

Elena Zotenko

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2517396/publications.pdf>

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 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Enduring epigenetic landmarks define the cancer microenvironment. <i>Genome Research</i> , 2018, 28, 625-638. | 5.5 | 74 |
| 6 | Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. <i>Epigenetics and Chromatin</i> , 2017, 10, 16. | 3.9 | 68 |
| 7 | Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. <i>Clinical Epigenetics</i> , 2016, 8, 74. | 4.1 | 8 |
| 8 | 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 |
| 9 | Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208. | 8.8 | 912 |
| 10 | 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 |
| 11 | 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 |
| 12 | Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015, 6, 5899. | 12.8 | 162 |
| 13 | DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. <i>Nature Communications</i> , 2015, 6, 7758. | 12.8 | 105 |
| 14 | Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , 2015, 7, 52. | 4.1 | 26 |
| 15 | 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 |
| 16 | Identification of sequence-structure RNA binding motifs for SELEX-derived aptamers. <i>Bioinformatics</i> , 2012, 28, i215-i223. | 4.1 | 85 |
| 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 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | 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 |
| 20 | Graph Theoretical Approaches to Delineate Dynamics of Biological Processes. , 2007, , 29-54. | | 0 |
| 21 | Structural footprinting in protein structure comparison: the impact of structural fragments. <i>BMC Structural Biology</i> , 2007, 7, 53. | 2.3 | 13 |
| 22 | 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 |
| 23 | Predicting domain-domain interactions using a parsimony approach. <i>Genome Biology</i> , 2006, 7, R104. | 9.6 | 73 |
| 24 | 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 |
| 25 | COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations. <i>Bioinformatics</i> , 2006, 22, 779-788. | 4.1 | 61 |