

Thomas Illig

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

24,100
citations

81900

39
h-index

110387

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. <i>Blood Advances</i> , 2022, , .	5.2	5
2	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
3	The Hannover Unified Biobank (HUB) â€œ Centralized Standardised Biobanking at Hannover Medical School. <i>Open Journal of Bioresources</i> , 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. <i>Scientific Reports</i> , 2019, 9, 8887.	3.3	55
5	High-throughput DNA methylation analysis in anorexia nervosa confirms <i>TNXB</i> hypermethylation. <i>World Journal of Biological Psychiatry</i> , 2018, 19, 187-199.	2.6	28
6	Differentially expressed genes and canonical pathway expression in human atherosclerotic plaques â€œ Tampere Vascular Study. <i>Scientific Reports</i> , 2017, 7, 41483.	3.3	52
7	Stability of targeted metabolite profiles of urine samples under different storage conditions. <i>Metabolomics</i> , 2017, 13, 4.	3.0	50
8	Blood pathway analyses reveal differences between prediabetic subjects with or without dyslipidaemia. The Cardiovascular Risk in Young Finns Study. <i>Diabetes/Metabolism Research and Reviews</i> , 2017, 33, e2914.	4.0	3
9	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
10	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
11	Differentially expressed genes and canonical pathways in the ascending thoracic aortic aneurysm â€œ The Tampere Vascular Study. <i>Scientific Reports</i> , 2017, 7, 12127.	3.3	20
12	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
13	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
14	Metabolomic Signature of Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>International Journal of Endocrinology</i> , 2017, 2017, 1-9.	1.5	6
15	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , 2016, 11, e0153163.	2.5	13
16	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
17	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolismâ€œThe Young Finns Study. <i>Scientific Reports</i> , 2016, 6, 38262.	3.3	62
18	Association of common variants identified by recent genome-wide association studies with obesity in Chinese children: a case-control study. <i>BMC Medical Genetics</i> , 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. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
20	Talin and vinculin are downregulated in atherosclerotic plaque; Tampere Vascular Study. <i>Atherosclerosis</i> , 2016, 255, 43-53.	0.8	35
21	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131
22	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
23	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	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. <i>BMC Medical Genomics</i> , 2015, 8, 65.	1.5	40
25	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
26	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
27	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
28	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
29	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. <i>American Journal of Human Genetics</i> , 2015, 96, 104-120.	6.2	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. <i>Atherosclerosis</i> , 2015, 242, 145-154.	0.8	29
31	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. <i>European Heart Journal</i> , 2015, 36, 1669-1675.	2.2	26
32	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> , 2015, 38, 1858-1867.	8.6	97
33	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015, 8, 43.	3.9	176
34	Activated immune-inflammatory pathways are associated with long-standing depressive symptoms: Evidence from gene-set enrichment analyses in the Young Finns Study. <i>Journal of Psychiatric Research</i> , 2015, 71, 120-125.	3.1	19
35	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
36	Spinocerebellar ataxia type 36 exists in diverse populations and can be caused by a short hexanucleotide GGCCTG repeat expansion. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2015, 86, 986-995.	1.9	49

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37	Identification of novel immune phenotypes for allergic and nonallergic childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 81-91.	2.9	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. <i>PLoS ONE</i> , 2014, 9, e111156.	2.5	8
39	Antioxidant Defense Enzyme Genes and Asthma Susceptibility: Gender-Specific Effects and Heterogeneity in Gene-Gene Interactions between Pathogenetic Variants of the Disease. <i>BioMed Research International</i> , 2014, 2014, 1-17.	1.9	18
40	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. <i>American Journal of Human Genetics</i> , 2014, 94, 349-360.	6.2	158
41	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , 2014, 10, 141-151.	3.0	51
42	Associations between thyroid hormones and serum metabolite profiles in an euthyroid population. <i>Metabolomics</i> , 2014, 10, 152-164.	3.0	21
43	Changes in metabolite profiles caused by genetically determined obesity in mice. <i>Metabolomics</i> , 2014, 10, 461-472.	3.0	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. <i>Molecular and Cellular Endocrinology</i> , 2014, 391, 41-49.	3.2	65
45	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
46	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
47	Comparative analysis of plasma metabolomics response to metabolic challenge tests in healthy subjects and influence of the FTO obesity risk allele. <i>Metabolomics</i> , 2014, 10, 386-401.	3.0	16
48	Mitochondrial DNA Variants in Obesity. <i>PLoS ONE</i> , 2014, 9, e94882.	2.5	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. <i>PLoS ONE</i> , 2014, 9, e98092.	2.5	2
50	Metabolomics reveals determinants of weight loss during lifestyle intervention in obese children. <i>Metabolomics</i> , 2013, 9, 1157-1167.	3.0	22
51	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
52	Identification of Serum Metabolites Associated With Risk of Type 2 Diabetes Using a Targeted Metabolomic Approach. <i>Diabetes</i> , 2013, 62, 639-648.	0.6	820
53	Identification and MS-assisted interpretation of genetically influenced NMR signals in human plasma. <i>Genome Medicine</i> , 2013, 5, 13.	8.2	23
54	Human serum metabolic profiles are age dependent. <i>Aging Cell</i> , 2012, 11, 960-967.	6.7	271

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55	Novel biomarkers for pre-diabetes identified by metabolomics. <i>Molecular Systems Biology</i> , 2012, 8, 615.	7.2	605
56	Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011, 477, 54-60.	27.8	916
57	Discovery of Sexual Dimorphisms in Metabolic and Genetic Biomarkers. <i>PLoS Genetics</i> , 2011, 7, e1002215.	3.5	328
58	A genome-wide perspective of genetic variation in human metabolism. <i>Nature Genetics</i> , 2010, 42, 137-141.	21.4	618
59	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
60	Metabolic Footprint of Diabetes: A Multiplatform Metabolomics Study in an Epidemiological Setting. <i>PLoS ONE</i> , 2010, 5, e13953.	2.5	501
61	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
62	SNPs of the <i>FADS</i> Gene Cluster are Associated with Polyunsaturated Fatty Acids in a Cohort of Patients with Cardiovascular Disease. <i>Lipids</i> , 2008, 43, 289-299.	1.7	218