

Taru Tukiainen

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

18,586
citations

304743

22
h-index

526287

27
g-index

31
all docs

31
docs citations

31
times ranked

45689
citing authors

#	ARTICLE	IF	CITATIONS
1	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. <i>European Journal of Human Genetics</i> , 2021, 29, 615-624.	2.8	17
2	WGS and RNA Studies Diagnose Noncoding <i>DMMD</i> Variants in Males With High Creatine Kinase. <i>Neurology: Genetics</i> , 2021, 7, e554.	1.9	21
3	Molecular pathways behind acquired obesity: Adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI. <i>Cell Reports Medicine</i> , 2021, 2, 100226.	6.5	31
4	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002725.	3.6	60
5	Hydroxysteroid 17- β dehydrogenase 13 variant increases phospholipids and protects against fibrosis in nonalcoholic fatty liver disease. <i>JCI Insight</i> , 2020, 5, .	5.0	62
6	LIN28B affects gene expression at the hypothalamic-pituitary axis and serum testosterone levels. <i>Scientific Reports</i> , 2019, 9, 18060.	3.3	5
7	Transient modification of lin28b expression - permanent effects on zebrafish growth. <i>Molecular and Cellular Endocrinology</i> , 2019, 479, 61-70.	3.2	4
8	A recurrent COL6A1 pseudoexon insertion causes muscular dystrophy and is effectively targeted by splice-correction therapies. <i>JCI Insight</i> , 2019, 4, .	5.0	33
9	Impaired hepatic lipid synthesis from polyunsaturated fatty acids in TM6SF2 E167K variant carriers with NAFLD. <i>Journal of Hepatology</i> , 2017, 67, 128-136.	3.7	97
10	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	516
11	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
12	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	27.8	764
13	Variants in the Oxidoreductase PYROXD1 Cause Early-Onset Myopathy with Internalized Nuclei and Myofibrillar Disorganization. <i>American Journal of Human Genetics</i> , 2016, 99, 1086-1105.	6.2	45
14	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	27.8	9,051
15	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, 35278.	3.3	25
16	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016, 7, 11122.	12.8	576
17	Analysis of the <i>ACTN3</i> heterozygous genotype suggests that β -actinin-3 controls sarcomeric composition and muscle function in a dose-dependent fashion. <i>Human Molecular Genetics</i> , 2016, 25, 866-877.	2.9	35
18	Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. <i>PLoS Genetics</i> , 2016, 12, e1006379.	3.5	20

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19	The landscape of genomic imprinting across diverse adult human tissues. <i>Genome Research</i> , 2015, 25, 927-936.	5.5	216
20	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
21	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
22	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
23	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	3.5	351
24	Chromosome X-Wide Association Study Identifies Loci for Fasting Insulin and Height and Evidence for Incomplete Dosage Compensation. <i>PLoS Genetics</i> , 2014, 10, e1004127.	3.5	61
25	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. <i>Nature Genetics</i> , 2012, 44, 269-276.	21.4	516
26	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. <i>Human Molecular Genetics</i> , 2012, 21, 1444-1455.	2.9	89
27	High-throughput serum NMR metabonomics for cost-effective holistic studies on systemic metabolism. <i>Analyst</i> , The, 2009, 134, 1781.	3.5	491