Urmo VÃµsa

List of Publications by Year
in descending order

35 papers	7,065 citations	236833 25 h-index	330025 37 g-index
52 all docs	52 docs citations	52 times ranked	13513 citing authors

#	Article	IF	Citations
1	Genetic analysis of over half a million people characterises C-reactive protein loci. Nature Communications, 2022, 13, 2198.	5.8	48
2	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
3	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
4	Small RNA expression and miRNA modification dynamics in human oocytes and early embryos. Genome Research, 2021, 31, 1474-1485.	2.4	10
5	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
6	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
7	Differences in local population history at the finest level: the case of the Estonian population. European Journal of Human Genetics, 2020, 28, 1580-1591.	1.4	23
8	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	0.7	14
9	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	1.2	38
10	Systematic Prioritization of Candidate Genes in Disease Loci Identifies TRAFD1 as a Master Regulator of IFNÎ³ Signaling in Celiac Disease. Frontiers in Genetics, 2020, 11, 562434.	1.1	20
11	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. Nature Communications, 2019, 10, 3300.	5.8	193
12	High-throughput identification of human SNPs affecting regulatory element activity. Nature Genetics, 2019, 51, 1160-1169.	9.4	157
13	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
14	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. Human Genetics, 2019, 138, 375-388.	1.8	6
15	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. Nature Genetics, 2019, 51, 600-605.	9.4	854
16	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
17	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	2.8	170
18	Gene co-expression analysis for functional classification and geneâ€“disease predictions. Briefings in Bioinformatics, 2018, 19, bbw139.	3.2	718

#	Article	IF	Citations
19	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature Genetics, 2018, 50, 1524-1532.	9.4	97
20	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
21	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. Nature Immunology, 2018, 19, 776-786.	7.0	103
22	Endothelial TLR4 and the microbiome drive cerebral cavernous malformations. Nature, 2017, 545, 305-310.	13.7	247
23	Optimizing bone morphogenic protein 4-mediated human embryonic stem cell differentiation into trophoblast-like cells using fibroblast growth factor 2 and transforming growth factor-Î²/activin/nodal signalling inhibition. Reproductive BioMedicine Online, 2017, 35, 253-263.	1.1	11
24	Meta-signature of human endometrial receptivity: a meta-analysis and validation study of transcriptomic biomarkers. Scientific Reports, 2017, 7, 10077.	1.6	182
25	Whole-genome expression analysis reveals genes associated with treatment response to escitalopram in major depression. European Neuropsychopharmacology, 2016, 26, 1475-1483.	0.3	22
26	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	9.4	494
27	Altered Gene Expression Associated with microRNA Binding Site Polymorphisms. PLoS ONE, 2015, 10, e0141351.	1.1	29
28	Tissue-specific mitochondrial heteroplasmy at position 16,093 within the same individual. Current Genetics, 2014, 60, 11-16.	0.8	20
29	Comprehensive Meta-analysis of MicroRNA Expression Using a Robust Rank Aggregation Approach. Methods in Molecular Biology, 2014, 1182, 361-373.	0.4	36
30	Metaâ€analysis of microRNA expression in lung cancer. International Journal of Cancer, 2013, 132, 2884-2893.	2.3	195
31	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247
32	Whole-exome sequencing identifies a polymorphism in the BMP5 gene associated with SSRI treatment response in major depression. Journal of Psychopharmacology, 2013, 27, 915-920.	2.0	31
33	Methylation Markers of Early-Stage Non-Small Cell Lung Cancer. PLoS ONE, 2012, 7, e39813.	1.1	62
34	Identification of miRâ€374a as a prognostic marker for survival in patients with earlyâ€stage nonsmall cell lung cancer. Genes Chromosomes and Cancer, 2011, 50, 812-822.	1.5	116
35	Metagenes Associated with Survival in Non-Small Cell Lung Cancer. Cancer Informatics, 2011, 10, CIN.S7135.	0.9	9