Tom R Gaunt

List of Publications by Year
in descending order

261 papers	35,044 citations	10373 72 h-index	5118 166 g-index
332 all docs	332 docs citations	332 times ranked	45420 citing authors

#	Article	IF	Citations
1	Machine learning improves mortality risk prediction after cardiac surgery: Systematic review and meta-analysis. Journal of Thoracic and Cardiovascular Surgery, 2022, 163, 2075-2087.e9.	0.4	49
2	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	0.9	39
3	Linking Physical Activity to Breast Cancer via Sex Steroid Hormones, Part 2: The Effect of Sex Steroid Hormones on Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 28-37.	1.1	19
4	Linking Physical Activity to Breast Cancer via Sex Hormones, Part 1: The Effect of Physical Activity on Sex Steroid Hormones. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 16-27.	1.1	12
5	The Effect of Circulating Zinc, Selenium, Copper and Vitamin K1 on COVID-19 Outcomes: A Mendelian Randomization Study. Nutrients, 2022, 14, 233.	1.7	21
6	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
7	Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes. Diabetologia, 2022, 65, 790-799.	2.9	9
8	The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 2022, 7, 41.	0.9	45
9	Reply to Janssen et al. Comment on â€œSobczyk, M.K.; Gaunt, T.R. The Effect of Circulating Zinc, Selenium, Copper and Vitamin K1 on COVID-19 Outcomes: A Mendelian Randomization Study. Nutrients 2022, 14, 233â€. Nutrients, 2022, 14, 1113.	1.7	5
10	Phenotypic Causal Inference Using Genome-Wide Association Study Data: Mendelian Randomization and Beyond. Annual Review of Biomedical Data Science, 2022, 5, 1-17.	2.8	5
11	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. International Journal of Epidemiology, 2022, 51, 1254-1267.	0.9	20
12	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	1.5	12
13	The impact of fatty acids biosynthesis on the risk of cardiovascular diseases in Europeans and East Asians: a Mendelian randomization study. Human Molecular Genetics, 2022, 31, 4034-4054.	1.4	5
14	Multi-ancestry Mendelian randomization of omics traits revealing drug targets of COVID-19 severity. EBioMedicine, 2022, 81, 104112.	2.7	7
15	Prediction of driver variants in the cancer genome via machine learning methodologies. Briefings in Bioinformatics, 2021, 22, .	3.2	13
16	Platelet Glycoprotein Ib Î±â€Chain as a Putative Therapeutic Target for Juvenile Idiopathic Arthritis: A Mendelian Randomization Study. Arthritis and Rheumatology, 2021, 73, 693-701.	2.9	8
17	EpiGraphDB: a database and data mining platform for health data science. Bioinformatics, 2021, 37, 1304-1311.	1.8	30
18	Computational Tools for Causal Inference in Genetics. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039248.	2.9	3

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19	MELODI Presto: a fast and agile tool to explore semantic triples derived from biomedical literature. Bioinformatics, 2021, 37, 583-585.	1.8	14
20	Establishing reference intervals for triglyceride-containing lipoprotein subfraction metabolites measured using nuclear magnetic resonance spectroscopy in a UK population. Annals of Clinical Biochemistry, 2021, 58, 47-53.	0.8	2
21	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224.	1.5	43
22	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	1.4	32
23	The variant call format provides efficient and robust storage of GWAS summary statistics. Genome Biology, 2021, 22, 32.	3.8	82
24	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. Journal of Investigative Dermatology, 2021, 141, 2620-2629.	0.3	12
25	The causal effects of serum lipids and apolipoproteins on kidney function: multivariable and bidirectional Mendelian-randomization analyses. International Journal of Epidemiology, 2021, 50, 1569-1579.	0.9	18
26	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	2.8	23
27	Association of physical activity intensity and bout length with mortality: An observational study of 79,503 UK Biobank participants. PLoS Medicine, 2021, 18, e1003757.	3.9	17
28	221Association of physical activity bout length and changing intensity with mortality in UK Biobank. International Journal of Epidemiology, 2021, 50, .	0.9	0
29	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
30	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
31	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. Human Molecular Genetics, 2021, 30, 119-134.	1.4	65
32	MendelVar: gene prioritization at GWAS loci using phenotypic enrichment of Mendelian disease genes. Bioinformatics, 2021, 37, 1-8.	1.8	12
33	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. Nature Communications, 2021, 12, 5640.	5.8	57
34	Validation of lipid-related therapeutic targets for coronary heart disease prevention using human genetics. Nature Communications, 2021, 12, 6120.	5.8	13
35	An informatics consult approach for generating clinical evidence for treatment decisions. BMC Medical Informatics and Decision Making, 2021, 21, 281.	1.5	8
36	Linking Physical Activity to Breast Cancer: Text Mining Results and a Protocol for Systematically Reviewing Three Potential Mechanistic Pathways. Cancer Epidemiology Biomarkers and Prevention, 2021, , .	1.1	9

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37	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	9.4	223
38	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature Communications, 2020, 11, 185.	5.8	45
39	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
40	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131.	9.4	298
41	Can machine learning improve mortality prediction following cardiac surgery?. European Journal of Cardio-thoracic Surgery, 2020, 58, 1130-1136.	0.6	29
42	Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. American Journal of Human Genetics, 2020, 106, 885-892.	2.6	51
43	Haptoglobin genotype and outcome after spontaneous intracerebral haemorrhage. Journal of Neurology, Neurosurgery and Psychiatry, 2020, 91, 298-304.	0.9	4
44	Circulating Fatty Acids and Risk of Coronary Heart Disease and Stroke: Individual Participant Data Metaâ€Analysis in Up to 16Â126 Participants. Journal of the American Heart Association, 2020, 9, e013131.	1.6	36
45	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. Clinical Epigenetics, 2020, 12, 95.	1.8	6
46	Mendelian Randomization Analysis Reveals a Causal Effect of Urinary Sodium/Urinary Creatinine Ratio on Kidney Function in Europeans. Frontiers in Bioengineering and Biotechnology, 2020, 8, 662.	2.0	3
47	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. American Journal of Human Genetics, 2020, 106, 315-326.	2.6	32
48	Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. Nature Communications, 2020, 11, 1010.	5.8	58
49	Associations between high blood pressure and DNA methylation. PLoS ONE, 2020, 15, e0227728.	1.1	37
50	Haptoglobin genotype and outcome after aneurysmal subarachnoid haemorrhage. Journal of Neurology, Neurosurgery and Psychiatry, 2020, 91, 305-313.	0.9	11
51	CScape-somatic: distinguishing driver and passenger point mutations in the cancer genome. Bioinformatics, 2020, 36, 3637-3644.	1.8	19
52	Opportunities and Challenges in Functional Genomics Research in Osteoporosis: Report From a Workshop Held by the Causes Working Group of the Osteoporosis and Bone Research Academy of the Royal Osteoporosis Society on October 5th 2020. Frontiers in Endocrinology, 2020, 11, 630875.	1.5	5
53	Triglyceride-containing lipoprotein sub-fractions and risk of coronary heart disease and stroke: A prospective analysis in 11,560 adults. European Journal of Preventive Cardiology, 2020, 27, 1617-1626.	0.8	19
54	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0

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55	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
56	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
57	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
58	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
59	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
60	Integrating Mendelian randomization and multiple-trait colocalization to uncover cell-specific inflammatory drivers of autoimmune and atopic disease. Human Molecular Genetics, 2019, 28, 3293-3300.	1.4	27
61	Availability of public databases for triangulation of findings. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15766-15767.	3.3	2
62	Appraising the causal relevance of DNA methylation for risk of lung cancer. International Journal of Epidemiology, 2019, 48, 1493-1504.	0.9	53
63	Estimating the Frequency of Single Point Driver Mutations across Common Solid Tumours. Scientific Reports, 2019, 9, 13452.	1.6	6
64	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	5.8	30
65	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	9.4	331
66	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. Genome Medicine, 2019, 11, 6.	3.6	30
67	Searching for the causal effects of body mass index in over 300 000 participants in UK Biobank, using Mendelian randomization. PLoS Genetics, 2019, 15, e1007951.	1.5	70
68	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	1.3	73
69	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. Diabetes, 2019, 68, 1681-1691.	0.3	79
70	Genetic determinants of circulating haptoglobin concentration. Clinica Chimica Acta, 2019, 494, 138-142.	0.5	14
71	Leveraging brain cortex-derived molecular data to elucidate epigenetic and transcriptomic drivers of complex traits and disease. Translational Psychiatry, 2019, 9, 105.	2.4	15
72	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. Human Genomics, 2019, 13, 6.	1.4	25

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73	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113.	0.9	52
74	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113.	0.9	47
75	Association of copy number variation across the genome with neuropsychiatric traits in the general population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 489-502.	1.1	26
76	Longitudinal analysis strategies for modelling epigenetic trajectories. International Journal of Epidemiology, 2018, 47, 516-525.	0.9	10
77	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. Human Molecular Genetics, 2018, 27, 1301-1308.	1.4	102
78	MELODI: Mining Enriched Literature Objects to Derive Intermediates. International Journal of Epidemiology, 2018, 47, 369-379.	0.9	15
79	The long-term impact of folic acid in pregnancy on offspring DNA methylation: follow-up of the Aberdeen Folic Acid Supplementation Trial (AFAST). International Journal of Epidemiology, 2018, 47, 928-937.	0.9	56
80	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. Development and Psychopathology, 2018, 30, 383-397.	1.4	43
81	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
82	FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. Bioinformatics, 2018, 34, 511-513.	1.8	296
83	Cardiometabolic phenotypes and mitochondrial DNA copy number in two cohorts of UK women. Mitochondrion, 2018, 39, 9-19.	1.6	13
84	A Methylomeâ€Wide Association Study of Trajectories of Oppositional Defiant Behaviors and Biological Overlap With Attention Deficit Hyperactivity Disorder. Child Development, 2018, 89, 1839-1855.	1.7	17
85	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. Oral Oncology, 2018, 85, 87-94.	0.8	17
86	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 2018, 7, .	3.3	46
87	Software Application Profile: PHESANT: a tool for performing automated phenome scans in UK Biobank. International Journal of Epidemiology, 2018, 47, 29-35.	0.9	151
88	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	2.8	3,639
89	Inflammation-related epigenetic risk and child and adolescent mental health: A prospective study from pregnancy to middle adolescence. Development and Psychopathology, 2018, 30, 1145-1156.	1.4	39
90	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. Epigenetics and Chromatin, 2018, 11, 25.	1.8	130

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91	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	1.4	22
92	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. Human Molecular Genetics, 2018, 27, 3293-3304.	1.4	57
93	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. Molecular Psychiatry, 2017, 22, 250-256.	4.1	124
94	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. International Journal of Epidemiology, 2017, 46, dyw307.	0.9	86
95	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
96	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 2017, 66, 1713-1722.	0.3	32
97	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus. Circulation, 2017, 135, 2373-2388.	1.6	304
98	A pathway-centric approach to rare variant association analysis. European Journal of Human Genetics, 2017, 25, 123-129.	1.4	13
99	Identifying low density lipoprotein cholesterol associated variants in the Annexin A2 (ANXA2) gene. Atherosclerosis, 2017, 261, 60-68.	0.4	18
100	HIPred: an integrative approach to predicting haploinsufficient genes. Bioinformatics, 2017, 33, 1751-1757.	1.8	36
101	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
102	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
103	Does milk intake promote prostate cancer initiation or progression via effects on insulin-like growth factors (IGFs)? A systematic review and meta-analysis. Cancer Causes and Control, 2017, 28, 497-528.	0.8	65
104	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
105	Developing the WCRF International/University of Bristol Methodology for Identifying and Carrying Out Systematic Reviews of Mechanisms of Exposureâ€“Cancer Associations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1667-1675.	1.1	25
106	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. American Journal of Human Genetics, 2017, 101, 590-602.	2.6	65
107	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. Scientific Reports, 2017, 7, 11597.	1.6	52
108	Variation in DNA methylation of the oxytocin receptor gene predicts children's resilience to prenatal stress. Development and Psychopathology, 2017, 29, 1663-1674.	1.4	50

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109	GTB â€“ an online genome tolerance browser. BMC Bioinformatics, 2017, 18, 20.	1.2	3
110	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
111	Prenatal unhealthy diet, insulinâ€like growth factor 2 gene (<scp>IGF</scp>2) methylation, and attention deficit hyperactivity disorder symptoms in youth with earlyâ€onset conduct problems. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 19-27.	3.1	70
112	Frequency of KLK3 gene deletions in the general population. Annals of Clinical Biochemistry, 2017, 54, 472-480.	0.8	0
113	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. Bioinformatics, 2017, 33, 79-86.	1.8	4
114	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	1.8	822
115	Metabolic Profiling of Adiponectin Levels in Adults. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	26
116	Functional Analysis of the Coronary Heart Disease Risk Locus on Chromosome 21q22. Disease Markers, 2017, 2017, 1-10.	0.6	6
117	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
118	Maternal eating disorders affect offspring cord blood DNA methylation: a prospective study. Clinical Epigenetics, 2017, 9, 120.	1.8	15
119	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. Clinical Epigenetics, 2017, 9, 112.	1.8	60
120	An integrative approach to predicting the functional effects of small indels in non-coding regions of the human genome. BMC Bioinformatics, 2017, 18, 442.	1.2	34
121	Physical activity phenotyping with activity bigrams, and their association with BMI. International Journal of Epidemiology, 2017, 46, 1857-1870.	0.9	7
122	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. Wellcome Open Research, 2017, 2, 118.	0.9	3
123	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. Wellcome Open Research, 2017, 2, 118.	0.9	3
124	Predicting the Pathogenic Impact of Sequence Variation in the Human Genome. Studies in Health Technology and Informatics, 2017, 235, 91-95.	0.2	0
125	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. Human Molecular Genetics, 2016, 25, 4339-4349.	1.4	11
126	Diagnosis of Coronary Heart Diseases Using Gene Expression Profiling; Stable Coronary Artery Disease, Cardiac Ischemia with and without Myocardial Necrosis. PLoS ONE, 2016, 11, e0149475.	1.1	10

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127	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. PLoS ONE, 2016, 11, e0153803.	1.1	6
128	Texture analysis in gel electrophoresis images using an integrative kernel-based approach. Scientific Reports, 2016, 6, 19256.	1.6	17
129	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. Translational Psychiatry, 2016, 6, e976-e976.	2.4	86
130	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	1.6	14
131	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
132	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	3.8	489
133	Metabolic Characterization of a Rare Genetic Variation Within APOC3 and Its Lipoprotein Lipaseâ€"Independent Effects. Circulation: Cardiovascular Genetics, 2016, 9, 231-239.	5.1	28
134	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
135	Assessing the role of insulinâ€like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. International Journal of Cancer, 2016, 139, 1520-1533.	2.3	26
136	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. Annals of Human Genetics, 2016, 80, 187-196.	0.3	41
137	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	5.5	122
138	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	0.9	94
139	DNA Methylation and BMI: Investigating Identified Methylation Sites at HIF3A in a Causal Framework. Diabetes, 2016, 65, 1231-1244.	0.3	95
140	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. Epigenetics, 2016, 11, 140-149.	1.3	80
141	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
142	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
143	Prenatal and early life influences on epigenetic age in children: a study of motherâ€"offspring pairs from two cohort studies. Human Molecular Genetics, 2016, 25, 191-201.	1.4	205
144	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. European Journal of Human Genetics, 2016, 24, 106-112.	1.4	23

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145	Incorporating Non-Coding Annotations into Rare Variant Analysis. PLoS ONE, 2016, 11, e0154181.	1.1	10
146	Replication and Characterization of Association between ABO SNPs and Red Blood Cell Traits by Meta-Analysis in Europeans. PLoS ONE, 2016, 11, e0156914.	1.1	22
147	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.2	2
148	Proxy Molecular Diagnosis from Whole-Exome Sequencing Reveals Papillon-Lefevre Syndrome Caused by a Missense Mutation in CTSC. PLoS ONE, 2015, 10, e0121351.	1.1	4
149	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. BioMed Research International, 2015, 2015, 1-16.	0.9	7
150	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
151	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	3.8	143
152	Maternal pre-pregnancy BMI and gestational weight gain, offspring DNA methylation and later offspring adiposity: findings from the Avon Longitudinal Study of Parents and Children. International Journal of Epidemiology, 2015, 44, 1288-1304.	0.9	244
153	Sequential data selection for predicting the pathogenic effects of sequence variation. , 2015, , .		1
154	Longitudinal analysis of DNA methylation associated with birth weight and gestational age. Human Molecular Genetics, 2015, 24, 3752-3763.	1.4	120
155	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
156	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
157	Mosaic structural variation in children with developmental disorders. Human Molecular Genetics, 2015, 24, 2733-2745.	1.4	54
158	Texture classification using feature selection and kernel-based techniques. Soft Computing, 2015, 19, 2469-2480.	2.1	30
159	Metabolite Profiling and Cardiovascular Event Risk. Circulation, 2015, 131, 774-785.	1.6	547
160	Prenatal exposure to maternal smoking and offspring DNA methylation across the lifecourse: findings from the Avon Longitudinal Study of Parents and Children (ALSPAC). Human Molecular Genetics, 2015, 24, 2201-2217.	1.4	345
161	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 526-534.	5.5	396
162	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	1.5	107

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163	Prenatal Exposure to Maternal Cigarette Smoking and DNA Methylation: Epigenome-Wide Association in a Discovery Sample of Adolescents and Replication in an Independent Cohort at Birth through 17 Years of Age. Environmental Health Perspectives, 2015, 123, 193-199.	2.8	178
164	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
165	An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics, 2015, 31, 1536-1543.	1.8	524
166	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
167	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. Cancer Causes and Control, 2015, 26, 1603-1616.	0.8	77
168	TCTEX1D2 mutations underlie Jeune asphyxiating thoracic dystrophy with impaired retrograde intraflagellar transport. Nature Communications, 2015, 6, 7074.	5.8	51
169	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
170	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300
171	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.3	91
172	eNOS and coronary artery disease: Publication bias and the eclipse of hypothesis-driven meta-analysis in genetic association studies. Gene, 2015, 556, 257-258.	1.0	9
173	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
174	Influence of Adiposity-Related Genetic Markers in a Population of Saudi Arabians Where Other Variables Influencing Obesity May Be Reduced. Disease Markers, 2014, 2014, 1-6.	0.6	21
175	Haptoglobin Duplicon, Hemoglobin, and Vitamin C: Analyses in the British Womenâ€™s Heart and Health Study and Caerphilly Prospective Study. Disease Markers, 2014, 2014, 1-5.	0.6	5
176	Canonical Correlation Analysis for Gene-Based Pleiotropy Discovery. PLoS Computational Biology, 2014, 10, e1003876.	1.5	27
177	A pathway-based data integration framework for prediction of disease progression. Bioinformatics, 2014, 30, 838-845.	1.8	67
178	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
179	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	1.4	28
180	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62

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