Ran Elkon

List of Publications by Year
in descending order

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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	CT-FOCS: a novel method for inferring cell type-specific enhancerâ€“promoter maps. Nucleic Acids Research, 2022, 50, e55-e55.	14.5	2
2	The DOMINO web-server for active module identification analysis. Bioinformatics, 2022, 38, 2364-2366.	4.1	2
3	Gene architecture directs splicing outcome in separate nuclear spatial regions. Molecular Cell, 2022, 82, 1021-1034.e8.	9.7	26
4	Incorporating regulatory interactions into gene-set analyses for GWAS data: A controlled analysis with the MAGMA tool. PLoS Computational Biology, 2022, 18, e1009908.	3.2	3
5	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. American Journal of Human Genetics, 2022, 109, 1077-1091.	6.2	27
6	Identification and characterization of key long non-coding RNAs in the mouse cochlea. RNA Biology, 2021, 18, 1160-1169.	3.1	4
7	Expression pattern of cochlear microRNAs in the mammalian auditory hindbrain. Cell and Tissue Research, 2021, 383, 655-666.	2.9	7
8	A comprehensive enhancer screen identifies TRAM2 as a key and novel mediator of YAP oncogenesis. Genome Biology, 2021, 22, 54.	8.8	16
9	DOMINO: a networkâ€based active module identification algorithm with reduced rate of false calls. Molecular Systems Biology, 2021, 17, e9593.	7.2	36
10	Genetic mapping of developmental trajectories for complex traits and diseases. Computational and Structural Biotechnology Journal, 2021, 19, 3458-3469.	4.1	1
11	A CRISPR knockout screen reveals new regulators of canonical Wnt signaling. Oncogenesis, 2021, 10, 63.	4.9	4
12	A cell-type-specific atlas of the inner ear transcriptional response to acoustic trauma. Cell Reports, 2021, 36, 109758.	6.4	59
13	Lineage-tracing and translatomic analysis of damage-inducible mitotic cochlear progenitors identifies candidate genes regulating regeneration. PLoS Biology, 2021, 19, e3001445.	5.6	12
14	GFI1 functions to repress neuronal gene expression in the developing inner ear hair cells. Development (Cambridge), 2020, 147, .	2.5	38
15	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. PLoS Genetics, 2020, 16, e1008977.	3.5	30
16	Transcription Dynamics Regulate Poly(A) Tails and Expression of the RNA Degradation Machinery to Balance mRNA Levels. Molecular Cell, 2020, 78, 434-444.e5.	9.7	50
17	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. , 2020, 16, e1008977.		0
18	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. , 2020, 16, e1008977.		0

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19	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. , 2020, 16, e1008977.		0
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21	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. , 2020, 16, e1008977.		0
22	Systematic identification of functional SNPs interrupting 3â€™UTR polyadenylation signals. , 2020, 16, e1008977.		0
23	Activity-dependent neuroprotective protein (ADNP) is an alcohol-responsive gene and negative regulator of alcohol consumption in female mice. Neuropsychopharmacology, 2019, 44, 415-424.	5.4	15
24	A CRISPR-Cas9 screen identifies essential CTCF anchor sites for estrogen receptor-driven breast cancer cell proliferation. Nucleic Acids Research, 2019, 47, 9557-9572.	14.5	21
25	The EXPANDER Integrated Platform for Transcriptome Analysis. Journal of Molecular Biology, 2019, 431, 2398-2406.	4.2	24
26	Recurrent functional misinterpretation of RNA-seq data caused by sample-specific gene length bias. PLoS Biology, 2019, 17, e3000481.	5.6	53
27	Cell-type-specific analysis of alternative polyadenylation using single-cell transcriptomics data. Nucleic Acids Research, 2019, 47, 10027-10039.	14.5	71
28	LncRNA-OIS1 regulates DPP4 activation to modulate senescence induced by RAS. Nucleic Acids Research, 2018, 46, 4213-4227.	14.5	40
29	Nuclear poly(A)-binding protein 1 is an ATM target and essential for DNA double-strand break repair. Nucleic Acids Research, 2018, 46, 730-747.	14.5	15
30	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancerâ€“promoter map. Genome Biology, 2018, 19, 56.	8.8	63
31	Helios is a key transcriptional regulator of outer hair cell maturation. Nature, 2018, 563, 696-700.	27.8	90
32	Genomic meta-analysis of the interplay between 3D chromatin organization and gene expression programs under basal and stress conditions. Epigenetics and Chromatin, 2018, 11, 49.	3.9	5
33	Pax6 regulation of <i>Sox9</i> in the retinal pigmented epithelium controls its timely differentiation and choroid vasculature development. Development (Cambridge), 2018, 145, .	2.5	15
34	Functional CRISPR screen identifies AP1-associated enhancer regulating FOXF1 to modulate oncogene-induced senescence. Genome Biology, 2018, 19, 118.	8.8	38
35	CUEDC1 is a primary target of ERÎ± essential for the growth of breast cancer cells. Cancer Letters, 2018, 436, 87-95.	7.2	7
36	Gfi1Cre mice have early onset progressive hearing loss and induce recombination in numerous inner ear non-hair cells. Scientific Reports, 2017, 7, 42079.	3.3	53

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37	Proteomic analysis of polyribosomes identifies splicing factors as potential regulators of translation during mitosis. Nucleic Acids Research, 2017, 45, 5945-5957.	14.5	35
38	Transcription Impacts the Efficiency of mRNA Translation via Co-transcriptional N6-adenosine Methylation. Cell, 2017, 169, 326-337.e12.	28.9	372
39	Characterization of noncoding regulatory DNA in the human genome. Nature Biotechnology, 2017, 35, 732-746.	17.5	79
40	Redifferentiation of expanded human islet Î² cells by inhibition of ARX. Scientific Reports, 2016, 6, 20698.	3.3	18
41	Functional genetic screens for enhancer elements in the human genome using CRISPR-Cas9. Nature Biotechnology, 2016, 34, 192-198.	17.5	352
42	Genome-Wide Polyadenylation Maps Reveal Dynamic mRNA 3â€²-End Formation in the Failing Human Heart. Circulation Research, 2016, 118, 433-438.	4.5	41
43	BRCA1185delAG tumors may acquire therapy resistance through expression of RING-less BRCA1. Journal of Clinical Investigation, 2016, 126, 2903-2918.	8.2	105
44	3â€™UTR Shortening Potentiates MicroRNA-Based Repression of Pro-differentiation Genes in Proliferating Human Cells. PLoS Genetics, 2016, 12, e1005879.	3.5	77
45	Myc coordinates transcription and translation to enhance transformation and suppress invasiveness. EMBO Reports, 2015, 16, 1723-1736.	4.5	42
46	RFX transcription factors are essential for hearing in mice. Nature Communications, 2015, 6, 8549.	12.8	142
47	Parallel Profiling of the Transcriptome, Cistrome, and Epigenome in the Cellular Response to Ionizing Radiation. Science Signaling, 2014, 7, rs3.	3.6	51
48	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. Molecular Cell, 2013, 49, 524-535.	9.7	484
49	Alternative cleavage and polyadenylation: extent, regulation and function. Nature Reviews Genetics, 2013, 14, 496-506.	16.3	712
50	Alternative Cleavage and Polyadenylation during Colorectal Cancer Development. Clinical Cancer Research, 2012, 18, 5256-5266.	7.0	108
51	E2F mediates enhanced alternative polyadenylation in proliferation. Genome Biology, 2012, 13, R59.	9.6	137
52	High throughput gene expression analysis of the inner ear. Hearing Research, 2012, 288, 77-88.	2.0	33
53	The Poly(A)-Binding Protein Nuclear 1 Suppresses Alternative Cleavage and Polyadenylation Sites. Cell, 2012, 149, 538-553.	28.9	309
54	Transcriptional modulation induced by ionizing radiation: p53 remains a central player. Molecular Oncology, 2011, 5, 336-348.	4.6	82

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55	Cell Typeâ€"Specific Transcriptome Analysis Reveals a Major Role for Zeb1 and miR-200b in Mouse Inner Ear Morphogenesis. PLoS Genetics, 2011, 7, e1002309.	3.5	90
56	Integration of Transcriptomics, Proteomics, and MicroRNA Analyses Reveals Novel MicroRNA Regulation of Targets in the Mammalian Inner Ear. PLoS ONE, 2011, 6, e18195.	2.5	74
57	Matrin 3 Binds and Stabilizes mRNA. PLoS ONE, 2011, 6, e23882.	2.5	136
58	BRD7 is a candidate tumour suppressor gene required for p53 function. Nature Cell Biology, 2010, 12, 380-389.	10.3	194
59	A Pumilio-induced RNA structure switch in p27-3â€² UTR controls miR-221 and miR-222 accessibility. Nature Cell Biology, 2010, 12, 1014-1020.	10.3	369
60	Expander: from expression microarrays to networks and functions. Nature Protocols, 2010, 5, 303-322.	12.0	183
61	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. Science Signaling, 2010, 3, rs3.	3.6	245
62	SPIKE â€" a database, visualization and analysis tool of cellular signaling pathways. BMC Bioinformatics, 2008, 9, 110.	2.6	65
63	Removal of AU Bias from Microarray mRNA Expression Data Enhances Computational Identification of Active MicroRNAs. PLoS Computational Biology, 2008, 4, e1000189.	3.2	8
64	Gene Expression Signature of Human Cancer Cell Lines Treated with the Ras Inhibitor Salirasib (S-Farnesylthiosalicylic Acid). Cancer Research, 2007, 67, 3320-3328.	0.9	48
65	Functional genomic delineation of TLR-induced transcriptional networks. BMC Genomics, 2007, 8, 394.	2.8	28
66	Comparative gene expression profiling reveals partially overlapping but distinct genomic actions of different antiestrogens in human breast cancer cells. Journal of Cellular Biochemistry, 2006, 98, 1163-1184.	2.6	43
67	E2F1 identified by promoter and biochemical analysis as a central target of glioblastoma cell-cycle arrest in response to ras inhibition. International Journal of Cancer, 2006, 119, 527-538.	5.1	26
68	Impaired genomic stability and increased oxidative stress exacerbate different features of Ataxia-telangiectasia. Human Molecular Genetics, 2005, 14, 2929-2943.	2.9	28
69	Deciphering Transcriptional Regulatory Elements That Encode Specific Cell-Cycle Phasing by Comparative Genomics Analysis. Cell Cycle, 2005, 4, 1788-1797.	2.6	42
70	Apolipoprotein E4 enhances brain inflammation by modulation of the NF-Î°B signaling cascade. Neurobiology of Disease, 2005, 20, 709-718.	4.4	142
71	Dissection of a DNA-damage-induced transcriptional network using a combination of microarrays, RNA interference and computational promoter analysis. Genome Biology, 2005, 6, R43.	9.6	71
72	In silico identification of transcriptional regulators associated with c-Myc. Nucleic Acids Research, 2004, 32, 4955-4961.	14.5	26

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73	Genome-Wide In Silico Identification of Transcriptional Regulators Controlling the Cell Cycle in Human Cells. Genome Research, 2003, 13, 773-780.	5.5	275