Lude Franke

List of Publications by Year
in descending order

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271 papers	60,367 citations	1883 102 h-index	1413 221 g-index
323 all docs	323 docs citations	323 times ranked	67454 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	Bayesian Test for Colocalisation between Pairs of Genetic Association Studies Using Summary Statistics. PLoS Genetics, 2014, 10, e1004383.	1.5	2,012
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
4	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	9.4	1,965
5	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
6	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
7	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	6.0	1,398
8	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
9	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
10	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
11	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
12	Proton pump inhibitors affect the gut microbiome. Gut, 2016, 65, 740-748.	6.1	885
13	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
14	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
15	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. Nature Genetics, 2019, 51, 600-605.	9.4	854
16	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
17	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
18	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743

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19	Gene co-expression analysis for functional classification and geneâ€“disease predictions. Briefings in Bioinformatics, 2018, 19, bbw139.	3.2	718
20	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
21	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
22	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
23	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	9.4	672
24	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
25	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
26	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
27	Newly identified genetic risk variants for celiac disease related to the immune response. Nature Genetics, 2008, 40, 395-402.	9.4	599
28	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. Nature Genetics, 2007, 39, 827-829.	9.4	592
29	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. Gut, 2018, 67, 108-119.	6.1	590
30	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
31	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
32	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
33	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	9.4	558
34	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
35	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. Circulation Research, 2015, 117, 817-824.	2.0	534
36	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533

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37	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
38	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	9.4	494
39	Reconstruction of a Functional Human Gene Network, with an Application for Prioritizing Positional Candidate Genes. American Journal of Human Genetics, 2006, 78, 1011-1025.	2.6	456
40	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.	9.4	426
41	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
42	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
43	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
44	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
45	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. Science Translational Medicine, 2018, 10, .	5.8	351
46	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
47	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
48	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	1.5	324
49	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
50	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
51	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
52	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
53	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	1.5	307
54	Identification of novel autism candidate regions through analysis of reported cytogenetic abnormalities associated with autism. Molecular Psychiatry, 2006, 11, 18-28.	4.1	296

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55	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
56	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. Nature Genetics, 2018, 50, 493-497.	9.4	289
57	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
58	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
59	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
60	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	13.5	275
61	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
62	Genome-Wide Association Study Identifies Variants Associated With Autoimmune Hepatitis Type 1. Gastroenterology, 2014, 147, 443-452.e5.	0.6	268
63	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247
64	Endothelial TLR4 and the microbiome drive cerebral cavernous malformations. Nature, 2017, 545, 305-310.	13.7	247
65	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
66	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
67	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
68	Genetic Analysis of Innate Immunity in Crohn's Disease and Ulcerative Colitis Identifies Two Susceptibility Loci Harboring CARD9 and IL18RAP. American Journal of Human Genetics, 2008, 82, 1202-1210.	2.6	229
69	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	9.4	223
70	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
71	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. Nature Genetics, 2005, 37, 1341-1344.	9.4	211
72	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. BMJ Open, 2015, 5, e006772.	0.8	207

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73	Genetic variation in DPP6 is associated with susceptibility to amyotrophic lateral sclerosis. Nature Genetics, 2008, 40, 29-31.	9.4	205
74	Wnt Signaling and Dupuytren's Disease. New England Journal of Medicine, 2011, 365, 307-317.	13.9	201
75	Genome-wide analysis of allelic expression imbalance in human primary cells by high-throughput transcriptome resequencing. Human Molecular Genetics, 2010, 19, 122-134.	1.4	197
76	ITPR2 as a susceptibility gene in sporadic amyotrophic lateral sclerosis: a genome-wide association study. Lancet Neurology, The, 2007, 6, 869-877.	4.9	195
77	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	1.5	194
78	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
79	Novel Association in Chromosome 4q27 Region with Rheumatoid Arthritis and Confirmation of Type 1 Diabetes Point to a General Risk Locus for Autoimmune Diseases. American Journal of Human Genetics, 2007, 81, 1284-1288.	2.6	189
80	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
81	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
82	Overview of cytogenetic regions of interest (CROIs) associated with the autism phenotype across the human genome. Molecular Psychiatry, 2006, 11, 1-1.	4.1	179
83	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	5.8	178
84	Using genomeâ€wide pathway analysis to unravel the etiology of complex diseases. Genetic Epidemiology, 2009, 33, 419-431.	0.6	173
85	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-ÂB signalling. Gut, 2009, 58, 1078-1083.	6.1	170
86	Evolutionary and Functional Analysis of Celiac Risk Loci Reveals SH2B3 as a Protective Factor against Bacterial Infection. American Journal of Human Genetics, 2010, 86, 970-977.	2.6	168
87	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	5.8	168
88	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
89	High-throughput identification of human SNPs affecting regulatory element activity. Nature Genetics, 2019, 51, 1160-1169.	9.4	157
90	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	3.8	154

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91	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. Cell Reports, 2016, 17, 2474-2487.	2.9	154
92	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
93	The single-cell eQTLGen consortium. ELife, 2020, 9, .	2.8	150
94	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	15.2	148
95	From genome to function by studying eQTLs. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1896-1902.	1.8	137
96	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	4.1	134
97	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. Nature Genetics, 2022, 54, 143-151.	9.4	132
98	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. BMC Genomics, 2014, 15, 860.	1.2	124
99	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	0.6	122
100	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	3.8	120
101	Gene-Network Analysis Identifies Susceptibility Genes Related to Glycobiology in Autism. PLoS ONE, 2009, 4, e5324.	1.1	119
102	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
103	Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465.	1.4	119
104	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
105	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
106	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. Gut, 2014, 63, 415-422.	6.1	113
107	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
108	A linear mixed-model approach to study multivariate geneâ€“environment interactions. Nature Genetics, 2019, 51, 180-186.	9.4	112

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109	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL , and CARD9. Hepatology, 2011, 53, 1977-1985.	3.6	110
110	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
111	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. PLoS Genetics, 2017, 13, e1006643.	1.5	110
112	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.	2.6	109
113	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
114	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. Microbiome, 2018, 6, 101.	4.9	109
115	Improving the diagnostic yield of exome- sequencing by predicting geneâ€“phenotype associations using large-scale gene expression analysis. Nature Communications, 2019, 10, 2837.	5.8	107
116	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
117	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	9.4	104
118	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. Nature Immunology, 2018, 19, 776-786.	7.0	103
119	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
120	Exome sequencing and network analysis identifies shared mechanisms underlying spinocerebellar ataxia. Brain, 2017, 140, 2860-2878.	3.7	98
121	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. Nature Genetics, 2014, 46, 957-963.	9.4	97
122	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature Genetics, 2018, 50, 1524-1532.	9.4	97
123	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96
124	Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model. BMC Medical Genomics, 2014, 7, 57.	0.7	96
125	HLA-DRB1*03:01 and HLA-DRB1*04:01 modify the presentation and outcome in autoimmune hepatitis type-1. Genes and Immunity, 2015, 16, 247-252.	2.2	96
126	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. Genome Medicine, 2014, 6, 88.	3.6	95

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127	Analysis of SNPs with an effect on gene expression identifies UBE2L3 and BCL3 as potential new risk genes for Crohn's disease. Human Molecular Genetics, 2010, 19, 3482-3488.	1.4	92
128	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	1.4	92
129	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. Genome Medicine, 2015, 7, 30.	3.6	91
130	Genome-wide association study in premature ovarian failure patients suggests ADAMTS19 as a possible candidate gene. Human Reproduction, 2009, 24, 2372-2378.	0.4	90
131	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. Thorax, 2015, 70, 21-32.	2.7	89
132	Mediation Analysis Demonstrates That Trans-eQTLs Are Often Explained by Cis-Mediation: A Genome-Wide Analysis among 1,800 South Asians. PLoS Genetics, 2014, 10, e1004818.	1.5	88
133	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	0.7	86
134	Copy-number variation in sporadic amyotrophic lateral sclerosis: a genome-wide screen. Lancet Neurology, The, 2008, 7, 319-326.	4.9	85
135	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
136	Unintended Side Effects of the Digital Transition: European Scientistsâ€™ Messages from a Proposition-Based Expert Round Table. Sustainability, 2018, 10, 2001.	1.6	82
137	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	1.8	81
138	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
139	ATR inhibition preferentially targets homologous recombination-deficient tumor cells. Oncogene, 2015, 34, 3474-3481.	2.6	80
140	A meta-analysis of Hodgkin lymphoma reveals 19p13.3 TCF3 as a novel susceptibility locus. Nature Communications, 2014, 5, 3856.	5.8	78
141	Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia. Nature Communications, 2014, 5, 4675.	5.8	76
142	A microarray screen for novel candidate genes in coeliac disease pathogenesis. Gut, 2004, 53, 944-951.	6.1	71
143	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
144	An epigenome-wide association study meta-analysis of educational attainment. Molecular Psychiatry, 2017, 22, 1680-1690.	4.1	70

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145	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
146	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. Human Molecular Genetics, 2016, 25, 1247-1254.	1.4	69
147	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. American Journal of Human Genetics, 2015, 96, 695-708.	2.6	67
148	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. European Journal of Human Genetics, 2017, 25, 877-885.	1.4	67
149	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
150	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	3.0	64
151	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
152	Understanding human immune function using the resources from the Human Functional Genomics Project. Nature Medicine, 2016, 22, 831-833.	15.2	63
153	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
154	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. Nature Communications, 2017, 8, 1584.	5.8	61
155	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
156	eQTL Analysis in Humans. Methods in Molecular Biology, 2009, 573, 311-328.	0.4	55
157	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. Genome Biology, 2017, 18, 6.	3.8	55
158	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. Human Molecular Genetics, 2015, 24, 397-409.	1.4	54
159	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. SSM - Population Health, 2021, 15, 100878.	1.3	53
160	Human Genetics in Rheumatoid Arthritis Guides a High-Throughput Drug Screen of the CD40 Signaling Pathway. PLoS Genetics, 2013, 9, e1003487.	1.5	52
161	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. PLoS ONE, 2012, 7, e35333.	1.1	50
162	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. European Respiratory Journal, 2014, 44, 860-872.	3.1	49

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163	An integrative approach for building personalized gene regulatory networks for precision medicine. Genome Medicine, 2018, 10, 96.	3.6	49
164	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
165	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. BMJ Open, 2021, 11, e044474.	0.8	49
166	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	1.5	47
167	A SNP panel for identification of DNA and RNA specimens. BMC Genomics, 2018, 19, 90.	1.2	47
168	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	0.7	47
169	Neutrophil Recruitment and Barrier Impairment in Celiac Disease: A Genomic Study. Clinical Gastroenterology and Hepatology, 2007, 5, 574-581.e5.	2.4	46
170	DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. PLoS Genetics, 2013, 9, e1003594.	1.5	45
171	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. Frontiers in Genetics, 2020, 11, 613.	1.1	45
172	Co-expressed immune and metabolic genes in visceral and subcutaneous adipose tissue from severely obese individuals are associated with plasma HDL and glucose levels: a microarray study. BMC Medical Genomics, 2010, 3, 34.	0.7	43
173	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. Nature Communications, 2016, 7, 12160.	5.8	43
174	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	2.7	43
175	A strategy to search for common obesity and type 2 diabetes genes. Trends in Endocrinology and Metabolism, 2007, 18, 19-26.	3.1	42
176	DNA methylation signatures of educational attainment. Npj Science of Learning, 2018, 3, 7.	1.5	42
177	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. Neurology, 2019, 92, e1899-e1911.	1.5	42
178	A Genome-Wide Association Study of Circulating Galectin-3. PLoS ONE, 2012, 7, e47385.	1.1	41
179	Genetic variants in the region of the C1q genes are associated with rheumatoid arthritis. Clinical and Experimental Immunology, 2013, 173, 76-83.	1.1	41
180	Detection, Imputation, and Association Analysis of Small Deletions and Null Alleles on Oligonucleotide Arrays. American Journal of Human Genetics, 2008, 82, 1316-1333.	2.6	40

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181	Determining the association between adipokine expression in multiple tissues and phenotypic features of non-alcoholic fatty liver disease in obesity. Nutrition and Diabetes, 2015, 5, e146-e146.	1.5	40
182	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. PLoS Genetics, 2017, 13, e1006587.	1.5	40
183	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. Nature Communications, 2022, 13, .	5.8	39
184	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	1.2	38
185	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	5.8	38
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