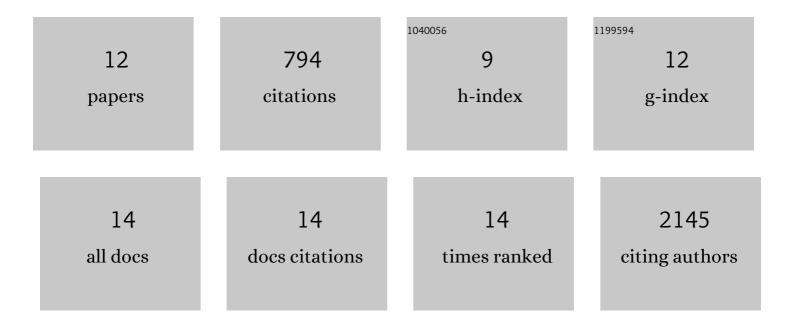
## Aliaksei Z Holik

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4098217/publications.pdf Version: 2024-02-01



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#	Article	IF	CITATIONS
1	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. Nucleic Acids Research, 2015, 43, e97-e97.	14.5	430
2	Dual inhibition of BCL-XL and MCL-1 is required to induce tumour regression in lung squamous cell carcinomas sensitive to FGFR inhibition. Oncogene, 2018, 37, 4475-4488.	5.9	75
3	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. Epigenetics and Chromatin, 2016, 9, 16.	3.9	63
4	Repression of <i>lgf1</i> expression by Ezh2 prevents basal cell differentiation in the developing lung. Development (Cambridge), 2015, 142, 1458-69.	2.5	48
5	Brg1 Loss Attenuates Aberrant Wnt-Signalling and Prevents Wnt-Dependent Tumourigenesis in the Murine Small Intestine. PLoS Genetics, 2014, 10, e1004453.	3.5	37
6	Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, Iqaa073.	3.2	37
7	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	14.5	34
8	Brg1 is required for stem cell maintenance in the murine intestinal epithelium in a tissue-specific manner. Stem Cells, 2013, 31, 2457-2466.	3.2	31
9	Cisplatin Increases Sensitivity to FGFR Inhibition in Patient-Derived Xenograft Models of Lung Squamous Cell Carcinoma. Molecular Cancer Therapeutics, 2017, 16, 1610-1622.	4.1	22
10	The LIM-domain only protein 4 contributes to lung epithelial cell proliferation but is not essential for tumor progression. Respiratory Research, 2015, 16, 67.	3.6	6
11	Quantitative proteomic analysis of EZH2 inhibition in acute myeloid leukemia reveals the targets and pathways that precede the induction of cell death. Proteomics - Clinical Applications, 2017, 11, 1700013.	1.6	5
12	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. Genomics Data, 2015, 5, 346-351.	1.3	2