Thomas Meitinger

List of Publications by Citations

585 papers	83,802 citations	139 h-index	280 g-index
629 ext. papers	98,147 ext. citations	12.6 avg, IF	6.43 L-index

#	Paper	IF	Citations
585	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
584	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
583	Mutations in LRRK2 cause autosomal-dominant parkinsonism with pleomorphic pathology. *Neuron*, **2004**, 44, 601-7	13.9	2228
582	Genomewide association analysis of coronary artery disease. *New England Journal of Medicine*, **2007** , 357, 443-53	59.2	1608
581	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
580	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
579	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
578	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
577	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
576	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
575	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
574	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-11	50.4	1323
573	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
572	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
571	Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23. *Nature Genetics*, **2000**, 26, 345-8	36.3	1224
570	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
569	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970

568	A gene (PEX) with homologies to endopeptidases is mutated in patients with X-linked hypophosphatemic rickets. The HYP Consortium. *Nature Genetics*, **1995**, 11, 130-6	36.3	912
567	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
566	The DNA sequence of the human X chromosome. *Nature*, **2005**, 434, 325-37	50.4	822
565	Polymorphisms in FKBP5 are associated with increased recurrence of depressive episodes and rapid response to antidepressant treatment. *Nature Genetics*, **2004**, 36, 1319-25	36.3	769
564	Range of genetic mutations associated with severe non-syndromic sporadic intellectual disability: an exome sequencing study. *Lancet, The*, **2012**, 380, 1674-82	40	765
563	Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60	50.4	728
562	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
561	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
560	An unusual member of the nuclear hormone receptor superfamily responsible for X-linked adrenal hypoplasia congenita. *Nature*, **1994**, 372, 635-41	50.4	720
559	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708
558	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
557	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675
556	Hypothetical LOC387715 is a second major susceptibility gene for age-related macular degeneration, contributing independently of complement factor H to disease risk. *Human Molecular Genetics*, **2005**, 14, 3227-36	5.6	656
555	Mutations in the DAX-1 gene give rise to both X-linked adrenal hypoplasia congenita and hypogonadotropic hypogonadism. *Nature*, **1994**, 372, 672-6	50.4	656
554	A mutation in VPS35, encoding a subunit of the retromer complex, causes late-onset Parkinson disease. *American Journal of Human Genetics*, **2011**, 89, 168-75	11	624
553	A common genetic variant is associated with adult and childhood obesity. *Science*, **2006**, 312, 279-83	33.3	584
552	Genome-wide, large-scale production of mutant mice by ENU mutagenesis. *Nature Genetics*, **2000**, 25, 444-7	36.3	578
551	Seven new loci associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 433-9, 439e1-2	36.3	577

550	Genome-wide association study of restless legs syndrome identifies common variants in three genomic regions. *Nature Genetics*, **2007**, 39, 1000-6	36.3	545
549	Genetics meets metabolomics: a genome-wide association study of metabolite profiles in human serum. *PLoS Genetics*, **2008**, 4, e1000282	6	538
548	Haploinsufficiency of TBK1 causes familial ALS and fronto-temporal dementia. *Nature Neuroscience*, **2015**, 18, 631-6	25.5	522
547	A genome-wide perspective of genetic variation in human metabolism. *Nature Genetics*, **2010**, 42, 137-41	36.3	515
546	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
545	Mutations in the CEP290 (NPHP6) gene are a frequent cause of Leber congenital amaurosis. *American Journal of Human Genetics*, **2006**, 79, 556-61	11	500
544	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genetics*, **2009**, 5, e1000504	6	495
543	Y-chromosomal diversity in Europe is clinal and influenced primarily by geography, rather than by language. *American Journal of Human Genetics*, **2000**, 67, 1526-43	11	471
542	Novel biomarkers for pre-diabetes identified by metabolomics. *Molecular Systems Biology*, **2012**, 8, 615	12.2	468
541	Mutations in the gene encoding epsilon-sarcoglycan cause myoclonus-dystonia syndrome. *Nature Genetics*, **2001**, 29, 66-9	36.3	458
540	Mutations of SURF-1 in Leigh disease associated with cytochrome c oxidase deficiency. *American Journal of Human Genetics*, **1998**, 63, 1609-21	11	454
539	A common genetic variant in the NOS1 regulator NOS1AP modulates cardiac repolarization. *Nature Genetics*, **2006**, 38, 644-51	36.3	438
538	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
537	Human TUBB3 mutations perturb microtubule dynamics, kinesin interactions, and axon guidance. *Cell*, **2010**, 140, 74-87	56.2	418
536	A gene (RPGR) with homology to the RCC1 guanine nucleotide exchange factor is mutated in X-linked retinitis pigmentosa (RP3). *Nature Genetics*, **1996**, 13, 35-42	36.3	415
535	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	37	414
534	An L-type calcium-channel gene mutated in incomplete X-linked congenital stationary night blindness. *Nature Genetics*, **1998**, 19, 260-3	36.3	400
533	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393

532	The Parkinson disease causing LRRK2 mutation I2020T is associated with increased kinase activity. *Human Molecular Genetics*, **2006**, 15, 223-32	5.6	393
531	New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nature Genetics*, **2009**, 41, 280-2	36.3	389
530	Narcolepsy is strongly associated with the T-cell receptor alpha locus. *Nature Genetics*, **2009**, 41, 708-11	36.3	380
529	Somatic mutations in ATP1A1 and ATP2B3 lead to aldosterone-producing adenomas and secondary hypertension. *Nature Genetics*, **2013**, 45, 440-4, 444e1-2	36.3	375
528	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. *Nature Genetics*, **2009**, 41, 283-5	36.3	374
527	Common variants in KCNN3 are associated with lone atrial fibrillation. *Nature Genetics*, **2010**, 42, 240-4	36.3	362
526	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355
525	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
524	Mutational hot spot within a new RPGR exon in X-linked retinitis pigmentosa. *Nature Genetics*, **2000**, 25, 462-6	36.3	345
523	Genome-wide association study of PR interval. *Nature Genetics*, **2010**, 42, 153-9	36.3	340
522	Mutations in the deubiquitinase gene USP8 cause Cushing© disease. *Nature Genetics*, **2015**, 47, 31-8	36.3	339
521	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
520	Diabetes insipidus, diabetes mellitus, optic atrophy and deafness (DIDMOAD) caused by mutations in a novel gene (wolframin) coding for a predicted transmembrane protein. *Human Molecular Genetics*, **1998**, 7, 2021-8	5.6	330
519	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
518	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
517	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
516	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. *Nature*, **2011**, 478, 97-102	50.4	322
515	SLC2A9 influences uric acid concentrations with pronounced sex-specific effects. *Nature Genetics*, **2008**, 40, 430-6	36.3	317

514	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nature Genetics*, **2013**, 45, 314-8	36.3	314
513	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
512	Genome-wide association study identifies two susceptibility loci for nonsyndromic cleft lip with or without cleft palate. *Nature Genetics*, **2010**, 42, 24-6	36.3	312
511	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. *Nature Genetics*, **2009**, 41, 407-14	36.3	308
510	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
509	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. *Nature Genetics*, **2009**, 41, 879-81	36.3	307
508	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. *Neuron*, **2018**, 97, 1268-1283.e6	13.9	296
507	Constitutive activation of PKA catalytic subunit in adrenal Cushing© syndrome. *New England Journal of Medicine*, **2014**, 370, 1019-28	59.2	284
506	Genetic diagnosis of Mendelian disorders via RNA sequencing. *Nature Communications*, **2017**, 8, 15824	17.4	277
505	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. *Nature Genetics*, **2010**, 42, 869-73	36.3	277
504	Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nature Genetics*, **2013**, 45, 912-917	36.3	276
503	Exome sequencing reveals de novo WDR45 mutations causing a phenotypically distinct, X-linked dominant form of NBIA. *American Journal of Human Genetics*, **2012**, 91, 1144-9	11	268
502	Mutations in a new gene in Ellis-van Creveld syndrome and Weyers acrodental dysostosis. *Nature Genetics*, **2000**, 24, 283-6	36.3	267
501	The autosomal dominant hypophosphatemic rickets (ADHR) gene is a secreted polypeptide overexpressed by tumors that cause phosphate wasting. *Journal of Clinical Endocrinology and Metabolism*, **2001**, 86, 497-500	5.6	264
500	Calmodulin mutations associated with recurrent cardiac arrest in infants. *Circulation*, **2013**, 127, 1009-17	16.7	262
499	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
498	Discovery of sexual dimorphisms in metabolic and genetic biomarkers. *PLoS Genetics*, **2011**, 7, e10022156		256
497	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249

496	Genome-wide association analysis identifies susceptibility loci for migraine without aura. *Nature Genetics*, **2012**, 44, 777-82	36.3	243
495	Genetic structure of Europeans: a view from the North-East. *PLoS ONE*, **2009**, 4, e5472	3.7	237
494	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
493	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. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
492	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
491	Genome-wide scan on total serum IgE levels identifies FCER1A as novel susceptibility locus. *PLoS Genetics*, **2008**, 4, e1000166	6	218
490	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
489	PTPRD (protein tyrosine phosphatase receptor type delta) is associated with restless legs syndrome. *Nature Genetics*, **2008**, 40, 946-8	36.3	217
488	Exome sequencing identifies ACAD9 mutations as a cause of complex I deficiency. *Nature Genetics*, **2010**, 42, 1131-4	36.3	210
487	Isolation of a candidate gene for Norrie disease by positional cloning. *Nature Genetics*, **1992**, 1, 199-203	36.3	207
486	Multiple regions of alpha-synuclein are associated with Parkinson© disease. *Annals of Neurology*, **2005**, 57, 535-41	9.4	206
485	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
484	A common region of 10p deleted in DiGeorge and velocardiofacial syndromes. *Nature Genetics*, **1996**, 13, 458-60	36.3	195
483	Prevalence of refractive error in Europe: the European Eye Epidemiology (E(3)) Consortium. *European Journal of Epidemiology*, **2015**, 30, 305-15	12.1	193
482	Characterization of circular RNAs in human, mouse and rat hearts. *Journal of Molecular and Cellular Cardiology*, **2016**, 98, 103-7	5.8	193
481	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. *Nature*, **2013**, 504, 432-6	50.4	185
480	Sequence variants on chromosome 9p21.3 confer risk for atherosclerotic stroke. *Annals of Neurology*, **2009**, 65, 531-9	9.4	185
479	Common variants in P2RY11 are associated with narcolepsy. *Nature Genetics*, **2011**, 43, 66-71	36.3	184

478	Absence of an orphan mitochondrial protein, c19orf12, causes a distinct clinical subtype of neurodegeneration with brain iron accumulation. *American Journal of Human Genetics*, **2011**, 89, 543-50	11	182
477	Pex gene deletions in Gy and Hyp mice provide mouse models for X-linked hypophosphatemia. *Human Molecular Genetics*, **1997**, 6, 165-71	5.6	181
476	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
475	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
474	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. *BMC Genomics*, **2014**, 15, 823	4.5	168
473	Propeller protein-associated neurodegeneration: a new X-linked dominant disorder with brain iron accumulation. *Brain*, **2013**, 136, 1708-17	11.2	167
472	Loss-of-function mutations in MGME1 impair mtDNA replication and cause multisystemic mitochondrial disease. *Nature Genetics*, **2013**, 45, 214-9	36.3	166
471	Large scale replication and meta-analysis of variants on chromosome 4q25 associated with atrial fibrillation. *European Heart Journal*, **2009**, 30, 813-9	9.5	165
470	Integrative analysis of the mitochondrial proteome in yeast. *PLoS Biology*, **2004**, 2, e160	9.7	165
469	Brief report: intragenic deletion of the KALIG-1 gene in Kallmann© syndrome. *New England Journal of Medicine*, **1992**, 326, 1752-5	59.2	165
468	Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA - Journal of the American Medical Association*, **2009**, 302, 168-78	27.4	164
467	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. *Mechanisms of Ageing and Development*, **2011**, 132, 324-30	5.6	162
466	ALOX5AP gene and the PDE4D gene in a central European population of stroke patients. *Stroke*, **2005**, 36, 731-6	6.7	161
465	Lack of the mitochondrial protein acylglycerol kinase causes Sengers syndrome. *American Journal of Human Genetics*, **2012**, 90, 314-20	11	160
464	Genotypic and phenotypic spectrum of PANK2 mutations in patients with neurodegeneration with brain iron accumulation. *Annals of Neurology*, **2006**, 59, 248-56	9.4	158
463	Prevalence, spectrum, and functional characterization of melanocortin-4 receptor gene mutations in a representative population-based sample and obese adults from Germany. *Journal of Clinical Endocrinology and Metabolism*, **2006**, 91, 1761-9	5.6	158
462	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. *Human Molecular Genetics*, **2009**, 18, 2288-96	5.6	154
461	Molecular modelling of the Norrie disease protein predicts a cystine knot growth factor tertiary structure. *Nature Genetics*, **1993**, 5, 376-80	36.3	154

460	Chronic recurrent multifocal osteomyelitis (CRMO): evidence for a susceptibility gene located on chromosome 18q21.3-18q22. *European Journal of Human Genetics*, **2002**, 10, 217-21	5.3	152
459	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
458	Genetic determinants of circulating sphingolipid concentrations in European populations. *PLoS Genetics*, **2009**, 5, e1000672	6	150
457	NEK1 variants confer susceptibility to amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1037-42	36.3	149
456	Distribution of mutations in the PEX gene in families with X-linked hypophosphataemic rickets (HYP). *Human Molecular Genetics*, **1997**, 6, 539-49	5.6	149
455	Genetic adaptation of fatty-acid metabolism: a human-specific haplotype increasing the biosynthesis of long-chain omega-3 and omega-6 fatty acids. *American Journal of Human Genetics*, **2012**, 90, 809-20	11	148
454	Genetic determinants of serum testosterone concentrations in men. *PLoS Genetics*, **2011**, 7, e1002313	6	148
453	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With ´Coronary Artery ´Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
452	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
451	Molecular diagnosis in mitochondrial complex I deficiency using exome sequencing. *Journal of Medical Genetics*, **2012**, 49, 277-83	5.8	145
450	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
449	Genome-wide association studies of serum magnesium, potassium, and sodium concentrations identify six Loci influencing serum magnesium levels. *PLoS Genetics*, **2010**, 6, e1001045	6	144
448	Novel (ovario) leukodystrophy related to AARS2 mutations. *Neurology*, **2014**, 82, 2063-71	6.5	142
447	Mutations of the mitochondrial-tRNA modifier MTO1 cause hypertrophic cardiomyopathy and lactic acidosis. *American Journal of Human Genetics*, **2012**, 90, 1079-87	11	140
446	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
445	Genomic organization of the human PEX gene mutated in X-linked dominant hypophosphatemic rickets. *Genome Research*, **1997**, 7, 573-85	9.7	137
444	Genome-wide association study identifies novel restless legs syndrome susceptibility loci on 2p14 and 16q12.1. *PLoS Genetics*, **2011**, 7, e1002171	6	135
443	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135

442	Improved proteome analysis of Saccharomyces cerevisiae mitochondria by free-flow electrophoresis. *Proteomics*, **2003**, 3, 906-16	4.8	134
441	Novel calmodulin mutations associated with congenital arrhythmia susceptibility. *Circulation: Cardiovascular Genetics*, **2014**, 7, 466-74		133
440	Genome-wide association study identifies a susceptibility locus at 21q21 for ventricular fibrillation in acute myocardial infarction. *Nature Genetics*, **2010**, 42, 688-691	36.3	132
439	Norrie disease is caused by mutations in an extracellular protein resembling C-terminal globular domain of mucins. *Nature Genetics*, **1992**, 2, 139-43	36.3	132
438	Exome sequencing of 20,791´cases of type 2 diabetes and 24,440´controls. *Nature*, **2019**, 570, 71-76	50.4	129
437	A large candidate gene survey identifies the KCNE1 D85N polymorphism as a possible modulator of drug-induced torsades de pointes. *Circulation: Cardiovascular Genetics*, **2012**, 5, 91-9		127
436	The epsilon-sarcoglycan gene (SGCE), mutated in myoclonus-dystonia syndrome, is maternally imprinted. *European Journal of Human Genetics*, **2003**, 11, 138-44	5.3	124
435	Genetic variation at chromosome 1p13.3 affects sortilin mRNA expression, cellular LDL-uptake and serum LDL levels which translates to the risk of coronary artery disease. *Atherosclerosis*, **2010**, 208, 183-9	3.1	123
434	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
433	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
432	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13127-32	11.5	121
431	Common variants in myocardial ion channel genes modify the QT interval in the general population: results from the KORA study. *Circulation Research*, **2005**, 96, 693-701	15.7	120
430	Directional dominance on stature and cognition in´diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
429	The association of a SNP upstream of INSIG2 with body mass index is reproduced in several but not all cohorts. *PLoS Genetics*, **2007**, 3, e61	6	119
428	Lifelong reduction of LDL-cholesterol related to a common variant in the LDL-receptor gene decreases the risk of coronary artery disease--a Mendelian Randomisation study. *PLoS ONE*, **2008**, 3, e2986	3.7	117
427	Nine loci for ocular axial length identified through genome-wide association studies, including shared loci with refractive error. *American Journal of Human Genetics*, **2013**, 93, 264-77	11	116
426	Genetic regulation of serum phytosterol levels and risk of coronary artery disease. *Circulation: Cardiovascular Genetics*, **2010**, 3, 331-9		116
425	Ghrelin receptor gene: identification of several sequence variants in extremely obese children and adolescents, healthy normal-weight and underweight students, and children with short normal stature. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 157-62	5.6	115

424	CLOCK gene variants associate with sleep duration in two independent populations. *Biological Psychiatry*, **2010**, 67, 1040-7	7.9	114
423	A K(ATP) channel gene effect on sleep duration: from genome-wide association studies to function in Drosophila. *Molecular Psychiatry*, **2013**, 18, 122-32	15.1	113
422	Mutations in the candidate gene for Norrie disease. *Human Molecular Genetics*, **1992**, 1, 461-5	5.6	112
421	The retinitis pigmentosa GTPase regulator, RPGR, interacts with the delta subunit of rod cyclic GMP phosphodiesterase. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 1315-20	11.5	110
420	SNP-based analysis of genetic substructure in the German population. *Human Heredity*, **2006**, 62, 20-9	1.1	109
419	Genome-wide association study of survival from sepsis due to pneumonia: an observational cohort study. *Lancet Respiratory Medicine,the*, **2015**, 3, 53-60	35.1	108
418	Linkage disequilibrium patterns and tagSNP transferability among European populations. *American Journal of Human Genetics*, **2005**, 76, 387-98	11	108
417	Mutations in FBXL4, encoding a mitochondrial protein, cause early-onset mitochondrial encephalomyopathy. *American Journal of Human Genetics*, **2013**, 93, 482-95	11	106
416	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
415	Copy-number variations measured by single-nucleotide-polymorphism oligonucleotide arrays in patients with mental retardation. *American Journal of Human Genetics*, **2007**, 81, 768-79	11	106
414	Hot-spot KIF5A mutations cause familial ALS. *Brain*, **2018**, 141, 688-697	11.2	105
413	ELAC2 mutations cause a mitochondrial RNA processing defect associated with hypertrophic cardiomyopathy. *American Journal of Human Genetics*, **2013**, 93, 211-23	11	104
412	Expression analysis of dopaminergic neurons in Parkinson© disease and aging links transcriptional dysregulation of energy metabolism to cell death. *Acta Neuropathologica*, **2011**, 122, 75-86	14.3	102
411	A new family of interspersed repetitive DNA sequences in the mouse genome. *Journal of Molecular Biology*, **1982**, 157, 453-71	6.5	102
410	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. *PLoS Genetics*, **2013**, 9, e1003796	6	100
409	Riboflavin-Responsive and -Non-responsive Mutations in FAD Synthase Cause Multiple Acyl-CoA Dehydrogenase and Combined Respiratory-Chain Deficiency. *American Journal of Human Genetics*, **2016**, 98, 1130-1145	11	97
408	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. *European Heart Journal*, **2014**, 35, 1069-77	9.5	97
407	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96

406	An isoform of hPANK2, deficient in pantothenate kinase-associated neurodegeneration, localizes to mitochondria. *Human Molecular Genetics*, **2003**, 12, 321-7	5.6	96
405	Mutations in GTPBP3 cause a mitochondrial translation defect associated with hypertrophic cardiomyopathy, lactic acidosis, and encephalopathy. *American Journal of Human Genetics*, **2014**, 95, 708-20	11	95
404	A genome-wide association study identifies three loci associated with mean platelet volume. *American Journal of Human Genetics*, **2009**, 84, 66-71	11	94
403	A novel deletion in progranulin gene is associated with FTDP-17 and CBS. *Neurobiology of Aging*, **2008**, 29, 427-35	5.6	94
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