Andrew A Hicks

List of Publications by Year
in descending order

178	44,732	9756 73	3714 179
papers	citations	h-index	g-index

199	199	199	46647
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. Pathogens and Global Health, 2022, 116, 128-136.	1.0	4
2	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
3	Generation and characterization of induced pluripotent stem cell (iPSC) lines of two asymptomatic individuals carrying a heterozygous exon 7 deletion in Parkin (PRKN) and two non-carriers from the same family. Stem Cell Research, 2022, 60, 102692.	0.3	1
4	Dihydroceramide- and ceramide-profiling provides insights into human cardiometabolic disease etiology. Nature Communications, 2022, 13, 936.	5.8	28
5	Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. Human Molecular Genetics, 2022, , .	1.4	3
6	Generation of an induced pluripotent stem cell line (EURACi014-A) from a Parkinsonâ€™s disease patient with an A53T mutation in the SNCA gene by an integration-free reprogramming method. Stem Cell Research, 2022, 60, 102713.	0.3	0
7	A genome on shaky ground: exploring the impact of mitochondrial DNA integrity on Parkinsonâ€™s disease by highlighting the use of cybrid models. Cellular and Molecular Life Sciences, 2022, 79, 283.	2.4	1
8	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
9	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
10	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
11	Association of mitochondrial DNA copy number with metabolic syndrome and type 2 diabetes in 14Â176 individuals. Journal of Internal Medicine, 2021, 290, 190-202.	2.7	61
12	Genetic variants in levodopa-induced dyskinesia (LID): A systematic review and meta-analysis. Parkinsonism and Related Disorders, 2021, 84, 52-60.	1.1	13
13	Task matters - challenging the motor system allows distinguishing unaffected Parkin mutation carriers from mutation-free controls. Parkinsonism and Related Disorders, 2021, 86, 101-104.	1.1	6
14	Balancing scientific interests and the rights of participants in designing a recall by genotype study. European Journal of Human Genetics, 2021, 29, 1146-1157.	1.4	6
15	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
16	Frequency of Heterozygous Parkin (PRKN) Variants and Penetrance of Parkinson's Disease Risk Markers in the Population-Based CHRIS Cohort. Frontiers in Neurology, 2021, 12, 706145.	1.1	14
17	Generation of hiPSC-Derived Functional Dopaminergic Neurons in Alginate-Based 3D Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 708389.	1.8	13
18	Exome-wide association study of levodopa-induced dyskinesia in Parkinsonâ€™s disease. Scientific Reports, 2021, 11, 19582.	1.6	3

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19	The SZT2 Interactome Unravels New Functions of the KICSTOR Complex. Cells, 2021, 10, 2711.	1.8	7
20	Interaction of Alpha-Synuclein With Lipids: Mitochondrial Cardiolipin as a Critical Player in the Pathogenesis of Parkinsonâ€™s Disease. Frontiers in Neuroscience, 2020, 14, 578993.	1.4	29
21	Interleukin-6 Signaling Effects on Ischemic Stroke and Other Cardiovascular Outcomes. Circulation Genomic and Precision Medicine, 2020, 13, e002872.	1.6	90
22	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
23	Silencing of CCR4-NOT complex subunits affect heart structure and function. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	18
24	Kinase inhibition of G2019S-LRRK2 enhances autolysosome formation and function to reduce endogenous alpha-synuclein intracellular inclusions. Cell Death Discovery, 2020, 6, 45.	2.0	30
25	Evaluation of the role of STAP1 in Familial Hypercholesterolemia. Scientific Reports, 2019, 9, 11995.	1.6	17
26	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	1.6	9
27	Mitochondrial DNA copy number is associated with mortality and infections in a large cohort of patients with chronic kidney disease. Kidney International, 2019, 96, 480-488.	2.6	53
28	Application of CRISPR/Cas9 editing and digital droplet PCR in human iPSCs to generate novel knock-in reporter lines to visualize dopaminergic neurons. Stem Cell Research, 2019, 41, 101656.	0.3	11
29	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
30	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
31	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
32	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
33	Modeling Parkinsonâ€™s disease in midbrain-like organoids. Npj Parkinson's Disease, 2019, 5, 5.	2.5	204
34	Parkin Interacts with Apoptosis-Inducing Factor and Interferes with Its Translocation to the Nucleus in Neuronal Cells. International Journal of Molecular Sciences, 2019, 20, 748.	1.8	9
35	Generation of an induced pluripotent stem cell line (EURACi005-A) from a Parkinson's disease patient carrying a homozygous exon 3 deletion in the PRKNgene. Stem Cell Research, 2019, 41, 101624.	0.3	5
36	Compound heterozygous SZT2 mutations in two siblings with early-onset epilepsy, intellectual disability and macrocephaly. Seizure: the Journal of the British Epilepsy Association, 2019, 66, 81-85.	0.9	14

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37	The PPARGC1A locus and CNS-specific PGC-1Î± isoforms are associated with Parkinson's Disease. Neurobiology of Disease, 2019, 121, 34-46.	2.1	23
38	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
39	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
40	Plasmid-normalized quantification of relative mitochondrial DNA copy number. Scientific Reports, 2018, 8, 15347.	1.6	61
41	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
42	Influence of collection tubes during quantitative targeted metabolomics studies in human blood samples. Clinica Chimica Acta, 2018, 486, 320-328.	0.5	44
43	Environmental and Genetic Variables Influencing Mitochondrial Health and Parkinsonâ€™s Disease Penetrance. Parkinson's Disease, 2018, 2018, 1-8.	0.6	13
44	A new hypothesis for Parkinsonâ€™s disease pathogenesis: GTPase-p38 MAPK signaling and autophagy as convergence points of etiology and genomics. Molecular Neurodegeneration, 2018, 13, 40.	4.4	69
45	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
46	Structural Consistency of the Pain Sensitivity Questionnaire in the Cooperative Health Research In South Tyrol (CHRIS) Population-Based Study. Journal of Pain, 2018, 19, 1424-1434.	0.7	15
47	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
48	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
49	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	3.0	24
50	SLP-2 interacts with Parkin in mitochondria and prevents mitochondrial dysfunction in Parkin-deficient human iPSC-derived neurons andDrosophila. Human Molecular Genetics, 2017, 26, 2412-2425.	1.4	48
51	32-channel time-correlated-single-photon-counting system for high-throughput lifetime imaging. Review of Scientific Instruments, 2017, 88, 083704.	0.6	11
52	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
53	Pre-analytic evaluation of volumetric absorptive microsampling and integration in a mass spectrometry-based metabolomics workflow. Analytical and Bioanalytical Chemistry, 2017, 409, 6263-6276.	1.9	44
54	CADPS2 gene expression is oppositely regulated by LRRK2 and alpha-synuclein. Biochemical and Biophysical Research Communications, 2017, 490, 876-881.	1.0	17

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55	Plasma and White Blood Cells Show Different miRNA Expression Profiles in Parkinsonâ€™s Disease. Journal of Molecular Neuroscience, 2017, 62, 244-254.	1.1	49
56	Elevated levels of alpha-synuclein blunt cellular signal transduction downstream of Gq protein-coupled receptors. Cellular Signalling, 2017, 30, 82-91.	1.7	9
57	The Impact of CRISPR/Cas9 Technology on Cardiac Research: From Disease Modelling to Therapeutic Approaches. Stem Cells International, 2017, 2017, 1-13.	1.2	36
58	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106
59	SLP-2: a potential new target for improving mitochondrial function in Parkinson's disease. Neural Regeneration Research, 2017, 12, 1435.	1.6	4
60	Deregulation of miRNAs 103a, 30b and 29a in peripheral blood of L-dopa treated Parkinson's patients. Parkinsonism and Related Disorders, 2016, 22, e189-e190.	1.1	0
61	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	1.4	27
62	Primary familial brain calcification in the â€˜IBGC2â€™ kindred: All linkage roads lead toSLC20A2. Movement Disorders, 2016, 31, 1901-1904.	2.2	16
63	PLA2G6mutations and Parkinsonism: Long-term follow-up of clinical features and neuropathology. Movement Disorders, 2016, 31, 1927-1929.	2.2	18
64	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	3.0	83
65	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
66	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
67	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
68	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
69	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
70	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
71	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	1.8	63
72	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

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73	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
74	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
75	Generation of Induced Pluripotent Stem Cells from Frozen Buffy Coats using Non-integrating Episomal Plasmids. Journal of Visualized Experiments, 2015, , e52885.	0.2	17
76	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
77	Overexpression of blood microRNAs 103a, 30b, and 29a in <scp>l</scp> -dopaâ€“treated patients with PD. Neurology, 2015, 84, 645-653.	1.5	102
78	Large-scale assessment of polyglutamine repeat expansions in Parkinson disease. Neurology, 2015, 85, 1283-1292.	1.5	25
79	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
80	Identification of a set of endogenous reference genes for miRNA expression studies in Parkinsonâ€™s disease blood samples. BMC Research Notes, 2014, 7, 715.	0.6	34
81	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. Human Molecular Genetics, 2014, 23, 3054-3068.	1.4	90
82	The Arachidonic Acid Metabolome Serves as a Conserved Regulator of Cholesterol Metabolism. Cell Metabolism, 2014, 20, 787-798.	7.2	92
83	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
84	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
85	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
86	Meta-analysis of genome-wide association studies identifies two loci associated with circulating osteoprotegerin levels. Human Molecular Genetics, 2014, 23, 6684-6693.	1.4	14
87	Fine-Mapping of Restless Legs Locus 4 (RLS4) Identifies a Haplotype over the SPATS2L and KCTD18 Genes. Journal of Molecular Neuroscience, 2013, 49, 600-605.	1.1	12
88	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
89	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
90	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	0.6	13

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91	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	0.6	14
92	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
93	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
94	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
95	Involvement of proprotein convertase PCSK7 in the regulation of systemic iron homeostasis. Hepatology, 2013, 58, 1860-1861.	3.6	4
96	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
97	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	1.5	194
98	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	3.9	116
99	A KATP channel gene effect on sleep duration: from genome-wide association studies to function in Drosophila. Molecular Psychiatry, 2013, 18, 122-132.	4.1	132
100	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	1.1	38
101	Sequencing of high-complexity DNA pools for identification of nucleotide and structural variants in regions associated with complex traits. European Journal of Human Genetics, 2012, 20, 77-83.	1.4	10
102	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
103	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
104	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
105	Genome-wide analysis of epistasis in body mass index using multiple human populations. European Journal of Human Genetics, 2012, 20, 857-862.	1.4	33
106	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
107	A multi-centre clinico-genetic analysis of the VPS35 gene in Parkinson disease indicates reduced penetrance for disease-associated variants. Journal of Medical Genetics, 2012, 49, 721-726.	1.5	94
108	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320

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109	Large-scale replication and heterogeneity in Parkinson disease genetic loci. Neurology, 2012, 79, 659-667.	1.5	119
110	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	2.6	85
111	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
112	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
113	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
114	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. PLoS ONE, 2012, 7, e46501.	1.1	111
115	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
116	Genetic Adaptation of Fatty-Acid Metabolism: A Human-Specific Haplotype Increasing the Biosynthesis of Long-Chain Omega-3 and Omega-6 Fatty Acids. American Journal of Human Genetics, 2012, 90, 809-820.	2.6	205
117	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	1.1	3
118	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
119	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
120	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
121	Copy Number Variation across European Populations. PLoS ONE, 2011, 6, e23087.	1.1	25
122	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
123	Variation in the Uric Acid Transporter Gene SLC2A9 and Its Association with AAO of Parkinsonâ€™s Disease. Journal of Molecular Neuroscience, 2011, 43, 246-250.	1.1	44
124	Variants in STAT5B Associate with Serum TC and LDL-C Levels. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E1496-E1501.	1.8	5
125	Linkage and association analysis of hyperthyrotropinaemia in an Alpine population reveal two novel loci on chromosomes 3q28-29 and 6q26-27. Journal of Medical Genetics, 2011, 48, 549-556.	1.5	6
126	Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. Human Molecular Genetics, 2011, 20, 1660-1671.	1.4	47

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127	Novel association to the proprotein convertase PCSK7 gene locus revealed by analysing soluble transferrin receptor (sTfR) levels. Human Molecular Genetics, 2011, 20, 1042-1047.	1.4	62
128	Identification of a common variant in the TFR2 gene implicated in the physiological regulation of serum iron levels. Human Molecular Genetics, 2011, 20, 1232-1240.	1.4	67
129	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	1.1	15
130	Parkin gene modifies the effect of RLS4 on the age at onset of restless legs syndrome (RLS). American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 350-355.	1.1	3
131	Copy number variation and association over T-cell receptor genesâ€"influence of DNA source. Immunogenetics, 2010, 62, 561-567.	1.2	14
132	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	1.4	22
133	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
134	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
135	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
136	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
137	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
138	Update on the management of restless legs syndrome: existing and emerging treatment options. Nature and Science of Sleep, 2010, 2, 199.	1.4	3
139	Modeling of Environmental Effects in Genome-Wide Association Studies Identifies SLC2A2 and HP as Novel Loci Influencing Serum Cholesterol Levels. PLoS Genetics, 2010, 6, e1000798.	1.5	51
140	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	1.4	133
141	A Global In Vivo Drosophila RNAi Screen Identifies NOT3 as a Conserved Regulator of Heart Function. Cell, 2010, 141, 142-153.	13.5	199
142	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
143	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: Results of genome-wide association analyses including 4659 European individuals. Atherosclerosis, 2010, 208, 412-420.	0.4	146
144	Linkage and Genomeâ€wide Association Analysis of Obesityâ€related Phenotypes: Association of Weight With the MGAT1 Gene. Obesity, 2010, 18, 803-808.	1.5	54

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145	Genome-Wide Association Study Identifies Multiple Genetic Loci for Activated Partial Thromboplastin Time and Prothrombin Time. Blood, 2010, 116, 4222-4222.	0.6	0
146	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	1.5	184
147	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Human Molecular Genetics, 2009, 18, 373-380.	1.4	88
148	A Genome-Wide Association Scan of RR and QT Interval Duration in 3 European Genetically Isolated Populations. Circulation: Cardiovascular Genetics, 2009, 2, 322-328.	5.1	67
149	ParkScreen: A Low-Cost Rapid Linkage Marker Panel for Parkinsonâ€™s Disease. Journal of Molecular Neuroscience, 2009, 39, 235-241.	1.1	0
150	2q37 as a Susceptibility Locus for Idiopathic Basal Ganglia Calcification (IBGC) in a Large South Tyrolean Family. Journal of Molecular Neuroscience, 2009, 39, 346-353.	1.1	49
151	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
152	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	9.4	356
153	Genome-wide linkage analysis of serum creatinine in three isolated European populations. Kidney International, 2009, 76, 297-306.	2.6	71
154	Restless legs syndrome: an update on genetics and future perspectives. Clinical Genetics, 2008, 73, 297-305.	1.0	33
155	Informed Consent in the Genomics Era. PLoS Medicine, 2008, 5, e192.	3.9	81
156	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
157	PARK10 Candidate RNF11 Is Expressed by Vulnerable Neurons and Localizes to Lewy Bodies in Parkinson Disease Brain. Journal of Neuropathology and Experimental Neurology, 2007, 66, 955-964.	0.9	28
158	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	9.4	339
159	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
160	A genome wide linkage disequilibrium screen in Parkinsonâ€™s disease. Journal of Neurology, 2005, 252, 597-602.	1.8	7
161	A susceptibility gene for late-onset idiopathic Parkinson's disease. Annals of Neurology, 2002, 52, 549-555.	2.8	239
162	Familial Aggregation of Parkinson's Disease in Iceland. New England Journal of Medicine, 2000, 343, 1765-1770.	13.9	271

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163	Genomic mapping and evolution of human GABA A receptor subunit gene clusters. Mammalian Genome, 1999, 10, 839-843.	1.0	30
164	Increase in syntaxin 1B and glutamate release in mossy fibre terminals following induction of LTP in the dentate gyrus: a candidate molecular mechanism underlying transsynaptic plasticity. European Journal of Neuroscience, 1998, 10, 2231-2237.	1.2	32
165	Induction of Longâ€Term Potentiation In Vivo Regulates Alternate Splicing to Alter Syntaxin 3 Isoform Expression in Rat Dentate Gyrus. Journal of Neurochemistry, 1998, 71, 666-675.	2.1	21
166	Increase in Syntaxin 1B mRNA in Hippocampal and Cortical Circuits During Spatial Learning Reflects a Mechanism of Trans-synaptic Plasticity Involved in Establishing a Memory Trace. Learning and Memory, 1998, 5, 375-390.	0.5	24
167	Synapsin I and syntaxin 1B: Key elements in the control of neurotransmitter release are regulated by neuronal activation and long-term potentiation in vivo. Neuroscience, 1997, 79, 329-340.	1.1	66
168	A Gene Map of the Human Genome. Science, 1996, 274, 540-546.	6.0	985
169	Brain Structure and Task-specific Increase in Expression of the Gene Encoding Syntaxin 1B During Learning in the Rat: A Potential Molecular Marker for Learning-induced Synaptic Plasticity in Neural Networks. European Journal of Neuroscience, 1996, 8, 2068-2074.	1.2	32
170	Schizophrenia and GABAA receptor subunit genes. Psychiatric Genetics, 1995, 5, 23-30.	0.6	14
171	Further Evidence for Clustering of Human GABAA Receptor Subunit Genes: Localization of the Î±6-Subunit Gene (GABRA6) to Distal Chromosome 5q by Linkage Analysis. Genomics, 1994, 20, 285-288.	1.3	53
172	Analysis of GABAA receptor subunit genes in multiplex pedigrees with manic depression. Psychiatric Genetics, 1994, 4, 185-191.	0.6	18
173	Transsynaptic expression of a presynaptic glutamate receptor during hippocampal long-term potentiation. Science, 1993, 262, 433-436.	6.0	87
174	Confirmation of the localization of the human GABAA receptor Î±1-subunit gene (GABRA1) to distal 5q by linkage analysis. Genomics, 1992, 14, 745-748.	1.3	45
175	The chicken GABAA receptor Î±1 subunit: cDNA sequence and localization of the corresponding mRNA. Molecular Brain Research, 1991, 9, 333-339.	2.5	45
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