

Ran Elkon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8827646/publications.pdf>

Version: 2024-02-01

73
papers

6,104
citations

109321

35
h-index

98798

67
g-index

79
all docs

79
docs citations

79
times ranked

10705
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternative cleavage and polyadenylation: extent, regulation and function. <i>Nature Reviews Genetics</i> , 2013, 14, 496-506.	16.3	712
2	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. <i>Molecular Cell</i> , 2013, 49, 524-535.	9.7	484
3	Transcription Impacts the Efficiency of mRNA Translation via Co-transcriptional N6-adenosine Methylation. <i>Cell</i> , 2017, 169, 326-337.e12.	28.9	372
4	A Pumilio-induced RNA structure switch in p27-3' UTR controls miR-221 and miR-222 accessibility. <i>Nature Cell Biology</i> , 2010, 12, 1014-1020.	10.3	369
5	Functional genetic screens for enhancer elements in the human genome using CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016, 34, 192-198.	17.5	352
6	The Poly(A)-Binding Protein Nuclear 1 Suppresses Alternative Cleavage and Polyadenylation Sites. <i>Cell</i> , 2012, 149, 538-553.	28.9	309
7	Genome-Wide In Silico Identification of Transcriptional Regulators Controlling the Cell Cycle in Human Cells. <i>Genome Research</i> , 2003, 13, 773-780.	5.5	275
8	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. <i>Science Signaling</i> , 2010, 3, rs3.	3.6	245
9	BRD7 is a candidate tumour suppressor gene required for p53 function. <i>Nature Cell Biology</i> , 2010, 12, 380-389.	10.3	194
10	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010, 5, 303-322.	12.0	183
11	Apolipoprotein E4 enhances brain inflammation by modulation of the NF- κ B signaling cascade. <i>Neurobiology of Disease</i> , 2005, 20, 709-718.	4.4	142
12	RFX transcription factors are essential for hearing in mice. <i>Nature Communications</i> , 2015, 6, 8549.	12.8	142
13	E2F mediates enhanced alternative polyadenylation in proliferation. <i>Genome Biology</i> , 2012, 13, R59.	9.6	137
14	Matrin 3 Binds and Stabilizes mRNA. <i>PLoS ONE</i> , 2011, 6, e23882.	2.5	136
15	Alternative Cleavage and Polyadenylation during Colorectal Cancer Development. <i>Clinical Cancer Research</i> , 2012, 18, 5256-5266.	7.0	108
16	BRCA1185delAG tumors may acquire therapy resistance through expression of RING-less BRCA1. <i>Journal of Clinical Investigation</i> , 2016, 126, 2903-2918.	8.2	105
17	Cell Type-Specific Transcriptome Analysis Reveals a Major Role for Zeb1 and miR-200b in Mouse Inner Ear Morphogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002309.	3.5	90
18	Helios is a key transcriptional regulator of outer hair cell maturation. <i>Nature</i> , 2018, 563, 696-700.	27.8	90

#	ARTICLE	IF	CITATIONS
19	Transcriptional modulation induced by ionizing radiation: p53 remains a central player. <i>Molecular Oncology</i> , 2011, 5, 336-348.	4.6	82
20	Characterization of noncoding regulatory DNA in the human genome. <i>Nature Biotechnology</i> , 2017, 35, 732-746.	17.5	79
21	3'UTR Shortening Potentiates MicroRNA-Based Repression of Pro-differentiation Genes in Proliferating Human Cells. <i>PLoS Genetics</i> , 2016, 12, e1005879.	3.5	77
22	Integration of Transcriptomics, Proteomics, and MicroRNA Analyses Reveals Novel MicroRNA Regulation of Targets in the Mammalian Inner Ear. <i>PLoS ONE</i> , 2011, 6, e18195.	2.5	74
23	Dissection of a DNA-damage-induced transcriptional network using a combination of microarrays, RNA interference and computational promoter analysis. <i>Genome Biology</i> , 2005, 6, R43.	9.6	71
24	Cell-type-specific analysis of alternative polyadenylation using single-cell transcriptomics data. <i>Nucleic Acids Research</i> , 2019, 47, 10027-10039.	14.5	71
25	SPIKE – a database, visualization and analysis tool of cellular signaling pathways. <i>BMC Bioinformatics</i> , 2008, 9, 110.	2.6	65
26	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. <i>Genome Biology</i> , 2018, 19, 56.	8.8	63
27	A cell-type-specific atlas of the inner ear transcriptional response to acoustic trauma. <i>Cell Reports</i> , 2021, 36, 109758.	6.4	59
28	Gfi1Cre mice have early onset progressive hearing loss and induce recombination in numerous inner ear non-hair cells. <i>Scientific Reports</i> , 2017, 7, 42079.	3.3	53
29	Recurrent functional misinterpretation of RNA-seq data caused by sample-specific gene length bias. <i>PLoS Biology</i> , 2019, 17, e3000481.	5.6	53
30	Parallel Profiling of the Transcriptome, Cistrome, and Epigenome in the Cellular Response to Ionizing Radiation. <i>Science Signaling</i> , 2014, 7, rs3.	3.6	51
31	Transcription Dynamics Regulate Poly(A) Tails and Expression of the RNA Degradation Machinery to Balance mRNA Levels. <i>Molecular Cell</i> , 2020, 78, 434-444.e5.	9.7	50
32	Gene Expression Signature of Human Cancer Cell Lines Treated with the Ras Inhibitor Salirasib (S-Farnesylthiosalicylic Acid). <i>Cancer Research</i> , 2007, 67, 3320-3328.	0.9	48
33	Comparative gene expression profiling reveals partially overlapping but distinct genomic actions of different antiestrogens in human breast cancer cells. <i>Journal of Cellular Biochemistry</i> , 2006, 98, 1163-1184.	2.6	43
34	Deciphering Transcriptional Regulatory Elements That Encode Specific Cell-Cycle Phasing by Comparative Genomics Analysis. <i>Cell Cycle</i> , 2005, 4, 1788-1797.	2.6	42
35	Myc coordinates transcription and translation to enhance transformation and suppress invasiveness. <i>EMBO Reports</i> , 2015, 16, 1723-1736.	4.5	42
36	Genome-Wide Polyadenylation Maps Reveal Dynamic mRNA 3'-End Formation in the Failing Human Heart. <i>Circulation Research</i> , 2016, 118, 433-438.	4.5	41

#	ARTICLE	IF	CITATIONS
37	LncRNA-OIS1 regulates DPP4 activation to modulate senescence induced by RAS. <i>Nucleic Acids Research</i> , 2018, 46, 4213-4227.	14.5	40
38	Functional CRISPR screen identifies AP1-associated enhancer regulating FOXF1 to modulate oncogene-induced senescence. <i>Genome Biology</i> , 2018, 19, 118.	8.8	38
39	GFI1 functions to repress neuronal gene expression in the developing inner ear hair cells. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	38
40	DOMINO: a network-based active module identification algorithm with reduced rate of false calls. <i>Molecular Systems Biology</i> , 2021, 17, e9593.	7.2	36
41	Proteomic analysis of polyribosomes identifies splicing factors as potential regulators of translation during mitosis. <i>Nucleic Acids Research</i> , 2017, 45, 5945-5957.	14.5	35
42	High throughput gene expression analysis of the inner ear. <i>Hearing Research</i> , 2012, 288, 77-88.	2.0	33
43	Systematic identification of functional SNPs interrupting 3' UTR polyadenylation signals. <i>PLoS Genetics</i> , 2020, 16, e1008977.	3.5	30
44	Impaired genomic stability and increased oxidative stress exacerbate different features of Ataxia-telangiectasia. <i>Human Molecular Genetics</i> , 2005, 14, 2929-2943.	2.9	28
45	Functional genomic delineation of TLR-induced transcriptional networks. <i>BMC Genomics</i> , 2007, 8, 394.	2.8	28
46	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. <i>American Journal of Human Genetics</i> , 2022, 109, 1077-1091.	6.2	27
47	In silico identification of transcriptional regulators associated with c-Myc. <i>Nucleic Acids Research</i> , 2004, 32, 4955-4961.	14.5	26
48	E2F1 identified by promoter and biochemical analysis as a central target of glioblastoma cell-cycle arrest in response to ras inhibition. <i>International Journal of Cancer</i> , 2006, 119, 527-538.	5.1	26
49	Gene architecture directs splicing outcome in separate nuclear spatial regions. <i>Molecular Cell</i> , 2022, 82, 1021-1034.e8.	9.7	26
50	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	4.2	24
51	A CRISPR-Cas9 screen identifies essential CTCF anchor sites for estrogen receptor-driven breast cancer cell proliferation. <i>Nucleic Acids Research</i> , 2019, 47, 9557-9572.	14.5	21
52	Redifferentiation of expanded human islet β^2 cells by inhibition of ARX. <i>Scientific Reports</i> , 2016, 6, 20698.	3.3	18
53	A comprehensive enhancer screen identifies TRAM2 as a key and novel mediator of YAP oncogenesis. <i>Genome Biology</i> , 2021, 22, 54.	8.8	16
54	Nuclear poly(A)-binding protein 1 is an ATM target and essential for DNA double-strand break repair. <i>Nucleic Acids Research</i> , 2018, 46, 730-747.	14.5	15

#	ARTICLE	IF	CITATIONS
55	Pax6 regulation of <i>Sox9</i> in the retinal pigmented epithelium controls its timely differentiation and choroid vasculature development. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	15
56	Activity-dependent neuroprotective protein (ADNP) is an alcohol-responsive gene and negative regulator of alcohol consumption in female mice. <i>Neuropsychopharmacology</i> , 2019, 44, 415-424.	5.4	15
57	Lineage-tracing and translomic analysis of damage-inducible mitotic cochlear progenitors identifies candidate genes regulating regeneration. <i>PLoS Biology</i> , 2021, 19, e3001445.	5.6	12
58	Removal of AU Bias from Microarray mRNA Expression Data Enhances Computational Identification of Active MicroRNAs. <i>PLoS Computational Biology</i> , 2008, 4, e1000189.	3.2	8
59	CUEDC1 is a primary target of ER α essential for the growth of breast cancer cells. <i>Cancer Letters</i> , 2018, 436, 87-95.	7.2	7
60	Expression pattern of cochlear microRNAs in the mammalian auditory hindbrain. <i>Cell and Tissue Research</i> , 2021, 383, 655-666.	2.9	7
61	Genomic meta-analysis of the interplay between 3D chromatin organization and gene expression programs under basal and stress conditions. <i>Epigenetics and Chromatin</i> , 2018, 11, 49.	3.9	5
62	Identification and characterization of key long non-coding RNAs in the mouse cochlea. <i>RNA Biology</i> , 2021, 18, 1160-1169.	3.1	4
63	A CRISPR knockout screen reveals new regulators of canonical Wnt signaling. <i>Oncogenesis</i> , 2021, 10, 63.	4.9	4
64	Incorporating regulatory interactions into gene-set analyses for GWAS data: A controlled analysis with the MAGMA tool. <i>PLoS Computational Biology</i> , 2022, 18, e1009908.	3.2	3
65	CT-FOCS: a novel method for inferring cell type-specific enhancer-promoter maps. <i>Nucleic Acids Research</i> , 2022, 50, e55-e55.	14.5	2
66	The DOMINO web-server for active module identification analysis. <i>Bioinformatics</i> , 2022, 38, 2364-2366.	4.1	2
67	Genetic mapping of developmental trajectories for complex traits and diseases. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3458-3469.	4.1	1
68	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. , 2020, 16, e1008977.		0
69	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. , 2020, 16, e1008977.		0
70	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. , 2020, 16, e1008977.		0
71	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. , 2020, 16, e1008977.		0
72	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. , 2020, 16, e1008977.		0

#	ARTICLE	IF	CITATIONS
73	Systematic identification of functional SNPs interrupting 3' UTR polyadenylation signals. , 2020, 16, e1008977.		0