Daniel I Chasman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8787748/publications.pdf

Version: 2024-02-01

218 papers 53,815 citations

83 h-index 210 g-index

232 all docs 232 docs citations

times ranked

232

58402 citing authors

#	Article	IF	CITATIONS
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
5	A comprehensive 1000 Genomes–based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
6	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	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.	21.4	1,818
8	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
9	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	21.4	1,285
10	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
11	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
12	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
13	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
14	Genetic Risk, Adherence to a Healthy Lifestyle, and Coronary Disease. New England Journal of Medicine, 2016, 375, 2349-2358.	27.0	979
15	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
16	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
17	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
18	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552

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19	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
20	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
21	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
22	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520
23	Sugar-Sweetened Beverages and Genetic Risk of Obesity. New England Journal of Medicine, 2012, 367, 1387-1396.	27.0	517
24	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21,4	492
25	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
26	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21,4	470
27	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
28	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
29	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
30	Pharmacogenetic Study of Statin Therapy and Cholesterol Reduction. JAMA - Journal of the American Medical Association, 2004, 291, 2821.	7.4	407
31	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
32	Genome-wide association studies identify four ER negative–specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21,4	374
33	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
34	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
35	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
36	Genome-wide association study reveals three susceptibility loci for common migraine in the general population. Nature Genetics, 2011, 43, 695-698.	21.4	355

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37	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
38	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
39	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338
40	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
41	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
42	Forty-Three Loci Associated with Plasma Lipoprotein Size, Concentration, and Cholesterol Content in Genome-Wide Analysis. PLoS Genetics, 2009, 5, e1000730.	3.5	300
43	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
44	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
45	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
46	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
47	Genetic Determinants of Statin-Induced Low-Density Lipoprotein Cholesterol Reduction. Circulation: Cardiovascular Genetics, 2012, 5, 257-264.	5.1	231
48	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
49	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	21.4	227
50	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
51	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
52	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
53	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
54	$\langle i \rangle$ KLB $\langle i \rangle$ is associated with alcohol drinking, and its gene product \hat{l}^2 -Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208

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55	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	12.8	183
56	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
57	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
58	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
59	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
60	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
61	Rationale, Design, and Methodology of the Women's Genome Health Study: A Genome-Wide Association Study of More Than 25 000 Initially Healthy American Women. Clinical Chemistry, 2008, 54, 249-255.	3.2	167
62	Novel locus including FGF21 is associated with dietary macronutrient intake. Human Molecular Genetics, 2013, 22, 1895-1902.	2.9	167
63	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
64	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
65	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	21.4	158
66	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
67	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
68	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
69	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
70	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144
71	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	21.4	135
72	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	2.8	127

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73	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
74	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
75	Genetic Loci Associated With Plasma Concentration of Low-Density Lipoprotein Cholesterol, High-Density Lipoprotein Cholesterol, Triglycerides, Apolipoprotein A1, and Apolipoprotein B Among 6382 White Women in Genome-Wide Analysis With Replication. Circulation: Cardiovascular Genetics, 2008. 1. 21-30.	5.1	117
76	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
77	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
78	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
79	A genome-wide association study of bitter and sweet beverage consumption. Human Molecular Genetics, 2019, 28, 2449-2457.	2.9	108
80	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
81	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
82	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99
83	Atherogenic Lipoprotein Determinants of Cardiovascular Disease and Residual Risk Among Individuals With Low Lowâ€Density Lipoprotein Cholesterol. Journal of the American Heart Association, 2017, 6, .	3.7	98
84	Genetic Obesity and the Risk of Atrial Fibrillation. Circulation, 2017, 135, 741-754.	1.6	96
85	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
86	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.1	91
87	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
88	Cumulative psychological stress and cardiovascular disease risk in middle aged and older women: Rationale, design, and baseline characteristics. American Heart Journal, 2017, 192, 1-12.	2.7	90
89	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
90	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84

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91	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
92	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
93	Association of Variation at the <i>ABO</i> Locus With Circulating Levels of Soluble Intercellular Adhesion Molecule-1, Soluble P-selectin, and Soluble E-selectin. Circulation: Cardiovascular Genetics, 2011, 4, 681-686.	5.1	77
94	Genome-Wide Association Analysis of Soluble ICAM-1 Concentration Reveals Novel Associations at the NFKBIK, PNPLA3, RELA, and SH2B3 Loci. PLoS Genetics, 2011, 7, e1001374.	3.5	76
95	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
96	Discordance between Circulating Atherogenic Cholesterol Mass and Lipoprotein Particle Concentration in Relation to Future Coronary Events in Women. Clinical Chemistry, 2017, 63, 870-879.	3.2	74
97	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	7 3
98	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
99	Genome-wide association study of selenium concentrations. Human Molecular Genetics, 2015, 24, 1469-1477.	2.9	67
100	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	1.3	67
101	Assessment of Risk Factors and Biomarkers Associated With Risk of Cardiovascular Disease Among Women Consuming a Mediterranean Diet. JAMA Network Open, 2018, 1, e185708.	5.9	65
102	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
103	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation. JAMA Cardiology, 2019, 4, 144.	6.1	64
104	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
105	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	8.1	63
106	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	1.9	61
107	Residual Risk of Atherosclerotic Cardiovascular Events in Relation to Reductions in Very‣owâ€Density Lipoproteins. Journal of the American Heart Association, 2017, 6, .	3.7	61
108	Fish Intake, Genetic Predisposition to Alzheimer Disease, and Decline in Global Cognition and Memory in 5 Cohorts of Older Persons. American Journal of Epidemiology, 2018, 187, 933-940.	3.4	61

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109	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
110	Using genetics to test the causal relationship of total adiposity and periodontitis: Mendelian randomization analyses in the Gene-Lifestyle Interactions and Dental Endpoints (GLIDE) Consortium. International Journal of Epidemiology, 2015, 44, 638-650.	1.9	54
111	Shared Molecular Genetic Mechanisms Underlie Endometriosis and Migraine Comorbidity. Genes, 2020, 11, 268.	2.4	53
112	On the utility of gene set methods in genomewide association studies of quantitative traits. Genetic Epidemiology, 2008, 32, 658-668.	1.3	52
113	Genetic loci associated with circulating phospholipid trans fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. American Journal of Clinical Nutrition, 2015, 101, 398-406.	4.7	49
114	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11 , 3368.	12.8	49
115	New Blood Pressure–Associated Loci Identified in Meta-Analyses of 475 000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
116	Genetic analysis of over half a million people characterises C-reactive protein loci. Nature Communications, 2022, 13, 2198.	12.8	48
117	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	3.9	47
118	Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. Human Genetics, 2016, 135, 425-439.	3.8	47
119	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	3.8	46
120	Selectivity in Genetic Association with Sub-classified Migraine in Women. PLoS Genetics, 2014, 10, e1004366.	3.5	45
121	Plasma Levels of the Proinflammatory Chitinâ€Binding Glycoprotein YKLâ€40, Variation in the Chitinase 3â€Like 1 Gene (<i>CHI3L1</i>), and Incident Cardiovascular Events. Journal of the American Heart Association, 2014, 3, e000897.	3.7	44
122	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. PLoS ONE, 2017, 12, e0185663.	2.5	44
123	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
124	Pleiotropy among Common Genetic Loci Identified for Cardiometabolic Disorders and C-Reactive Protein. PLoS ONE, 2015, 10, e0118859.	2.5	43
125	Thyroid function, sex hormones and sexual function: a Mendelian randomization study. European Journal of Epidemiology, 2021, 36, 335-344.	5.7	43
126	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	1.9	43

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127	Association of cyclooxygenase-2 genetic variant with cardiovascular disease. European Heart Journal, 2014, 35, 2242-2248.	2.2	42
128	A Common Variant in <i>MIR182</i> Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium., 2016, 57, 4528.		42
129	A common missense variant of LILRB5 is associated with statin intolerance and myalgia. European Heart Journal, 2017, 38, 3569-3575.	2.2	41
130	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
131	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
132	Dietary fatty acids modulate associations between genetic variants and circulating fatty acids in plasma and erythrocyte membranes: Metaâ€analysis of nine studies in the CHARGE consortium. Molecular Nutrition and Food Research, 2015, 59, 1373-1383.	3.3	37
133	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
134	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	3.8	36
135	Polymorphisms in Catechol- <i>O</i> -Methyltransferase Modify Treatment Effects of Aspirin on Risk of Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2160-2167.	2.4	35
136	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant at <i>SLC39A8</i> in Europeans. Schizophrenia Bulletin, 2016, 42, sbv070.	4.3	35
137	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	1.9	34
138	Common Genetic Variations in the Vitamin D Pathway in Relation to Blood Pressure. American Journal of Hypertension, 2014, 27, 1387-1395.	2.0	33
139	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	3.9	32
140	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
141	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
142	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
143	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
144	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28

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145	Are Genetic Tests for Atherosclerosis Ready for Routine Clinical Use?. Circulation Research, 2016, 118, 607-619.	4. 5	28
146	Could vitamin D reduce obesity-associated inflammation? Observational and Mendelian randomization study. American Journal of Clinical Nutrition, 2020, 111, 1036-1047.	4.7	28
147	Association of the Mediterranean Diet With Onset of Diabetes in the Women's Health Study. JAMA Network Open, 2020, 3, e2025466.	5.9	28
148	Rare Genetic Variants Associated With Sudden Cardiac Death in Adults. Journal of the American College of Cardiology, 2019, 74, 2623-2634.	2.8	27
149	Hypothyroidism and Kidney Function: A Mendelian Randomization Study. Thyroid, 2020, 30, 365-379.	4. 5	27
150	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. American Journal of Human Genetics, 2022, 109, 1077-1091.	6.2	27
151	Investigating methotrexate toxicity within a randomized double-blinded, placebo-controlled trial: Rationale and design of the Cardiovascular Inflammation Reduction Trial-Adverse Events (CIRT-AE) Study. Seminars in Arthritis and Rheumatism, 2017, 47, 133-142.	3.4	26
152	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
153	Genetic variation at the coronary artery disease risk locus <i>GUCY1A3</i> modifies cardiovascular disease prevention effects of aspirin. European Heart Journal, 2019, 40, 3385-3392.	2.2	25
154	Group IIA Secretory Phospholipase A ₂ , Vascular Inflammation, and Incident Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1182-1190.	2.4	25
155	Prospective Study of Common Variants in <i>CX3CR1</i> and Risk of Macular Degeneration. JAMA Ophthalmology, 2014, 132, 84.	2.5	24
156	Interaction of methylation-related genetic variants with circulating fatty acids on plasma lipids: a meta-analysis of 7 studies and methylation analysis of 3 studies in the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. American Journal of Clinical Nutrition, 2016, 103, 567-578.	4.7	24
157	COMT and Alpha-Tocopherol Effects in Cancer Prevention: Gene-Supplement Interactions in Two Randomized Clinical Trials. Journal of the National Cancer Institute, 2019, 111, 684-694.	6.3	24
158	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	3 . 5	24
159	Migraine genetics: from genome-wide association studies to translational insights. Genome Medicine, 2016, 8, 86.	8.2	22
160	Association between Vitamin D Genetic Risk Score and Cancer Risk in a Large Cohort of U.S. Women. Nutrients, 2018, 10, 55.	4.1	22
161	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
162	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22

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163	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
164	Effect of Vitamin D and ω-3 Fatty Acid Supplementation on Risk of Age-Related Macular Degeneration. JAMA Ophthalmology, 2020, 138, 1280.	2.5	20
165	Mitochondrial genome-wide association study of migraine – the HUNT Study. Cephalalgia, 2020, 40, 625-634.	3.9	19
166	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	1.4	19
167	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
168	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
169	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. PLoS ONE, 2017, 12, e0186456.	2.5	18
170	Statin-induced LDL cholesterol response and type 2 diabetes: a bidirectional two-sample Mendelian randomization study. Pharmacogenomics Journal, 2020, 20, 462-470.	2.0	18
171	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	3.7	18
172	Migraine, Stroke, and Cervical Arterial Dissection. Neurology: Genetics, 2022, 8, 00.	1.9	18
173	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
174	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
175	Pleiotropy-Based Decomposition of Genetic Risk Scores: Association and Interaction Analysis for Type 2 Diabetes and CAD. American Journal of Human Genetics, 2020, 106, 646-658.	6.2	17
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177	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	3.3	16
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