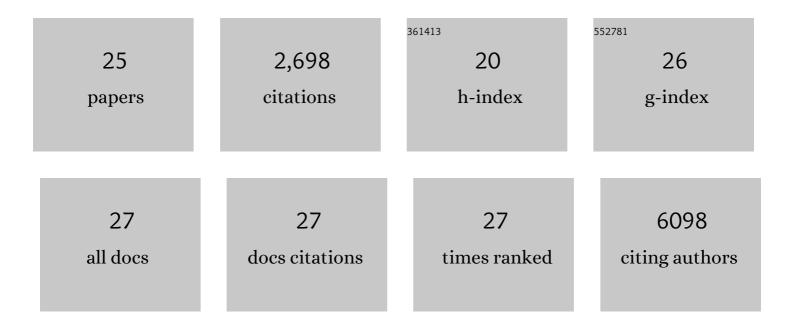
Elena Zotenko

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2517396/publications.pdf Version: 2024-02-01



FLENA ZOTENKO

#	Article	IF	CITATIONS
1	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. Genome Biology, 2016, 17, 208.	8.8	912
2	Why Do Hubs in the Yeast Protein Interaction Network Tend To Be Essential: Reexamining the Connection between the Network Topology and Essentiality. PLoS Computational Biology, 2008, 4, e1000140.	3.2	373
3	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome Research, 2016, 26, 719-731.	5.5	312
4	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. Nature Communications, 2015, 6, 5899.	12.8	162
5	DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. Nature Communications, 2015, 6, 7758.	12.8	105
6	Identification of sequence–structure RNA binding motifs for SELEX-derived aptamers. Bioinformatics, 2012, 28, i215-i223.	4.1	85
7	Enduring epigenetic landmarks define the cancer microenvironment. Genome Research, 2018, 28, 625-638.	5.5	74
8	Predicting domain-domain interactions using a parsimony approach. Genome Biology, 2006, 7, R104.	9.6	73
9	Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. Nature Communications, 2019, 10, 416.	12.8	71
10	Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. Epigenetics and Chromatin, 2017, 10, 16.	3.9	68
11	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. Cancer Cell, 2019, 35, 297-314.e8.	16.8	62
12	COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations. Bioinformatics, 2006, 22, 779-788.	4.1	61
13	A bioengineered microenvironment to quantitatively measure the tumorigenic properties of cancer-associated fibroblasts in human prostate cancer. Biomaterials, 2013, 34, 4777-4785.	11.4	53
14	MicroRNA profiling of the pubertal mouse mammary gland identifies miR-184 as a candidate breast tumour suppressor gene. Breast Cancer Research, 2015, 17, 83.	5.0	44
15	Decomposition of overlapping protein complexes: a graph theoretical method for analyzing static and dynamic protein associations. Algorithms for Molecular Biology, 2006, 1, 7.	1.2	43
16	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. Cell Reports, 2021, 36, 109722.	6.4	39
17	On the Applicability of Elastic Network Normal Modes in Small-Molecule Docking. Journal of Chemical Information and Modeling, 2012, 52, 844-856.	5.4	27
18	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. Clinical Epigenetics, 2015, 7, 52.	4.1	26

Elena Zotenko

#	Article	IF	CITATIONS
19	Genome-wide DNA methylation profiling in triple-negative breast cancer reveals epigenetic signatures with important clinical value. Molecular and Cellular Oncology, 2016, 3, e1038424.	0.7	24
20	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. Scientific Reports, 2019, 9, 9511.	3.3	24
21	Secondary structure spatial conformation footprint: a novel method for fast protein structure comparison and classification. BMC Structural Biology, 2006, 6, 12.	2.3	19
22	Inferring Physical Protein Contacts from Large-Scale Purification Data of Protein Complexes. Molecular and Cellular Proteomics, 2011, 10, M110.004929.	3.8	16
23	Structural footprinting in protein structure comparison: the impact of structural fragments. BMC Structural Biology, 2007, 7, 53.	2.3	13
24	Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. Clinical Epigenetics, 2016, 8, 74.	4.1	8
25	Graph Theoretical Approaches to Delineate Dynamics of Biological Processes. , 2007, , 29-54.		0