

Elena Zotenko

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

2,698
citations

361413

20
h-index

552781

26
g-index

27
all docs

27
docs citations

27
times ranked

6098
citing authors

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

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