

Massimo Mangino

List of Publications by Year in descending order

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Version: 2024-02-01

270
papers

77,620
citations

1704

104
h-index

584

262
g-index

305
all docs

305
docs citations

305
times ranked

72862
citing authors

#	ARTICLE	IF	CITATIONS
1	Body mass index mediates the effect of the DASH diet on hypertension: Common metabolites underlying the association. <i>Journal of Human Nutrition and Dietetics</i> , 2022, 35, 214-222.	2.5	6
2	Analysis of antibody binding specificities in twin and SNP-genotyped cohorts reveals that antiviral antibody epitope selection is a heritable trait. <i>Immunity</i> , 2022, 55, 174-184.e5.	14.3	22
3	Metabolome Genome-Wide Association Study Identifies 74 Novel Genomic Regions Influencing Plasma Metabolites Levels. <i>Metabolites</i> , 2022, 12, 61.	2.9	18
4	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	12.8	21
5	Incremental Value of a Panel of Serum Metabolites for Predicting Risk of Atherosclerotic Cardiovascular Disease. <i>Journal of the American Heart Association</i> , 2022, 11, e024590.	3.7	1
6	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. <i>Nature Communications</i> , 2022, 13, 1222.	12.8	5
7	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	3.8	12
8	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	21.4	215
9	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. <i>International Journal of Epidemiology</i> , 2022, 51, 1254-1267.	1.9	20
10	Genome-wide Association Study of Liking for Several Types of Physical Activity in the UK Biobank and Two Replication Cohorts. <i>Medicine and Science in Sports and Exercise</i> , 2022, 54, 1252-1260.	0.4	3
11	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	21.4	142
12	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits. <i>Nature Communications</i> , 2022, 13, 2743.	12.8	22
13	Cross-Sectional Blood Metabolite Markers of Hypertension: A Multicohort Analysis of 44,306 Individuals from the Consortium of METabolomics Studies. <i>Metabolites</i> , 2022, 12, 601.	2.9	6
14	Probable delirium is a presenting symptom of COVID-19 in frail, older adults: a cohort study of 322 hospitalised and 535 community-based older adults. <i>Age and Ageing</i> , 2021, 50, 40-48.	1.6	82
15	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	12.0	79
16	High intake of vegetables is linked to lower white blood cell profile and the effect is mediated by the gut microbiome. <i>BMC Medicine</i> , 2021, 19, 37.	5.5	30
17	Immune Trait Shifts in Association With Tobacco Smoking: A Study in Healthy Women. <i>Frontiers in Immunology</i> , 2021, 12, 637974.	4.8	18
18	The trans-ancestral genomic architecture of glyceic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341

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19	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
20	A Bidirectional Mendelian Randomization Study to evaluate the causal role of reduced blood vitamin D levels with type 2 diabetes risk in South Asians and Europeans. <i>Nutrition Journal</i> , 2021, 20, 71.	3.4	9
21	Vaccine side-effects and SARS-CoV-2 infection after vaccination in users of the COVID Symptom Study app in the UK: a prospective observational study. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 939-949.	9.1	744
22	N-glycosylation of immunoglobulin G predicts incident hypertension. <i>Journal of Hypertension</i> , 2021, 39, 2527-2533.	0.5	13
23	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
24	Genome-Wide Association Study Identifies Two Novel Loci Associated with Female Stress and Urgency Urinary Incontinence. <i>Journal of Urology</i> , 2021, 206, 679-687.	0.4	5
25	Plasma N-glycome shows continuous deterioration as the diagnosis of insulin resistance approaches. <i>BMJ Open Diabetes Research and Care</i> , 2021, 9, e002263.	2.8	13
26	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	28.9	188
27	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. <i>Journal of Human Genetics</i> , 2021, 66, 625-636.	2.3	40
28	Differential associations between a priori diet quality scores and markers of cardiovascular health in women: cross-sectional analyses from TwinsUK. <i>British Journal of Nutrition</i> , 2021, 126, 1017-1027.	2.3	5
29	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
30	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
31	Dietary Influence on Systolic and Diastolic Blood Pressure in the TwinsUK Cohort. <i>Nutrients</i> , 2020, 12, 2130.	4.1	9
32	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.6	26
33	Real-time tracking of self-reported symptoms to predict potential COVID-19. <i>Nature Medicine</i> , 2020, 26, 1037-1040.	30.7	1,173
34	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
35	Human postprandial responses to food and potential for precision nutrition. <i>Nature Medicine</i> , 2020, 26, 964-973.	30.7	418
36	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	9.8	65

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37	Dysregulated Antibody, Natural Killer Cell and Immune Mediator Profiles in Autoimmune Thyroid Diseases. <i>Cells</i> , 2020, 9, 665.	4.1	18
38	Consumption of Stilbenes and Flavonoids is Linked to Reduced Risk of Obesity Independently of Fiber Intake. <i>Nutrients</i> , 2020, 12, 1871.	4.1	19
39	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.	10.3	90
40	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.2	118
41	Genome-wide scan identifies novel genetic loci regulating salivary metabolite levels. <i>Human Molecular Genetics</i> , 2020, 29, 864-875.	2.9	13
42	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	1.9	34
43	Self-Reported Symptoms of COVID-19, Including Symptoms Most Predictive of SARS-CoV-2 Infection, Are Heritable. <i>Twin Research and Human Genetics</i> , 2020, 23, 316-321.	0.6	57
44	Genetic and Environmental Influences of Dietary Indices in a UK Female Twin Cohort. <i>Twin Research and Human Genetics</i> , 2020, 23, 330-337.	0.6	4
45	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. <i>Scientific Reports</i> , 2019, 9, 11623.	3.3	13
46	The CODATwins Project: The Current Status and Recent Findings of COllaborative Project of Development of Anthropometrical Measures in Twins. <i>Twin Research and Human Genetics</i> , 2019, 22, 800-808.	0.6	19
47	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	12.0	75
48	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.	2.8	27
49	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019, 22, 523-529.	0.6	116
50	Metabolomic profiling identifies novel associations with Electrolyte and Acid-Base Homeostatic patterns. <i>Scientific Reports</i> , 2019, 9, 15088.	3.3	7
51	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.2	21
52	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019, 28, 2062-2077.	2.9	40
53	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. <i>American Journal of Epidemiology</i> , 2019, 188, 991-1012.	3.4	81
54	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	21.4	328

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55	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.	1.3	69
56	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
57	A genetic IFN/STAT1/FAS axis determines CD4 T stem cell memory levels and apoptosis in healthy controls and Adult T-cell Leukemia patients. <i>OncoImmunology</i> , 2018, 7, e1426423.	4.6	17
58	Genome-wide association study identifies nine novel loci for 2D:4D finger ratio, a putative retrospective biomarker of testosterone exposure in utero. <i>Human Molecular Genetics</i> , 2018, 27, 2025-2038.	2.9	36
59	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
60	Obligatory and facilitative allelic variation in the DNA methylome within common disease-associated loci. <i>Nature Communications</i> , 2018, 9, 8.	12.8	107
61	Better governance, better access: practising responsible data sharing in the METADAC governance infrastructure. <i>Human Genomics</i> , 2018, 12, 24.	2.9	36
62	Glycosylation Profile of Immunoglobulin G Is Cross-Sectionally Associated With Cardiovascular Disease Risk Score and Subclinical Atherosclerosis in Two Independent Cohorts. <i>Circulation Research</i> , 2018, 122, 1555-1564.	4.5	87
63	Definitive Zygosity Scores in the Peas in the Pod Questionnaire is a Sensitive and Accurate Assessment of the Zygosity of Adult Twins. <i>Twin Research and Human Genetics</i> , 2018, 21, 146-154.	0.6	12
64	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.	3.6	27
65	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
66	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018, 10, 126.	4.1	110
67	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
68	Body mass index is negatively associated with telomere length: a collaborative cross-sectional meta-analysis of 87 observational studies. <i>American Journal of Clinical Nutrition</i> , 2018, 108, 453-475.	4.7	137
69	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	21.4	482
70	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	3.6	19
71	Omega-6 oxylipins generated by soluble epoxide hydrolase are associated with knee osteoarthritis. <i>Journal of Lipid Research</i> , 2018, 59, 1763-1770.	4.2	41
72	Plasma N-glycome composition associates with chronic low back pain. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2124-2133.	2.4	18

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73	Gut microbial diversity is associated with lower arterial stiffness in women. <i>European Heart Journal</i> , 2018, 39, 2390-2397.	2.2	181
74	Reduced telomere length is associated with fibrotic joint disease suggesting that impaired telomere repair contributes to joint fibrosis. <i>PLoS ONE</i> , 2018, 13, e0190120.	2.5	8
75	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	7.1	376
76	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. <i>Nature Genetics</i> , 2017, 49, 568-578.	21.4	341
77	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	2.9	29
78	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
79	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.	12.8	169
80	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
81	Innate and adaptive immune traits are differentially affected by genetic and environmental factors. <i>Nature Communications</i> , 2017, 8, 13850.	12.8	107
82	Higher Nevus Count Exhibits a Distinct DNA Methylation Signature in Healthy Human Skin: Implications for Melanoma. <i>Journal of Investigative Dermatology</i> , 2017, 137, 910-920.	0.7	26
83	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017, 8, 744.	12.8	64
84	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. <i>Nature Communications</i> , 2017, 8, 447.	12.8	102
85	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	2.7	123
86	2SNP heritability and effects of genetic variants for neutrophil-to-lymphocyte and platelet-to-lymphocyte ratio. <i>Journal of Human Genetics</i> , 2017, 62, 979-988.	2.3	32
87	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017, 8, 16015.	12.8	149
88	Differences in genetic and environmental variation in adult BMI by sex, age, time period, and region: an individual-based pooled analysis of 40 twin cohorts. <i>American Journal of Clinical Nutrition</i> , 2017, 106, 457-466.	4.7	107
89	PopPAnTe: population and pedigree association testing for quantitative data. <i>BMC Genomics</i> , 2017, 18, 150.	2.8	6
90	Influence of acquired obesity on coronary vessel wall late gadolinium enhancement in discordant monozygote twins. <i>European Radiology</i> , 2017, 27, 4612-4618.	4.5	4

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91	Acne and Telomere Length: A New Spectrum between Senescence and Apoptosis Pathways. <i>Journal of Investigative Dermatology</i> , 2017, 137, 513-515.	0.7	6
92	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
93	Positive Association Between Vitamin D Serum Levels and Naevus Counts. <i>Acta Dermato-Venereologica</i> , 2017, 97, 321-324.	1.3	6
94	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
95	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. <i>PLoS ONE</i> , 2017, 12, e0167742.	2.5	29
96	Telomeres and the natural lifespan limit in humans. <i>Aging</i> , 2017, 9, 1130-1142.	3.1	82
97	Genetic and environmental influences on adult human height across birth cohorts from 1886 to 1994. <i>ELife</i> , 2016, 5, .	6.0	42
98	Characterizing Blood Metabolomics Profiles Associated with Self-Reported Food Intakes in Female Twins. <i>PLoS ONE</i> , 2016, 11, e0158568.	2.5	92
99	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , 2016, 11, e0153163.	2.5	13
100	Integrated multiomics approach identifies calcium and integrin-binding protein-2 as a novel gene for pulse wave velocity. <i>Journal of Hypertension</i> , 2016, 34, 79-87.	0.5	18
101	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
102	Association of Cross-Sectional and Longitudinal Change in Arterial Stiffness With Gene Expression in the Twins UK Cohort. <i>Hypertension</i> , 2016, 67, 70-76.	2.7	10
103	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
104	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	8.8	183
105	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. <i>Human Molecular Genetics</i> , 2016, 25, ddd334.	2.9	107
106	<sc>GWAS</sc> analysis of handgrip and lower body strength in older adults in the <sc>CHARGE</sc> consortium. <i>Aging Cell</i> , 2016, 15, 792-800.	6.7	51
107	Novel regional age-associated DNA methylation changes within human common disease-associated loci. <i>Genome Biology</i> , 2016, 17, 193.	8.8	29
108	Genetic and environmental effects on body mass index from infancy to the onset of adulthood: an individual-based pooled analysis of 45 twin cohorts participating in the COllaborative project of Development of Anthropometrical measures in Twins (CODATwins) study. <i>American Journal of Clinical Nutrition</i> , 2016, 104, 371-379.	4.7	175

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109	<i>KLB</i> is associated with alcohol drinking, and its gene product β -Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	7.1	208
110	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
111	Genetic and environmental influences on height from infancy to early adulthood: An individual-based pooled analysis of 45 twin cohorts. <i>Scientific Reports</i> , 2016, 6, 28496.	3.3	133
112	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. <i>Scientific Reports</i> , 2016, 6, 20092.	3.3	42
113	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
114	Skin phenotypes can offer some insight about the association between telomere length and cancer susceptibility. <i>Medical Hypotheses</i> , 2016, 97, 7-10.	1.5	10
115	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	12.6	438
116	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	12.8	245
117	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
118	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	2.9	73
119	Glycosylation Profile of IgG in Moderate Kidney Dysfunction. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 933-941.	6.1	75
120	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	2.5	69
121	Metabolomics profiling reveals novel markers for leukocyte telomere length. <i>Aging</i> , 2016, 8, 77-86.	3.1	33
122	Zygoty Differences in Height and Body Mass Index of Twins From Infancy to Old Age: A Study of the CODATwins Project. <i>Twin Research and Human Genetics</i> , 2015, 18, 557-570.	0.6	24
123	The CODATwins Project: The Cohort Description of Collaborative Project of Development of Anthropometrical Measures in Twins to Study Macro-Environmental Variation in Genetic and Environmental Effects on Anthropometric Traits. <i>Twin Research and Human Genetics</i> , 2015, 18, 348-360.	0.6	55
124	Decreasing initial telomere length in humans intergenerationally understates age-associated telomere shortening. <i>Aging Cell</i> , 2015, 14, 669-677.	6.7	24
125	ID: 239. <i>Cytokine</i> , 2015, 76, 109.	3.2	0
126	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.	0.4	0

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127	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.	3.5	331
128	Circulating Proteomic Signatures of Chronological Age. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 809-816.	3.6	106
129	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2015, 44, 578-586.	1.9	123
130	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. <i>Human Genetics</i> , 2015, 134, 823-835.	3.8	133
131	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	12.8	178
132	<i>DCAF4</i> , a novel gene associated with leucocyte telomere length. <i>Journal of Medical Genetics</i> , 2015, 52, 157-162.	3.2	66
133	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
134	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
135	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. <i>Diabetes</i> , 2015, 64, 1841-1852.	0.6	63
136	The Genetic Architecture of the Human Immune System: A Bioresource for Autoimmunity and Disease Pathogenesis. <i>Cell</i> , 2015, 161, 387-403.	28.9	292
137	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
138	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.	3.5	95
139	Paternal age and telomere length in twins: the germ stem cell selection paradigm. <i>Aging Cell</i> , 2015, 14, 701-703.	6.7	38
140	Metabolomic study of carotid-femoral pulse-wave velocity in women. <i>Journal of Hypertension</i> , 2015, 33, 791-796.	0.5	57
141	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.	21.4	357
142	Metabolomic Identification of a Novel Pathway of Blood Pressure Regulation Involving Hexadecanedioate. <i>Hypertension</i> , 2015, 66, 422-429.	2.7	90
143	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	27.8	1,014
144	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. <i>Molecular Psychiatry</i> , 2015, 20, 1232-1239.	7.9	112

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145	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
146	The Rate of Nonallelic Homologous Recombination in Males Is Highly Variable, Correlated between Monozygotic Twins and Independent of Age. PLoS Genetics, 2014, 10, e1004195.	3.5	17
147	Salt-inducible kinase 3, SIK3, is a new gene associated with hearing. Human Molecular Genetics, 2014, 23, 6407-6418.	2.9	30
148	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
149	Estimating telomere length from whole genome sequence data. Nucleic Acids Research, 2014, 42, e75-e75.	14.5	151
150	Genomics of ageing in twins. Proceedings of the Nutrition Society, 2014, 73, 526-531.	1.0	4
151	Interaction between allelic variations in vitamin D receptor and retinoid X receptor genes on metabolic traits. BMC Genetics, 2014, 15, 37.	2.7	12
152	Glycans Are a Novel Biomarker of Chronological and Biological Ages. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2014, 69, 779-789.	3.6	297
153	Lipidomics Profiling and Risk of Cardiovascular Disease in the Prospective Population-Based Bruneck Study. Circulation, 2014, 129, 1821-1831.	1.6	445
154	Gender and telomere length: Systematic review and meta-analysis. Experimental Gerontology, 2014, 51, 15-27.	2.8	394
155	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	21.4	214
156	Association of adiponectin and leptin with relative telomere length in seven independent cohorts including 11,448 participants. European Journal of Epidemiology, 2014, 29, 629-638.	5.7	23
157	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62
158	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
159	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
160	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	6.7	103
161	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology, 2014, 2, 719-729.	11.4	319
162	Genome-Wide Association Study Identifies Variants in Casein Kinase II (<i>CSNK2A2</i>) to be Associated With Leukocyte Telomere Length in a Punjabi Sikh Diabetic Cohort. Circulation: Cardiovascular Genetics, 2014, 7, 287-295.	5.1	46

#	ARTICLE	IF	CITATIONS
163	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
164	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	6.2	104
165	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
166	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
167	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
168	An investigation of rheumatoid arthritis loci in patients with early-onset psoriasis validates association of the <i>REL</i> gene. British Journal of Dermatology, 2013, 168, 864-866.	1.5	11
169	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
170	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
171	Meta-analysis of telomere length in 19,713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	2.8	380
172	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
173	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
174	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
175	Heritability analyses show visit-to-visit blood pressure variability reflects different pathological phenotypes in younger and older adults. Journal of Hypertension, 2013, 31, 2356-2361.	0.5	36
176	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	2.9	104
177	Lower Urinary Tract Symptoms in Men With Parkinson Disease. Journal of Neuroscience Nursing, 2013, 45, 382-392.	1.1	14
178	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. American Journal of Epidemiology, 2013, 178, 451-460.	3.4	51
179	Alcohol-induced metabolomic differences in humans. Translational Psychiatry, 2013, 3, e276-e276.	4.8	79
180	Understanding coronary artery disease using twin studies: Table 1. Heart, 2013, 99, 373-375.	2.9	29

#	ARTICLE	IF	CITATIONS
181	Genome Wide Association Analysis of a Founder Population Identified TAF3 as a Gene for MCHC in Humans. PLoS ONE, 2013, 8, e69206.	2.5	9
182	Glycosylation of Immunoglobulin G: Role of Genetic and Epigenetic Influences. PLoS ONE, 2013, 8, e82558.	2.5	105
183	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormone-Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
184	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	3.5	92
185	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
186	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. Molecular Psychiatry, 2012, 17, 1116-1129.	7.9	112
187	Genome-wide association and functional studies identify the <i>DOT1L</i> gene to be involved in cartilage thickness and hip osteoarthritis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8218-8223.	7.1	154
188	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. Human Molecular Genetics, 2012, 21, 5385-5394.	2.9	210
189	A Discovery Genome-Wide Association Study of Entrepreneurship. International Journal of Developmental Sciences, 2012, 6, 127-135.	0.5	10
190	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
191	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
192	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	3.5	620
193	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
194	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
195	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
196	Differential profile analysis of urinary cytokines in patients with overactive bladder: comment. International Urogynecology Journal, 2012, 23, 1141-1141.	1.4	4
197	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289
198	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855

#	ARTICLE	IF	CITATIONS
199	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	27.8	401
200	Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011, 477, 54-60.	27.8	916
201	Genetic architecture of circulating lipid levels. <i>European Journal of Human Genetics</i> , 2011, 19, 813-819.	2.8	23
202	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	2.8	460
203	A polymorphism associated with entrepreneurship: evidence from dopamine receptor candidate genes. <i>Small Business Economics</i> , 2011, 36, 151-155.	6.7	53
204	Leukocyte telomere length and marital status among middle-aged adults. <i>Age and Ageing</i> , 2011, 40, 73-78.	1.6	35
205	Genome-wide association and genetic functional studies identify <i>AUTS2</i> gene (<i>AUTS2</i>) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7119-7124.	7.1	258
206	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403
207	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	21.4	367
208	Multiple Loci Are Associated with White Blood Cell Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002113.	3.5	106
209	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. <i>PLoS Genetics</i> , 2011, 7, e1002333.	3.5	29
210	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. <i>PLoS Genetics</i> , 2011, 7, e1002025.	3.5	87
211	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. <i>PLoS Medicine</i> , 2011, 8, e1001116.	8.4	446
212	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. <i>PLoS ONE</i> , 2011, 6, e19382.	2.5	56
213	Large Scale Replication Study of the Association between HLA Class II/BTNL2 Variants and Osteoarthritis of the Knee in European-Descent Populations. <i>PLoS ONE</i> , 2011, 6, e23371.	2.5	32
214	Quantitative Trait Loci for CD4:CD8 Lymphocyte Ratio Are Associated with Risk of Type 1 Diabetes and HIV-1 Immune Control. <i>American Journal of Human Genetics</i> , 2010, 86, 88-92.	6.2	80
215	IRF4 Variants Have Age-Specific Effects on Nevus Count and Predispose to Melanoma. <i>American Journal of Human Genetics</i> , 2010, 87, 6-16.	6.2	114
216	Genetic variation in the <i>SMAD3</i> gene is associated with hip and knee osteoarthritis. <i>Arthritis and Rheumatism</i> , 2010, 62, 2347-2352.	6.7	145

#	ARTICLE	IF	CITATIONS
217	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	27.8	3,249
218	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
219	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	21.4	518
220	Sequence variants at CHRN3, CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	21.4	649
221	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
222	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
223	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
224	A Common Variant in the Telomerase RNA Component Is Associated with Short Telomere Length. <i>PLoS ONE</i> , 2010, 5, e13048.	2.5	39
225	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387
226	Genome-wide association identifies <i>OBFC1</i> as a locus involved in human leukocyte telomere biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9293-9298.	7.1	244
227	Genome-Wide Association Study Identifies Two Novel Regions at 11p15.5-p13 and 1p31 with Major Impact on Acute-Phase Serum Amyloid A. <i>PLoS Genetics</i> , 2010, 6, e1001213.	3.5	24
228	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
229	Common variants near TERC are associated with mean telomere length. <i>Nature Genetics</i> , 2010, 42, 197-199.	21.4	296
230	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. <i>Lancet</i> , 2010, 376, 180-188.	13.7	1,385
231	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.5	453
232	A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. <i>Journal of Medical Genetics</i> , 2009, 46, 451-454.	3.2	76
233	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. <i>PLoS Genetics</i> , 2009, 5, e1000504.	3.5	572
234	An obesogenic postnatal environment is more important than the fetal environment for the development of adult adiposity: a study of female twins. <i>American Journal of Clinical Nutrition</i> , 2009, 90, 401-406.	4.7	29

#	ARTICLE	IF	CITATIONS
235	Bivariate genetic modelling of the response to an oral glucose tolerance challenge: A gene × environment interaction approach. <i>Diabetologia</i> , 2009, 52, 1048-1055.	6.3	5
236	Heritability of insulin sensitivity and lipid profile depend on BMI: evidence for gene × obesity interaction. <i>Diabetologia</i> , 2009, 52, 2578-2584.	6.3	24
237	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	21.4	1,572
238	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. <i>Nature Genetics</i> , 2009, 41, 1182-1190.	21.4	481
239	Association analysis of IL-12B and IL-23R polymorphisms in myocardial infarction. <i>Journal of Molecular Medicine</i> , 2008, 86, 99-103.	3.9	20
240	Lack of association of genetic variants in the LRP8 gene with familial and sporadic myocardial infarction. <i>Journal of Molecular Medicine</i> , 2008, 86, 1163-1170.	3.9	6
241	The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. <i>Journal of Molecular Medicine</i> , 2008, 86, 1233-1241.	3.9	80
242	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	21.4	742
243	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	21.4	1,179
244	Arachidonate 5-lipoxygenase (5-LO) promoter genotype and risk of myocardial infarction: A case × control study. <i>Atherosclerosis</i> , 2008, 199, 328-332.	0.8	23
245	Repeated Replication and a Prospective Meta-Analysis of the Association Between Chromosome 9p21.3 and Coronary Artery Disease. <i>Circulation</i> , 2008, 117, 1675-1684.	1.6	356
246	A regulatory SNP of the BICD1 gene contributes to telomere length variation in humans. <i>Human Molecular Genetics</i> , 2008, 17, 2518-2523.	2.9	58
247	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. <i>PLoS ONE</i> , 2008, 3, e2986.	2.5	137
248	Genomewide Association Analysis of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2007, 357, 443-453.	27.0	1,865
249	Leukotriene B4 production in healthy subjects carrying variants of the arachidonate 5-lipoxygenase-activating protein gene associated with a risk of myocardial infarction. <i>Clinical Science</i> , 2007, 112, 411-416.	4.3	17
250	LGALS2 functional variant rs7291467 is not associated with susceptibility to myocardial infarction in Caucasians. <i>Atherosclerosis</i> , 2007, 194, 112-115.	0.8	20
251	Enhanced linkage of a locus on chromosome 2 to premature coronary artery disease in the absence of hypercholesterolemia. <i>European Journal of Human Genetics</i> , 2007, 15, 313-319.	2.8	16
252	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. <i>Nature</i> , 2007, 447, 661-678.	27.8	8,895

#	ARTICLE	IF	CITATIONS
253	Mapping of a Major Locus that Determines Telomere Length in Humans. American Journal of Human Genetics, 2005, 76, 147-151.	6.2	243
254	A Genomewide Linkage Study of 1,933 Families Affected by Premature Coronary Artery Disease: The British Heart Foundation (BHF) Family Heart Study. American Journal of Human Genetics, 2005, 77, 1011-1020.	6.2	105
255	Hereditary gingival fibromatosis (HGF) with hypertrichosis is unlinked to the HGF1 and HGF2 loci. American Journal of Medical Genetics Part A, 2003, 116A, 312-314.	2.4	16
256	A gene for familial isolated chronic nail candidiasis maps to chromosome 11p12-q12.1. European Journal of Human Genetics, 2003, 11, 433-436.	2.8	10
257	Mapping of a new autosomal dominant non-syndromic hearing loss locus (DFNA43) to chromosome 2p12. Journal of Medical Genetics, 2003, 40, 278-281.	3.2	8
258	Familial chronic nail candidiasis with ICAM-1 deficiency: a new form of chronic mucocutaneous candidiasis. Journal of Medical Genetics, 2002, 39, 671-675.	3.2	25
259	Identification of a novel NOG gene mutation (P35S) in an Italian family with symphalangism. Human Mutation, 2002, 19, 308-308.	2.5	102
260	Assignment of a locus for autosomal dominant idiopathic scoliosis (IS) to human chromosome 17p11. Human Genetics, 2002, 111, 401-404.	3.8	125
261	Three novel mutations causing a truncated protein within the RP2 gene in Italian families with X-linked retinitis pigmentosa. Mutation Research - Mutation Research Genomics, 2001, 432, 79-82.	1.1	1
262	Identification of novel RP2 mutations in a subset of X-linked retinitis pigmentosa families and prediction of new domains. Human Mutation, 2001, 18, 109-119.	2.5	39
263	Mapping of a new autosomal dominant nonsyndromic hearing loss locus (DFNA30) to chromosome 15q25-26. European Journal of Human Genetics, 2001, 9, 667-671.	2.8	11
264	A Novel Mutation (R271X) in the Myotubularin Gene Causes a Severe Miotubular Myopathy. Human Heredity, 1999, 49, 59-60.	0.8	8
265	Mutation analysis of the RPGR gene reveals novel mutations in south European patients with X-linked retinitis pigmentosa. European Journal of Human Genetics, 1999, 7, 687-694.	2.8	30
266	A single-nucleotide polymorphism in the human bone morphogenetic protein-4 (BMP 4) gene. Journal of Human Genetics, 1999, 44, 76-77.	2.3	19
267	Localization of a Gene for Familial Patella Aplasia-Hypoplasia (PTLAH) to Chromosome 17q21-q22. American Journal of Human Genetics, 1999, 65, 441-447.	6.2	27
268	First-trimester prenatal diagnosis of Ellis-van Creveld syndrome using linked microsatellite markers. Prenatal Diagnosis, 1998, 18, 504-506.	2.3	0
269	Two new missense mutations (A105T and C110G) in the Norrin gene in two Italian families with Norrie disease and familial exudative vitreoretinopathy. , 1997, 72, 242-244.		17
270	Real-time tracking of self-reported symptoms to predict potential COVID-19. , 0, .		1