Lude Franke

List of Publications by Year in Descending Order

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	Functional genomics analysis identifies T and NK cell activation as a driver of epigenetic clock progression.. *Genome Biology*, **2022**, 23, 24	18.3	6
282	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project.. *Nature Genetics*, **2022**, 54, 143-151	36.3	7
281	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. *Science Translational Medicine*, **2022**, 14, eabj0264	17.5	4
280	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
279	DNA methylation in peripheral tissues and left-handedness.. *Scientific Reports*, **2022**, 12, 5606	4.9	0
278	Increased genetic contribution to wellbeing during the COVID-19 pandemic.. *PLoS Genetics*, **2022**, 18, e1010135	6	0
277	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. *Nature Communications*, **2022**, 13,	17.4	2
276	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
275	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	3	18
274	Correction for both common and rare cell types in blood is important to identify genes that correlate with age. *BMC Genomics*, **2021**, 22, 184	4.5	0
273	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. *Biological Psychiatry*, **2021**, 90, 611-620	7.9	17
272	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. *Nature Communications*, **2021**, 12, 2830	17.4	9
271	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. *Scientific Reports*, **2021**, 11, 10606	4.9	0
270	Habitual dietary intake of IBD patients differs from population controls: a case-control study. *European Journal of Nutrition*, **2021**, 60, 345-356	5.2	10
269	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. *Molecular Psychiatry*, **2021**, 26, 2148-2162	15.1	7
268	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80
267	Translational insights from single-cell technologies across the cardiovascular disease continuum. *Trends in Cardiovascular Medicine*, **2021**,	6.9	1

266	Integration of metabolomics, genomics, and immune phenotypes reveals the causal roles of metabolites in disease. *Genome Biology*, **2021**, 22, 198	18.3	6
265	Mapping the human genetic architecture of COVID-19. *Nature*, **2021**,	50.4	162
264	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PLoS ONE*, **2021**, 16, e0255402	3.7	3
263	Inflammatory Protein Profiles in Plasma of Candidaemia Patients and the Contribution of Host Genetics to Their Variability. *Frontiers in Immunology*, **2021**, 12, 662171	8.4	2
262	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
261	Phantom epistasis between unlinked loci. *Nature*, **2021**, 596, E1-E3	50.4	1
260	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. *Journal of Women's Health*, **2021**,	3	6
259	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. *SSM - Population Health*, **2021**, 15, 100878	3.8	9
258	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
257	Meta-analyses identify DNA methylation associated with kidney function and damage. *Nature Communications*, **2021**, 12, 7174	17.4	0
256	Habitual sleep disturbances and migraine: a Mendelian randomization study. *Annals of Clinical and Translational Neurology*, **2020**, 7, 2370-2380	5.3	6
255	Predicted efficacy of a pharmacogenetic passport for inflammatory bowel disease. *Alimentary Pharmacology and Therapeutics*, **2020**, 51, 1105-1115	6.1	7
254	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. *Hypertension*, **2020**, 76, 195-205	8.5	12
253	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. *BMC Bioinformatics*, **2020**, 21, 243	3.6	15
252	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. *Nature Communications*, **2020**, 11, 3368	17.4	22
251	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
250	Practical Barriers and Facilitators Experienced by Patients, Pharmacists and Physicians to the Implementation of Pharmacogenomic Screening in Dutch Outpatient Hospital Care-An Explorative Pilot Study. *Journal of Personalized Medicine*, **2020**, 10,	3.6	1
249	The single-cell eQTLGen consortium. *ELife*, **2020**, 9,	8.9	68

248	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. *European Journal of Human Genetics*, **2020**, 28, 253-263	5.3	8
247	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
246	An epigenome-wide association study identifies multiple DNA methylation markers of exposure to endocrine disruptors. *Environment International*, **2020**, 144, 106016	12.9	6
245	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. *International Journal of Epidemiology*, **2020**, 49, 1022-1031	7.8	15
244	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response. *PLoS Pathogens*, **2020**, 16, e1008408	7.6	11
243	Systematic Prioritization of Candidate Genes in Disease Loci Identifies as a Master Regulator of IFN Signaling in Celiac Disease. *Frontiers in Genetics*, **2020**, 11, 562434	4.5	9
242	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response **2020**, 16, e1008408		
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238	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response **2020**, 16, e1008408		
237	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. *Genetics*, **2019**, 212, 905-918	4	13
236	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. *Human Genetics*, **2019**, 138, 375-388	6.3	4
235	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. *Neurology*, **2019**, 92, e1899-e1911	6.5	26
234	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 223-231	3.5	2
233	RNA-Seq in 296 phased trios provides a high-resolution map of genomic imprinting. *BMC Biology*, **2019**, 17, 50	7.3	10
232	High-throughput identification of human SNPs affecting regulatory element activity. *Nature Genetics*, **2019**, 51, 1160-1169	36.3	87
231	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

230	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
229	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. *Biological Psychiatry*, **2019**, 86, 599-607	7.9	24
228	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. *Nature Genetics*, **2019**, 51, 600-605	36.3	378
227	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. *Genome Biology*, **2019**, 20, 235	18.3	12
226	Relationship between gut microbiota and circulating metabolites in population-based cohorts. *Nature Communications*, **2019**, 10, 5813	17.4	63
225	Skewed X-inactivation is common in the general female population. *European Journal of Human Genetics*, **2019**, 27, 455-465	5.3	41
224	A linear mixed-model approach to study multivariate gene-environment interactions. *Nature Genetics*, **2019**, 51, 180-186	36.3	63
223	Gene co-expression analysis for functional classification and gene-disease predictions. *Briefings in Bioinformatics*, **2018**, 19, 575-592	13.4	377
222	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. *Nature Genetics*, **2018**, 50, 493-497	36.3	164
221	Generalized Ichthyotic Peeling Skin Syndrome due to FLG2 Mutations. *Journal of Investigative Dermatology*, **2018**, 138, 1881-1884	4.3	10
220	DNA methylation signatures of educational attainment. *Npj Science of Learning*, **2018**, 3, 7	6	14
219	Blood Eosinophil Count and Metabolic, Cardiac and Pulmonary Outcomes: A Mendelian Randomization Study. *Twin Research and Human Genetics*, **2018**, 21, 89-100	2.2	6
218	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
217	A SNP panel for identification of DNA and RNA specimens. *BMC Genomics*, **2018**, 19, 90	4.5	17
216	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
215	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. *Microbiome*, **2018**, 6, 101	16.6	53
214	Unintended Side Effects of the Digital Transition: European Scientists Messages from a Proposition-Based Expert Round Table. *Sustainability*, **2018**, 10, 2001	3.6	55
213	Genome-wide identification of directed gene networks using large-scale population genomics data. *Nature Communications*, **2018**, 9, 3097	17.4	13

212	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. *Cell*, **2018**, 173, 1705-1715.e16	56.2	360
211	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. *EBioMedicine*, **2018**, 38, 206-216	8.8	19
210	An integrative approach for building personalized gene regulatory networks for precision medicine. *Genome Medicine*, **2018**, 10, 96	14.4	19
209	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. *Science Translational Medicine*, **2018**, 10,	17.5	159
208	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. *Nature Genetics*, **2018**, 50, 1524-1532	36.3	54
207	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. *Nature Communications*, **2018**, 9, 3738	17.4	12
206	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. *Nature Immunology*, **2018**, 19, 776-786	19.1	63
205	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
204	Reply to 'Misestimation of heritability and prediction accuracy of male-pattern baldness'. *Nature Communications*, **2018**, 9, 2538	17.4	
203	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. *Genome Biology*, **2017**, 18, 6	18.3	36
202	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 771-781	11.5	36
201	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
200	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
199	Endothelial TLR4 and the microbiome drive cerebral cavernous malformations. *Nature*, **2017**, 545, 305-310	50.4	166
198	Disease variants alter transcription factor levels and methylation of their binding sites. *Nature Genetics*, **2017**, 49, 131-138	36.3	252
197	Identification of context-dependent expression quantitative trait loci in whole blood. *Nature Genetics*, **2017**, 49, 139-145	36.3	240
196	The genetic architecture of molecular traits. *Current Opinion in Systems Biology*, **2017**, 1, 25-31	3.2	3
195	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511

194	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
193	Exome sequencing and network analysis identifies shared mechanisms underlying spinocerebellar ataxia. *Brain*, **2017**, 140, 2860-2878	11.2	68
192	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. *PLoS Genetics*, **2017**, 13, e1006587	6	24
191	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. *PLoS Genetics*, **2017**, 13, e1006643	6	75
190	Overlapping SETBP1 gain-of-function mutations in Schinzel-Giedion syndrome and hematologic malignancies. *PLoS Genetics*, **2017**, 13, e1006683	6	17
189	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
188	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nature Communications*, **2017**, 8, 1584	17.4	37
187	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
186	An epigenome-wide association study meta-analysis of educational attainment. *Molecular Psychiatry*, **2017**, 22, 1680-1690	15.1	46
185	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
184	An integrative genomics approach identifies novel pathways that influence candidaemia susceptibility. *PLoS ONE*, **2017**, 12, e0180824	3.7	17
183	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. *PLoS ONE*, **2017**, 12, e0182472	3.7	8
182	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. *Molecular Psychiatry*, **2016**, 21, 189-197	15.1	85
181	Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes. *European Journal of Human Genetics*, **2016**, 24, 263-70	5.3	14
180	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
179	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
178	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
177	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. *Nature Communications*, **2016**, 7, 12160	17.4	36

176	Evidence for mitochondrial genetic control of autosomal gene expression. *Human Molecular Genetics*, **2016**, 25, 5332-5338	5.6	4
175	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. *Cell Reports*, **2016**, 17, 2474-2487	10.6	100
174	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
173	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
172	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. *Cell*, **2016**, 167, 1099-1110.e14	56.2	163
171	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. *Human Molecular Genetics*, **2016**, 25, 2093-2103	5.6	20
170	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355
169	Proton pump inhibitors affect the gut microbiome. *Gut*, **2016**, 65, 740-8	19.2	575
168	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
167	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
166	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
165	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
164	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
163	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
162	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
161	Eosinophil Count Is a Common Factor for Complex Metabolic and Pulmonary Traits and Diseases: The LifeLines Cohort Study. *PLoS ONE*, **2016**, 11, e0168480	3.7	18
160	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. *PLoS ONE*, **2016**, 11, e0167519	3.7	18
159	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. *Nature Medicine*, **2016**, 22, 952-60	50.5	106

158	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
157	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
156	Genetic variants in RBFOX3 are associated with sleep latency. *European Journal of Human Genetics*, **2016**, 24, 1488-95	5.3	18
155	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
154	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
153	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. *Genome Biology*, **2016**, 17, 191	18.3	80
152	The effect of host genetics on the gut microbiome. *Nature Genetics*, **2016**, 48, 1407-1412	36.3	434
151	Blood lipids influence DNA methylation in circulating cells. *Genome Biology*, **2016**, 17, 138	18.3	118
150	Understanding human immune function using the resources from the Human Functional Genomics Project. *Nature Medicine*, **2016**, 22, 831-3	50.5	43
149	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
148	Gene expression analysis identifies global gene dosage sensitivity in cancer. *Nature Genetics*, **2015**, 47, 115-25	36.3	219
147	Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications*, **2015**, 6, 5890	17.4	489
146	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81
145	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
144	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
143	Evaluation of European coeliac disease risk variants in a north Indian population. *European Journal of Human Genetics*, **2015**, 23, 530-5	5.3	11
142	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
141	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229

140	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
139	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
138	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
137	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. *Circulation Research*, **2015**, 117, 817-24	15.7	368
136	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
135	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
134	ATR inhibition preferentially targets homologous recombination-deficient tumor cells. *Oncogene*, **2015**, 34, 3474-81	9.2	60
133	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
132	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
131	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
130	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. *Genome Medicine*, **2015**, 7, 105	14.4	26
129	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
128	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. *Nature Communications*, **2015**, 6, 7208	17.4	126
127	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. *Journal of Allergy and Clinical Immunology*, **2015**, 135, 556-8	11.5	3
126	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
125	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
124	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
123	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

122	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
121	Detection and replication of epistasis influencing transcription in humans. *Nature*, **2014**, 508, 249-53	50.4	149
120	Genome-wide association study identifies variants associated with autoimmune hepatitis type 1. *Gastroenterology*, **2014**, 147, 443-52.e5	13.3	201
119	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
118	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
117	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
116	Correlation of genetic risk and messenger RNA expression in a Th17/IL23 pathway analysis in inflammatory bowel disease. *Inflammatory Bowel Diseases*, **2014**, 20, 777-82	4.5	16
115	Proteomic studies related to genetic determinants of variability in protein concentrations. *Journal of Proteome Research*, **2014**, 13, 5-14	5.6	12
114	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
113	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
112	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. *Nature Genetics*, **2014**, 46, 957-63	36.3	81
111	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
110	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. *European Respiratory Journal*, **2014**, 44, 860-72	13.6	35
109	A meta-analysis of Hodgkin lymphoma reveals 19p13.3 TCF3 as a novel susceptibility locus. *Nature Communications*, **2014**, 5, 3856	17.4	55
108	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. *Nature Genetics*, **2014**, 46, 901-4	36.3	75
107	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
106	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
105	From genome to function by studying eQTLs. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2014**, 1842, 1896-1902	6.9	95

104	Ciliary genes are down-regulated in bronchial tissue of primary ciliary dyskinesia patients. *PLoS ONE* , **2014**, 9, e88216	3.7	13
103	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. *BMC Genomics*, **2014**, 15, 860	4.5	90
102	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
101	Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia. *Nature Communications*, **2014**, 5, 4675	17.4	62
100	Bayesian test for colocalisation between pairs of genetic association studies using summary statistics. *PLoS Genetics*, **2014**, 10, e1004383	6	868
99	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
98	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
97	Hemani et al. reply. *Nature*, **2014**, 514, E5-6	50.4	8
96	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
95	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. *Gut*, **2014**, 63, 415-22	19.2	92
94	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
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19	Genome-wide identification of directed gene networks using large-scale population genomics data		1
18	Discovering patterns of pleiotropy in genome-wide association studies		1
17	Disease variants alter transcription factor levels and methylation of their binding sites		6
16	Hypothesis-free identification of modulators of genetic risk factors		7
15	Systematic prioritization of candidate genes in disease loci identifies TRAFD1 as a master regulator of IFN signalling in celiac disease		4

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