

# Alexanda Teumer

## List of Publications by Year in descending order

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Version: 2024-02-01

318  
papers

57,785  
citations

1798

103  
h-index

1595

216  
g-index

366  
all docs

366  
docs citations

366  
times ranked

59539  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
3	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
4	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
5	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
6	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	9.4	1,544
7	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
8	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
9	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	9.4	1,104
10	A mega-analysis of genome-wide association studies for major depressive disorder. <i>Molecular Psychiatry</i> , 2013, 18, 497-511.	4.1	1,002
11	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
12	Cohort Profile: The Study of Health in Pomerania. <i>International Journal of Epidemiology</i> , 2011, 40, 294-307.	0.9	876
13	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
14	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015, 520, 224-229.	13.7	772
15	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
16	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 376-384.	9.4	710
17	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. <i>Brain Imaging and Behavior</i> , 2014, 8, 153-182.	1.1	696
18	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675

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19	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	13.7	640
20	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012, 44, 552-561.	9.4	594
21	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	9.4	590
22	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	9.4	581
23	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
24	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. <i>PLoS Genetics</i> , 2009, 5, e1000504.	1.5	572
25	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
26	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
27	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
28	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
29	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
30	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
31	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. <i>Nature Genetics</i> , 2009, 41, 1182-1190.	9.4	481
32	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
33	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. <i>Circulation</i> , 2011, 123, 731-738.	1.6	461
34	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	6.0	450
35	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
36	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412

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37	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	13.7	401
38	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
39	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
40	Meta-analysis of genome-wide association studies of anxiety disorders. <i>Molecular Psychiatry</i> , 2016, 21, 1391-1399.	4.1	373
41	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
42	ENIGMA and global neuroscience: A decade of large-scale studies of the brain in health and disease across more than 40 countries. <i>Translational Psychiatry</i> , 2020, 10, 100.	2.4	365
43	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
44	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
45	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
46	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
47	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 2009, 41, 1191-1198.	9.4	324
48	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
49	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. <i>PLoS Genetics</i> , 2010, 6, e1001177.	1.5	312
50	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010, 42, 1068-1076.	9.4	308
51	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2017, 5, 97-105.	5.5	298
52	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	6.0	289
53	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
54	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279

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55	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
56	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	5.8	250
57	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
58	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
59	A genome-wide association study of metabolic traits in human urine. <i>Nature Genetics</i> , 2011, 43, 565-569.	9.4	224
60	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	9.4	215
61	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	7.1	213
62	Moderation of Adult Depression by a Polymorphism in the FKBP5 Gene and Childhood Physical Abuse in the General Population. <i>Neuropsychopharmacology</i> , 2011, 36, 1982-1991.	2.8	209
63	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	3.0	208
64	<i>KLB</i> is associated with alcohol drinking, and its gene product $\beta$ -Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	3.3	208
65	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , 2016, 19, 420-431.	7.1	204
66	Genetic Variants Associated With Cardiac Structure and Function. <i>JAMA - Journal of the American Medical Association</i> , 2009, 302, 168.	3.8	202
67	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	9.4	192
68	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773.	5.8	183
69	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
70	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	5.8	181
71	Genetic Determinants of Serum Testosterone Concentrations in Men. <i>PLoS Genetics</i> , 2011, 7, e1002313.	1.5	178
72	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178

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73	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017, 81, 325-335.	0.7	175
74	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. <i>JAMA Psychiatry</i> , 2017, 74, 1214.	6.0	174
75	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
76	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. <i>PLoS Genetics</i> , 2011, 7, e1002292.	1.5	172
77	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. <i>ELife</i> , 2019, 8, .	2.8	170
78	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
79	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
80	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	1.5	166
81	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.	5.1	162
82	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
83	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormone-Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. <i>PLoS Genetics</i> , 2012, 8, e1002805.	1.5	151
84	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. <i>PLoS Genetics</i> , 2014, 10, e1004123.	1.5	150
85	A Genome-Wide Association Study of Depressive Symptoms. <i>Biological Psychiatry</i> , 2013, 73, 667-678.	0.7	149
86	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 2044.	3.8	143
87	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. <i>Alzheimer's and Dementia</i> , 2018, 14, 707-722.	0.4	143
88	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	1.5	142
89	Identification of Genetic Loci Associated With <i>Helicobacter pylori</i> Serologic Status. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1912.	3.8	142
90	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. <i>European Heart Journal</i> , 2014, 35, 1069-1077.	1.0	137

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91	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
92	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	4.1	134
93	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
94	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
95	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
96	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	4.9	130
97	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. <i>Circulation</i> , 2013, 128, 1310-1324.	1.6	128
98	White Blood Cells and Blood Pressure. <i>Circulation</i> , 2020, 141, 1307-1317.	1.6	125
99	Genome-wide association study of chronic periodontitis in a general German population. <i>Journal of Clinical Periodontology</i> , 2013, 40, 977-985.	2.3	123
100	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
101	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018, 9, 5141.	5.8	119
102	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. <i>Human Molecular Genetics</i> , 2013, 22, 3597-3607.	1.4	116
103	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020, 25, 1430-1446.	4.1	116
104	Asymmetry within and around the human planum temporale is sexually dimorphic and influenced by genes involved in steroid hormone receptor activity. <i>Cortex</i> , 2015, 62, 41-55.	1.1	114
105	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. <i>Nature Genetics</i> , 2014, 46, 629-634.	9.4	113
106	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015, 87, 1017-1029.	2.6	113
107	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012, 17, 1116-1129.	4.1	112
108	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 427-436.	0.5	112

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109	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. <i>Molecular Psychiatry</i> , 2015, 20, 1232-1239.	4.1	112
110	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	3.3	110
111	Cystatin C and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2016, 68, 934-945.	1.2	109
112	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	5.8	108
113	Multiple Loci Are Associated with White Blood Cell Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002113.	1.5	106
114	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.	2.6	106
115	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
116	Measuring Biological Age via Metabonomics: The Metabolic Age Score. <i>Journal of Proteome Research</i> , 2016, 15, 400-410.	1.8	105
117	Common Methods for Performing Mendelian Randomization. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 51.	1.1	105
118	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. <i>Neuron</i> , 2015, 86, 1189-1202.	3.8	102
119	Childhood maltreatment, the corticotropin-releasing hormone receptor gene and adult depression in the general population. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 1483-1493.	1.1	98
120	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 100-112.	5.1	98
121	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	1.6	98
122	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
123	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. <i>Psychological Science</i> , 2014, 25, 1975-1986.	1.8	92
124	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. <i>Human Molecular Genetics</i> , 2014, 23, 3054-3068.	1.4	90
125	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	89
126	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89



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127	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	5.8	89
128	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	6.0	88
129	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. <i>PLoS Genetics</i> , 2011, 7, e1002025.	1.5	87
130	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. <i>Human Molecular Genetics</i> , 2017, 26, 2577-2588.	1.4	87
131	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	0.7	87
132	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019, 29, 120-127.e5.	1.8	86
133	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. <i>Nature Communications</i> , 2020, 11, 3981.	5.8	86
134	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	0.7	84
135	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
136	Genomewide meta-analysis identifies loci associated with $IGF$ and $IGFBP$ levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	3.0	83
137	Fucosyltransferase 2 (FUT2) non-secretor status and blood group B are associated with elevated serum lipase activity in asymptomatic subjects, and an increased risk for chronic pancreatitis: a genetic association study. <i>Gut</i> , 2015, 64, 646-656.	6.1	82
138	Association of Telomere Length With Risk of Disease and Mortality. <i>JAMA Internal Medicine</i> , 2022, 182, 291.	2.6	81
139	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	1.5	80
140	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
141	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	6.2	75
142	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	5.8	75
143	Genetic variants associated with longitudinal changes in brain structure across the lifespan. <i>Nature Neuroscience</i> , 2022, 25, 421-432.	7.1	75
144	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. <i>Gastroenterology</i> , 2016, 151, 351-363.e28.	0.6	74

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145	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
146	Genetic epistasis between the brain-derived neurotrophic factor Val66Met polymorphism and the 5-HTT promoter polymorphism moderates the susceptibility to depressive disorders after childhood abuse. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2012, 36, 264-270.	2.5	73
147	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. <i>American Journal of Human Genetics</i> , 2014, 95, 49-65.	2.6	73
148	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
149	Cohort Profile Update: The Study of Health in Pomerania (SHIP). <i>International Journal of Epidemiology</i> , 2022, 51, e372-e383.	0.9	73
150	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. <i>Archives of General Psychiatry</i> , 2012, 69, 854.	13.8	71
151	Analyzing Illumina Gene Expression Microarray Data from Different Tissues: Methodological Aspects of Data Analysis in the MetaXpress Consortium. <i>PLoS ONE</i> , 2012, 7, e50938.	1.1	71
152	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	5.8	71
153	A bidirectional Mendelian randomization study supports causal effects of kidney function on blood pressure. <i>Kidney International</i> , 2020, 98, 708-716.	2.6	70
154	A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. <i>Human Molecular Genetics</i> , 2011, 20, 1241-1251.	1.4	67
155	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	0.7	67
156	Multiethnic Meta-Analysis Identifies <i>RAI1</i> as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 391-401.	1.4	65
157	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	1.4	64
158	Myocardial gene expression profiles and cardiodepressant autoantibodies predict response of patients with dilated cardiomyopathy to immunoadsorption therapy. <i>European Heart Journal</i> , 2013, 34, 666-675.	1.0	64
159	Genetic effects influencing risk for major depressive disorder in China and Europe. <i>Translational Psychiatry</i> , 2017, 7, e1074-e1074.	2.4	64
160	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
161	Liver Phenotypes of European Adults Heterozygous or Homozygous for Pi <sup>1</sup> -Z Variant of AAT (Pi <sup>1</sup> -MZ vs Tj ETQq <sup>1</sup> 0.784314 rgB / 0.6 63	0.6	63
162	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61

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