-metabolism disorders. *DMM Disease Models and Mechanisms*, **2016**, 9, 25-38	4.1	46
138	Genetic evidence for a role of adiponutrin in the metabolism of apolipoprotein B-containing lipoproteins. *Human Molecular Genetics*, **2009**, 18, 4669-76	5.6	45
137	Transferrin and HFE genes interact in Alzheimer's disease risk: the Epistasis Project. *Neurobiology of Aging*, **2012**, 33, 202.e1-13	5.6	43
136	The dopamine hydroxylase -1021C/T polymorphism is associated with the risk of Alzheimer's disease in the Epistasis Project. *BMC Medical Genetics*, **2010**, 11, 162	2.1	43
135	Association of the gene encoding neurogranin with schizophrenia in males. *Journal of Psychiatric Research*, **2008**, 42, 125-33	5.2	43
134	Linkage and association studies identify a novel locus for Alzheimer disease at 7q36 in a Dutch population-based sample. *American Journal of Human Genetics*, **2005**, 77, 643-52	11	43
133	LPIN2 is associated with type 2 diabetes, glucose metabolism, and body composition. *Diabetes*, **2007**, 56, 3020-6	0.9	42
132	Replication by the Epistasis Project of the interaction between the genes for IL-6 and IL-10 in the risk of Alzheimer's disease. *Journal of Neuroinflammation*, **2009**, 6, 22	10.1	41
131	Familial aggregation, the PDE4D gene, and ischemic stroke in a genetically isolated population. *Neurology*, **2005**, 65, 1203-9	6.5	41
130	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2 with serum creatinine level. *BMC Medical Genetics*, **2010**, 11, 41	2.1	39
129	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. *Science Advances*, **2020**, 6, eaax0301	14.3	38

128	A common biological basis of obesity and nicotine addiction. *Translational Psychiatry*, **2013**, 3, e308	8.6	37
127	Linkage and genome-wide association analysis of obesity-related phenotypes: association of weight with the MGAT1 gene. *Obesity*, **2010**, 18, 803-8	8	37
126	Heritability estimates of body size in fetal life and early childhood. *PLoS ONE*, **2012**, 7, e39901	3.7	36
125	The GenABEL Project for statistical genomics. *F1000Research*, **2016**, 5, 914	3.6	35
124	Insight into the genetic architecture of back pain and its risk factors from a study of 509,000 individuals. *Pain*, **2019**, 160, 1361-1373	8	34
123	Prevalence of the variant allele rs61764370 T>G in the 3'UTR of KRAS among Dutch BRCA1, BRCA2 and non-BRCA1/BRCA2 breast cancer families. *Breast Cancer Research and Treatment*, **2011**, 128, 79-84	4.4	33
122	The cholesteryl ester transfer protein (CETP) gene and the risk of Alzheimer's disease. *Neurogenetics*, **2007**, 8, 189-93	3	33
121	Heritability of serum iron, ferritin and transferrin saturation in a genetically isolated population, the Erasmus Rucphen Family (ERF) Study. *Human Heredity*, **2006**, 61, 222-8	1.1	33
120	Linkage and association analyses of glaucoma related traits in a large pedigree from a Dutch genetically isolated population. *Journal of Medical Genetics*, **2011**, 48, 802-9	5.8	32
119	A study of the SORL1 gene in Alzheimer's disease and cognitive function. *Journal of Alzheimer's Disease*, **2009**, 18, 51-64	4.3	32
118	Detection, imputation, and association analysis of small deletions and null alleles on oligonucleotide arrays. *American Journal of Human Genetics*, **2008**, 82, 1316-33	11	32
117	Hearing impairment in Dutch patients with connexin 26 (GJB2) and connexin 30 (GJB6) mutations. *International Journal of Pediatric Otorhinolaryngology*, **2005**, 69, 165-74	1.7	31
116	Genome-wide study links MTMR7 gene to variant Creutzfeldt-Jakob risk. *Neurobiology of Aging*, **2012**, 33, 1487.e21-8	5.6	30
115	The TCF7L2 diabetes risk variant is associated with HbA(1C) levels: a genome-wide association meta-analysis. *Annals of Human Genetics*, **2010**, 74, 471-8	2.2	29
114	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. *Human Molecular Genetics*, **2019**, 28, 2062-2077	5.6	28
113	Tag SNPs chosen from HapMap perform well in several population isolates. *Genetic Epidemiology*, **2007**, 31, 189-94	2.6	28
112	Heritability of fasting glucose levels in a young genetically isolated population. *Diabetologia*, **2006**, 49, 667-72	10.3	28
111	Common variants in Mendelian kidney disease genes and their association with renal function. *Journal of the American Society of Nephrology: JASN*, **2013**, 24, 2105-17	12.7	27

110	A genome-wide screen for interactions reveals a new locus on 4p15 modifying the effect of waist-to-hip ratio on total cholesterol. *PLoS Genetics*, **2011**, 7, e1002333	6	25
109	Region-based association analysis of human quantitative traits in related individuals. *PLoS ONE*, **2013**, 8, e65395	3.7	25
108	Association of SNPs of CD40 gene with multiple sclerosis in Russians. *PLoS ONE*, **2013**, 8, e61032	3.7	24
107	Novel strategy to identify genetic risk factors for COPD severity: a genetic isolate. *European Respiratory Journal*, **2010**, 35, 768-75	13.6	24
106	A genome-wide search for genes involved in type 2 diabetes in a recently genetically isolated population from the Netherlands. *Diabetes*, **2003**, 52, 3001-4	0.9	24
105	An R package "VariABEL" for genome-wide searching of potentially interacting loci by testing genotypic variance heterogeneity. *BMC Genetics*, **2012**, 13, 4	2.6	23
104	Association of FGFR2 gene polymorphisms with the risk of breast cancer in population of West Siberia. *European Journal of Human Genetics*, **2009**, 17, 1688-91	5.3	23
103	Linkage disequilibrium and haplotype homozygosity in population samples genotyped at a high marker density. *Human Heredity*, **2006**, 62, 175-89	1.1	23
102	Angiotensinogen promoter B-haplotype associated with cerebral small vessel disease enhances basal transcriptional activity. *Stroke*, **2004**, 35, 2592-7	6.7	23
101	Familial clustering of multiple sclerosis in a Dutch genetic isolate. *Multiple Sclerosis Journal*, **2007**, 13, 17-24	5	22
100	Epistatic effect of cholesteryl ester transfer protein and hepatic lipase on serum high-density lipoprotein cholesterol levels. *Journal of Clinical Endocrinology and Metabolism*, **2007**, 92, 2680-7	5.6	22
99	A genome-wide linkage study of individuals with high scores on NEO personality traits. *Molecular Psychiatry*, **2012**, 17, 1031-41	15.1	21
98	Heritabilities, apolipoprotein E, and effects of inbreeding on plasma lipids in a genetically isolated population: the Erasmus Rucphen Family Study. *European Journal of Epidemiology*, **2007**, 22, 99-105	12.1	21
97	A genome-wide screen for depression in two independent Dutch populations. *Biological Psychiatry*, **2010**, 68, 187-96	7.9	20
96	Interaction of insulin and PPAR-□genes in Alzheimer's disease: the Epistasis Project. *Journal of Neural Transmission*, **2012**, 119, 473-9	4.3	19
95	Genetic architecture of circulating lipid levels. *European Journal of Human Genetics*, **2011**, 19, 813-9	5.3	19
94	Genes predict village of origin in rural Europe. *European Journal of Human Genetics*, **2010**, 18, 1269-70	5.3	19
93	Detecting low frequent loss-of-function alleles in genome wide association studies with red hair color as example. *PLoS ONE*, **2011**, 6, e28145	3.7	19

92	A genome wide association study links glutamate receptor pathway to sporadic Creutzfeldt-Jakob disease risk. *PLoS ONE*, **2014**, 10, e0123654	3.7	18
91	Association of HSP70 and its co-chaperones with Alzheimer's disease. *Journal of Alzheimer's Disease*, **2011**, 25, 93-102	4.3	18
90	Genetic architecture of open angle glaucoma and related determinants. *Journal of Medical Genetics*, **2011**, 48, 190-6	5.8	18
89	Cerebrovascular risk factors do not contribute to genetic variance of cognitive function: the ERF study. *Neurobiology of Aging*, **2007**, 28, 735-41	5.6	18
88	Ignoring distant genealogic loops leads to false-positives in homozygosity mapping. *Annals of Human Genetics*, **2006**, 70, 965-70	2.2	18
87	Genetic variants in RBFOX3 are associated with sleep latency. *European Journal of Human Genetics*, **2016**, 24, 1488-95	5.3	18
86	Refining genome-wide linkage intervals using a meta-analysis of genome-wide association studies identifies loci influencing personality dimensions. *European Journal of Human Genetics*, **2013**, 21, 876-82	5.3	17
85	Shared genetic factors in the co-occurrence of symptoms of depression and cardiovascular risk factors. *Journal of Affective Disorders*, **2010**, 122, 247-52	6.6	17
84	Angiotensin converting enzyme gene, smoking and mortality in a population-based study. *European Journal of Clinical Investigation*, **2005**, 35, 444-9	4.6	16
83	Association between type 2 diabetes loci and measures of fatness. *PLoS ONE*, **2010**, 5, e8541	3.7	15
82	Nonadditive Effects of Genes in Human Metabolomics. *Genetics*, **2015**, 200, 707-18	4	14
81	Linkage analysis of adult height in a large pedigree from a Dutch genetically isolated population. *Human Genetics*, **2009**, 126, 457-71	6.3	14
80	Suggestive linkage of ADHD to chromosome 18q22 in a young genetically isolated Dutch population. *European Journal of Human Genetics*, **2009**, 17, 958-66	5.3	14
79	Rapid and robust association mapping of expression quantitative trait loci. *BMC Proceedings*, **2007**, 1 Suppl 1, S144	2.3	14
78	Chromosome-wise dissection of the genome of the extremely big mouse line DU6i. *Genetics*, **2006**, 172, 401-10	4	14
77	Relationship of the Ubiquilin 1 gene with Alzheimer's and Parkinson's disease and cognitive function. *Neuroscience Letters*, **2007**, 424, 1-5	3.3	14
76	'Omics' biomarkers associated with chronic low back pain: protocol of a retrospective longitudinal study. *BMJ Open*, **2016**, 6, e012070	3	14
75	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. *BMC Genomics*, **2013**, 14, 865	4.5	13

74	Development and application of genomic control methods for genome-wide association studies using non-additive models. *PLoS ONE*, **2013**, 8, e81431	3.7	13
73	Role of shared genetic and environmental factors in symptoms of depression and body composition. *Psychiatric Genetics*, **2009**, 19, 32-8	2.9	13
72	Chromosomal segregation and fertility in Robertsonian chromosomal heterozygotes of the house musk shrew (Suncus murinus, Insectivora, Soricidae). *Heredity*, **1998**, 81 (Pt 3), 335-41	3.6	13
71	The alpha-adducin gene is associated with macrovascular complications and mortality in patients with type 2 diabetes. *Diabetes*, **2006**, 55, 2922-7	0.9	13
70	High-Performance Mixed Models Based Genome-Wide Association Analysis with omicABEL software. *F1000Research*, **2014**, 3, 200	3.6	13
69	Interactions between PPAR-□and inflammation-related cytokine genes on the development of Alzheimer's disease, observed by the Epistasis Project. *International Journal of Molecular Epidemiology and Genetics*, **2012**, 3, 39-47	0.9	13
68	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. *Communications Biology*, **2020**, 3, 329	6.7	12
67	Plasma N-glycome composition associates with chronic low back pain. *Biochimica Et Biophysica Acta - General Subjects*, **2018**, 1862, 2124-2133	4	12
66	Genetic Sharing with Cardiovascular Disease Risk Factors and Diabetes Reveals Novel Bone Mineral Density Loci. *PLoS ONE*, **2015**, 10, e0144531	3.7	12
65	PedStr software for cutting large pedigrees for haplotyping, IBD computation and multipoint linkage analysis. *Annals of Human Genetics*, **2009**, 73, 527-31	2.2	12
64	Breaking loops in large complex pedigrees. *Human Heredity*, **2008**, 65, 57-65	1.1	12
63	Inheritance of litter size at birth in the house musk shrew (Suncus murinus, Insectivora, Soricidae). *Genetical Research*, **1998**, 71, 65-72	1.1	12
62	Cyclin-dependent kinase 5 is associated with risk for Alzheimer's disease in a Dutch population-based study. *Journal of Neurology*, **2008**, 255, 655-62	5.5	11
61	Identifying genetic risk variants for coronary heart disease in familial hypercholesterolemia: an extreme genetics approach. *European Journal of Human Genetics*, **2015**, 23, 381-7	5.3	10
60	Effects of the renin-angiotensin system genes and salt sensitivity genes on blood pressure and atherosclerosis in the total population and patients with type 2 diabetes. *Diabetes*, **2007**, 56, 1905-12	0.9	10
59	Genetic factors influence the clustering of depression among individuals with lower socioeconomic status. *PLoS ONE*, **2009**, 4, e5069	3.7	10
58	Validation of standard operating procedures in a multicenter retrospective study to identify -omics biomarkers for chronic low back pain. *PLoS ONE*, **2017**, 12, e0176372	3.7	10
57	ISSLS Prize in Clinical Science 2020. Examining causal effects of body mass index on back pain: a Mendelian randomization study. *European Spine Journal*, **2020**, 29, 686-691	2.7	10

56	A powerful genome-wide feasible approach to detect parent-of-origin effects in studies of quantitative traits. *European Journal of Human Genetics*, **2010**, 18, 379-84	5.3	9
55	Reply to Lack of support for association between the KIF1B rs10492972[C] variant and multiple sclerosis *Nature Genetics*, **2010**, 42, 470-471	36.3	9
54	Angiotensinogen M235T polymorphism and symptoms of depression in a population-based study and a family-based study. *Psychiatric Genetics*, **2008**, 18, 162-6	2.9	9
53	Replication of 15 loci involved in human plasma protein N-glycosylation in 4802 samples from four cohorts. *Glycobiology*, **2021**, 31, 82-88	5.8	9
52	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. *Scientific Reports*, **2020**, 10, 10486	4.9	8
51	Inheritance of litter size at birth in the Brazilian grass mouse (Akodon cursor, Sigmodontinae, Rodentia). *Genetical Research*, **2002**, 80, 55-62	1.1	8
50	Beyond power: Multivariate discovery, replication, and interpretation of pleiotropic loci using summary association statistics		8
49	A genetic epidemiologic study of candidate genes involved in the optic nerve head morphology **2012**, 53, 1485-91		7
48	Familial aggregation of preeclampsia and intrauterine growth restriction in a genetically isolated population in The Netherlands. *European Journal of Human Genetics*, **2008**, 16, 1437-42	5.3	7
47	miLD and booLD programs for calculation and analysis of corrected linkage disequilibrium. *Annals of Human Genetics*, **2003**, 67, 372-5	2.2	7
46	A network-based conditional genetic association analysis of the human metabolome. *GigaScience*, **2018**, 7,	7.6	7
45	Solving sequences of generalized least-squares problems on multi-threaded architectures. *Applied Mathematics and Computation*, **2014**, 234, 606-617	2.7	6
44	Linkage analysis for plasma amyloid beta levels in persons with hypertension implicates A40 levels to presenilin 2. *Human Genetics*, **2012**, 131, 1869-76	6.3	6
43	Low-density lipoprotein receptor mutations generate synthetic genome-wide associations. *European Journal of Human Genetics*, **2013**, 21, 563-6	5.3	6
42	Inheritance of Oligodontia in Kerry Blue Terrier Dogs. *Russian Journal of Genetics*, **2003**, 39, 669-675	0.6	6
41	Sex- and age-specific genetic analysis of chronic back pain. *Pain*, **2021**, 162, 1176-1187	8	6
40	A deletion in DJ-1 and the risk of dementia--a population-based survey. *Neuroscience Letters*, **2004**, 372, 196-9	3.3	5
39	Estimation of Allele Frequencies in Indigenous Populations of Siberia Based on Pedigree Data. *Russian Journal of Genetics*, **2001**, 37, 1293-1298	0.6	5

38	Twenty loci associated with bone mineral density identified by large-scale meta-analysis of genome-wide association datasets. *Bone*, **2009**, 44, S230-S231	4.7	4
37	ParallABEL: an R library for generalized parallelization of genome-wide association studies. *BMC Bioinformatics*, **2010**, 11, 217	3.6	4
36	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. *American Journal of Human Genetics*, **2008**, 82, 801	11	4
35	Evidence for novel loci for late-onset Parkinson's disease in a genetic isolate from the Netherlands. *Human Genetics*, **2006**, 119, 51-60	6.3	4
34	Genome-wide association study identifies locus as associated with chronic widespread musculoskeletal pain. *Annals of the Rheumatic Diseases*, **2021**, 80, 1227-1235	2.4	4
33	MQScore_SNP software for multipoint parametric linkage analysis of quantitative traits in large pedigrees. *Annals of Human Genetics*, **2010**, 74, 286-9	2.2	3
32	Solution for underflow problem in linkage and segregation analysis. *Computational Biology and Chemistry*, **2006**, 30, 382-5	3.6	3
31	Inheritance of Hypodontia in Kerry Blue Terrier Dogs. *Russian Journal of Genetics*, **2004**, 40, 529-536	0.6	3
30	A Method for Pooling Alleles from Different Genotyping Experiments. *Annals of Human Genetics*, **2005**, 69, 233-238	2.2	3
29	A method for pooling alleles from different genotyping experiments. *Annals of Human Genetics*, **2005**, 69, 233-8	2.2	3
28	The case for launch of an international DNA-based birth cohort study. *Journal of Global Health*, **2011**, 1, 39-45	4.3	3
27	Chromosomal and genic mechanisms of reproductive isolation: the case of Suncus murinus. *Acta Theriologica*, **2000**, 45, 147-159		3
26	The New Coronavirus COVID-19 Infection. *Molecular Genetics, Microbiology and Virology*, **2020**, 35, 53-60	0.4	3
25	Effects of Population Structure in Genome-wide Association Studies **2011**, 123-156		2
24	Correction for Schumann et al., Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 9316-9316	11.5	2
23	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain at different anatomic sites		2
22	Genome-wide association study identifies RNF123 locus as associated with chronic widespread musculoskeletal pain		2
21	Genome-wide association studies of low back pain and lumbar spinal disorders using electronic health record data identify a locus associated with lumbar spinal stenosis. *Pain*, **2021**, 162, 2263-2272	8	2

20	Comparison of methods used for recovering the line origin of alleles in a cross between outbred lines. *Genetical Research*, **2002**, 79, 75-83	1.1	1
19	Defining the genetic control of human blood plasma N-glycome using genome-wide association study		1
18	Sequence variation at 8q24.21 and risk of back pain. *F1000Research*,9, 424	3.6	1
17	The GWAS-MAP platform for aggregation of results of genome-wide association studies and the GWAS-MAP|homo database of 70 billion genetic associations of human traits.. *Vavilovskii Zhurnal Genetiki I Selektsii*, **2020**, 24, 876-884	0.9	1
16	Chromosomal segregation and fertility in Robertsonian chromosomal heterozygotes of the house musk shrew (Suncus murinus, Insectivora, Soricidae)		1
15	PheLiGe: an interactive database of billions of human genotype-phenotype associations. *Nucleic Acids Research*, **2021**, 49, D1347-D1350	20.1	1
14	Network based conditional genome wide association analysis of human metabolomics		1
13	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. *Human Molecular Genetics*, **2021**, 30, 1259-1270	5.6	0
12	Nontrivial Replication of Loci Detected by Multi-Trait Methods. *Frontiers in Genetics*, **2021**, 12, 627989	4.5	0
11	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. *Epigenetics and Chromatin*, **2021**, 14, 44	5.8	0
10	Genetic regulation of post-translational modification of two distinct proteins.. *Nature Communications*, **2022**, 13, 1586	17.4	0
9	Association Between Human Gut Microbiome and N-Glycan Composition of Total Plasma Proteome.. *Frontiers in Microbiology*, **2022**, 13, 811922	5.7	0
8	A protocol for recruiting and analyzing the disease-oriented Russian disc degeneration study (RuDDS) biobank for functional omics studies of lumbar disc degeneration.. *PLoS ONE*, **2022**, 17, e0267384	3.7	0
7	Population specific analysis of Yakut exomes. *Doklady Biochemistry and Biophysics*, **2017**, 474, 213-216	0.8	
6	Ped_Outlier software for automatic identification of within-family outliers. *Computational Biology and Chemistry*, **2010**, 34, 242-3	3.6	
5	Segregation analysis of animal pedigree data from inter-population crosses. *Genes and Genetic Systems*, **1997**, 72, 291-6	1.4	
4	Quantitative Genetics of Human Protein N-Glycosylation. *Advances in Experimental Medicine and Biology*, **2021**, 1325, 151-171	3.6	
3	THE INFLUENCE OF GENETIC AND ENVIRONMENTAL FACTORS ON BLOOD PRESSURE VARIANCE IN A GENETICALLY ISOLATED POPULATION. *Journal of Hypertension*, **2004**, 22, S215	1.9	

2	FREQUENCY AND HERITABILITY OF THE METABOLIC SYNDROME IN A GENETICALLY ISOLATED POPULATION. *Journal of Hypertension*, **2004**, 22, S146	1.9
1	The limits of normal approximation for adult height. *European Journal of Human Genetics*, **2021**, 29, 1082–1091	5.5