Aravinda Chakravarti

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4437471/publications.pdf

Version: 2024-02-01

316	79,251	2423	567
papers	citations	97 h-index	263 g-index

330	330	330	80436
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Interferon pathway lupus risk alleles modulate risk of death from acute COVID-19. Translational Research, 2022, 244, 47-55.	2.2	9
2	C. Thomas Caskey (1938â€“2022). Genome Research, 2022, 32, vii-viii.	2.4	1
3	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
4	The Compleat Human Genome. , 2022, 1, 234-236.		1
5	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
6	Pathogenic alleles in microtubule, secretory granule and extracellular matrix-related genes in familial keratoconus. Human Molecular Genetics, 2021, 30, 658-671.	1.4	12
7	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.	0.8	3
8	Sequence-based correction of barcode bias in massively parallel reporter assays. Genome Research, 2021, 31, 1638-1645.	2.4	3
9	Magnitude of Mendelian versus complex inheritance of rare disorders. American Journal of Medical Genetics, Part A, 2021, 185, 3287-3293.	0.7	12
10	A multi-enhancer RET regulatory code is disrupted in Hirschsprung disease. Genome Research, 2021, 31, 2199-2208.	2.4	10
11	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	7.7	118
12	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	1.4	7
13	MicroRNA-4516-mediated regulation of MAPK10 relies on 3â€² UTR cis-acting variants and contributes to the altered risk of Hirschsprung disease. Journal of Medical Genetics, 2020, 57, 634-642.	1.5	6
14	A gene regulatory network explains RETâ€“EDNRB epistasis in Hirschsprung disease. Human Molecular Genetics, 2019, 28, 3137-3147.	1.4	25
15	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.	1.2	10
16	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.	1.8	29
17	Multiple SCN5A 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.	3.3	22
18	Molecular Genetic Anatomy and Risk Profile of Hirschsprungâ€™s Disease. New England Journal of Medicine, 2019, 380, 1421-1432.	13.9	131

#	Article	IF	Citations
19	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
20	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.	0.9	3
21	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, 116, 26697-26708.	3.3	16
22	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
23	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.	1.4	5
24	Cardiomyocytes have mosaic patterns of protein expression. Cardiovascular Pathology, 2018, 34, 50-57.	0.7	18
25	Response to Brosens et al. Genetics in Medicine, 2018, 20, 1479-1480.	1.1	0
26	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.	2.6	123
27	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.	1.4	24
28	RET somatic mutations are underrecognized in Hirschsprung disease. Genetics in Medicine, 2018, 20, 770-777.	1.1	24
29	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59
30	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
31	Newton E. Morton (1929â€“2018). American Journal of Human Genetics, 2018, 102, 1011-1017.	2.6	0
32	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.	1.1	25
33	Human cardiac cis-regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. Genome Research, 2018, 28, 1577-1588.	2.4	25
34	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
35	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
36	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. Genome Biology, 2017, 18, 48.	3.8	72

#	Article	IF	Citations
37	Testing the Ret and Sema3d genetic interaction in mouse enteric nervous system development. Human Molecular Genetics, 2017, 26, 1811-1820.	1.4	8
38	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	9.4	281
39	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, 1596.	1.2	5
40	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
41	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
42	MicroRNAs in the miR-17 and miR-15 families are downregulated in chronic kidney disease with hypertension. PLoS ONE, 2017, 12, e0176734.	1.1	38
43	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	1.1	24
44	Revealing rateâ€limiting steps in complex disease biology: The crucial importance of studying rare, extremeâ€phenotype families. BioEssays, 2016, 38, 578-586.	1.2	47
45	Commentary: The central questions of human genetics: Richard Lewontinâ€™s 1968 senior lecture in Victor McKusickâ€™s Bar Harbor short course. International Journal of Epidemiology, 2016, 45, 668-672.	0.9	2
46	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. Cell, 2016, 167, 355-368.e10.	13.5	112
47	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. Human Molecular Genetics, 2016, 25, ddw333.	1.4	38
48	A PIGN mutation responsible for multiple congenital anomaliesâ€“hypotoniaâ€“seizures syndrome 1 (MCAHS1) in an Israeliâ€“Arab family. American Journal of Medical Genetics, Part A, 2016, 170, 176-182.	0.7	26
49	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
50	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
51	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
52	Transcriptional regulation of PRPF31 gene expression by MSR1 repeat elements causes incomplete penetrance in retinitis pigmentosa. Scientific Reports, 2016, 6, 19450.	1.6	42
53	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. Scientific Reports, 2016, 6, 28356.	1.6	6
54	The Genome Project-Write. Science, 2016, 353, 126-127.	6.0	194

#	Article	IF	Citations
55	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
56	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
57	RET Mutation and Function in HSCR, MEN2, and Other Cancers. , 2016, , 517-523.		1
58	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
59	Population variation in total genetic risk of Hirschsprung disease from common RET, SEMA3 and NRG1 susceptibility polymorphisms. Human Molecular Genetics, 2015, 24, 2997-3003.	1.4	66
60	Global implementation of genomic medicine: We are not alone. Science Translational Medicine, 2015, 7, 290ps13.	5.8	146
61	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, 581-596.	2.6	118
62	Intestinal Neuronal Dysplasia-Like Submucosal Ganglion Cell Hyperplasia at the Proximal Margins of Hirschsprung Disease Resections. Pediatric and Developmental Pathology, 2015, 18, 466-476.	0.5	21
63	The Role of Rare Variants in Systolic Blood Pressure: Analysis of ExomeChip Data in HyperGEN African Americans. Human Heredity, 2015, 79, 20-27.	0.4	13
64	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
65	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
66	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, 283-294.	2.6	225
67	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
68	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. American Journal of Human Genetics, 2015, 97, 199-215.	2.6	574
69	Loss of Î´-catenin function in severe autism. Nature, 2015, 520, 51-56.	13.7	145
70	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
71	Proteins linked to autosomal dominant and autosomal recessive disorders harbor characteristic rare missense mutation distribution patterns. Human Molecular Genetics, 2015, 24, 5995-6002.	1.4	40
72	Perspectives on Human Variation through the Lens of Diversity and Race: Figure 1.. Cold Spring Harbor Perspectives in Biology, 2015, 7, a023358.	2.3	16

#	Article	IF	Citations
73	Direct Estimates of the Genomic Contributions to Blood Pressure Heritability within a Population-Based Cohort (ARIC). PLoS ONE, 2015, 10, e0133031.	1.1	47
74	HPASubC: A suite of tools for user subclassification of human protein atlas tissue images. Journal of Pathology Informatics, 2015, 6, 36.	0.8	14
75	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
76	Effects of RET and NRG1 polymorphisms in Indonesian patients with Hirschsprung disease. Journal of Pediatric Surgery, 2014, 49, 1614-1618.	0.8	37
77	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, 17690-17692.	3.3	0
78	A population-based study of KCNH7 p.Arg394His and bipolar spectrum disorder. Human Molecular Genetics, 2014, 23, 6395-6406.	1.4	48
79	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
80	Linkage analysis incorporating geneâ€“age interactions identifies seven novel lipid loci: The Family Blood Pressure Program. Atherosclerosis, 2014, 235, 84-93.	0.4	11
81	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.	2.6	109
82	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.	2.6	73
83	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
84	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
85	2013 William Allan Award: My Multifactorial Journey. American Journal of Human Genetics, 2014, 94, 326-333.	2.6	2
86	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. Heart Rhythm, 2014, 11, 471-477.	0.3	16
87	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, 854-869.	2.6	72
88	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.	1.1	19
89	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, 545-554.	2.6	189
90	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641

#	Article	IF	Citations
91	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
92	Distilling Pathophysiology from Complex Disease Genetics. Cell, 2013, 155, 21-26.	13.5	67
93	Contribution of rare and common variants determine complex diseasesâ€"Hirschsprung disease as a model. Developmental Biology, 2013, 382, 320-329.	0.9	119
94	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
95	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
96	Genetics and Genomics for the Prevention and Treatment of Cardiovascular Disease: Update. Circulation, 2013, 128, 2813-2851.	1.6	100
97	Associations between NOS1AP Single Nucleotide Polymorphisms (SNPs) and QT Interval Duration in Four Racial/Ethnic Groups in the Multiâ€Ethnic Study of Atherosclerosis (MESA). Annals of Noninvasive Electrocardiology, 2013, 18, 29-40.	0.5	10
98	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.	1.5	112
99	Effects of Rare and Common Blood Pressure Gene Variants on Essential Hypertension. Circulation Research, 2013, 112, 318-326.	2.0	24
100	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	1.4	56
101	Chromosome 21 Scan in Down Syndrome Reveals DSCAM as a Predisposing Locus in Hirschsprung Disease. PLoS ONE, 2013, 8, e62519.	1.1	22
102	A Polymorphic 3â€™UTR Element in ATP1B1 Regulates Alternative Polyadenylation and Is Associated with Blood Pressure. PLoS ONE, 2013, 8, e76290.	1.1	17
103	Defining the Contribution of CNTNAP2 to Autism Susceptibility. PLoS ONE, 2013, 8, e77906.	1.1	33
104	Next-Generation Sequencing of Human Mitochondrial Reference Genomes Uncovers High Heteroplasmy Frequency. PLoS Computational Biology, 2012, 8, e1002737.	1.5	61
105	Male and female differential reproductive rate could explain parental transmission asymmetry of mutation origin in Hirschsprung disease. European Journal of Human Genetics, 2012, 20, 917-920.	1.4	8
106	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	9.4	533
107	Mendelian Puzzles. Science, 2012, 335, 930-931.	6.0	17
108	2011 Introduction to Curt Stern Award 1. American Journal of Human Genetics, 2012, 90, 405-406.	2.6	0

#	Article	IF	Citations
109	Rapid and efficient human mutation detection using a bench-top next-generation DNA sequencer. Human Mutation, 2012, 33, 281-289.	1.1	33
110	Quantifying and Modeling Birth Order Effects in Autism. PLoS ONE, 2011, 6, e26418.	1.1	23
111	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.	1.1	4
112	Mining gold dust under the genome wide significance level: a twoâ€stage approach to analysis of GWAS. Genetic Epidemiology, 2011, 35, 111-118.	0.6	46
113	A multilevel model to address batch effects in copy number estimation using SNP arrays. Biostatistics, 2011, 12, 33-50.	0.9	43
114	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	1.3	181
115	Widespread Promiscuous Genetic Information Transfer From DNA to RNA. Circulation Research, 2011, 109, 1202-1203.	2.0	29
116	A Bivariate Genome-Wide Approach to Metabolic Syndrome. Diabetes, 2011, 60, 1329-1339.	0.3	226
117	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, 2285-2295.	1.4	77
118	Genomic contributions to Mendelian disease. Genome Research, 2011, 21, 643-644.	2.4	17
119	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
120	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, 347-354.	1.0	17
121	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
122	Genomics Is Not Enough. Science, 2011, 334, 15-15.	6.0	39
123	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
124	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. PLoS Genetics, 2011, 7, e1002158.	1.5	117
125	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.	1.5	290
126	Copy Number Variants in Candidate Genes Are Genetic Modifiers of Hirschsprung Disease. PLoS ONE, 2011, 6, e21219.	1.1	56

#	Article	IF	Citations
127	2008 Presidential Address: Principia Genetica: Our Future Science. American Journal of Human Genetics, 2010, 86, 302-308.	2.6	4
128	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.	2.6	230
129	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	9.4	400
130	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	9.4	438
131	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
132	Mendelian disorders and multifactorial traits: the big divide or one for all?. Nature Reviews Genetics, 2010, 11, 380-384.	7.7	76
133	Genome-Wide Association Study Identifies GPC5 as a Novel Genetic Locus Protective against Sudden Cardiac Arrest. PLoS ONE, 2010, 5, e9879.	1.1	54
134	Parent-Of-Origin Effects in Autism Identified through Genome-Wide Linkage Analysis of 16,000 SNPs. PLoS ONE, 2010, 5, e12513.	1.1	33
135	Polymorphisms in the Mitochondrial DNA Control Region and Frailty in Older Adults. PLoS ONE, 2010, 5, e11069.	1.1	44
136	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. PLoS Genetics, 2010, 6, e1001045.	1.5	185
137	Polymorphisms in the NOS1APGene Modulate QT Interval Duration and Risk of Arrhythmias in the Long QT Syndrome. Journal of the American College of Cardiology, 2010, 55, 2745-2752.	1.2	163
138	Multiple Independent Genetic Factors at NOS1AP Modulate the QT Interval in a Multi-Ethnic Population. PLoS ONE, 2009, 4, e4333.	1.1	27
139	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.	1.1	89
140	Genetic Variations in Nitric Oxide Synthase 1 Adaptor Protein Are Associated With Sudden Cardiac Death in US White Community-Based Populations. Circulation, 2009, 119, 940-951.	1.6	167
141	Positional identification of variants of Adamts16 linked to inherited hypertension. Human Molecular Genetics, 2009, 18, 2825-2838.	1.4	57
142	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, 226-231.	3.3	280
143	Hybrids of aneuploid human cancer cells permit complementation of simple and complex cancer defects. Cancer Biology and Therapy, 2009, 8, 347-355.	1.5	3
144	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, 552-558.	1.0	1

#	Article	IF	Citations
145	Hemostasis, Inflammation, and Fatal and Nonfatal Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2009, 29, 2182-2190.	1.1	41
146	Drug-Sensitized Zebrafish Screen Identifies Multiple Genes, Including GINS3 , as Regulators of Myocardial Repolarization. Circulation, 2009, 120, 553-559.	1.6	106
147	Understanding cardiovascular disease through the lens of genome-wide association studies. Trends in Genetics, 2009, 25, 387-394.	2.9	68
148	Interaction between a chromosome 10RETenhancer and chromosome 21 in the Down syndrome-Hirschsprung disease association. Human Mutation, 2009, 30, 771-775.	1.1	57
149	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, 1650-1657.	1.4	52
150	A genome-wide linkage and association scan reveals novel loci for autism. Nature, 2009, 461, 802-808.	13.7	570
151	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	13.7	7,490
152	Kinship: Race relations. Nature, 2009, 457, 380-381.	13.7	17
153	Tracing India's invisible threads. Nature, 2009, 461, 487-488.	13.7	17
154	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	9.4	356
155	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	9.4	1,224
156	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	9.4	363
157	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
158	Association between Microdeletion and Microduplication at 16p11.2 and Autism. New England Journal of Medicine, 2008, 358, 667-675.	13.9	1,476
159	Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. European Journal of Human Genetics, 2008, 16, 1507-1511.	1.4	64
160	Victor Almon McKusick (1921â€“2008). Nature, 2008, 455, 46-46.	13.7	1
161	A Common Genetic Variant in the Neurexin Superfamily Member CNTNAP2 Increases Familial Risk of Autism. American Journal of Human Genetics, 2008, 82, 160-164.	2.6	566
162	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, 135-144.	1.5	42

#	Article	IF	Citations
163	Estimating Genome-Wide Copy Number Using Allele-Specific Mixture Models. Journal of Computational Biology, 2008, 15, 857-866.	0.8	17
164	Population Bottlenecks as a Potential Major Shaping Force of Human Genome Architecture. PLoS Genetics, 2007, 3, e119.	1.5	55
165	Associations between Genetic Variants in the NOS1AP (CAPON) Gene and Cardiac Repolarization in the Old Order Amish. Human Heredity, 2007, 64, 214-219.	0.4	71
166	An ancestral variant of Secretogranin II confers regulation by PHOX2 transcription factors and association with hypertension. Human Molecular Genetics, 2007, 16, 1752-1764.	1.4	29
167	Multiple Genes for Essential-Hypertension Susceptibility on Chromosome 1q. American Journal of Human Genetics, 2007, 80, 253-264.	2.6	102
168	Genome-Wide Association Scan Shows Genetic Variants in the FTO Gene Are Associated with Obesity-Related Traits. PLoS Genetics, 2007, 3, e115.	1.5	1,446
169	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
170	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
171	An investigation of genome-wide associations of hypertension with microsatellite markers in the family blood pressure program (FBPP). Human Genetics, 2007, 121, 577-590.	1.8	26
172	Human embryonic stem cells have a unique epigenetic signature. Genome Research, 2006, 16, 1075-1083.	2.4	250
173	Variation in the Ciliary Neurotrophic Factor Gene and Muscle Strength in Older Caucasian Women. Journal of the American Geriatrics Society, 2006, 54, 823-826.	1.3	32
174	A common genetic variant in the NOS1 regulator NOS1AP modulates cardiac repolarization. Nature Genetics, 2006, 38, 644-651.	9.4	500
175	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, 469-477.	1.4	19
176	Identifying Allelic Loss and Homozygous Deletions in Pancreatic Cancer without Matched Normals Using High-Density Single-Nucleotide Polymorphism Arrays. Cancer Research, 2006, 66, 7920-7928.	0.4	78
177	High Incidence of Deafness from Three Frequent Connexin 26 Mutations in an Isolated Community. Genetic Testing and Molecular Biomarkers, 2006, 10, 40-43.	1.7	12
178	Genomic alterations in cultured human embryonic stem cells. Nature Genetics, 2005, 37, 1099-1103.	9.4	592
179	A common sex-dependent mutation in a RET enhancer underlies Hirschsprung disease risk. Nature, 2005, 434, 857-863.	13.7	438
180	A Population Association Study of Angiotensinogen Polymorphisms and Haplotypes With Left Ventricular Phenotypes. Hypertension, 2005, 46, 1294-1299.	1.3	16

#	Article	IF	Citations
181	Evaluation of the RET regulatory landscape reveals the biological relevance of a HSCR-implicated enhancer. Human Molecular Genetics, 2005, 14, 3837-3845.	1.4	75
182	On the probability that a novel variant is a disease-causing mutation. Genome Research, 2005, 15, 960-966.	2.4	24
183	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, 15960-15964.	3.3	423
184	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, 8949-8954.	3.3	36
185	Haplotype Association Analysis of AGT Variants with Hypertension-Related Traits: The HyperGEN Study. Human Heredity, 2005, 60, 164-176.	0.4	22
186	Differential Susceptibility to Hypertension Is Due to Selection during the Out-of-Africa Expansion. PLoS Genetics, 2005, 1, e82.	1.5	208
187	Finding Needles in Haystacks â€"IRF6Gene Variants in Isolated Cleft Lip or Cleft Palate. New England Journal of Medicine, 2004, 351, 822-824.	13.9	11
188	Haplotype and Missing Data Inference in Nuclear Families. Genome Research, 2004, 14, 1624-1632.	2.4	42
189	The Human MitoChip: A High-Throughput Sequencing Microarray for Mitochondrial Mutation Detection. Genome Research, 2004, 14, 812-819.	2.4	218
190	Positional Identification of Hypertension Susceptibility Genes on Chromosome 2. Hypertension, 2004, 43, 477-482.	1.3	85
191	From The Cover: The gene for soluble N-ethylmaleimide sensitive factor attachment protein Â is mutated in hydrocephaly with hop gait (hyh) mice. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1748-1753.	3.3	65
192	Genomics in Sudden Cardiac Death. Circulation Research, 2004, 94, 712-723.	2.0	88
193	Exhaustive allelic transmission disequilibrium tests as a new approach to genome-wide association studies. Nature Genetics, 2004, 36, 1181-1188.	9.4	154
194	Ching Chun Li (1912â€“2003):A Personal Remembrance of a Hero of Genetics. American Journal of Human Genetics, 2004, 74, 789-792.	2.6	4
195	Nature, nurture and human disease. Nature, 2003, 421, 412-414.	13.7	129
196	Safety issues in cell-based intervention trials. Fertility and Sterility, 2003, 80, 1077-1085.	0.5	72
197	Undetected Genotyping Errors Cause Apparent Overtransmission of Common Alleles in the Transmission/Disequilibrium Test. American Journal of Human Genetics, 2003, 72, 598-610.	2.6	157
198	A Genome-Wide Linkage Analysis Investigating the Determinants of Blood Pressure in Whites and African Americans. American Journal of Hypertension, 2003, 16, 151-153.	1.0	60

#	Article	IF	Citations
199	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. Genome Research, 2003, 13, 2363-2371.	2.4	954
200	Erythrocyte Sodium-Lithium Countertransport and Blood Pressure. Hypertension, 2003, 41, 842-846.	1.3	21
201	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, 376-381.	3.3	113
202	Linkage Disequilibrium and Haplotype Diversity in the Genes of the Renin-Angiotensin System: Findings From the Family Blood Pressure Program. Genome Research, 2003, 13, 173-181.	2.4	71
203	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, 1826-1831.	3.3	133
204	A BDNF Coding Variant is Associated with the NEO Personality Inventory Domain Neuroticism, a Risk Factor for Depression. Neuropsychopharmacology, 2003, 28, 397-401.	2.8	321
205	Associations Between Hypertension and Genes in the Renin-Angiotensin System. Hypertension, 2003, 41, 1027-1034.	1.3	116
206	Public stem cell banks: considerations of justice in stem cell research and therapy. Hastings Center Report, 2003, 33, 13-27.	0.7	22
207	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, 4755-4756.	3.3	35
208	viewGene: A Graphical Tool for Polymorphism Visualization and Characterization. Genome Research, 2002, 12, 333-338.	2.4	16
209	An Evaluation of the Assembly of an Approximately 15-Mb Region on Human Chromosome 13q32â€“q33 Linked to Bipolar Disorder and Schizophrenia. Genomics, 2002, 79, 635-658.	1.3	18
210	Future of genetics of mood disorders research. Biological Psychiatry, 2002, 52, 457-477.	0.7	116
211	A Genome-Wide Scan for Obesity in African-Americans. Diabetes, 2002, 51, 541-544.	0.3	60
212	Haplotype Inference in Random Population Samples. American Journal of Human Genetics, 2002, 71, 1129-1137.	2.6	176
213	Cloning of rat thymic stromal lymphopoietin receptor (TSLPR) and characterization of genomic structure of murine Tslpr gene. Gene, 2002, 284, 161-168.	1.0	7
214	Chronic constipation due to Hirschsprung's disease and desmosis coli in a family. Pediatric Surgery International, 2002, 18, 110-114.	0.6	8
215	Segregation at three loci explains familial and population risk in Hirschsprung disease. Nature Genetics, 2002, 31, 89-93.	9.4	269
216	Genome-wide association study and mouse model identify interaction between RET and EDNRB pathways in Hirschsprung disease. Nature Genetics, 2002, 32, 237-244.	9.4	255

#	Article	IF	Citations
217	High-Throughput Variation Detection and Genotyping Using Microarrays. Genome Research, 2001, 11, 1913-1925.	2.4	258
218	EDNRB/EDN3 and Hirschsprung Disease Type II. Pigment Cell & Melanoma Research, 2001, 14, 161-169.	4.0	97
219	. . .to a future of genetic medicine. Nature, 2001, 409, 822-823.	13.7	164
220	Testing for Colon Neoplasia Susceptibility Variants at the Human COX2 Locus. Journal of the National Cancer Institute, 2001, 93, 635-639.	3.0	15
221	Sequence Variation Within the Fragile X Locus. Genome Research, 2001, 11, 1382-1391.	2.4	12
222	Parallel Genotyping of Human SNPs Using Generic High-density Oligonucleotide Tag Arrays. Genome Research, 2000, 10, 853-860.	2.4	273
223	Patterns of Meiotic Recombination on the Long Arm of Human Chromosome 21. Genome Research, 2000, 10, 1319-1332.	2.4	47
224	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, 1807-1820.	2.6	246
225	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, 1208-1218.	2.6	84
226	PATTERNS OFGENETICVARIATION INMENDELIAN ANDCOMPLEXTRAITS. Annual Review of Genomics and Human Genetics, 2000, 1, 387-407.	2.5	78
227	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, 693-698.	1.0	28
228	GIST: A web tool for collecting gene information. Physiological Genomics, 1999, 1, 75-81.	1.0	11
229	Pleiotropic Skeletal and Ocular Phenotypes of the Mouse Mutation Congenital Hydrocephalus (ch/Mf1) Arise from a Winged Helix/Forkhead Transcription Factor Gene. Human Molecular Genetics, 1999, 8, 625-637.	1.4	100
230	Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis. Nature Genetics, 1999, 22, 239-247.	9.4	1,040
231	Identifying disease alleles by genome sharing. Nature Genetics, 1999, 23, 25-25.	9.4	228
232	Population geneticsâ€"making sense out of sequence. Nature Genetics, 1999, 21, 56-60.	9.4	561
233	Professor Ching Chun Li, Courageous Scholar and Educator. American Journal of Human Genetics, 1999, 64, 14-15.	2.6	4
234	Elevated Frequency and Allelic Heterogeneity of Congenital Nephrotic Syndrome, Finnish Type, in the Old Order Mennonites. American Journal of Human Genetics, 1999, 65, 1785-1790.	2.6	55

#	Article	IF	Citations
235	A Radiation Hybrid Map of 48 Loci Including the Clouston Hidrotic Ectodermal Dysplasia Locus in the Pericentromeric Region of Chromosome 13q. Genomics, 1999, 56, 127-130.	1.3	26
236	A DNA Polymorphism Discovery Resource for Research on Human Genetic Variation: Table 1.. Genome Research, 1998, 8, 1229-1231.	2.4	750
237	Schizophrenia susceptibility loci on chromosomes 13q32 and 8p21. Nature Genetics, 1998, 20, 70-73.	9.4	506
238	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, 3065-3070.	2.6	27
239	It's raining SNPs, hallelujah?. Nature Genetics, 1998, 19, 216-217.	9.4	139
240	An integrated genetic linkage map of the laboratory rat. Mammalian Genome, 1998, 9, 521-530.	1.0	92
241	HumanGFRA1: Cloning, Mapping, Genomic Structure, and Evaluation as a Candidate Gene for Hirschsprung Disease Susceptibility. Genomics, 1998, 48, 354-362.	1.3	58
242	New Goals for the U.S. Human Genome Project: 1998-2003. , 1998, 282, 682-689.		711
243	Allele Frequency Distributions in Pooled DNA Samples: Applications to Mapping Complex Diseaseâ€‰Genes. Genome Research, 1998, 8, 111-123.	2.4	120
244	Variations on a Theme: Cataloging Human DNA Sequence Variation. Science, 1997, 278, 1580-1581.	6.0	979
245	Cloning of a Novel Homeobox-Containing Gene,PKNOX1,and Mapping to Human Chromosome 21q22.3. Genomics, 1997, 41, 193-200.	1.3	58
246	A PvuII polymorphism detected by a cDNA clone of the gene encoding the human spasmolytic protein (SML1 gene), one of three members of the trefoil peptide gene family clustered on chromosome 21q22.3. Clinical Genetics, 1997, 52, 247-248.	1.0	1
247	Age, Sex, and the Familial Risk of Rheumatoid Arthritis. American Journal of Epidemiology, 1996, 144, 15-24.	1.6	25
248	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, 445-447.	9.4	296
249	Endothelinâ€“3 frameshift mutation in congenital central hypoventilation syndrome. Nature Genetics, 1996, 13, 395-396.	9.4	89
250	Germline mutations in glial cell line-derived neurotrophic factor (GDNF) and RET in a Hirschsprung disease patient. Nature Genetics, 1996, 14, 341-344.	9.4	269
251	Down syndrome consequent to a cryptic maternal 12p;21q chromosome translocation. American Journal of Medical Genetics Part A, 1995, 56, 67-71.	2.4	70
252	The CD4/CD8 ratio: Message in a bottle?. Nature Medicine, 1995, 1, 1240-1241.	15.2	17

#	Article	IF	Citations
253	Chromosomal Localization of the Mouse Src-like Adapter Protein (Slap) Gene and Its Putative Human Homolog SLA. Genomics, 1995, 30, 623-625.	1.3	13
254	DNA Profile Similarity in a Subdivided Population. Human Heredity, 1994, 44, 100-109.	0.4	10
255	Identity-by-descent and association mapping of a recessive gene for Hirschsprung disease on human chromosome 13q22. Human Molecular Genetics, 1994, 3, 1217-1225.	1.4	241
256	Automated construction of genetic linkage maps using an expert system (MultiMap): a human genome linkage map. Nature Genetics, 1994, 6, 384-390.	9.4	440
257	Cytogenetics and origins of pediatric germ cell tumors. Cancer Genetics and Cytogenetics, 1994, 74, 54-58.	1.0	48
258	A missense mutation of the endothelin-B receptor gene in multigenic hirschsprung's disease. Cell, 1994, 79, 1257-1266.	13.5	877
259	Linkage mapping of the cystathionine ?-synthase (CBS) gene on human chromosome 21 using a DNA polymorphism in the 3? untranslated region. Human Genetics, 1993, 90, 566-8.	1.8	19
260	D21S210: A highly polymorphic (GT)n marker closely linked to the ?-amyloid protein precursor (APP) gene. Human Genetics, 1993, 91, 87-8.	1.8	8
261	A gene for Hirschsprung disease (megacolon) in the pericentromeric region of human chromosome 10. Nature Genetics, 1993, 4, 351-356.	9.4	154
262	DNA Polymorphisms in the 3â€² Untranslated Region of Genes on Human Chromosome 21. Genomics, 1993, 15, 98-102.	1.3	8
263	Microsatellite Polymorphism Linkage Map of Human Chromosome 13q. Genomics, 1993, 15, 376-386.	1.3	55
264	A Linkage Map of Human Chromosome 21: 43 PCR Markers at Average Intervals of 2.5 cM. Genomics, 1993, 16, 562-571.	1.3	73
265	Efficient Construction of High-Resolution Regular Article from Yeast Artificial Chromosomes Using Radiation Hybrids: Inner Product Mapping. Genomics, 1993, 18, 283-289.	1.3	13
266	A somatic cell hybrid map of human chromosome 13. Genomics, 1993, 18, 486-495.	1.3	6
267	Dinucleotide repeat polymorphism at the DXS1146 locus. Human Molecular Genetics, 1993, 2, 1078-1078.	1.4	2
268	Multiplex PCR of three dinucleotide repeats in the Prader-Willi/Angelman critical region (15q11â€“q13): molecular diagnosis and mechanism of uniparental disomy. Human Molecular Genetics, 1993, 2, 143-151.	1.4	174
269	Dinucleotide repeat polymorphisms at the D13S192 and D13S193 loci. Human Molecular Genetics, 1993, 2, 86-86.	1.4	4
270	D21S215 is a (GT)n polymorphic marker close to centromeric alphoid sequences on chromosome 21. Genomics, 1992, 13, 1365-1367.	1.3	14

#	Article	IF	Citations
271	Linkage mapping of the AML1 gene on human chromosome 21 using a DNA polymorphism in the 3â€² untranslated region. Genomics, 1992, 14, 506-507.	1.3	5
272	Linkage mapping of the carbonyl reductase (CBR) gene on human chromosome 21 using a DNA polymorphism in the 3â€² untranslated region. Genomics, 1992, 13, 447-448.	1.3	7
273	Schizophrenia and porphobilinogen deaminase gene polymorphisms: an association study. Schizophrenia Research, 1992, 8, 51-58.	1.1	9
274	Dinucleotide repeat (GT)n markers on chromosome 21. Genomics, 1992, 14, 818-819.	1.3	13
275	Cloning and linkage mapping of three polymorphic tetranucleotide (TAAA)n repeats on human chromosome 21. Genomics, 1992, 14, 1071-1075.	1.3	6
276	Genetics and biology of human ovarian teratomas. Cancer Genetics and Cytogenetics, 1992, 62, 58-65.	1.0	43
277	Fragile X founder effect?. Nature Genetics, 1992, 1, 237-238.	9.4	42
278	Genetic Epidemiology and genetic Epidemiology. Genetic Epidemiology, 1992, 9, i-ii.	0.6	0
279	Detection of genetic heterogeneity for complex quantitative phenotypes. Genetic Epidemiology, 1992, 9, 207-223.	0.6	6
280	Pedigree analysis of blood pressure in subjects from rural Greece and relatives who migrated to Melbourne, Australia. Genetic Epidemiology, 1992, 9, 225-238.	0.6	12
281	Estimation of the frequency of isoform-genotype discrepancies at the apolipoprotein E locus in heterozygotes for the isoforms. Genetic Epidemiology, 1992, 9, 239-248.	0.6	21
282	Dietary intake and gene variation influence the response of plasma lipids to dietary intervention. Genetic Epidemiology, 1992, 9, 249-260.	0.6	21
283	Elementary methods for the analysis of dichotomous outcomes in unselected samples of Twins. Genetic Epidemiology, 1992, 9, 273-287.	0.6	45
284	Segregation analysis of 159 soft tissue sarcoma kindreds: Comparison of fixed and sequential sampling schemes. Genetic Epidemiology, 1992, 9, 291-304.	0.6	14
285	Commingling analysis of memory performance in offspring of Alzheimer patients. Genetic Epidemiology, 1992, 9, 333-345.	0.6	12
286	Two-Locus models of disease. Genetic Epidemiology, 1992, 9, 347-365.	0.6	96
287	Preliminary ordering of multiple linked loci using pairwise linkage data. Genetic Epidemiology, 1992, 9, 367-375.	0.6	27
288	A genetic linkage map of 27 markers on human chromosome 21. Genomics, 1991, 9, 407-419.	1.3	82

#	Article	IF	Citations
289	Guidelines for human linkage maps An International System for Human Linkage Maps (ISLM, 1990). Annals of Human Genetics, 1991, 55, 1-6.	0.3	27
290	DNA duplication associated with Charcot-Marie-Tooth disease type 1A. Cell, 1991, 66, 219-232.	13.5	1,313
291	Linkage mapping of highly informative DNA polymorphisms within the human interferon-Î± receptor gene on chromosome 21. Genomics, 1991, 11, 573-576.	1.3	35
292	A graphical representation of genetic and physical maps: The Marey map. Genomics, 1991, 11, 219-222.	1.3	67
293	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.	1.8	14
294	Information content of the Centre d'Etude du Polymorphisme Humain (CEPH) family structures for linkage studies. Human Genetics, 1991, 87, 721-4.	1.8	9
295	Waardenburg syndrome and Hirschsprung disease: Evidence for pleiotropic effects of a single dominant gene. American Journal of Medical Genetics Part A, 1990, 35, 100-104.	2.4	48
296	Phylogeny of human Î²-globin haplotypes and its implications for recent human evolution. American Journal of Physical Anthropology, 1990, 81, 113-130.	2.1	66
297	Linkage analysis of the human HMG14 gene on chromosome 21 using a GT dinucleotide repeat as polymorphic marker. Genomics, 1990, 7, 136-138.	1.3	60
298	Linkage mapping of the highly informative DNA marker D21S156 to human chromosome 21 using a polymorphic GT dinucleotide repeat. Genomics, 1990, 8, 400-402.	1.3	28
299	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.	0.7	21
300	A genetic linkage map of 17 markers on human chromosome 21. Genomics, 1989, 4, 579-591.	1.3	82
301	DNA polymorphism haplotypes of the human apolipoprotein APOA1-APOC3-APOA4 gene cluster. Human Genetics, 1988, 80, 265-273.	1.8	67
302	Methods for studying recombination on chromosomes that undergo nondisjunction. Genomics, 1987, 1, 35-42.	1.3	47
303	Estimation of segregation and ascertainment probabilities by discarding the single probands. Genetic Epidemiology, 1987, 4, 185-191.	0.6	7
304	Tests of linkage and heterogeneity in Mendelian diseases using identity by descent scores. Genetic Epidemiology, 1987, 4, 255-266.	0.6	18
305	Etiological heterogeneity in Hodgkin's disease: HLA linked and unlinked determinants of susceptibility independent of histological concordance. Genetic Epidemiology, 1986, 3, 407-415.	0.6	25
306	A genetic map of human chromosome 11p. Genetic Epidemiology, 1986, 3, 135-140.	0.6	1

#	Article	IF	Citations
307	Linkage analysis between Huntington disease and the G8 marker locus. Genetic Epidemiology, 1986, 3, 211-216.	0.6	0
308	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.	1.8	5
309	Aggregation of colon cancer in family data. Genetic Epidemiology, 1984, 1, 53-61.	0.6	14
310	A test of nonrandom segregation. Genetic Epidemiology, 1984, 1, 329-340.	0.6	12
311	Identity of different mutations for deleterious genes (reply). Nature, 1983, 301, 176-177.	13.7	2
312	Variation in allele frequencies among caste groups of the Dhangars of Maharashtra, India: An analysis with Wright'sFSTstatistic. Annals of Human Biology, 1977, 4, 275-280.	0.4	19
313	Mean and variance of FST in a finite number of incompletely isolated populations. Theoretical Population Biology, 1977, 11, 291-306.	0.5	88
314	Drift variances of FSTand GST statistics obtained from a finite number of isolated populations. Theoretical Population Biology, 1977, 11, 307-325.	0.5	93
315	Genetic differentiation in the colonising lizard Anolis grahami. Heredity, 1977, 38, 121-123.	1.2	7
316	On consanguineous marriages and the genetic load. Human Genetics, 1977, 36, 47-54.	1.8	81