Tuuli Lappalainen

List of Publications by Year
in descending order

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75 papers	34,561 citations	50170 46 h-index	71532 76 g-index
102 all docs	102 docs citations	102 times ranked	57484 citing authors

#	Article	IF	Citations
1	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	1.5	14
2	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	1.1	13
3	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	2.6	7
4	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131, .	2.0	20
5	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. Cell, 2021, 184, 92-105.e16.	13.5	480
6	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	3.8	150
7	Genetic and non-genetic factors affecting the expression of COVID-19-relevant genes in the large airway epithelium. Genome Medicine, 2021, 13, 66.	3.6	21
8	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
9	An autoimmune disease risk variant: A trans master regulatory effect mediated by IRF1 under immune stimulation?. PLoS Genetics, 2021, 17, e1009684.	1.5	17
10	From variant to function in human disease genetics. Science, 2021, 373, 1464-1468.	6.0	75
11	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
12	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
13	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	6.0	89
14	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	6.0	210
15	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
16	A polyclonal allelic expression assay for detecting regulatory effects of transcript variants. Genome Medicine, 2020, 12, 79.	3.6	5
17	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
18	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	13.5	147

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19	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	6.0	99
20	Genomic Analysis in the Age of Human Genome Sequencing. Cell, 2019, 177, 70-84.	13.5	205
21	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS Genetics, 2019, 15, e1008481.	1.5	20
22	Identifying Genes Whose Mutant Transcripts Cause Dominant Disease Traits by Potential Gain-of-Function Alleles. American Journal of Human Genetics, 2018, 103, 171-187.	2.6	160
23	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	9.4	167
24	MBV: a method to solve sample mislabeling and detect technical bias in large combined genotype and sequencing assay datasets. Bioinformatics, 2017, 33, 1895-1897.	1.8	43
25	Associating cellular epigenetic models with human phenotypes. Nature Reviews Genetics, 2017, 18, 441-451.	7.7	257
26	SnapShot: Discovering Genetic Regulatory Variants by QTL Analysis. Cell, 2017, 171, 980-980.e1.	13.5	10
27	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
28	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
29	Quantifying the regulatory effect size of cis-acting genetic variation using allelic fold change. Genome Research, 2017, 27, 1872-1884.	2.4	114
30	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	5.8	157
31	Preeclampsia does not share common risk alleles in 9p21 with coronary artery disease and type 2 diabetes. Annals of Medicine, 2016, 48, 330-336.	1.5	2
32	DNA Methylation Profiling of Uniparental Disomy Subjects Provides a Map of Parental Epigenetic Bias in the Human Genome. American Journal of Human Genetics, 2016, 99, 555-566.	2.6	66
33	Concerted Genetic Function in Blood Traits. Cell, 2016, 167, 1167-1169.	13.5	4
34	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	1.6	28
35	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. Nature Communications, 2016, 7, 12817.	5.8	105
36	Voices of biotech. Nature Biotechnology, 2016, 34, 270-275.	9.4	4

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37	From trainee to tenure-track: ten tips. Genome Biology, 2015, 16, 132.	3.8	2
38	Tools and best practices for data processing in allelic expression analysis. Genome Biology, 2015, 16, 195.	3.8	335
39	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	2.4	216
40	Tissue-Specific Effects of Genetic and Epigenetic Variation on Gene Regulation and Splicing. PLoS Genetics, 2015, 11, e1004958.	1.5	185
41	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	6.0	1,127
42	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
43	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
44	Assessing allele-specific expression across multiple tissues from RNA-seq read data. Bioinformatics, 2015, 31, 2497-2504.	1.8	90
45	Functional genomics bridges the gap between quantitative genetics and molecular biology. Genome Research, 2015, 25, 1427-1431.	2.4	63
46	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. Nature Genetics, 2015, 47, 88-91.	9.4	215
47	Tandem RNA Chimeras Contribute to Transcriptome Diversity in Human Population and Are Associated with Intronic Genetic Variants. PLoS ONE, 2014, 9, e104567.	1.1	31
48	Allelic mapping bias in RNA-sequencing is not a major confounder in eQTL studies. Genome Biology, 2014, 15, 467.	3.8	67
49	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. PLoS Genetics, 2014, 10, e1004549.	1.5	49
50	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
51	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	1.5	55
52	Gene Age Predicts the Strength of Purifying Selection Acting on Gene Expression Variation in Humans. American Journal of Human Genetics, 2014, 95, 660-674.	2.6	35
53	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. Bioinformatics, 2014, 30, 165-171.	1.8	21
54	Genetic interactions affecting human gene expression identified by variance association mapping. ELife, 2014, 3, e01381.	2.8	137

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55	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
56	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. Science, 2013, 342, 744-747.	6.0	364
57	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	9.4	251
58	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
59	Janusâ€"a comprehensive tool investigating the two faces of transcription. Bioinformatics, 2013, 29, 1600-1606.	1.8	2
60	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
61	Passive and active DNA methylation and the interplay with genetic variation in gene regulation. ELife, 2013, 2, e00523.	2.8	374
62	Sex-biased genetic effects on gene regulation in humans. Genome Research, 2012, 22, 2368-2375.	2.4	92
63	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
64	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
65	Swedish Population Substructure Revealed by Genome-Wide Single Nucleotide Polymorphism Data. PLoS ONE, 2011, 6, e16747.	1.1	39
66	Epistatic Selection between Coding and Regulatory Variation in Human Evolution and Disease. American Journal of Human Genetics, 2011, 89, 459-463.	2.6	73
67	Rare and Common Regulatory Variation in Population-Scale Sequenced Human Genomes. PLoS Genetics, 2011, 7, e1002144.	1.5	98
68	Distinct Variants at LIN28B Influence Growth in Height from Birth to Adulthood. American Journal of Human Genetics, 2010, 86, 773-782.	2.6	81
69	Genomic landscape of positive natural selection in Northern European populations. European Journal of Human Genetics, 2010, 18, 471-478.	1.4	31
70	Evolutionary history of regulatory variation in human populations. Human Molecular Genetics, 2010, 19, R197-R203.	1.4	10
71	Population Structure in Contemporary Swedenâ€"A Yâ€€Chromosomal and Mitochondrial DNA Analysis. Annals of Human Genetics, 2009, 73, 61-73.	0.3	36
72	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. BMC Genetics, 2008, 9, 54.	2.7	31

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73	Migration Waves to the Baltic Sea Region. Annals of Human Genetics, 2008, 72, 337-348.	0.3	63
74	Genome-Wide Analysis of Single Nucleotide Polymorphisms Uncovers Population Structure in Northern Europe. PLoS ONE, 2008, 3, e3519.	1.1	112
75	Regional differences among the Finns: A Y-chromosomal perspective. Gene, 2006, 376, 207-215.	1.0	67