

Igor Ulitsky

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

13,599
citations

41344

49
h-index

48315

88
g-index

112
all docs

112
docs citations

112
times ranked

20664
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovering functional motifs in long noncoding RNAs. Wiley Interdisciplinary Reviews RNA, 2022, , e1708.	6.4	10
2	Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors. Cell Reports, 2022, 38, 110418.	6.4	12
3	Transcriptome and chromatin alterations in social fear indicate association of MEG3 with successful extinction of fear. Molecular Psychiatry, 2022, 27, 4064-4076.	7.9	3
4	Unique features of transcription termination and initiation at closely spaced tandem human genes. Molecular Systems Biology, 2022, 18, e10682.	7.2	2
5	Context-specific effects of sequence elements on subcellular localization of linear and circular RNAs. Nature Communications, 2022, 13, 2481.	12.8	13
6	Substoichiometric action of long noncoding RNAs. Nature Cell Biology, 2022, 24, 608-615.	10.3	31
7	OCT4 activates a <i>Suv39h1</i> -repressive antisense lncRNA to couple histone H3 Lysine 9 methylation to pluripotency. Nucleic Acids Research, 2022, 50, 7367-7379.	14.5	7
8	Unique features of transcription termination and initiation at closely spaced tandem human genes. Molecular Systems Biology, 2022, 18, .	7.2	2
9	Identification and characterization of key long non-coding RNAs in the mouse cochlea. RNA Biology, 2021, 18, 1160-1169.	3.1	4
10	SCIRT lncRNA Restrains Tumorigenesis by Opposing Transcriptional Programs of Tumor-Initiating Cells. Cancer Research, 2021, 81, 580-593.	0.9	18
11	Novel Transcript Discovery Expands the Repertoire of Pathologically-Associated, Long Non-Coding RNAs in Vascular Smooth Muscle Cells. International Journal of Molecular Sciences, 2021, 22, 1484.	4.1	5
12	Inefficient splicing curbs noncoding RNA transcription. Nature Structural and Molecular Biology, 2021, 28, 327-328.	8.2	1
13	The evolutionarily conserved long non-coding RNA <i>LINC00261</i> drives neuroendocrine prostate cancer proliferation and metastasis via distinct nuclear and cytoplasmic mechanisms. Molecular Oncology, 2021, 15, 1921-1941.	4.6	22
14	MIR503HG Loss Promotes Endothelial-to-Mesenchymal Transition in Vascular Disease. Circulation Research, 2021, 128, 1173-1190.	4.5	41
15	High-resolution mapping of function and protein binding in an RNA nuclear enrichment sequence. EMBO Journal, 2021, 40, e106357.	7.8	11
16	SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. Nature, 2021, 594, 240-245.	27.8	182
17	Highly conserved and cis-acting lncRNAs produced from paralogous regions in the center of HOXA and HOXB clusters in the endoderm lineage. PLoS Genetics, 2021, 17, e1009681.	3.5	12
18	Therapy based on functional RNA elements. Science, 2021, 373, 623-624.	12.6	5

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19	Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. <i>Genome Biology</i> , 2021, 22, 29.	8.8	27
20	Regulation of gene expression by cis-acting long non-coding RNAs. <i>Nature Reviews Genetics</i> , 2020, 21, 102-117.	16.3	479
21	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
22	Targeting purine synthesis in ASS1-expressing tumors enhances the response to immune checkpoint inhibitors. <i>Nature Cancer</i> , 2020, 1, 894-908.	13.2	43
23	Gene Architecture and Sequence Composition Underpin Selective Dependency of Nuclear Export of Long RNAs on NXF1 and the TREX Complex. <i>Molecular Cell</i> , 2020, 79, 251-267.e6.	9.7	87
24	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020, 39, e103777.	7.8	77
25	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
26	A MAFG-lncRNA axis links systemic nutrient abundance to hepatic glucose metabolism. <i>Nature Communications</i> , 2020, 11, 644.	12.8	29
27	Regulation of neuronal commitment in mouse embryonic stem cells by the <i>Reno1/Bahcc1</i> locus. <i>EMBO Reports</i> , 2020, 21, e51264.	4.5	15
28	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	4.2	24
29	The Human-Specific and Smooth Muscle Cell-Enriched lncRNA SMILR Promotes Proliferation by Regulating Mitotic CENPF mRNA and Drives Cell-Cycle Progression Which Can Be Targeted to Limit Vascular Remodeling. <i>Circulation Research</i> , 2019, 125, 535-551.	4.5	100
30	Regulation of CHD2 expression by the Chaserr long noncoding RNA gene is essential for viability. <i>Nature Communications</i> , 2019, 10, 5092.	12.8	71
31	Endothelial function and dysfunction in the cardiovascular system: the long non-coding road. <i>Cardiovascular Research</i> , 2019, 115, 1692-1704.	3.8	43
32	Predictive models of subcellular localization of long RNAs. <i>Rna</i> , 2019, 25, 557-572.	3.5	75
33	Long Noncoding RNAs in Development and Regeneration of the Neural Lineage. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 165-177.	1.1	9
34	In-cell identification and measurement of RNA-protein interactions. <i>Nature Communications</i> , 2019, 10, 5317.	12.8	43
35	Alternative 3' UTRs direct localization of functionally diverse protein isoforms in neuronal compartments. <i>Nucleic Acids Research</i> , 2019, 47, 2560-2573.	14.5	86
36	Aging well with Norad. <i>ELife</i> , 2019, 8, .	6.0	6

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37	SAM68 is required for regulation of Pumilio by the NORAD long noncoding RNA. <i>Genes and Development</i> , 2018, 32, 70-78.	5.9	61
38	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells. <i>Nature</i> , 2018, 555, 107-111.	27.8	268
39	Production of Spliced Long Noncoding RNAs Specifies Regions with Increased Enhancer Activity. <i>Cell Systems</i> , 2018, 7, 537-547.e3.	6.2	63
40	Predicting microRNA targeting efficacy in <i>Drosophila</i> . <i>Genome Biology</i> , 2018, 19, 152.	8.8	91
41	Regulation of Neuroregeneration by Long Noncoding RNAs. <i>Molecular Cell</i> , 2018, 72, 553-567.e5.	9.7	83
42	Interactions between short and long noncoding RNAs. <i>FEBS Letters</i> , 2018, 592, 2874-2883.	2.8	88
43	Altered p53 functionality in cancer-associated fibroblasts contributes to their cancer-supporting features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6410-6415.	7.1	81
44	Efficient and Accurate Translation Initiation Directed by TISU Involves RPS3 and RPS10e Binding and Differential Eukaryotic Initiation Factor 1A Regulation. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	33
45	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017, 89, 1676-1683.	1.1	112
46	Genome-wide identification and expression profiling of long non-coding RNAs in auditory and vestibular systems. <i>Scientific Reports</i> , 2017, 7, 8637.	3.3	20
47	A subset of conserved mammalian long non-coding RNAs are fossils of ancestral protein-coding genes. <i>Genome Biology</i> , 2017, 18, 162.	8.8	57
48	The human lncRNA LINC-PINT inhibits tumor cell invasion through a highly conserved sequence element. <i>Genome Biology</i> , 2017, 18, 202.	8.8	161
49	Cap-proximal nucleotides via differential eIF4E binding and alternative promoter usage mediate translational response to energy stress. <i>ELife</i> , 2017, 6, .	6.0	75
50	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016, 8, 1052-1064.	6.9	77
51	Evolution to the rescue: using comparative genomics to understand long non-coding RNAs. <i>Nature Reviews Genetics</i> , 2016, 17, 601-614.	16.3	480
52	The functions of long noncoding RNAs in development and stem cells. <i>Development (Cambridge)</i> , 2016, 143, 3882-3894.	2.5	180
53	Circular RNAs are long-lived and display only minimal early alterations in response to a growth factor. <i>Nucleic Acids Research</i> , 2016, 44, 1370-1383.	14.5	484
54	Methods for distinguishing between protein-coding and long noncoding RNAs and the elusive biological purpose of translation of long noncoding RNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 31-40.	1.9	82

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55	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells. <i>Nature Communications</i> , 2016, 7, 12209.	12.8	192
56	Nuclear Retention of mRNA in Mammalian Tissues. <i>Cell Reports</i> , 2015, 13, 2653-2662.	6.4	233
57	Principles of Long Noncoding RNA Evolution Derived from Direct Comparison of Transcriptomes in 17 Species. <i>Cell Reports</i> , 2015, 11, 1110-1122.	6.4	565
58	Recurrent inactivating RASA2 mutations in melanoma. <i>Nature Genetics</i> , 2015, 47, 1408-1410.	21.4	90
59	Diversion of aspartate in ASS1-deficient tumours fosters de novo pyrimidine synthesis. <i>Nature</i> , 2015, 527, 379-383.	27.8	271
60	Beyond Secondary Structure: Primary-Sequence Determinants License Pri-miRNA Hairpins for Processing. <i>Cell</i> , 2013, 152, 844-858.	28.9	373
61	lincRNAs: Genomics, Evolution, and Mechanisms. <i>Cell</i> , 2013, 154, 26-46.	28.9	2,337
62	Extensive alternative polyadenylation during zebrafish development. <i>Genome Research</i> , 2012, 22, 2054-2066.	5.5	305
63	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. <i>Cell</i> , 2011, 147, 1537-1550.	28.9	1,072
64	Dynamic Changes in the Copy Number of Pluripotency and Cell Proliferation Genes in Human ESCs and iPSCs during Reprogramming and Time in Culture. <i>Cell Stem Cell</i> , 2011, 8, 106-118.	11.1	819
65	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011, 39, D793-D799.	14.5	74
66	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
67	A Point Mutation in Translation Initiation Factor eIF2B Leads to Function- and Time-Specific Changes in Brain Gene Expression. <i>PLoS ONE</i> , 2011, 6, e26992.	2.5	13
68	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 901-908.	8.2	93
69	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010, 5, 303-322.	12.0	183
70	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , 2010, 38, e160-e160.	14.5	84
71	Propagation of human embryonic and induced pluripotent stem cells in an indirect co-culture system. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 211-216.	2.1	20
72	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 346.	7.2	28

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73	DEGAS: De Novo Discovery of Dysregulated Pathways in Human Diseases. PLoS ONE, 2010, 5, e13367.	2.5	113
74	Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences. Lecture Notes in Computer Science, 2010, , 578-579.	1.3	0
75	Identifying functional modules using expression profiles and confidence-scored protein interactions. Bioinformatics, 2009, 25, 1158-1164.	4.1	111
76	Allegro: Analyzing expression and sequence in concert to discover regulatory programs. Nucleic Acids Research, 2009, 37, 1566-1579.	14.5	40
77	Towards accurate imputation of quantitative genetic interactions. Genome Biology, 2009, 10, R140.	9.6	24
78	Comprehensive MicroRNA Profiling Reveals a Unique Human Embryonic Stem Cell Signature Dominated by a Single Seed Sequence. Stem Cells, 2008, 26, 1506-1516.	3.2	202
79	SPIKE â€“ a database, visualization and analysis tool of cellular signaling pathways. BMC Bioinformatics, 2008, 9, 110.	2.6	65
80	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. Genome Biology, 2008, 9, R1.	9.6	18
81	Regulatory networks define phenotypic classes of human stem cell lines. Nature, 2008, 455, 401-405.	27.8	321
82	From Eâ€™MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. Molecular Systems Biology, 2008, 4, 209.	7.2	69
83	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles. Lecture Notes in Computer Science, 2008, , 347-359.	1.3	37
84	DETECTING PATHWAYS TRANSCRIPTIONALLY CORRELATED WITH CLINICAL PARAMETERS. , 2008, , .		4
85	Detecting pathways transcriptionally correlated with clinical parameters. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 249-58.	0.4	6
86	Networkâ€‘based prediction of protein function. Molecular Systems Biology, 2007, 3, 88.	7.2	918
87	Identification of functional modules using network topology and high-throughput data. BMC Systems Biology, 2007, 1, 8.	3.0	267
88	The Average Common Substring Approach to Phylogenomic Reconstruction. Journal of Computational Biology, 2006, 13, 336-350.	1.6	184
89	The Molecular and Functional Foundations of Conductive Somatic Cell Reprogramming to Ground State Pluripotency. SSRN Electronic Journal, 0, , .	0.4	0