Thomas Illig

List of Publications by Year in descending order

62 papers	24,100 citations	81743 39 h-index	110170 64 g-index
65 all docs	65 docs citations	65 times ranked	33864 citing authors

#	Article	IF	Citations
1	Validation and clinical application of transactivation assays for RUNX1 variant classification. Blood Advances, 2022, , .	2.5	5
2	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
3	The Hannover Unified Biobank (HUB) â€“ Centralized Standardised Biobanking at Hannover Medical School. Open Journal of Bioresources, 2021, 8, .	1.5	1
4	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. Scientific Reports, 2019, 9, 8887.	1.6	55
5	High-throughput DNA methylation analysis in anorexia nervosa confirms TNXB hypermethylation. World Journal of Biological Psychiatry, 2018, 19, 187-199.	1.3	28
6	Differentially expressed genes and canonical pathway expression in human atherosclerotic plaques â€“ Tampere Vascular Study. Scientific Reports, 2017, 7, 41483.	1.6	52
7	Stability of targeted metabolite profiles of urine samples under different storage conditions. Metabolomics, 2017, 13, 4.	1.4	50
8	Blood pathway analyses reveal differences between prediabetic subjects with or without dyslipidaemia. The Cardiovascular Risk in Young Finns Study. Diabetes/Metabolism Research and Reviews, 2017, 33, e2914.	1.7	3
9	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
10	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
11	Differentially expressed genes and canonical pathways in the ascending thoracic aortic aneurysm â€“ The Tampere Vascular Study. Scientific Reports, 2017, 7, 12127.	1.6	20
12	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
13	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
14	Metabolomic Signature of Coronary Artery Disease in Type 2 Diabetes Mellitus. International Journal of Endocrinology, 2017, 2017, 1-9.	0.6	6
15	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. PLoS ONE, 2016, 11, e0153163.	1.1	13
16	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
17	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolismâ€”The Young Finns Study. Scientific Reports, 2016, 6, 38262.	1.6	62
18	Association of common variants identified by recent genome-wide association studies with obesity in Chinese children: a case-control study. BMC Medical Genetics, 2016, 17, 7.	2.1	35

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19	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
20	Talin and vinculin are downregulated in atherosclerotic plaque; Tampere Vascular Study. Atherosclerosis, 2016, 255, 43-53.	0.4	35
21	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
22	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
23	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
24	Extensive alterations of the whole-blood transcriptome are associated with body mass index: results of an mRNA profiling study involving two large population-based cohorts. BMC Medical Genomics, 2015, 8, 65.	0.7	40
25	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
26	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	5.8	178
27	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
28	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
29	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	2.6	163
30	Kindlin 3 (FERMT3) is associated with unstable atherosclerotic plaques, anti-inflammatory type II macrophages and upregulation of beta-2 integrins in all major arterial beds. Atherosclerosis, 2015, 242, 145-154.	0.4	29
31	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. European Heart Journal, 2015, 36, 1669-1675.	1.0	26
32	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. Diabetes Care, 2015, 38, 1858-1867.	4.3	97
33	Characterization of whole-genome autosomal differences of DNA methylation between men and women. Epigenetics and Chromatin, 2015, 8, 43.	1.8	176
34	Activated immuneâ€“inflammatory pathways are associated with long-standing depressive symptoms: Evidence from gene-set enrichment analyses in the Young Finns Study. Journal of Psychiatric Research, 2015, 71, 120-125.	1.5	19
35	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
36	Spinocerebellar ataxia type 36 exists in diverse populations and can be caused by a short hexanucleotide GGCCTG repeat expansion. Journal of Neurology, Neurosurgery and Psychiatry, 2015, 86, 986-995.	0.9	49

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37	Identification of novel immune phenotypes for allergic andÂnonallergic childhood asthma. Journal of Allergy and Clinical Immunology, 2015, 135, 81-91.	1.5	132
38	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	1.1	8
39	Antioxidant Defense Enzyme Genes and Asthma Susceptibility: Gender-Specific Effects and Heterogeneity in Gene-Gene Interactions between Pathogenetic Variants of the Disease. BioMed Research International, 2014, 2014, 1-17.	0.9	18
40	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
41	Metabolite profiling reveals new insights into the regulation of serum urate in humans. Metabolomics, 2014, 10, 141-151.	1.4	51
42	Associations between thyroid hormones and serum metabolite profiles in an euthyroid population. Metabolomics, 2014, 10, 152-164.	1.4	21
43	Changes in metabolite profiles caused by genetically determined obesity in mice. Metabolomics, 2014, 10, 461-472.	1.4	20
44	Blood microRNA profile associates with the levels of serum lipids and metabolites associated with glucose metabolism and insulin resistance and pinpoints pathways underlying metabolic syndrome. Molecular and Cellular Endocrinology, 2014, 391, 41-49.	1.6	65
45	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
46	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
47	Comparative analysis of plasma metabolomics response to metabolic challenge tests in healthy subjects and influence of the FTO obesity risk allele. Metabolomics, 2014, 10, 386-401.	1.4	16
48	Mitochondrial DNA Variants in Obesity. PLoS ONE, 2014, 9, e94882.	1.1	26
49	Blood cis-eQTL Analysis Fails to Identify Novel Association Signals among Sub-Threshold Candidates from Genome-Wide Association Studies in Restless Legs Syndrome. PLoS ONE, 2014, 9, e98092.	1.1	2
50	Metabolomics reveals determinants of weight loss during lifestyle intervention in obese children. Metabolomics, 2013, 9, 1157-1167.	1.4	22
51	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
52	Identification of Serum Metabolites Associated With Risk of Type 2 Diabetes Using a Targeted Metabolomic Approach. Diabetes, 2013, 62, 639-648.	0.3	820
53	Identification and MS-assisted interpretation of genetically influenced NMR signals in human plasma. Genome Medicine, 2013, 5, 13.	3.6	23
54	Human serum metabolic profiles are age dependent. Aging Cell, 2012, 11, 960-967.	3.0	271

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55	Novel biomarkers for preâ€diabetes identified by metabolomics. Molecular Systems Biology, 2012, 8, 615.	3.2	605
56	Human metabolic individuality in biomedical and pharmaceutical research. Nature, 2011, 477, 54-60.	13.7	916
57	Discovery of Sexual Dimorphisms in Metabolic and Genetic Biomarkers. PLoS Genetics, 2011, 7, e1002215.	1.5	328
58	A genome-wide perspective of genetic variation in human metabolism. Nature Genetics, 2010, 42, 137-141.	9.4	618
59	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
60	Metabolic Footprint of Diabetes: A Multiplatform Metabolomics Study in an Epidemiological Setting. PLoS ONE, 2010, 5, e13953.	1.1	501
61	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
62	SNPs of the FADS Gene Cluster are Associated with Polyunsaturated Fatty Acids in a Cohort of Patients with Cardiovascular Disease. Lipids, 2008, 43, 289-299.	0.7	218