

# Margus Lukk

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2730685/publications.pdf>

Version: 2024-02-01

18  
papers

2,772  
citations

567281

15  
h-index

839539

18  
g-index

20  
all docs

20  
docs citations

20  
times ranked

6181  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020, 583, 265-270.	27.8	36
2	Crisflash: open-source software to generate CRISPR guide RNAs against genomes annotated with individual variation. <i>Bioinformatics</i> , 2019, 35, 3146-3147.	4.1	31
3	Mutational landscape of a chemically-induced mouse model of liver cancer. <i>Journal of Hepatology</i> , 2018, 69, 840-850.	3.7	97
4	Identification of Cancer Related Genes Using a Comprehensive Map of Human Gene Expression. <i>PLoS ONE</i> , 2016, 11, e0157484.	2.5	36
5	Successful transmission and transcriptional deployment of a human chromosome via mouse male meiosis. <i>ELife</i> , 2016, 5, .	6.0	4
6	Enhancer Evolution across 20 Mammalian Species. <i>Cell</i> , 2015, 160, 554-566.	28.9	671
7	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. <i>ELife</i> , 2014, 3, e02626.	6.0	84
8	Aberrant methylation of tRNA links cellular stress to neurodevelopmental disorders. <i>EMBO Journal</i> , 2014, 33, 2020-2039.	7.8	490
9	Latent Regulatory Potential of Human-Specific Repetitive Elements. <i>Molecular Cell</i> , 2013, 49, 262-272.	9.7	62
10	AHT-ChIP-seq: a completely automated robotic protocol for high-throughput chromatin immunoprecipitation. <i>Genome Biology</i> , 2013, 14, R124.	9.6	28
11	Global Gene Expression Profiling Reveals SPINK1 as a Potential Hepatocellular Carcinoma Marker. <i>PLoS ONE</i> , 2013, 8, e59459.	2.5	67
12	MageComet-web application for harmonizing existing large-scale experiment descriptions. <i>Bioinformatics</i> , 2012, 28, 1402-1403.	4.1	1
13	Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , 2011, 12, 137.	2.6	71
14	ArrayExpress update--an archive of microarray and high-throughput sequencing-based functional genomics experiments. <i>Nucleic Acids Research</i> , 2011, 39, D1002-D1004.	14.5	285
15	A global map of human gene expression. <i>Nature Biotechnology</i> , 2010, 28, 322-324.	17.5	315
16	MAGETabulator, a suite of tools to support the microarray data format MAGE-TAB. <i>Bioinformatics</i> , 2009, 25, 279-280.	4.1	14
17	ArrayExpress update--from an archive of functional genomics experiments to the atlas of gene expression. <i>Nucleic Acids Research</i> , 2009, 37, D868-D872.	14.5	380
18	Importing ArrayExpress datasets into R/Bioconductor. <i>Bioinformatics</i> , 2009, 25, 2092-2094.	4.1	100