

Martina Mller-Nurasyid

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

207 papers	36,777 citations	77 h-index	191 g-index
233 ext. papers	46,729 ext. citations	15.5 avg, IF	6.08 L-index

#	Paper	IF	Citations
207	Genome-wide meta-analysis of phytosterols reveals five novel loci and a detrimental effect on coronary atherosclerosis.. <i>Nature Communications</i> , 2022 , 13, 143	17.4	3
206	ExomeChip-based rare variant association study in restless legs syndrome.. <i>Sleep Medicine</i> , 2022 , 94, 26-30	4.6	
205	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. <i>Circulation Research</i> , 2021 ,	15.7	2
204	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. <i>Nature Communications</i> , 2021 , 12, 6618	17.4	2
203	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. <i>European Heart Journal</i> , 2021 , 42, 2000-2011	9.5	14
202	Deoxyribonuclease 1 Q222R single nucleotide polymorphism and long-term mortality after acute myocardial infarction. <i>Basic Research in Cardiology</i> , 2021 , 116, 29	11.8	2
201	Cis-epistasis at the LPA locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2021 ,	9.9	6
200	Comparison of genetic risk prediction models to improve prediction of coronary heart disease in two large cohorts of the MONICA/KORA study. <i>Genetic Epidemiology</i> , 2021 , 45, 633-650	2.6	2
199	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
198	Chronically elevated branched chain amino acid levels are pro-arrhythmic. <i>Cardiovascular Research</i> , 2021 ,	9.9	6
197	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. <i>Movement Disorders</i> , 2021 , 36, 449-459	7	2
196	Exome-Wide Association Study Identifies FN3KRP and PGP as New Candidate Longevity Genes. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021 , 76, 786-795	6.4	4
195	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
194	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021 , 30, 393-409	5.6	6
193	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , 2021 , 13, 7	7.7	11
192	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
191	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60

190	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. <i>Biological Psychiatry</i> , 2020 , 88, 470-479	7.9	6
189	Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. <i>Circulation</i> , 2020 , 142, 324-338	16.7	27
188	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
187	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. <i>Diabetes Care</i> , 2020 , 43, 875-884	14.6	16
186	Genetic Susceptibility for Atrial Fibrillation in Patients Undergoing Atrial Fibrillation Ablation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020 , 13, e007676	6.4	12
185	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. <i>Movement Disorders</i> , 2020 , 35, 1245-1248	7	23
184	Private variants in PRKN are associated with late-onset Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2020 , 75, 24-26	3.6	2
183	Integrative clinical transcriptome analysis reveals TMPRSS2-ERG dependency of prognostic biomarkers in prostate adenocarcinoma. <i>International Journal of Cancer</i> , 2020 , 146, 2036-2046	7.5	7
182	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 145, 1208-1218	11.5	19
181	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
180	Genome-wide association meta-analysis for early age-related macular degeneration highlights novel loci and insights for advanced disease. <i>BMC Medical Genomics</i> , 2020 , 13, 120	3.7	19
179	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 387-395	5.2	4
178	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020 , 25, 2392-2409	15.1	45
177	National trends in total cholesterol obscure heterogeneous changes in HDL and non-HDL cholesterol and total-to-HDL cholesterol ratio: a pooled analysis of 458 population-based studies in Asian and Western countries. <i>International Journal of Epidemiology</i> , 2020 , 49, 173-192	7.8	25
176	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
175	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
174	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. <i>European Journal of Human Genetics</i> , 2019 , 27, 952-962	5.3	18
173	Rising rural body-mass index is the main driver of the global obesity epidemic in adults. <i>Nature</i> , 2019 , 569, 260-264	50.4	278

172	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019 , 14, e0216222	3.7	11
171	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181
170	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. <i>Nature Communications</i> , 2019 , 10, 3300	17.4	78
169	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. <i>Scientific Reports</i> , 2019 , 9, 9439	4.9	3
168	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 3118-3131	15.1	12
167	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. <i>ELife</i> , 2019 , 8,	8.9	82
166	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
165	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019 ,	6.5	17
164	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019 , 51, 245-257	36.3	259
163	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019 , 85, 946-955	7.9	35
162	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
161	Repolarization Heterogeneity Measured With T-Wave Area Dispersion in Standard 12-Lead ECG Predicts Sudden Cardiac Death in General Population. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2018 , 11, e005762	6.4	11
160	Contributions of mean and shape of blood pressure distribution to worldwide trends and variations in raised blood pressure: a pooled analysis of 1018 population-based measurement studies with 88.6 million participants. <i>International Journal of Epidemiology</i> , 2018 , 47, 872-883i	7.8	40
159	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
158	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 2941	17.4	262
157	Incidence of complications related to catheter ablation of atrial fibrillation and atrial flutter: a nationwide in-hospital analysis of administrative data for Germany in 2014. <i>European Heart Journal</i> , 2018 , 39, 4020-4029	9.5	62
156	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87	18.3	25
155	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018 , 9, 2282	17.4	147

154	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
153	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
152	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018 , 50, 524-537	36.3	536
151	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. <i>European Heart Journal</i> , 2018 , 39, 3961-3969	9.5	31
150	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. <i>Nature Communications</i> , 2018 , 9, 4919	17.4	4
149	Atrial fibrillation genetic risk differentiates cardioembolic stroke from other stroke subtypes. <i>Neurology: Genetics</i> , 2018 , 4, e293	3.8	19
148	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001758	5.2	14
147	Genetics of the thrombomodulin-endothelial cell protein C receptor system and the risk of early-onset ischemic stroke. <i>PLoS ONE</i> , 2018 , 13, e0206554	3.7	4
146	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
145	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002037	5.2	11
144	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. <i>Molecular Psychiatry</i> , 2017 , 22, 192-201	15.1	31
143	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
142	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. <i>European Journal of Preventive Cardiology</i> , 2017 , 24, 492-504	3.9	16
141	Common coding variant in increases the risk for large artery stroke. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 3613-3618	11.5	28
140	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836	15.1	146
139	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017 , 26, 2346-2363	5.6	17
138	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
137	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105

136	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017 , 8, 15805	17.4	50
135	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	29.02	414
134	and Loci Associate with Plasma Osmolality. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 2311-2321	12.7	14
133	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
132	Association of Atopic Dermatitis with Cardiovascular Risk Factors and Diseases. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 1074-1081	4.3	48
131	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	3.66	310
130	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017 , 8, 744	17.4	37
129	Worldwide trends in body-mass index, underweight, overweight, and obesity from 1975 to 2016: a pooled analysis of 2416 population-based measurement studies in 128.9 million children, adolescents, and adults. <i>Lancet, The</i> , 2017 , 390, 2627-2642	4.0	2980
128	is associated with lacunar ischemic stroke and deep ICH: Meta-analyses among 21,500 cases and 40,600 controls. <i>Neurology</i> , 2017 , 89, 1829-1839	6.5	46
127	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017 , 207, 1275-1283	4	12
126	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
125	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. <i>Scientific Reports</i> , 2017 , 7, 11303	4.9	14
124	Evaluating the Causal Relation of ApoA-IV with Disease-Related Traits - A Bidirectional Two-sample Mendelian Randomization Study. <i>Scientific Reports</i> , 2017 , 7, 8734	4.9	11
123	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017 , 7, 6037	4.9	10
122	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		24
121	Worldwide trends in blood pressure from 1975 to 2015: a pooled analysis of 1479 population-based measurement studies with 19.1 million participants. <i>Lancet, The</i> , 2017 , 389, 37-55	4.0	1100
120	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
119	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. <i>BMC Bioinformatics</i> , 2017 , 18, 429	3.6	0

118	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017 , 127, 1798-1812	15.9	68
117	C-reactive protein upregulates the whole blood expression of CD59 - an integrative analysis. <i>PLoS Computational Biology</i> , 2017 , 13, e1005766	5	19
116	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
115	Exome-wide association study reveals novel susceptibility genes to sporadic dilated cardiomyopathy. <i>PLoS ONE</i> , 2017 , 12, e0172995	3.7	66
114	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017 , 12, e0182472	3.7	8
113	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
112	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
111	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
110	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
109	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016 , 6, 35371	4.9	11
108	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016 , 8, 341ra76	17.5	77
107	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016 , 2, e1501678	14.3	75
106	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. <i>Stroke</i> , 2016 , 47, 307-16	6.7	39
105	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , 2016 , 15, 174-184	24.1	159
104	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016 , 351, 1166-71	33.3	325
103	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016 , 25, 358-70	5.6	54
102	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
101	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325

100	Worldwide trends in diabetes since 1980: a pooled analysis of 751 population-based studies with 4.4 million participants. <i>Lancet, The</i> , 2016 , 387, 1513-1530	40	2039
99	Genetic variants in RFX3 are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016 , 24, 1488-95	5.3	18
98	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016 , 25, 4094-4106	5.6	14
97	ImmunoChip analysis identifies association of the RAD50/IL13 region with human longevity. <i>Aging Cell</i> , 2016 , 15, 585-8	9.9	15
96	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015 , 6, 5890	17.4	489
95	Effects of diabetes definition on global surveillance of diabetes prevalence and diagnosis: a pooled analysis of 96 population-based studies with 331,288 participants. <i>Lancet Diabetes and Endocrinology, the</i> , 2015 , 3, 624-37	18.1	109
94	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
93	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology, the</i> , 2015 , 3, 243-53	18.1	81
92	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
91	Genetically determined height and coronary artery disease. <i>New England Journal of Medicine</i> , 2015 , 372, 1608-18	59.2	152
90	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
89	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
88	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
87	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015 , 87, 1017-29	9.9	83
86	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015 , 126, e19-29	2.2	45
85	Genome-wide association study identifies new susceptibility loci for cutaneous lupus erythematosus. <i>Experimental Dermatology</i> , 2015 , 24, 510-5	4	37
84	Heritability of young- and old-onset ischaemic stroke. <i>European Journal of Neurology</i> , 2015 , 22, 1488-91	6	11
83	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015 , 70, 758-762 ^{2,4}		

82	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
81	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015 , 11, e1005230	6	59
80	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
79	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
78	Heme oxygenase-1 gene promoter microsatellite polymorphism is associated with progressive atherosclerosis and incident cardiovascular disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 229-36	9.4	41
77	META-GSA: Combining Findings from Gene-Set Analyses across Several Genome-Wide Association Studies. <i>PLoS ONE</i> , 2015 , 10, e0140179	3.7	2
76	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. <i>Journal of the American College of Cardiology</i> , 2014 , 63, 1200-1210	15.1	102
75	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. <i>Cell</i> , 2014 , 156, 343-58	56.2	96
74	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. <i>Circulation</i> , 2014 , 130, 1225-35	16.7	143
73	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
72	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014 , 9, 1192-218	28.8	278
71	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
70	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
69	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. <i>Heart Rhythm</i> , 2014 , 11, 471-7	6.7	12
68	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. <i>American Journal of Human Genetics</i> , 2014 , 94, 710-20	11	19
67	No evidence for genome-wide interactions on plasma fibrinogen by smoking, alcohol consumption and body mass index: results from meta-analyses of 80,607 subjects. <i>PLoS ONE</i> , 2014 , 9, e111156	3.7	5
66	Controversial association results for INSIG2 on body mass index may be explained by interactions with age and with MC4R. <i>European Journal of Human Genetics</i> , 2014 , 22, 1217-24	5.3	7
65	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. <i>PLoS Genetics</i> , 2014 , 10, e1004508	6	45

64	Harmonization of study and reference data by PhaseLift: saving time when imputing study data. <i>Genetic Epidemiology</i> , 2014 , 38, 381-8	2.6	1
63	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13127-32	11.5	121
62	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. <i>American Journal of Human Genetics</i> , 2013 , 93, 236-48	11	49
61	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
60	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597
59	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
58	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
57	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
56	Low penetrance susceptibility to glioma is caused by the TP53 variant rs78378222. <i>British Journal of Cancer</i> , 2013 , 108, 2178-85	8.7	42
55	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
54	A regulatory variant in CCR6 is associated with susceptibility to antitopoisomerase-positive systemic sclerosis. <i>Arthritis and Rheumatism</i> , 2013 , 65, 3202-8		25
53	Deciphering the 8q24.21 association for glioma. <i>Human Molecular Genetics</i> , 2013 , 22, 2293-302	5.6	45
52	Empirical hierarchical bayes approach to gene-environment interactions: development and application to genome-wide association studies of lung cancer in TRICL. <i>Genetic Epidemiology</i> , 2013 , 37, 551-559	2.6	5
51	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. <i>Human Molecular Genetics</i> , 2013 , 22, 3381-93	5.6	18
50	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. <i>Blood</i> , 2012 , 120, 4873-81	2.2	65
49	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
48	TGF β receptor gene variants in systemic sclerosis-related pulmonary arterial hypertension: results from a multicentre EUSTAR study of European Caucasian patients. <i>Annals of the Rheumatic Diseases</i> , 2012 , 71, 1900-3	2.4	16
47	Acute air pollution effects on heart rate variability are modified by SNPs involved in cardiac rhythm in individuals with diabetes or impaired glucose tolerance. <i>Environmental Research</i> , 2012 , 112, 177-85	7.9	30

46	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012 , 44, 670-5	36.3	429
45	A meta-analysis of genome-wide association studies of the electrocardiographic early repolarization pattern. <i>Heart Rhythm</i> , 2012 , 9, 1627-34	6.7	53
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41	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012 , 44, 532-538	36.3	94
40	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2011 , 44, 187-92	36.3	244
39	Chromosome 7p11.2 (EGFR) variation influences glioma risk. <i>Human Molecular Genetics</i> , 2011 , 20, 2897-904	36.3	129
38	A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. <i>Human Molecular Genetics</i> , 2011 , 20, 1241-51	5.6	60
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6	Discovering patterns of pleiotropy in genome-wide association studies		1
5	Network reconstruction for trans acting genetic loci using multi-omics data and prior information		3
4	Genome wide association analysis in dilated cardiomyopathy reveals two new key players in systolic heart failure on chromosome 3p25.1 and 22q11.23		1
3	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
2	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
1	Cis-epistasis at the LPA locus and risk of coronary artery disease		1