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	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	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
5	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
6	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
7	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
8	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
9	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
10	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
11	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	21.4	776
12	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
13	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
14	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
15	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
16	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
17	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
18	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549

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19	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
20	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
21	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
22	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
23	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
24	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
25	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
26	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
27	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
28	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
29	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
30	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
31	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
32	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
33	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
34	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
35	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
36	Positron emission tomographic analysis of the nigrostriatal dopaminergic system in familial Parkinsonism associated with mutations in theParkin gene. Annals of Neurology, 2001, 49, 367-376.	5.3	257

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37	Lewy body Parkinson's disease in a large pedigree with 77Parkin mutation carriers. Annals of Neurology, 2005, 58, 411-422.	5.3	252
38	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
39	Parkin deletions in a family with adult-onset, tremor-dominant parkinsonism: Expanding the phenotype. Annals of Neurology, 2000, 48, 65-71.	5.3	247
40	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	3.5	230
41	Distribution, type, and origin ofParkin mutations: Review and case studies. Movement Disorders, 2004, 19, 1146-1157.	3.9	219
42	Corticobasal degeneration shares a common genetic background with progressive supranuclear palsy. Annals of Neurology, 2000, 47, 374-377.	5.3	216
43	Mutations in PINK1 and Parkin Impair Ubiquitination of Mitofusins in Human Fibroblasts. PLoS ONE, 2011, 6, e16746.	2.5	209
44	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
45	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
46	A Global In Vivo Drosophila RNAi Screen Identifies NOT3 as a Conserved Regulator of Heart Function. Cell, 2010, 141, 142-153.	28.9	199
47	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
48	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
49	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
50	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
51	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	3.5	184
52	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
53	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
54	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166

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55	Novel mutation in the TOR1A (DYT1) gene in atypical, early onset dystonia and polymorphisms in dystonia and early onset parkinsonism. Neurogenetics, 2001, 3, 133-143.	1.4	155
56	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
57	Mutant Parkin Impairs Mitochondrial Function and Morphology in Human Fibroblasts. PLoS ONE, 2010, 5, e12962.	2.5	140
58	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
59	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
60	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
61	Large-scale replication and heterogeneity in Parkinson disease genetic loci. Neurology, 2012, 79, 659-667.	1.1	119
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	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	8.4	116
64	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
65	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
66	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. PLoS ONE, 2012, 7, e46501.	2.5	111
67	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
68	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
69	Linkage Analysis Identifies a Novel Locus for Restless Legs Syndrome on Chromosome 2q in a South Tyrolean Population Isolate. American Journal of Human Genetics, 2006, 79, 716-723.	6.2	101
70	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
71	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
72	The Arachidonic Acid Metabolome Serves as a Conserved Regulator of Cholesterol Metabolism. Cell Metabolism, 2014, 20, 787-798.	16.2	92

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73	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
74	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
75	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
76	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
77	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€‐ and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
78	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
79	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
80	Genome-wide linkage analysis of serum creatinine in three isolated European populations. Kidney International, 2009, 76, 297-306.	5.2	71
81	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
82	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
83	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
84	Alginate Formulations: Current Developments in the Race for Hydrogel-Based Cardiac Regeneration. Frontiers in Bioengineering and Biotechnology, 2020, 8, 414.	4.1	69
85	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
86	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
87	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
88	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	4.4	63
89	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
90	Suggestive evidence for linkage for restless legs syndrome on chromosome 19p13. Neurogenetics, 2008, 9, 75-82.	1.4	61

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91	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
92	The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. BMC Medical Genetics, 2007, 8, 29.	2.1	56
93	Impaired sense of smell and color discrimination in monogenic and idiopathic Parkinson's disease. Movement Disorders, 2010, 25, 2665-2669.	3.9	53
94	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.	3.5	51
95	Structural findings in the basal ganglia in genetically determined and idiopathic Parkinson's disease. Movement Disorders, 2009, 24, 99-103.	3.9	50
96	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.	2.3	49
97	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
98	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
99	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
100	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
101	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
102	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
103	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
104	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
105	Influence of collection tubes during quantitative targeted metabolomics studies in human blood samples. Clinica Chimica Acta, 2018, 486, 320-328.	1.1	44
106	Structural imaging in the presymptomatic stage of genetically determined parkinsonism. Neurobiology of Disease, 2010, 39, 402-408.	4.4	43
107	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
108	Co-occurrence of restless legs syndrome andParkin mutations in two families. Movement Disorders, 2006, 21, 258-263.	3.9	38

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109	Restless legs syndrome: Epidemiological and clinicogenetic study in a South Tyrolean population isolate. Movement Disorders, 2006, 21, 1189-1195.	3.9	38
110	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	2.5	38
111	Frequency of heterozygous Parkin mutations in healthy subjects: Need for careful prospective follow-up examination of mutation carriers. Parkinsonism and Related Disorders, 2009, 15, 425-429.	2.2	37
112	Clinical and genetic evaluation of a family with a mixed dystonia phenotype from south tyrol. Annals of Neurology, 1998, 44, 394-398.	5.3	36
113	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
114	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
115	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
116	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
117	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
118	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
119	Nonmotor symptoms in Parkin geneâ€related parkinsonism. Movement Disorders, 2010, 25, 1279-1284.	3.9	31
120	Metabolic Signature of Dietary Iron Overload in a Mouse Model. Cells, 2018, 7, 264.	4.1	31
121	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
122	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
123	Phenotypic variability in a large kindred (Family LA) with deletions in theparkin gene. Movement Disorders, 2002, 17, 424-426.	3.9	27
124	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
125	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
126	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

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127	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
128	Association between restless legs syndrome and migraine: a populationâ€based study. European Journal of Neurology, 2014, 21, 1205-1210.	3.3	26
129	Using global team science to identify genetic parkinson's disease worldwide. Annals of Neurology, 2019, 86, 153-157.	5.3	26
130	Copy Number Variation across European Populations. PLoS ONE, 2011, 6, e23087.	2.5	25
131	Large-scale assessment of polyglutamine repeat expansions in Parkinson disease. Neurology, 2015, 85, 1283-1292.	1.1	25
132	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	2.8	23
133	Serum iron level and kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2016, 32, gfw215.	0.7	23
134	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
135	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	2.8	22
136	Exome sequencing in a family with restless legs syndrome. Movement Disorders, 2012, 27, 1686-1689.	3.9	22
137	Heterogeneous susceptibility for uraemic media calcification and concomitant inflammation within the arterial tree. Nephrology Dialysis Transplantation, 2015, 30, 1995-2005.	0.7	21
138	The arrhythmogenic cardiomyopathy-specific coding and non-coding transcriptome in human cardiac stromal cells. BMC Genomics, 2018, 19, 491.	2.8	21
139	HDAC Inhibition Improves the Sarcoendoplasmic Reticulum Ca2+-ATPase Activity in Cardiac Myocytes. International Journal of Molecular Sciences, 2018, 19, 419.	4.1	21
140	Sequential recruitment of study participants may inflate genetic heritability estimates. Human Genetics, 2017, 136, 743-757.	3.8	20
141	Silencing of CCR4-NOT complex subunits affect heart structure and function. DMM Disease Models and Mechanisms, 2020, 13, .	2.4	18
142	Age, Sex, Body Mass Index, Diet and Menopause Related Metabolites in a Large Homogeneous Alpine Cohort. Metabolites, 2022, 12, 205.	2.9	18
143	Genetic Structure in Contemporary South Tyrolean Isolated Populations Revealed by Analysis of Y-Chromosome, mtDNA, and Alu Polymorphisms. Human Biology, 2006, 78, 441-464.	0.2	17
144	Generation of Induced Pluripotent Stem Cells from Frozen Buffy Coats using Non-integrating Episomal Plasmids. Journal of Visualized Experiments, 2015, , e52885.	0.3	17

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145	CADPS2 gene expression is oppositely regulated by LRRK2 and alpha-synuclein. Biochemical and Biophysical Research Communications, 2017, 490, 876-881.	2.1	17
146	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
147	Primary familial brain calcification in the â€˜IBGC2â€™ kindred: All linkage roads lead toSLC20A2. Movement Disorders, 2016, 31, 1901-1904.	3.9	16
148	Abnormal premotorâ€“motor interaction in heterozygous Parkin - and Pink1 mutation carriers. Clinical Neurophysiology, 2017, 128, 275-280.	1.5	16
149	A network-based meta-analysis for characterizing the genetic landscape of human aging. Biogerontology, 2018, 19, 81-94.	3.9	16
150	Acetylation mediates Cx43 reduction caused by electrical stimulation. Journal of Molecular and Cellular Cardiology, 2015, 87, 54-64.	1.9	15
151	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
152	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
153	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
154	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	2.5	15
155	Copy number variation and association over T-cell receptor genesâ€”influence of DNA source. Immunogenetics, 2010, 62, 561-567.	2.4	14
156	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14
157	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
158	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
159	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
160	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
161	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13
162	Higher cardiogenic potential of iPSCs derived from cardiac versus skin stromal cells. Frontiers in Bioscience - Landmark, 2016, 21, 719-743.	3.0	13

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163	Environmental and Genetic Variables Influencing Mitochondrial Health and Parkinsonâ€™s Disease Penetrance. Parkinson's Disease, 2018, 2018, 1-8.	1.1	13
164	Generation of hiPSC-Derived Functional Dopaminergic Neurons in Alginate-Based 3D Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 708389.	3.7	13
165	Imaging movement-related activity in medicated Parkin-associated and sporadic Parkinsonâ€™s disease. Parkinsonism and Related Disorders, 2010, 16, 384-387.	2.2	12
166	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
167	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
168	Exclusion of linkage to chromosome 14q in a large South Tyrolean family with idiopathic basal ganglia calcification (IBGC). American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1319-1322.	1.7	10
169	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	3.3	10
170	Elevated levels of alpha-synuclein blunt cellular signal transduction downstream of Gq protein-coupled receptors. Cellular Signalling, 2017, 30, 82-91.	3.6	9
171	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	3.6	9
172	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
173	PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. Bioinformatics, 2008, 24, 279-281.	4.1	8
174	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
175	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
176	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
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