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	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	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
6	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
7	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
8	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
10	A Gene Map of the Human Genome. Science, 1996, 274, 540-546.	6.0	985
11	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
12	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
13	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
14	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
15	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
16	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
17	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
18	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675

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19	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
20	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
21	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
22	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
23	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
24	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
25	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
26	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
27	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
28	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
29	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
30	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	9.4	356
31	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
32	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
33	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
34	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
35	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
36	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308

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37	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
38	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
39	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
40	Familial Aggregation of Parkinson's Disease in Iceland. New England Journal of Medicine, 2000, 343, 1765-1770.	13.9	271
41	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
42	A susceptibility gene for late-onset idiopathic Parkinson's disease. Annals of Neurology, 2002, 52, 549-555.	2.8	239
43	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
44	Modeling Parkinsonâ€™s disease in midbrain-like organoids. Npj Parkinson's Disease, 2019, 5, 5.	2.5	204
45	A Global In Vivo Drosophila RNAi Screen Identifies NOT3 as a Conserved Regulator of Heart Function. Cell, 2010, 141, 142-153.	13.5	199
46	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
47	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
48	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
49	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	1.5	184
50	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
51	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
52	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
53	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
54	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

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55	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	1.4	133
56	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
57	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
58	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
59	Large-scale replication and heterogeneity in Parkinson disease genetic loci. Neurology, 2012, 79, 659-667.	1.5	119
60	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	3.9	116
61	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
62	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. PLoS ONE, 2012, 7, e46501.	1.1	111
63	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
64	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
65	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
66	The Arachidonic Acid Metabolome Serves as a Conserved Regulator of Cholesterol Metabolism. Cell Metabolism, 2014, 20, 787-798.	7.2	92
67	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
68	Interleukin-6 Signaling Effects on Ischemic Stroke and Other Cardiovascular Outcomes. Circulation Genomic and Precision Medicine, 2020, 13, e002872.	1.6	90
69	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
70	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
71	Transsynaptic expression of a presynaptic glutamate receptor during hippocampal long-term potentiation. Science, 1993, 262, 433-436.	6.0	87
72	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87

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73	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
74	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
75	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
76	Informed Consent in the Genomics Era. PLoS Medicine, 2008, 5, e192.	3.9	81
77	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
78	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
79	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
80	Genome-wide linkage analysis of serum creatinine in three isolated European populations. Kidney International, 2009, 76, 297-306.	2.6	71
81	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
82	Distinct regional expression of nicotinic acetylcholine receptor genes in chick brain. Molecular Brain Research, 1990, 7, 305-315.	2.5	70
83	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
84	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
85	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
86	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
87	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
88	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
89	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	1.8	63
90	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

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91	Plasmid-normalized quantification of relative mitochondrial DNA copy number. Scientific Reports, 2018, 8, 15347.	1.6	61
92	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
93	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
94	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
95	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
96	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
97	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
98	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
99	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
100	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
101	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
102	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
103	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
104	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
105	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
106	Influence of collection tubes during quantitative targeted metabolomics studies in human blood samples. Clinica Chimica Acta, 2018, 486, 320-328.	0.5	44
107	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	1.1	38
108	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

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109	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
110	Restless legs syndrome: an update on genetics and future perspectives. Clinical Genetics, 2008, 73, 297-305.	1.0	33
111	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
112	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
113	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
114	Genomic mapping and evolution of human GABA A receptor subunit gene clusters. Mammalian Genome, 1999, 10, 839-843.	1.0	30
115	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
116	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
117	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
118	Dihydroceramide- and ceramide-profiling provides insights into human cardiometabolic disease etiology. Nature Communications, 2022, 13, 936.	5.8	28
119	Dinucleotide repeat polymorphism in the human X-linked GABAAreceptora3-subunit gene. Nucleic Acids Research, 1991, 19, 4016-4016.	6.5	27
120	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	1.4	27
121	Copy Number Variation across European Populations. PLoS ONE, 2011, 6, e23087.	1.1	25
122	Large-scale assessment of polyglutamine repeat expansions in Parkinson disease. Neurology, 2015, 85, 1283-1292.	1.5	25
123	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	3.0	24
124	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
125	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
126	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

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127	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	1.4	22
128	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
129	Analysis of GABAA receptor subunit genes in multiplex pedigrees with manic depression. Psychiatric Genetics, 1994, 4, 185-191.	0.6	18
130	PLA2G6mutations and Parkinsonism: Long-term follow-up of clinical features and neuropathology. Movement Disorders, 2016, 31, 1927-1929.	2.2	18
131	Silencing of CCR4-NOT complex subunits affect heart structure and function. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	18
132	Generation of Induced Pluripotent Stem Cells from Frozen Buffy Coats using Non-integrating Episomal Plasmids. Journal of Visualized Experiments, 2015, , e52885.	0.2	17
133	CADPS2 gene expression is oppositely regulated by LRRK2 and alpha-synuclein. Biochemical and Biophysical Research Communications, 2017, 490, 876-881.	1.0	17
134	Evaluation of the role of STAP1 in Familial Hypercholesterolemia. Scientific Reports, 2019, 9, 11995.	1.6	17
135	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
136	Primary familial brain calcification in the â€˜IBGC2â€™ kindred: All linkage roads lead toSLC20A2. Movement Disorders, 2016, 31, 1901-1904.	2.2	16
137	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
138	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	1.1	15
139	Schizophrenia and GABAA receptor subunit genes. Psychiatric Genetics, 1995, 5, 23-30.	0.6	14
140	Copy number variation and association over T-cell receptor genesâ€”influence of DNA source. Immunogenetics, 2010, 62, 561-567.	1.2	14
141	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	0.6	14
142	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
143	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
144	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

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145	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	0.6	13
146	Environmental and Genetic Variables Influencing Mitochondrial Health and Parkinsonâ€™s Disease Penetrance. Parkinson's Disease, 2018, 2018, 1-8.	0.6	13
147	Genetic variants in levodopa-induced dyskinesia (LID): A systematic review and meta-analysis. Parkinsonism and Related Disorders, 2021, 84, 52-60.	1.1	13
148	Generation of hiPSC-Derived Functional Dopaminergic Neurons in Alginate-Based 3D Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 708389.	1.8	13
149	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
150	32-channel time-correlated-single-photon-counting system for high-throughput lifetime imaging. Review of Scientific Instruments, 2017, 88, 083704.	0.6	11
151	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
152	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
153	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
154	Elevated levels of alpha-synuclein blunt cellular signal transduction downstream of Gq protein-coupled receptors. Cellular Signalling, 2017, 30, 82-91.	1.7	9
155	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	1.6	9
156	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
157	A genome wide linkage disequilibrium screen in Parkinsonâ€™s disease. Journal of Neurology, 2005, 252, 597-602.	1.8	7
158	The SZT2 Interactome Unravels New Functions of the KICSTOR Complex. Cells, 2021, 10, 2711.	1.8	7
159	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
160	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
161	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
162	Variants in STAT5B Associate with Serum TC and LDL-C Levels. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E1496-E1501.	1.8	5

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163	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
164	Involvement of proprotein convertase PCSK7 in the regulation of systemic iron homeostasis. Hepatology, 2013, 58, 1860-1861.	3.6	4
165	SLP-2: a potential new target for improving mitochondrial function in Parkinson's disease. Neural Regeneration Research, 2017, 12, 1435.	1.6	4
166	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
167	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
168	Update on the management of restless legs syndrome: existing and emerging treatment options. Nature and Science of Sleep, 2010, 2, 199.	1.4	3
169	Exome-wide association study of levodopa-induced dyskinesia in Parkinsonâ€™s disease. Scientific Reports, 2021, 11, 19582.	1.6	3
170	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
171	Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. Human Molecular Genetics, 2022, , .	1.4	3
172	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
173	Caenorhabditis elegans Parkin: Regulators of its abundance and role in autophagy-lysosomal dynamics. Open Research Europe, 0, 2, 23.	2.0	1
174	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
175	ParkScreen: A Low-Cost Rapid Linkage Marker Panel for Parkinsonâ€™s Disease. Journal of Molecular Neuroscience, 2009, 39, 235-241.	1.1	0
176	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
177	Genome-Wide Association Study Identifies Multiple Genetic Loci for Activated Partial Thromboplastin Time and Prothrombin Time. Blood, 2010, 116, 4222-4222.	0.6	0
178	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