Jonas Carlsson AlmlÃ¶f

List of Publications by Year
in descending order

17 papers	3,067 citations	686830 13 h-index	887659 17 g-index
17 all docs	17 docs citations	17 times ranked	8049 citing authors

#	Article	IF	Citations
1	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
2	Transancestral mapping and genetic load in systemic lupus erythematosus. Nature Communications, 2017, 8, 16021.	5.8	314
3	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	9.4	251
4	Genome-wide DNA methylation analysis in multiple tissues in primary SjÃ¶gren's syndrome reveals regulatory effects at interferon-induced genes. Annals of the Rheumatic Diseases, 2016, 75, 2029-2036.	0.5	180
5	DNA methylation mapping identifies gene regulatory effects in patients with systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2018, 77, 736-743.	0.5	135
6	Whole-genome sequencing identifies complex contributions to genetic risk by variants in genes causing monogenic systemic lupus erythematosus. Human Genetics, 2019, 138, 141-150.	1.8	63
7	Novel risk genes for systemic lupus erythematosus predicted by random forest classification. Scientific Reports, 2017, 7, 6236.	1.6	54
8	Shared and Unique Patterns of DNA Methylation in Systemic Lupus Erythematosus and Primary SjÃ¶gren's Syndrome. Frontiers in Immunology, 2019, 10, 1686.	2.2	39
9	Powerful Identification of Cis-regulatory SNPs in Human Primary Monocytes Using Allele-Specific Gene Expression. PLoS ONE, 2012, 7, e52260.	1.1	36
10	Deep targeted sequencing in pediatric acute lymphoblastic leukemia unveils distinct mutational patterns between genetic subtypes and novel relapse-associated genes. Oncotarget, 2016, 7, 64071-64088.	0.8	36
11	CopyNumber450kCancer: baseline correction for accurate copy number calling from the 450k methylation array. Bioinformatics, 2016, 32, 1080-1082.	1.8	31
12	Allelic expression mapping across cellular lineages to establish impact of nonâ€coding <scp>SNP</scp>s. Molecular Systems Biology, 2014, 10, 754.	3.2	21
13	Basic Tilted Helix Bundle â€“ A new protein fold in human FKBP25/FKBP3 and HectD1. Biochemical and Biophysical Research Communications, 2014, 447, 26-31.	1.0	14
14	Function of multiple sclerosis-protective HLA class I alleles revealed by genome-wide protein-quantitative trait loci mapping of interferon signalling. PLoS Genetics, 2020, 16, e1009199.	1.5	12
15	Variants in BANK1 are associated with lupus nephritis of European ancestry. Genes and Immunity, 2021, 22, 194-202.	2.2	9
16	Single Nucleotide Polymorphisms with Cis-Regulatory Effects on Long Non-Coding Transcripts in Human Primary Monocytes. PLoS ONE, 2014, 9, e102612.	1.1	9
17	Contributions of de novo variants to systemic lupus erythematosus. European Journal of Human Genetics, 2021, 29, 184-193.	1.4	6