Peter P Pramstaller

List of Publications by Year
in descending order

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205 papers	42,208 citations	9264 74 h-index	2747 192 g-index
222 all docs	222 docs citations	222 times ranked	45177 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.	2.3	4
2	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	3.3	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.	0.7	1
4	Age, Sex, Body Mass Index, Diet and Menopause Related Metabolites in a Large Homogeneous Alpine Cohort. Metabolites, 2022, 12, 205.	2.9	18
5	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.	0.7	0
6	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.	5.4	1
7	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
8	Whole Exome Sequencing Enhanced Imputation Identifies 85 Metabolite Associations in the Alpine CHRIS Cohort. Metabolites, 2022, 12, 604.	2.9	6
9	Prevalence and determinants of serum antibodies to SARS-CoV-2 in the general population of the Gardena valley. Epidemiology and Infection, 2021, 149, e194.	2.1	8
10	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
11	Task matters - challenging the motor system allows distinguishing unaffected Parkin mutation carriers from mutation-free controls. Parkinsonism and Related Disorders, 2021, 86, 101-104.	2.2	6
12	Balancing scientific interests and the rights of participants in designing a recall by genotype study. European Journal of Human Genetics, 2021, 29, 1146-1157.	2.8	6
13	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
14	Return of research results (RoRR) to the healthy CHRIS cohort: designing a policy with the participants. Journal of Community Genetics, 2021, 12, 577-592.	1.2	6
15	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.	2.4	14
16	Generation of hiPSC-Derived Functional Dopaminergic Neurons in Alginate-Based 3D Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 708389.	3.7	13
17	Association between non-alcoholic fatty liver disease and impaired cardiac sympathetic/parasympathetic balance in subjects with and without type 2 diabetesâ€"The Cooperative Health Research in South Tyrol (CHRIS)-NAFLD sub-study. Nutrition, Metabolism and Cardiovascular Diseases, 2021, 31, 3464-3473.	2.6	14
18	Exome-wide association study of levodopa-induced dyskinesia in Parkinsonâ€™s disease. Scientific Reports, 2021, 11, 19582.	3.3	3

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19	Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. Biomolecules, 2021, 11, 1663.	4.0	5
20	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
21	Highly Elevated Plasma Î³â€Glutamyltransferase Elevations: A Trait Caused by Î³â€Glutamyltransferase 1 Transmembrane Mutations. Hepatology, 2020, 71, 1124-1127.	7.3	4
22	Alginate Formulations: Current Developments in the Race for Hydrogel-Based Cardiac Regeneration. Frontiers in Bioengineering and Biotechnology, 2020, 8, 414.	4.1	69
23	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
24	Silencing of CCR4-NOT complex subunits affect heart structure and function. DMM Disease Models and Mechanisms, 2020, 13, .	2.4	18
25	Kinase inhibition of G2019S-LRRK2 enhances autolysosome formation and function to reduce endogenous alpha-synuclein intracellular inclusions. Cell Death Discovery, 2020, 6, 45.	4.7	30
26	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	3.6	9
27	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
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.	0.7	11
29	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
30	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
31	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
32	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
33	Using global team science to identify genetic parkinson's disease worldwide. Annals of Neurology, 2019, 86, 153-157.	5.3	26
34	The Histone Deacetylase Inhibitor Suberoylanilide Hydroxamic Acid (SAHA) Restores Cardiomyocyte Contractility in a Rat Model of Early Diabetes. International Journal of Molecular Sciences, 2019, 20, 1873.	4.1	15
35	Effects of smoking status, history and intensity on heart rate variability in the general population: The CHRIS study. PLoS ONE, 2019, 14, e0215053.	2.5	33
36	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.	4.1	9

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37	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.	0.7	5
38	Microbiota, type 2 diabetes and non-alcoholic fatty liver disease: protocol of an observational study. Journal of Translational Medicine, 2019, 17, 408.	4.4	7
39	Comparative assessment of different familial aggregation methods in the context of large and unstructured pedigrees. Bioinformatics, 2019, 35, 69-76.	4.1	3
40	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.	2.0	14
41	The PPARGC1A locus and CNS-specific PGC-1Î± isoforms are associated with Parkinson's Disease. Neurobiology of Disease, 2019, 121, 34-46.	4.4	23
42	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
43	Are Requirements to Deposit Data in Research Repositories Compatible With the European Union's General Data Protection Regulation?. Annals of Internal Medicine, 2019, 170, 332.	3.9	27
44	A network-based meta-analysis for characterizing the genetic landscape of human aging. Biogerontology, 2018, 19, 81-94.	3.9	16
45	Generation of human induced pluripotent stem cells (EURACi001-A, EURACi002-A, EURACi003-A) from peripheral blood mononuclear cells of three patients carrying mutations in the CAV3 gene. Stem Cell Research, 2018, 27, 25-29.	0.7	4
46	Metabolic Signature of Dietary Iron Overload in a Mouse Model. Cells, 2018, 7, 264.	4.1	31
47	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
48	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.	6.2	326
49	Derivation of human induced pluripotent stem cell line EURACi004-A from skin fibroblasts of a patient with Arrhythmogenic Cardiomyopathy carrying the heterozygous PKP2 mutation c.2569_3018del50. Stem Cell Research, 2018, 32, 78-82.	0.7	2
50	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
51	Influence of collection tubes during quantitative targeted metabolomics studies in human blood samples. Clinica Chimica Acta, 2018, 486, 320-328.	1.1	44
52	Environmental and Genetic Variables Influencing Mitochondrial Health and Parkinsonâ€™s Disease Penetrance. Parkinson's Disease, 2018, 2018, 1-8.	1.1	13
53	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.	10.8	69
54	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71

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55	The arrhythmogenic cardiomyopathy-specific coding and non-coding transcriptome in human cardiac stromal cells. BMC Genomics, 2018, 19, 491.	2.8	21
56	HDAC Inhibition Improves the Sarcoendoplasmic Reticulum Ca2+-ATPase Activity in Cardiac Myocytes. International Journal of Molecular Sciences, 2018, 19, 419.	4.1	21
57	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.	1.4	15
58	A Web Resource for Levodopa-Induced Dyskinesia Genetics in Parkinsonâ€™s Disease. Neuroinformatics, 2017, 15, 297-300.	2.8	2
59	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
60	Sequential recruitment of study participants may inflate genetic heritability estimates. Human Genetics, 2017, 136, 743-757.	3.8	20
61	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.	2.9	48
62	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
63	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
64	Influence of L-dopa on subtle motor signs in heterozygous Parkin- and PINK1 mutation carriers. Parkinsonism and Related Disorders, 2017, 42, 95-99.	2.2	7
65	Exploring Approaches for Detecting Protein Functional Similarity within an Orthology-based Framework. Scientific Reports, 2017, 7, 381.	3.3	6
66	Pre-analytic evaluation of volumetric absorptive microsampling and integration in a mass spectrometry-based metabolomics workflow. Analytical and Bioanalytical Chemistry, 2017, 409, 6263-6276.	3.7	44
67	CADPS2 gene expression is oppositely regulated by LRRK2 and alpha-synuclein. Biochemical and Biophysical Research Communications, 2017, 490, 876-881.	2.1	17
68	Plasma and White Blood Cells Show Different miRNA Expression Profiles in Parkinsonâ€™s Disease. Journal of Molecular Neuroscience, 2017, 62, 244-254.	2.3	49
69	Abnormal premotorâ€“motor interaction in heterozygous Parkin - and Pink1 mutation carriers. Clinical Neurophysiology, 2017, 128, 275-280.	1.5	16
70	Elevated levels of alpha-synuclein blunt cellular signal transduction downstream of Gq protein-coupled receptors. Cellular Signalling, 2017, 30, 82-91.	3.6	9
71	The Impact of CRISPR/Cas9 Technology on Cardiac Research: From Disease Modelling to Therapeutic Approaches. Stem Cells International, 2017, 2017, 1-13.	2.5	36
72	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106

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73	SLP-2: a potential new target for improving mitochondrial function in Parkinson's disease. Neural Regeneration Research, 2017, 12, 1435.	3.0	4
74	Higher cardiogenic potential of iPSCs derived from cardiac versus skin stromal cells. Frontiers in Bioscience - Landmark, 2016, 21, 719-743.	3.0	13
75	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
76	Primary familial brain calcification in the â€˜IBGC2â€™ kindred: All linkage roads lead toSLC20A2. Movement Disorders, 2016, 31, 1901-1904.	3.9	16
77	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.	6.7	83
78	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
79	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
80	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
81	Serum iron level and kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2016, 32, gfw215.	0.7	23
82	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
83	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
84	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	4.4	63
85	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.	3.5	331
86	Haplotype analysis of the 4p16.3 region in Portuguese families with Huntington's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 135-143.	1.7	6
87	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
88	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
89	Generation of Induced Pluripotent Stem Cells from Frozen Buffy Coats using Non-integrating Episomal Plasmids. Journal of Visualized Experiments, 2015, , e52885.	0.3	17
90	Overexpression of blood microRNAs 103a, 30b, and 29a in <scp>l</scp> -dopaâ€“treated patients with PD. Neurology, 2015, 84, 645-653.	1.1	102

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91	Heterogeneous susceptibility for uraemic media calcification and concomitant inflammation within the arterial tree. Nephrology Dialysis Transplantation, 2015, 30, 1995-2005.	0.7	21
92	Acetylation mediates Cx43 reduction caused by electrical stimulation. Journal of Molecular and Cellular Cardiology, 2015, 87, 54-64.	1.9	15
93	Large-scale assessment of polyglutamine repeat expansions in Parkinson disease. Neurology, 2015, 85, 1283-1292.	1.1	25
94	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
95	Identification of a set of endogenous reference genes for miRNA expression studies in Parkinsonâ€™s disease blood samples. BMC Research Notes, 2014, 7, 715.	1.4	34
96	SNP-Based Linkage Analysis in Extended Pedigrees: Comparison between Two Alternative Approaches. Human Heredity, 2014, 78, 27-37.	0.8	1
97	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.	2.9	90
98	The Arachidonic Acid Metabolome Serves as a Conserved Regulator of Cholesterol Metabolism. Cell Metabolism, 2014, 20, 787-798.	16.2	92
99	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. BMC Endocrine Disorders, 2014, 14, 9.	2.2	440
100	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
101	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
102	Association between restless legs syndrome and migraine: a populationâ€based study. European Journal of Neurology, 2014, 21, 1205-1210.	3.3	26
103	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
104	Meta-analysis of genome-wide association studies identifies two loci associated with circulating osteoprotegerin levels. Human Molecular Genetics, 2014, 23, 6684-6693.	2.9	14
105	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.	2.3	12
106	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
107	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
108	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13

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109	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14
110	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
111	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
112	Plasma phosphatidylcholine and sphingomyelin concentrations are associated with depression and anxiety symptoms in a Dutch family-based lipidomics study. Journal of Psychiatric Research, 2013, 47, 357-362.	3.1	115
113	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
114	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
115	Involvement of proprotein convertase PCSK7 in the regulation of systemic iron homeostasis. Hepatology, 2013, 58, 1860-1861.	7.3	4
116	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
117	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.	3.5	194
118	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	8.4	116
119	Estimating the Glomerular Filtration Rate in the General Population Using Different Equations: Effects on Classification and Association. Nephron Clinical Practice, 2013, 123, 102-111.	2.3	33
120	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	2.5	38
121	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
122	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
123	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
124	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	3.5	190
125	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.	3.5	419
126	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64

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127	Methods for Meta-Analyses of Genome-wide Association Studies: Critical Assessment of Empirical Evidence. American Journal of Epidemiology, 2012, 175, 739-749.	3.4	42
128	Genome-wide analysis of epistasis in body mass index using multiple human populations. European Journal of Human Genetics, 2012, 20, 857-862.	2.8	33
129	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
130	"Patientcentricity": An Editorial. Studies in Ethics, Law, and Technology, 2012, 6, .	0.3	0
131	GWAtoolbox: an R package for fast quality control and handling of genome-wide association studies meta-analysis data. Bioinformatics, 2012, 28, 444-445.	4.1	46
132	Exome sequencing in a family with restless legs syndrome. Movement Disorders, 2012, 27, 1686-1689.	3.9	22
133	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.	3.2	94
134	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
135	Large-scale replication and heterogeneity in Parkinson disease genetic loci. Neurology, 2012, 79, 659-667.	1.1	119
136	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.	6.2	85
137	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
138	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
139	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
140	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. PLoS ONE, 2012, 7, e46501.	2.5	111
141	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.	21.4	762
142	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.	6.2	205
143	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	2.5	3
144	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

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145	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
146	Mutations in PINK1 and Parkin Impair Ubiquitination of Mitofusins in Human Fibroblasts. PLoS ONE, 2011, 6, e16746.	2.5	209
147	Copy Number Variation across European Populations. PLoS ONE, 2011, 6, e23087.	2.5	25
148	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	2.8	23
149	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.	2.3	44
150	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
151	Variants in STAT5B Associate with Serum TC and LDL-C Levels. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E1496-E1501.	3.6	5
152	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.	3.2	6
153	Heritability Analysis of Life Span in a Semi-isolated Population Followed Across Four Centuries Reveals the Presence of Pleiotropy Between Life Span and Reproduction. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2011, 66A, 26-37.	3.6	44
154	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.	2.9	47
155	Novel association to the proprotein convertase PCSK7 gene locus revealed by analysing soluble transferrin receptor (sTfR) levels. Human Molecular Genetics, 2011, 20, 1042-1047.	2.9	62
156	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.	2.9	67
157	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. PLoS Genetics, 2011, 7, e1002333.	3.5	29
158	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	2.5	15
159	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.	1.7	3
160	Copy number variation and association over T-cell receptor genesâ€”influence of DNA source. Immunogenetics, 2010, 62, 561-567.	2.4	14
161	Structural imaging in the presymptomatic stage of genetically determined parkinsonism. Neurobiology of Disease, 2010, 39, 402-408.	4.4	43
162	Nonmotor symptoms in Parkin geneâ€related parkinsonism. Movement Disorders, 2010, 25, 1279-1284.	3.9	31

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163	Impaired sense of smell and color discrimination in monogenic and idiopathic Parkinson's disease. Movement Disorders, 2010, 25, 2665-2669.	3.9	53
164	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2with serum creatinine level. BMC Medical Genetics, 2010, 11, 41.	2.1	48
165	Drawing the history of the Hutterite population on a genetic landscape: inference from Y-chromosome and mtDNA genotypes. European Journal of Human Genetics, 2010, 18, 463-470.	2.8	26
166	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	2.8	22
167	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
168	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
169	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
170	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
171	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.	21.4	836
172	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
173	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
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