Aravinda Chakravarti

List of Publications by Citations

304 papers	61,039 citations	92 h-index	246 g-index
330 ext. papers	72,375 ext. citations	13.4 avg, IF	6.58 L-index

#	Paper	IF	Citations
304	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
303	Finding the missing heritability of complex diseases. *Nature*, **2009**, 461, 747-53	50.4	6084
302	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
301	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
300	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
299	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94	36.3	1628
298	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
297	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
296	Association between microdeletion and microduplication at 16p11.2 and autism. *New England Journal of Medicine*, **2008**, 358, 667-75	59.2	1249
295	Genome-wide association scan shows genetic variants in the FTO gene are associated with obesity-related traits. *PLoS Genetics*, **2007**, 3, e115	6	1231
294	DNA duplication associated with Charcot-Marie-Tooth disease type 1A. *Cell*, **1991**, 66, 219-32	56.2	1161
293	Genome-wide association study of blood pressure and hypertension. *Nature Genetics*, **2009**, 41, 677-87	36.3	1065
292	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
291	Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis. *Nature Genetics*, **1999**, 22, 239-47	36.3	916
290	Variations on a theme: cataloging human DNA sequence variation. *Science*, **1997**, 278, 1580-1	33.3	849
289	Development of human protein reference database as an initial platform for approaching systems biology in humans. *Genome Research*, **2003**, 13, 2363-71	9.7	823
288	A missense mutation of the endothelin-B receptor gene in multigenic Hirschsprung's disease. *Cell*, **1994**, 79, 1257-66	56.2	796

287	A DNA polymorphism discovery resource for research on human genetic variation. *Genome Research*, **1998**, 8, 1229-31	9.7	627
286	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
285	New goals for the U.S. Human Genome Project: 1998-2003. *Science*, **1998**, 282, 682-9	33.3	540
284	Genomic alterations in cultured human embryonic stem cells. *Nature Genetics*, **2005**, 37, 1099-103	36.3	525
283	Population genetics--making sense out of sequence. *Nature Genetics*, **1999**, 21, 56-60	36.3	487
282	A common genetic variant in the neurexin superfamily member CNTNAP2 increases familial risk of autism. *American Journal of Human Genetics*, **2008**, 82, 160-4	11	482
281	A genome-wide linkage and association scan reveals novel loci for autism. *Nature*, **2009**, 461, 802-8	50.4	474
280	A common genetic variant in the NOS1 regulator NOS1AP modulates cardiac repolarization. *Nature Genetics*, **2006**, 38, 644-51	36.3	438
279	Schizophrenia susceptibility loci on chromosomes 13q32 and 8p21. *Nature Genetics*, **1998**, 20, 70-3	36.3	435
278	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. *American Journal of Human Genetics*, **2015**, 97, 199-215	11	432
277	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
276	Automated construction of genetic linkage maps using an expert system (MultiMap): a human genome linkage map. *Nature Genetics*, **1994**, 6, 384-90	36.3	408
275	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
274	A common sex-dependent mutation in a RET enhancer underlies Hirschsprung disease risk. *Nature*, **2005**, 434, 857-63	50.4	377
273	Haploinsufficiency of telomerase reverse transcriptase leads to anticipation in autosomal dominant dyskeratosis congenita. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 15960-4	11.5	365
272	Common variants in KCNN3 are associated with lone atrial fibrillation. *Nature Genetics*, **2010**, 42, 240-4	36.3	362
271	Genome-wide association study of PR interval. *Nature Genetics*, **2010**, 42, 153-9	36.3	340
270	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338

269	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
268	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
267	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. *Nature Genetics*, **2009**, 41, 407-14	36.3	308
266	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. *Nature Genetics*, **2009**, 41, 879-81	36.3	307
265	A BDNF coding variant is associated with the NEO personality inventory domain neuroticism, a risk factor for depression. *Neuropsychopharmacology*, **2003**, 28, 397-401	8.7	287
264	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
263	A homozygous mutation in the endothelin-3 gene associated with a combined Waardenburg type 2 and Hirschsprung phenotype (Shah-Waardenburg syndrome). *Nature Genetics*, **1996**, 12, 445-7	36.3	277
262	Germline mutations in glial cell line-derived neurotrophic factor (GDNF) and RET in a Hirschsprung disease patient. *Nature Genetics*, **1996**, 14, 341-4	36.3	252
261	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
260	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
259	Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARe Project. *PLoS Genetics*, **2011**, 7, e1001300	6	249
258	From the Cover: Whole-genome association study identifies STK39 as a hypertension susceptibility gene. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 226-31	11.5	240
257	High-throughput variation detection and genotyping using microarrays. *Genome Research*, **2001**, 11, 1913-25	9.7	239
256	Parallel genotyping of human SNPs using generic high-density oligonucleotide tag arrays. *Genome Research*, **2000**, 10, 853-60	9.7	232
255	Genome-wide association study and mouse model identify interaction between RET and EDNRB pathways in Hirschsprung disease. *Nature Genetics*, **2002**, 32, 237-44	36.3	229
254	Identity-by-descent and association mapping of a recessive gene for Hirschsprung disease on human chromosome 13q22. *Human Molecular Genetics*, **1994**, 3, 1217-25	5.6	228
253	Human embryonic stem cells have a unique epigenetic signature. *Genome Research*, **2006**, 16, 1075-83	9.7	224
252	Segregation at three loci explains familial and population risk in Hirschsprung disease. *Nature Genetics*, **2002**, 31, 89-93	36.3	223

251	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	6	220
250	Identifying disease alleles by genome sharing. *Nature Genetics*, **1999**, 23, 25-25	36.3	213
249	Parental origin and phenotype of triploidy in spontaneous abortions: predominance of diandry and association with the partial hydatidiform mole. *American Journal of Human Genetics*, **2000**, 66, 1807-20	11	208
248	The Human MitoChip: a high-throughput sequencing microarray for mitochondrial mutation detection. *Genome Research*, **2004**, 14, 812-9	9.7	201
247	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
246	Differential contributions of rare and common, coding and noncoding Ret mutations to multifactorial Hirschsprung disease liability. *American Journal of Human Genetics*, **2010**, 87, 60-74	11	198
245	A bivariate genome-wide approach to metabolic syndrome: STAMPEED consortium. *Diabetes*, **2011**, 60, 1329-39	0.9	194
244	Differential susceptibility to hypertension is due to selection during the out-of-Africa expansion. *PLoS Genetics*, **2005**, 1, e82	6	175
243	Haplotype inference in random population samples. *American Journal of Human Genetics*, **2002**, 71, 1129-37	11	164
242	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *American Journal of Human Genetics*, **2015**, 96, 283-94	11	161
241	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. *Nature Genetics*, **2017**, 49, 54-64	36.3	157
240	Association of hypertension drug target genes with blood pressure and hypertension in 86,588 individuals. *Hypertension*, **2011**, 57, 903-10	8.5	154
239	Multiplex PCR of three dinucleotide repeats in the Prader-Willi/Angelman critical region (15q11-q13): molecular diagnosis and mechanism of uniparental disomy. *Human Molecular Genetics*, **1993**, 2, 143-51	5.6	153
238	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
237	Undetected genotyping errors cause apparent overtransmission of common alleles in the transmission/disequilibrium test. *American Journal of Human Genetics*, **2003**, 72, 598-610	11	149
236	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
235	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*, **2013**, 93, 545-54	11	145
234	Genome-wide association studies of serum magnesium, potassium, and sodium concentrations identify six Loci influencing serum magnesium levels. *PLoS Genetics*, **2010**, 6, e1001045	6	144

233	Polymorphisms in the NOS1AP gene modulate QT interval duration and risk of arrhythmias in the long QT syndrome. *Journal of the American College of Cardiology*, **2010**, 55, 2745-52	15.1	143
232	Genetic variations in nitric oxide synthase 1 adaptor protein are associated with sudden cardiac death in US white community-based populations. *Circulation*, **2009**, 119, 940-51	16.7	141
231	GENOME ENGINEERING. The Genome Project-Write. *Science*, **2016**, 353, 126-7	33.3	138
230	Exhaustive allelic transmission disequilibrium tests as a new approach to genome-wide association studies. *Nature Genetics*, **2004**, 36, 1181-8	36.3	138
229	A gene for Hirschsprung disease (megacolon) in the pericentromeric region of human chromosome 10. *Nature Genetics*, **1993**, 4, 351-6	36.3	136
228	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
227	Phenotype variation in two-locus mouse models of Hirschsprung disease: tissue-specific interaction between Ret and Ednrb. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 1826-31	11.5	120
226	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
225	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
224	Global implementation of genomic medicine: We are not alone. *Science Translational Medicine*, **2015**, 7, 290ps13	17.5	112
223	Nature, nurture and human disease. *Nature*, **2003**, 421, 412-4	50.4	110
222	Future of genetics of mood disorders research. *Biological Psychiatry*, **2002**, 52, 457-77	7.9	108
221	Associations between hypertension and genes in the renin-angiotensin system. *Hypertension*, **2003**, 41, 1027-34	8.5	105
220	Allele frequency distributions in pooled DNA samples: applications to mapping complex disease genes. *Genome Research*, **1998**, 8, 111-23	9.7	104
219	Loss of β-catenin function in severe autism. *Nature*, **2015**, 520, 51-6	50.4	97
218	Identification of a sudden cardiac death susceptibility locus at 2q24.2 through genome-wide association in European ancestry individuals. *PLoS Genetics*, **2011**, 7, e1002158	6	95
217	Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PLoS Genetics*, **2013**, 9, e1003379	6	94
216	Multiple genes for essential-hypertension susceptibility on chromosome 1q. *American Journal of Human Genetics*, **2007**, 80, 253-64	11	93

215	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
214	Sequence variations in the public human genome data reflect a bottlenecked population history. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 376-81	11.5	92
213	Contribution of rare and common variants determine complex diseases-Hirschsprung disease as a model. *Developmental Biology*, **2013**, 382, 320-9	3.1	90
212	Pleiotropic skeletal and ocular phenotypes of the mouse mutation congenital hydrocephalus (ch/Mf1) arise from a winged helix/forkhead transcriptionfactor gene. *Human Molecular Genetics*, **1999**, 8, 625-37	5.6	88
211	EDNRB/EDN3 and Hirschsprung disease type II. *Pigment Cell & Melanoma Research*, **2001**, 14, 161-9		86
210	Drug-sensitized zebrafish screen identifies multiple genes, including GINS3, as regulators of myocardial repolarization. *Circulation*, **2009**, 120, 553-9	16.7	84
209	An integrated genetic linkage map of the laboratory rat. *Mammalian Genome*, **1998**, 9, 521-30	3.2	83
208	Functional loss of semaphorin 3C and/or semaphorin 3D and their epistatic interaction with ret are critical to Hirschsprung disease liability. *American Journal of Human Genetics*, **2015**, 96, 581-96	11	82
207	Endothelin-3 frameshift mutation in congenital central hypoventilation syndrome. *Nature Genetics*, **1996**, 13, 395-6	36.3	82
206	Two-locus models of disease. *Genetic Epidemiology*, **1992**, 9, 347-65	2.6	82
205	Linkage disequilibrium analysis of biallelic DNA markers, human quantitative trait loci, and threshold-defined case and control subjects. *American Journal of Human Genetics*, **2000**, 67, 1208-18	11	81
204	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. *American Journal of Human Genetics*, **2014**, 95, 24-38	11	80
203	Genomics in sudden cardiac death. *Circulation Research*, **2004**, 94, 712-23	15.7	80
202	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. *Cell*, **2016**, 167, 355-368.e10	56.2	80
201	Positional identification of hypertension susceptibility genes on chromosome 2. *Hypertension*, **2004** , 43, 477-82	8.5	79
200	A genetic linkage map of 27 markers on human chromosome 21. *Genomics*, **1991**, 9, 407-19	4.3	78
199	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
198	Genetics and genomics for the prevention and treatment of cardiovascular disease: update: a scientific statement from the American Heart Association. *Circulation*, **2013**, 128, 2813-51	16.7	76

197	A genetic linkage map of 17 markers on human chromosome 21. *Genomics*, **1989**, 4, 579-91	4.3	75
196	Drift variances of FST and GST statistics obtained from a finite number of isolated populations. *Theoretical Population Biology*, **1977**, 11, 307-25	1.2	75
195	Mitochondrial DNA variants of respiratory complex I that uniquely characterize haplogroup T2 are associated with increased risk of age-related macular degeneration. *PLoS ONE*, **2009**, 4, e5508	3.7	74
194	Identifying allelic loss and homozygous deletions in pancreatic cancer without matched normals using high-density single-nucleotide polymorphism arrays. *Cancer Research*, **2006**, 66, 7920-8	10.1	74
193	Molecular Genetic Anatomy and Risk Profile of Hirschsprung's Disease. *New England Journal of Medicine*, **2019**, 380, 1421-1432	59.2	71
192	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARe consortium. *Human Molecular Genetics*, **2011**, 20, 2285-95	5.6	70
191	Mean and variance of FST in a finite number of incompletely isolated populations. *Theoretical Population Biology*, **1977**, 11, 291-306	1.2	70
190	On consanguineous marriages and the genetic load. *Human Genetics*, **1977**, 36, 47-54	6.3	70
189	Evaluation of the RET regulatory landscape reveals the biological relevance of a HSCR-implicated enhancer. *Human Molecular Genetics*, **2005**, 14, 3837-45	5.6	67
188	Patterns of genetic variation in Mendelian and complex traits. *Annual Review of Genomics and Human Genetics*, **2000**, 1, 387-407	9.7	65
187	DNA polymorphism haplotypes of the human apolipoprotein APOA1-APOC3-APOA4 gene cluster. *Human Genetics*, **1988**, 80, 265-73	6.3	65
186	Associations between genetic variants in the NOS1AP (CAPON) gene and cardiac repolarization in the old order Amish. *Human Heredity*, **2007**, 64, 214-9	1.1	64
185	Distilling pathophysiology from complex disease genetics. *Cell*, **2013**, 155, 21-6	56.2	63
184	A linkage map of human chromosome 21:43 PCR markers at average intervals of 2.5 cM. *Genomics*, **1993**, 16, 562-71	4.3	62
183	Mendelian disorders and multifactorial traits: the big divide or one for all?. *Nature Reviews Genetics*, **2010**, 11, 380-4	30.1	60
182	Phylogeny of human beta-globin haplotypes and its implications for recent human evolution. *American Journal of Physical Anthropology*, **1990**, 81, 113-30	2.5	60
181	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59
180	Linkage disequilibrium and haplotype diversity in the genes of the renin-angiotensin system: findings from the family blood pressure program. *Genome Research*, **2003**, 13, 173-81	9.7	59

179	Linkage analysis of the human HMG14 gene on chromosome 21 using a GT dinucleotide repeat as polymorphic marker. *Genomics*, **1990**, 7, 136-8	4.3	59
178	Safety issues in cell-based intervention trials. *Fertility and Sterility*, **2003**, 80, 1077-85	4.8	58
177	A genome-wide scan for obesity in African-Americans. *Diabetes*, **2002**, 51, 541-4	0.9	58
176	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
175	Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. *European Journal of Human Genetics*, **2008**, 16, 1507-11	5.3	57
174	An enhancer polymorphism at the cardiomyocyte intercalated disc protein NOS1AP locus is a major regulator of the QT interval. *American Journal of Human Genetics*, **2014**, 94, 854-69	11	56
173	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. *Genome Biology*, **2017**, 18, 48	18.3	55
172	Understanding cardiovascular disease through the lens of genome-wide association studies. *Trends in Genetics*, **2009**, 25, 387-94	8.5	55
171	Next-generation sequencing of human mitochondrial reference genomes uncovers high heteroplasmy frequency. *PLoS Computational Biology*, **2012**, 8, e1002737	5	54
170	The gene for soluble N-ethylmaleimide sensitive factor attachment protein alpha is mutated in hydrocephaly with hop gait (hyh) mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 1748-53	11.5	54
169	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
168	Copy number variants in candidate genes are genetic modifiers of Hirschsprung disease. *PLoS ONE*, **2011**, 6, e21219	3.7	53
167	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52
166	Positional identification of variants of Adamts16 linked to inherited hypertension. *Human Molecular Genetics*, **2009**, 18, 2825-38	5.6	52
165	Elevated frequency and allelic heterogeneity of congenital nephrotic syndrome, Finnish type, in the old order Mennonites. *American Journal of Human Genetics*, **1999**, 65, 1785-90	11	52
164	Interaction between a chromosome 10 RET enhancer and chromosome 21 in the Down syndrome-Hirschsprung disease association. *Human Mutation*, **2009**, 30, 771-5	4.7	50
163	Follow-up of a major linkage peak on chromosome 1 reveals suggestive QTLs associated with essential hypertension: GenNet study. *European Journal of Human Genetics*, **2009**, 17, 1650-7	5.3	50
162	A genome-wide linkage analysis investigating the determinants of blood pressure in whites and African Americans. *American Journal of Hypertension*, **2003**, 16, 151-3	2.3	50

161	Human GFRA1: cloning, mapping, genomic structure, and evaluation as a candidate gene for Hirschsprung disease susceptibility. *Genomics*, **1998**, 48, 354-62	4.3	50
160	Population variation in total genetic risk of Hirschsprung disease from common RET, SEMA3 and NRG1 susceptibility polymorphisms. *Human Molecular Genetics*, **2015**, 24, 2997-3003	5.6	49
159	Microsatellite polymorphism linkage map of human chromosome 13q. *Genomics*, **1993**, 15, 376-86	4.3	49
158	Genome-wide association study identifies GPC5 as a novel genetic locus protective against sudden cardiac arrest. *PLoS ONE*, **2010**, 5, e9879	3.7	48
157	Genetic variation associated with circulating monocyte count in the eMERGE Network. *Human Molecular Genetics*, **2013**, 22, 2119-27	5.6	46
156	Population bottlenecks as a potential major shaping force of human genome architecture. *PLoS Genetics*, **2007**, 3, e119	6	46
155	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508	6	45
154	Down syndrome consequent to a cryptic maternal 12p;21q chromosome translocation. *American Journal of Medical Genetics Part A*, **1995**, 56, 67-71		45
153	A graphical representation of genetic and physical maps: the Marey map. *Genomics*, **1991**, 11, 219-22	4.3	45
152	Cytogenetics and origins of pediatric germ cell tumors. *Cancer Genetics and Cytogenetics*, **1994**, 74, 54-8		44
151	Waardenburg syndrome and Hirschsprung disease: evidence for pleiotropic effects of a single dominant gene. *American Journal of Medical Genetics Part A*, **1990**, 35, 100-4		44
150	Methods for studying recombination on chromosomes that undergo nondisjunction. *Genomics*, **1987**, 1, 35-42	4.3	43
149	The road ahead in genetics and genomics. *Nature Reviews Genetics*, **2020**, 21, 581-596	30.1	43
148	Mining gold dust under the genome wide significance level: a two-stage approach to analysis of GWAS. *Genetic Epidemiology*, **2011**, 35, 111-8	2.6	41
147	Cloning of a novel homeobox-containing gene, PKNOX1, and mapping to human chromosome 21q22.3. *Genomics*, **1997**, 41, 193-200	4.3	39
146	A multilevel model to address batch effects in copy number estimation using SNP arrays. *Biostatistics*, **2011**, 12, 33-50	3.7	38
145	Polymorphisms in the mitochondrial DNA control region and frailty in older adults. *PLoS ONE*, **2010**, 5, e11069	3.7	37
144	Hemostasis, inflammation, and fatal and nonfatal coronary heart disease: long-term follow-up of the atherosclerosis risk in communities (ARIC) cohort. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2009**, 29, 2182-90	9.4	37

143	Allele-specific expression in the germline of patients with familial pancreatic cancer: an unbiased approach to cancer gene discovery. *Cancer Biology and Therapy*, **2008**, 7, 135-44	4.6	37
142	Patterns of meiotic recombination on the long arm of human chromosome 21. *Genome Research*, **2000**, 10, 1319-32	9.7	37
141	Haplotype and missing data inference in nuclear families. *Genome Research*, **2004**, 14, 1624-32	9.7	36
140	Elementary methods for the analysis of dichotomous outcomes in unselected samples of twins. *Genetic Epidemiology*, **1992**, 9, 273-87	2.6	36
139	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. *Circulation: Cardiovascular Genetics*, **2016**, 9, 64-70		35
138	Genetics and biology of human ovarian teratomas. III. Cytogenetics and origins of malignant ovarian germ cell tumors. *Cancer Genetics and Cytogenetics*, **1992**, 62, 58-65		34
137	Effects of RET and NRG1 polymorphisms in Indonesian patients with Hirschsprung disease. *Journal of Pediatric Surgery*, **2014**, 49, 1614-8	2.6	33
136	Phenotype-genotype correlation in Hirschsprung disease is illuminated by comparative analysis of the RET protein sequence. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 8949-54	11.5	32
135	Direct Estimates of the Genomic Contributions to Blood Pressure Heritability within a Population-Based Cohort (ARIC). *PLoS ONE*, **2015**, 10, e0133031	3.7	32
134	Revealing rate-limiting steps in complex disease biology: The crucial importance of studying rare, extreme-phenotype families. *BioEssays*, **2016**, 38, 578-86	4.1	32
133	Transcriptional regulation of PRPF31 gene expression by MSR1 repeat elements causes incomplete penetrance in retinitis pigmentosa. *Scientific Reports*, **2016**, 6, 19450	4.9	31
132	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
131	Rapid and efficient human mutation detection using a bench-top next-generation DNA sequencer. *Human Mutation*, **2012**, 33, 281-9	4.7	31
130	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. *European Heart Journal*, **2018**, 39, 3961-3969	9.5	31
129	A population-based study of KCNH7 p.Arg394His and bipolar spectrum disorder. *Human Molecular Genetics*, **2014**, 23, 6395-406	5.6	30
128	Variation in the ciliary neurotrophic factor gene and muscle strength in older Caucasian women. *Journal of the American Geriatrics Society*, **2006**, 54, 823-6	5.6	30
127	Linkage mapping of highly informative DNA polymorphisms within the human interferon-alpha receptor gene on chromosome 21. *Genomics*, **1991**, 11, 573-6	4.3	30
126	A compelling genetic hypothesis for a complex disease: PRODH2/DGCR6 variation leads to schizophrenia susceptibility. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 4755-6	11.5	29

125	Parent-of-origin effects in autism identified through genome-wide linkage analysis of 16,000 SNPs. *PLoS ONE*, **2010**, 5, e12513	3.7	28
124	Linkage mapping of the highly informative DNA marker D21S156 to human chromosome 21 using a polymorphic GT dinucleotide repeat. *Genomics*, **1990**, 8, 400-2	4.3	28
123	MicroRNAs in the miR-17 and miR-15 families are downregulated in chronic kidney disease with hypertension. *PLoS ONE*, **2017**, 12, e0176734	3.7	27
122	Lack of association between a biallelic polymorphism in the adducin gene and blood pressure in whites and African Americans. *American Journal of Hypertension*, **2000**, 13, 693-8	2.3	26
121	A radiation hybrid map of 48 loci including the clouston hidrotic ectodermal dysplasia locus in the pericentromeric region of chromosome 13q. *Genomics*, **1999**, 56, 127-30	4.3	26
120	Guidelines for human linkage maps. An International System for Human Linkage Maps (ISLM, 1990). *Annals of Human Genetics*, **1991**, 55, 1-6	2.2	26
119	Multiple independent genetic factors at NOS1AP modulate the QT interval in a multi-ethnic population. *PLoS ONE*, **2009**, 4, e4333	3.7	25
118	Defining the contribution of CNTNAP2 to autism susceptibility. *PLoS ONE*, **2013**, 8, e77906	3.7	25
117	Proteins linked to autosomal dominant and autosomal recessive disorders harbor characteristic rare missense mutation distribution patterns. *Human Molecular Genetics*, **2015**, 24, 5995-6002	5.6	24
116	An ancestral variant of Secretogranin II confers regulation by PHOX2 transcription factors and association with hypertension. *Human Molecular Genetics*, **2007**, 16, 1752-64	5.6	24
115	Preliminary ordering of multiple linked loci using pairwise linkage data. *Genetic Epidemiology*, **1992**, 9, 367-75	2.6	24
114	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. *Human Molecular Genetics*, **2016**, 25, 5265-5275	5.6	23
113	Age, sex, and the familial risk of rheumatoid arthritis. *American Journal of Epidemiology*, **1996**, 144, 15-24	3.8	22
112	A PIGN mutation responsible for multiple congenital anomalies-hypotonia-seizures syndrome 1 (MCAHS1) in an Israeli-Arab family. *American Journal of Medical Genetics, Part A*, **2016**, 170A, 176-82	2.5	22
111	An investigation of genome-wide associations of hypertension with microsatellite markers in the family blood pressure program (FBPP). *Human Genetics*, **2007**, 121, 577-90	6.3	21
110	Haplotype association analysis of AGT variants with hypertension-related traits: the HyperGEN study. *Human Heredity*, **2005**, 60, 164-76	1.1	21
109	On the probability that a novel variant is a disease-causing mutation. *Genome Research*, **2005**, 15, 960-6	9.7	21
108	Effects of rare and common blood pressure gene variants on essential hypertension: results from the Family Blood Pressure Program, CLUE, and Atherosclerosis Risk in Communities studies. *Circulation Research*, **2013**, 112, 318-26	15.7	20

107	Genomic structure of the gene for the SH2 and pleckstrin homology domain-containing protein GRB10 and evaluation of its role in Hirschsprung disease. *Oncogene*, **1998**, 17, 3065-70	9.2	20
106	Erythrocyte sodium-lithium countertransport and blood pressure: a genome-wide linkage study. *Hypertension*, **2003**, 41, 842-6	8.5	20
105	RET somatic mutations are underrecognized in Hirschsprung disease. *Genetics in Medicine*, **2018**, 20, 770-777	8.1	20
104	Public stem cell banks: considerations of justice in stem cell research and therapy. *Hastings Center Report*, **2003**, 33, 13-27	3.3	20
103	Linkage mapping of the cystathionine beta-synthase (CBS) gene on human chromosome 21 using a DNA polymorphism in the 3R untranslated region. *Human Genetics*, **1993**, 90, 566-8	6.3	19
102	Evidence against close linkage of unipolar affective illness to human chromosome 11p markers HRAS1 and INS and chromosome Xq marker DXS52. *Biological Psychiatry*, **1990**, 28, 63-72	7.9	19
101	Etiological heterogeneity in Hodgkin's disease: HLA linked and unlinked determinants of susceptibility independent of histological concordance. *Genetic Epidemiology*, **1986**, 3, 407-15	2.6	19
100	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. *PLoS ONE*, **2016**, 11, e0164132	3.7	19
99	Intestinal Neuronal Dysplasia-Like Submucosal Ganglion Cell Hyperplasia at the Proximal Margins of Hirschsprung Disease Resections. *Pediatric and Developmental Pathology*, **2015**, 18, 466-76	2.2	18
98	Chromosome 21 scan in Down syndrome reveals DSCAM as a predisposing locus in Hirschsprung disease. *PLoS ONE*, **2013**, 8, e62519	3.7	18
97	The impact of data quality on the identification of complex disease genes: experience from the Family Blood Pressure Program. *European Journal of Human Genetics*, **2006**, 14, 469-77	5.3	18
96	An evaluation of the assembly of an approximately 15-Mb region on human chromosome 13q32-q33 linked to bipolar disorder and schizophrenia. *Genomics*, **2002**, 79, 635-56	4.3	18
95	Estimating genome-wide copy number using allele-specific mixture models. *Journal of Computational Biology*, **2008**, 15, 857-66	1.7	17
94	Estimation of the frequency of isoform-genotype discrepancies at the apolipoprotein E locus in heterozygotes for the isoforms. *Genetic Epidemiology*, **1992**, 9, 239-48	2.6	17
93	Genetics. Mendelian puzzles. *Science*, **2012**, 335, 930-1	33.3	16
92	Quantifying and modeling birth order effects in autism. *PLoS ONE*, **2011**, 6, e26418	3.7	16
91	Being human: kinship: race relations. *Nature*, **2009**, 457, 380-1	50.4	15
90	Five blood pressure loci identified by an updated genome-wide linkage scan: meta-analysis of the Family Blood Pressure Program. *American Journal of Hypertension*, **2011**, 24, 347-54	2.3	15

89	Dietary intake and gene variation influence the response of plasma lipids to dietary intervention. *Genetic Epidemiology*, **1992**, 9, 249-60	2.6	15
88	Tests of linkage and heterogeneity in Mendelian diseases using identity by descent scores. *Genetic Epidemiology*, **1987**, 4, 255-66	2.6	15
87	Variation in allele frequencies among caste groups of the Dhangars of Maharashtra, India: an analysis with Wright's Fst statistic. *Annals of Human Biology*, **1977**, 4, 275-80	1.7	15
86	Sequence analysis of six blood pressure candidate regions in 4,178 individuals: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. *PLoS ONE*, **2014**, 9, e109155	3.7	15
85	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. *Human Genetics*, **2019**, 138, 199-210	6.3	14
84	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
83	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. *PLoS ONE*, **2018**, 13, e0200486	3.7	14
82	Genomic contributions to Mendelian disease. *Genome Research*, **2011**, 21, 643-4	9.7	14
81	D21S215 is a (GT)n polymorphic marker close to centromeric alphoid sequences on chromosome 21. *Genomics*, **1992**, 13, 1365-7	4.3	14
80	Multiple variant enhancers modulate its cardiac gene expression and the QT interval. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 10636-10645	11.5	13
79	The CD4/CD8 ratio: message in a bottle?. *Nature Medicine*, **1995**, 1, 1240-1	50.5	13
78	Aggregation of colon cancer in family data. *Genetic Epidemiology*, **1984**, 1, 53-61	2.6	13
77	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. *Heart Rhythm*, **2014**, 11, 471-7	6.7	12
76	A polymorphic 3'UTR element in ATP1B1 regulates alternative polyadenylation and is associated with blood pressure. *PLoS ONE*, **2013**, 8, e76290	3.7	12
75	A population association study of angiotensinogen polymorphisms and haplotypes with left ventricular phenotypes. *Hypertension*, **2005**, 46, 1294-9	8.5	12
74	Linkage mapping of D21S171 to the distal long arm of human chromosome 21 using a polymorphic (AC)n dinucleotide repeat. *Human Genetics*, **1991**, 87, 401-4	6.3	12
73	Perspectives on Human Variation through the Lens of Diversity and Race. *Cold Spring Harbor Perspectives in Biology*, **2015**, 7, a023358	10.2	11
72	Genome-wide association study of Hirschsprung disease detects a novel low-frequency variant at the RET locus. *European Journal of Human Genetics*, **2018**, 26, 561-569	5.3	11

71	Human cardiac -regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. *Genome Research*, **2018**, 28, 1577-1588	9.7	11
70	Testing for colon neoplasia susceptibility variants at the human COX2 locus. *Journal of the National Cancer Institute*, **2001**, 93, 635-9	9.7	11
69	ViewGene: a graphical tool for polymorphism visualization and characterization. *Genome Research*, **2002**, 12, 333-8	9.7	11
68	Efficient construction of high-resolution physical maps from yeast artificial chromosomes using radiation hybrids: inner product mapping. *Genomics*, **1993**, 18, 283-9	4.3	11
67	Segregation analysis of 159 soft tissue sarcoma kindreds: comparison of fixed and sequential sampling schemes. *Genetic Epidemiology*, **1992**, 9, 291-304	2.6	11
66	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. *PLoS Genetics* , **2017**, 13, e1006678	6	11
65	Sequence variation within the fragile X locus. *Genome Research*, **2001**, 11, 1382-91	9.7	11
64	High incidence of deafness from three frequent connexin 26 mutations in an isolated community. *Genetic Testing and Molecular Biomarkers*, **2006**, 10, 40-3		10
63	Finding needles in haystacks--IRF6 gene variants in isolated cleft lip or cleft palate. *New England Journal of Medicine*, **2004**, 351, 822-4	59.2	10
62	Dinucleotide repeat (GT)n markers on chromosome 21. *Genomics*, **1992**, 14, 818-9	4.3	10
61	Commingling analysis of memory performance in offspring of Alzheimer patients. *Genetic Epidemiology*, **1992**, 9, 333-45	2.6	10
60	Cardiomyocytes have mosaic patterns of protein expression. *Cardiovascular Pathology*, **2018**, 34, 50-57	3.8	9
59	Associations between NOS1AP single nucleotide polymorphisms (SNPs) and QT interval duration in four racial/ethnic groups in the Multi-Ethnic Study of Atherosclerosis (MESA). *Annals of Noninvasive Electrocardiology*, **2013**, 18, 29-40	1.5	9
58	Linkage analysis incorporating gene-age interactions identifies seven novel lipid loci: the Family Blood Pressure Program. *Atherosclerosis*, **2014**, 235, 84-93	3.1	9
57	GIST: A web tool for collecting gene information. *Physiological Genomics*, **1999**, 1, 75-81	3.6	9
56	Chromosomal localization of the mouse Src-like adapter protein (Slap) gene and its putative human homolog SLA. *Genomics*, **1995**, 30, 623-5	4.3	9
55	DNA profile similarity in a subdivided population. *Human Heredity*, **1994**, 44, 100-9	1.1	9
54	Schizophrenia and porphobilinogen deaminase gene polymorphisms: an association study. *Schizophrenia Research*, **1992**, 8, 51-8	3.6	9

53	Pedigree analysis of blood pressure in subjects from rural Greece and relatives who migrated to Melbourne, Australia. *Genetic Epidemiology*, **1992**, 9, 225-38	2.6	9
52	A test of nonrandom segregation. *Genetic Epidemiology*, **1984**, 1, 329-40	2.6	9
51	HPASubC: A suite of tools for user subclassification of human protein atlas tissue images. *Journal of Pathology Informatics*, **2015**, 6, 36	4.4	9
50	A gene regulatory network explains RET-EDNRB epistasis in Hirschsprung disease. *Human Molecular Genetics*, **2019**, 28, 3137-3147	5.6	8
49	Information content of the Centre dEtude du Polymorphisme Humain (CEPH) family structures for linkage studies. *Human Genetics*, **1991**, 87, 721-4	6.3	8
48	Male and female differential reproductive rate could explain parental transmission asymmetry of mutation origin in Hirschsprung disease. *European Journal of Human Genetics*, **2012**, 20, 917-20	5.3	7
47	Cloning of rat thymic stromal lymphopoietin receptor (TSLPR) and characterization of genomic structure of murine Tslpr gene. *Gene*, **2002**, 284, 161-8	3.8	7
46	Linkage mapping of the carbonyl reductase (CBR) gene on human chromosome 21 using a DNA polymorphism in the 3Runtranslated region. *Genomics*, **1992**, 13, 447-8	4.3	7
45	DNA polymorphisms in the 3Runtranslated region of genes on human chromosome 21. *Genomics*, **1993**, 15, 98-102	4.3	6
44	Detection of genetic heterogeneity for complex quantitative phenotypes. *Genetic Epidemiology*, **1992**, 9, 207-23	2.6	6
43	D21S210: a highly polymorphic (GT)n marker closely linked to the beta-amyloid protein precursor (APP) gene. *Human Genetics*, **1993**, 91, 87-8	6.3	6
42	Estimation of segregation and ascertainment probabilities by discarding the single probands. *Genetic Epidemiology*, **1987**, 4, 185-91	2.6	6
41	Genetic differentiation in the colonising lizard Anolis grahami. *Heredity*, **1977**, 38, 121-123	3.6	6
40	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. *Scientific Reports*, **2016**, 6, 28356	4.9	5
39	Sequence characterization of RET in 117 Chinese Hirschsprung disease families identifies a large burden of de novo and parental mosaic mutations. *Orphanet Journal of Rare Diseases*, **2019**, 14, 237	4.2	5
38	The role of rare variants in systolic blood pressure: analysis of ExomeChip data in HyperGEN African Americans. *Human Heredity*, **2015**, 79, 20-7	1.1	5
37	Chronic constipation due to Hirschsprungs disease and desmosis coli in a family. *Pediatric Surgery International*, **2002**, 18, 110-4	2.1	5
36	Cloning and linkage mapping of three polymorphic tetranucleotide (TAAA)n repeats on human chromosome 21. *Genomics*, **1992**, 14, 1071-5	4.3	5

35	Linkage map on chromosome 21q and the association of a DNA haplotype with a propensity to nondisjunction and trisomy 21. *Annals of the New York Academy of Sciences*, **1985**, 450, 95-107	6.5	5
34	Gene- and tissue-level interactions in normal gastrointestinal development and Hirschsprung disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**,	11.5	5
33	Widespread promiscuous genetic information transfer from DNA to RNA. *Circulation Research*, **2011**, 109, 1202-3	15.7	4
32	Ching Chun Li (1912–2003):A Personal Remembrance of a Hero of Genetics. *American Journal of Human Genetics*, **2004**, 74, 789-792	11	4
31	A somatic cell hybrid map of human chromosome 13. *Genomics*, **1993**, 18, 486-95	4.3	4
30	Linkage mapping of the AML1 gene on human chromosome 21 using a DNA polymorphism in the 3R untranslated region. *Genomics*, **1992**, 14, 506-7	4.3	4
29	Testing the Ret and Sema3d genetic interaction in mouse enteric nervous system development. *Human Molecular Genetics*, **2017**, 26, 1811-1820	5.6	3
28	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. *International Journal of Environmental Research and Public Health*, **2017**, 14,	4.6	3
27	SNPs and other features as they predispose to complex disease: genome-wide predictive analysis of a quantitative phenotype for hypertension. *PLoS ONE*, **2011**, 6, e27891	3.7	3
26	1998 ASHG Award for Excellence in Education. Professor Ching Chun Li, courageous scholar and educator. *American Journal of Human Genetics*, **1999**, 64, 14-5	11	3
25	Dinucleotide repeat polymorphisms at the D13S192 and D13S193 loci. *Human Molecular Genetics*, **1993**, 2, 86	5.6	3
24	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. *European Journal of Human Genetics*, **2019**, 27, 269-277	5.3	3
23	MicroRNA-4516-mediated regulation of relies on 3RUTR -acting variants and contributes to the altered risk of Hirschsprung disease. *Journal of Medical Genetics*, **2020**, 57, 634-642	5.8	2
22	2013 William Allan Award: My multifactorial journey. *American Journal of Human Genetics*, **2014**, 94, 326-33	11	2
21	Hybrids of aneuploid human cancer cells permit complementation of simple and complex cancer defects. *Cancer Biology and Therapy*, **2009**, 8, 347-55	4.6	2
20	2008 Presidential Address: Principia Genetica: Our Future Science. *American Journal of Human Genetics*, **2010**, 86, 302-308	11	2
19	Dinucleotide repeat polymorphism at the DXS1146 locus. *Human Molecular Genetics*, **1993**, 2, 1078	5.6	2
18	Identity of different mutations for deleterious genes (reply). *Nature*, **1983**, 301, 176-177	50.4	2

17	A multi-enhancer regulatory code is disrupted in Hirschsprung disease. *Genome Research*, **2021**,	9.7	2
16	Magnitude of Mendelian versus complex inheritance of rare disorders. *American Journal of Medical Genetics, Part A*, **2021**, 185, 3287-3293	2.5	2
15	The association of cell cycle checkpoint 2 variants and kidney function: findings of the Family Blood Pressure Program and the Atherosclerosis Risk In Communities study. *American Journal of Hypertension*, **2009**, 22, 552-8	2.3	1
14	A PvuII polymorphism detected by a cDNA clone of the gene encoding the human spasmolytic protein protein (SML1 gene), one of three members of the trefoil peptide gene family clustered on chromosome 21q22.3. *Clinical Genetics*, **1997**, 52, 247-8	4	1
13	A genetic map of human chromosome 11p. *Genetic Epidemiology*, **1986**, 1, 135-40	2.6	1
12	Pathogenic alleles in microtubule, secretory granule and extracellular matrix-related genes in familial keratoconus. *Human Molecular Genetics*, **2021**, 30, 658-671	5.6	1
11	Multiple, independent, common variants at RET, SEMA3 and NRG1 gut enhancers specify Hirschsprung disease risk in European ancestry subjects. *Journal of Pediatric Surgery*, **2021**, 56, 2286-2294	2.6	1
10	Commentary: The central questions of human genetics: Richard Lewontin's 1968 senior lecture in Victor McKusick's Bar Harbor short course. *International Journal of Epidemiology*, **2016**, 45, 668-72	7.8	1
9	Analysis of putative cis-regulatory elements regulating blood pressure variation. *Human Molecular Genetics*, **2020**, 29, 1922-1932	5.6	0
8	Sequence-based correction of barcode bias in massively parallel reporter assays. *Genome Research*, **2021**, 31, 1638-1645	9.7	0
7	High Levels of Interest in Reproductive Genetic Information in Parents of Children and Adults With Hirschsprung Disease. *Journal of Pediatric Gastroenterology and Nutrition*, **2019**, 69, 299-305	2.8	0
6	Response to Brosens et al. *Genetics in Medicine*, **2018**, 20, 1479-1480	8.1	
5	Profile of Mary-Claire King, 2014 Lasker-Koshland Special Achievement in Medical Science awardee. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 17690-2	11.5	
4	2011 introduction to Curt Stern Award. *American Journal of Human Genetics*, **2012**, 90, 405-6	11	
3	Linkage analysis between Huntington disease and the G8 marker locus. *Genetic Epidemiology*, **1986**, 1, 211-6	2.6	
2	Newton E. Morton (1929-2018). *American Journal of Human Genetics*, **2018**, 102, 1011-1017	11	
1	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	