Lude Franke

List of Publications by Citations

283 papers	39,978 citations	90 h-index	198 g-index
323 ext. papers	52,232 ext. citations	16 avg, IF	6.25 L-index

#	Paper	IF	Citations
283	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
282	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
281	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
280	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. *Nature Genetics*, **2015**, 47, 979-986	36.3	1278
279	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
278	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. *Nature Genetics*, **2011**, 43, 246-52	36.3	1028
277	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
276	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
275	Bayesian test for colocalisation between pairs of genetic association studies using summary statistics. *PLoS Genetics*, **2014**, 10, e1004383	6	868
274	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
273	Multiple common variants for celiac disease influencing immune gene expression. *Nature Genetics*, **2010**, 42, 295-302	36.3	727
272	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
271	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
270	Proton pump inhibitors affect the gut microbiome. *Gut*, **2016**, 65, 740-8	19.2	575
269	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
268	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. *Nature Genetics*, **2011**, 43, 1193-201	36.3	535
267	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530

266	Newly identified genetic risk variants for celiac disease related to the immune response. *Nature Genetics*, **2008**, 40, 395-402	36.3	524
265	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. *Nature Genetics*, **2007**, 39, 827-9	36.3	518
264	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
263	Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications*, **2015**, 6, 5890	17.4	489
262	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
261	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
260	The effect of host genetics on the gut microbiome. *Nature Genetics*, **2016**, 48, 1407-1412	36.3	434
259	Reconstruction of a functional human gene network, with an application for prioritizing positional candidate genes. *American Journal of Human Genetics*, **2006**, 78, 1011-25	11	420
258	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
257	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. *Nature Genetics*, **2016**, 48, 510-8	36.3	404
256	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
255	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. *Nature Genetics*, **2019**, 51, 600-605	36.3	378
254	Gene co-expression analysis for functional classification and gene-disease predictions. *Briefings in Bioinformatics*, **2018**, 19, 575-592	13.4	377
253	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. *Circulation Research*, **2015**, 117, 817-24	15.7	368
252	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. *Gut*, **2018**, 67, 108-119	19.2	368
251	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. *Cell*, **2018**, 173, 1705-1715.e16	56.2	360
250	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355
249	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335

248	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1043-8	36.3	328
247	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
246	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	6	261
245	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. *PLoS Genetics*, **2011**, 7, e1002004	6	260
244	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	36.3	257
243	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
242	Identification of novel autism candidate regions through analysis of reported cytogenetic abnormalities associated with autism. *Molecular Psychiatry*, **2006**, 11, 18-28	15.1	256
241	Disease variants alter transcription factor levels and methylation of their binding sites. *Nature Genetics*, **2017**, 49, 131-138	36.3	252
240	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
239	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
238	Identification of context-dependent expression quantitative trait loci in whole blood. *Nature Genetics*, **2017**, 49, 139-145	36.3	240
237	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
236	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	36.3	223
235	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	6	220
234	Gene expression analysis identifies global gene dosage sensitivity in cancer. *Nature Genetics*, **2015**, 47, 115-25	36.3	219
233	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
232	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. *PLoS Genetics*, **2013**, 9, e1003201	6	209
231	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202

230	Genome-wide association study identifies variants associated with autoimmune hepatitis type 1. *Gastroenterology*, **2014**, 147, 443-52.e5	13.3	201
229	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
228	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
227	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, 1202-10	11	196
226	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. *Nature Genetics*, **2005**, 37, 1341-4	36.3	184
225	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, 13790-4	11.5	181
224	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
223	Genetic variation in DPP6 is associated with susceptibility to amyotrophic lateral sclerosis. *Nature Genetics*, **2008**, 40, 29-31	36.3	177
222	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
221	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, 1284-8	11	171
220	Identification of novel autism candidate regions through analysis of reported cytogenetic abnormalities associated with autism. *Molecular Psychiatry*, **2006**, 11, 1, 18-28	15.1	169
219	ITPR2 as a susceptibility gene in sporadic amyotrophic lateral sclerosis: a genome-wide association study. *Lancet Neurology, The*, **2007**, 6, 869-77	24.1	168
218	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
217	Endothelial TLR4 and the microbiome drive cerebral cavernous malformations. *Nature*, **2017**, 545, 305-310	50.4	166
216	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. *Nature Genetics*, **2018**, 50, 493-497	36.3	164
215	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. *Cell*, **2016**, 167, 1099-1110.e14	56.2	163
214	Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression. *PLoS Genetics*, **2012**, 8, e1002431	6	163
213	Mapping the human genetic architecture of COVID-19. *Nature*, **2021**,	50.4	162

212	Using genome-wide pathway analysis to unravel the etiology of complex diseases. *Genetic Epidemiology*, **2009**, 33, 419-31	2.6	159
211	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. *Science Translational Medicine*, **2018**, 10,	17.5	159
210	Wnt signaling and Dupuytren's disease. *New England Journal of Medicine*, **2011**, 365, 307-17	59.2	153
209	Genome-wide analysis of allelic expression imbalance in human primary cells by high-throughput transcriptome resequencing. *Human Molecular Genetics*, **2010**, 19, 122-34	5.6	152
208	Detection and replication of epistasis influencing transcription in humans. *Nature*, **2014**, 508, 249-53	50.4	149
207	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-kappaB signalling. *Gut*, **2009**, 58, 1078-83	19.2	147
206	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
205	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137
204	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. *BMJ Open*, **2015**, 5, e006772	3	136
203	Evolutionary and functional analysis of celiac risk loci reveals SH2B3 as a protective factor against bacterial infection. *American Journal of Human Genetics*, **2010**, 86, 970-7	11	130
202	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. *Nature Communications*, **2015**, 6, 7208	17.4	126
201	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
200	Blood lipids influence DNA methylation in circulating cells. *Genome Biology*, **2016**, 17, 138	18.3	118
199	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. *Nature Medicine*, **2016**, 22, 952-60	50.5	106
198	Gene-network analysis identifies susceptibility genes related to glycobiology in autism. *PLoS ONE*, **2009**, 4, e5324	3.7	104
197	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. *Cell Reports*, **2016**, 17, 2474-2487	10.6	100
196	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL, and CARD9. *Hepatology*, **2011**, 53, 1977-85	11.2	96
195	From genome to function by studying eQTLs. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2014**, 1842, 1896-1902	6.9	95

194	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. *Gut*, **2014**, 63, 415-22	19.2	92
193	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
192	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. *BMC Genomics*, **2014**, 15, 860	4.5	90
191	High-throughput identification of human SNPs affecting regulatory element activity. *Nature Genetics*, **2019**, 51, 1160-1169	36.3	87
190	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. *Molecular Psychiatry*, **2016**, 21, 189-197	15.1	85
189	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
188	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
187	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, 3482-8	5.6	82
186	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81
185	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. *Nature Genetics*, **2014**, 46, 957-63	36.3	81
184	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	11	80
183	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. *Genome Biology*, **2016**, 17, 191	18.3	80
182	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80
181	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. *Genome Medicine*, **2014**, 6, 88	14.4	79
180	Copy-number variation in sporadic amyotrophic lateral sclerosis: a genome-wide screen. *Lancet Neurology, The*, **2008**, 7, 319-26	24.1	78
179	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
178	SMIM1 underlies the Vel blood group and influences red blood cell traits. *Nature Genetics*, **2013**, 45, 542-545	36.3	77
177	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76

176	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. *PLoS Genetics*, **2017**, 13, e1006643	6	75
175	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. *Nature Genetics*, **2014**, 46, 901-4	36.3	75
174	Genome-wide association study in premature ovarian failure patients suggests ADAMTS19 as a possible candidate gene. *Human Reproduction*, **2009**, 24, 2372-8	5.7	75
173	Improved imputation quality of low-frequency and rare variants in European samples using the 'Genome of The Netherlands'. *European Journal of Human Genetics*, **2014**, 22, 1321-6	5.3	74
172	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. *BMC Research Notes*, **2014**, 7, 901	2.3	74
171	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. *BMC Medical Genomics*, **2009**, 2, 1	3.7	74
170	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. *Thorax*, **2015**, 70, 21-32	7.3	73
169	Exome sequencing and network analysis identifies shared mechanisms underlying spinocerebellar ataxia. *Brain*, **2017**, 140, 2860-2878	11.2	68
168	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
167	The single-cell eQTLGen consortium. *ELife*, **2020**, 9,	8.9	68
166	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	3.7	66
165	HLA-DRB1*03:01 and HLA-DRB1*04:01 modify the presentation and outcome in autoimmune hepatitis type-1. *Genes and Immunity*, **2015**, 16, 247-52	4.4	63
164	Relationship between gut microbiota and circulating metabolites in population-based cohorts. *Nature Communications*, **2019**, 10, 5813	17.4	63
163	A linear mixed-model approach to study multivariate gene-environment interactions. *Nature Genetics*, **2019**, 51, 180-186	36.3	63
162	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. *Nature Immunology*, **2018**, 19, 776-786	19.1	63
161	Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia. *Nature Communications*, **2014**, 5, 4675	17.4	62
160	A microarray screen for novel candidate genes in coeliac disease pathogenesis. *Gut*, **2004**, 53, 944-51	19.2	62
159	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61

158	ATR inhibition preferentially targets homologous recombination-deficient tumor cells. *Oncogene*, **2015**, 34, 3474-81	9.2	60
157	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. *Bioinformatics*, **2011**, 27, 2104-11	7.2	60
156	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	36.3	60
155	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *American Journal of Human Genetics*, **2012**, 91, 744-53	11	58
154	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	6	56
153	Unintended Side Effects of the Digital Transition: European Scientists Messages from a Proposition-Based Expert Round Table. *Sustainability*, **2018**, 10, 2001	3.6	55
152	Improving the diagnostic yield of exome- sequencing by predicting gene-phenotype associations using large-scale gene expression analysis. *Nature Communications*, **2019**, 10, 2837	17.4	55
151	A meta-analysis of Hodgkin lymphoma reveals 19p13.3 TCF3 as a novel susceptibility locus. *Nature Communications*, **2014**, 5, 3856	17.4	55
150	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. *American Journal of Human Genetics*, **2018**, 102, 1185-1194	11	55
149	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. *Nature Genetics*, **2018**, 50, 1524-1532	36.3	54
148	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. *Microbiome*, **2018**, 6, 101	16.6	53
147	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
146	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48	11	49
145	eQTL analysis in humans. *Methods in Molecular Biology*, **2009**, 573, 311-28	1.4	48
144	An epigenome-wide association study meta-analysis of educational attainment. *Molecular Psychiatry*, **2017**, 22, 1680-1690	15.1	46
143	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. *Genome Medicine*, **2015**, 7, 30	14.4	45
142	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508	6	45
141	Human genetics in rheumatoid arthritis guides a high-throughput drug screen of the CD40 signaling pathway. *PLoS Genetics*, **2013**, 9, e1003487	6	45

140	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	11	44
139	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	15.5	44
138	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	5.3	43
137	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	5.6	43
136	Understanding human immune function using the resources from the Human Functional Genomics Project. *Nature Medicine*, **2016**, 22, 831-3	50.5	43
135	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. *Human Molecular Genetics*, **2016**, 25, 1247-54	5.6	42
134	Mapping of gene expression reveals CYP27A1 as a susceptibility gene for sporadic ALS. *PLoS ONE*, **2012**, 7, e35333	3.7	41
133	Skewed X-inactivation is common in the general female population. *European Journal of Human Genetics*, **2019**, 27, 455-465	5.3	41
132	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
131	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
130	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
129	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nature Communications*, **2017**, 8, 1584	17.4	37
128	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	3.7	37
127	A strategy to search for common obesity and type 2 diabetes genes. *Trends in Endocrinology and Metabolism*, **2007**, 18, 19-26	8.8	37
126	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. *Genome Biology*, **2017**, 18, 6	18.3	36
125	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 771-781	11.5	36
124	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. *Nature Communications*, **2016**, 7, 12160	17.4	36
123	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 885-8	11.5	36

122	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. *European Respiratory Journal*, **2014**, 44, 860-72	13.6	35
121	A genome-wide association study of circulating galectin-3. *PLoS ONE*, **2012**, 7, e47385	3.7	34
120	Genetic variants in the region of the C1q genes are associated with rheumatoid arthritis. *Clinical and Experimental Immunology*, **2013**, 173, 76-83	6.2	33
119	DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. *PLoS Genetics*, **2013**, 9, e1003594	6	32
118	Detection, imputation, and association analysis of small deletions and null alleles on oligonucleotide arrays. *American Journal of Human Genetics*, **2008**, 82, 1316-33	11	32
117	Lack of Association Between Genetic Variants at and Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. *Frontiers in Genetics*, **2020**, 11, 613	4.5	31
116	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	4.7	29
115	Neutrophil recruitment and barrier impairment in celiac disease: a genomic study. *Clinical Gastroenterology and Hepatology*, **2007**, 5, 574-81	6.9	29
114	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
113	Extraintestinal manifestations and complications in inflammatory bowel disease: from shared genetics to shared biological pathways. *Inflammatory Bowel Diseases*, **2014**, 20, 987-94	4.5	27
112	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. *Neurology*, **2019**, 92, e1899-e1911	6.5	26
111	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. *Genome Medicine*, **2015**, 7, 105	14.4	26
110	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. *PLoS Genetics*, **2017**, 13, e1006587	6	24
109	Copper metabolism domain-containing 1 represses genes that promote inflammation and protects mice from colitis and colitis-associated cancer. *Gastroenterology*, **2014**, 147, 184-195.e3	13.3	24
108	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. *Biological Psychiatry*, **2019**, 86, 599-607	7.9	24
107	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. *Human Molecular Genetics*, **2014**, 23, 2481-9	5.6	23
106	Copy number variants on the X chromosome in women with primary ovarian insufficiency. *Fertility and Sterility*, **2011**, 95, 1584-8.e1	4.8	23
105	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. *Nature Communications*, **2020**, 11, 3368	17.4	22

104	TEAM: a tool for the integration of expression, and linkage and association maps. *European Journal of Human Genetics*, **2004**, 12, 633-8	5.3	22
103	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. *Human Molecular Genetics*, **2016**, 25, 2093-2103	5.6	20
102	Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. *Human Molecular Genetics*, **2016**, 25, 180-90	5.6	20
101	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. *Journal of Allergy and Clinical Immunology*, **2015**, 135, 1486-93.e8	11.5	19
100	Combination of text-mining algorithms increases the performance. *Bioinformatics*, **2006**, 22, 2151-7	7.2	19
99	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	36.3	19
98	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. *EBioMedicine*, **2018**, 38, 206-216	8.8	19
97	An integrative approach for building personalized gene regulatory networks for precision medicine. *Genome Medicine*, **2018**, 10, 96	14.4	19
96	Genome-wide analysis shows no genomic predictors of ovarian response to stimulation by exogenous FSH for IVF. *Reproductive BioMedicine Online*, **2011**, 22, 382-8	4	18
95	HHEX gene polymorphisms are associated with type 2 diabetes in the Dutch Breda cohort. *European Journal of Human Genetics*, **2008**, 16, 652-6	5.3	18
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