

# Igor Ulitsky

## List of Publications by Year in descending order

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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	lincRNAs: Genomics, Evolution, and Mechanisms. <i>Cell</i> , 2013, 154, 26-46.	28.9	2,337
2	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. <i>Cell</i> , 2011, 147, 1537-1550.	28.9	1,072
3	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007, 3, 88.	7.2	918
4	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
5	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
6	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
7	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
8	Regulation of gene expression by cis-acting long non-coding RNAs. <i>Nature Reviews Genetics</i> , 2020, 21, 102-117.	16.3	479
9	Beyond Secondary Structure: Primary-Sequence Determinants License Pri-miRNA Hairpins for Processing. <i>Cell</i> , 2013, 152, 844-858.	28.9	373
10	Regulatory networks define phenotypic classes of human stem cell lines. <i>Nature</i> , 2008, 455, 401-405.	27.8	321
11	Extensive alternative polyadenylation during zebrafish development. <i>Genome Research</i> , 2012, 22, 2054-2066.	5.5	305
12	Diversion of aspartate in ASS1-deficient tumours fosters de novo pyrimidine synthesis. <i>Nature</i> , 2015, 527, 379-383.	27.8	271
13	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells. <i>Nature</i> , 2018, 555, 107-111.	27.8	268
14	Identification of functional modules using network topology and high-throughput data. <i>BMC Systems Biology</i> , 2007, 1, 8.	3.0	267
15	Nuclear Retention of mRNA in Mammalian Tissues. <i>Cell Reports</i> , 2015, 13, 2653-2662.	6.4	233
16	Comprehensive MicroRNA Profiling Reveals a Unique Human Embryonic Stem Cell Signature Dominated by a Single Seed Sequence. <i>Stem Cells</i> , 2008, 26, 1506-1516.	3.2	202
17	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
18	The Average Common Substring Approach to Phylogenomic Reconstruction. <i>Journal of Computational Biology</i> , 2006, 13, 336-350.	1.6	184

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19	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010, 5, 303-322.	12.0	183
20	SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. <i>Nature</i> , 2021, 594, 240-245.	27.8	182
21	The functions of long noncoding RNAs in development and stem cells. <i>Development (Cambridge)</i> , 2016, 143, 3882-3894.	2.5	180
22	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
23	DEGAS: De Novo Discovery of Dysregulated Pathways in Human Diseases. <i>PLoS ONE</i> , 2010, 5, e13367.	2.5	113
24	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017, 89, 1676-1683.	1.1	112
25	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , 2009, 25, 1158-1164.	4.1	111
26	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
27	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
28	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
29	Predicting microRNA targeting efficacy in <i>Drosophila</i> . <i>Genome Biology</i> , 2018, 19, 152.	8.8	91
30	Recurrent inactivating RASA2 mutations in melanoma. <i>Nature Genetics</i> , 2015, 47, 1408-1410.	21.4	90
31	Interactions between short and long noncoding RNAs. <i>FEBS Letters</i> , 2018, 592, 2874-2883.	2.8	88
32	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
33	Alternative 5' UTRs direct localization of functionally diverse protein isoforms in neuronal compartments. <i>Nucleic Acids Research</i> , 2019, 47, 2560-2573.	14.5	86
34	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , 2010, 38, e160-e160.	14.5	84
35	Regulation of Neuroregeneration by Long Noncoding RNAs. <i>Molecular Cell</i> , 2018, 72, 553-567.e5.	9.7	83
36	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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37	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
38	<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
39	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020, 39, e103777.	7.8	77
40	Predictive models of subcellular localization of long RNAs. <i>Rna</i> , 2019, 25, 557-572.	3.5	75
41	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
42	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011, 39, D793-D799.	14.5	74
43	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
44	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
45	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , 2008, 4, 209.	7.2	69
46	SPIKE – a database, visualization and analysis tool of cellular signaling pathways. <i>BMC Bioinformatics</i> , 2008, 9, 110.	2.6	65
47	Production of Spliced Long Noncoding RNAs Specifies Regions with Increased Enhancer Activity. <i>Cell Systems</i> , 2018, 7, 537-547.e3.	6.2	63
48	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
49	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
50	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
51	Endothelial function and dysfunction in the cardiovascular system: the long non-coding road. <i>Cardiovascular Research</i> , 2019, 115, 1692-1704.	3.8	43
52	In-cell identification and measurement of RNA-protein interactions. <i>Nature Communications</i> , 2019, 10, 5317.	12.8	43
53	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
54	MIR503HG Loss Promotes Endothelial-to-Mesenchymal Transition in Vascular Disease. <i>Circulation Research</i> , 2021, 128, 1173-1190.	4.5	41

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55	Allegro: Analyzing expression and sequence in concert to discover regulatory programs. <i>Nucleic Acids Research</i> , 2009, 37, 1566-1579.	14.5	40
56	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles. <i>Lecture Notes in Computer Science</i> , 2008, , 347-359.	1.3	37
57	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
58	Substoichiometric action of long noncoding RNAs. <i>Nature Cell Biology</i> , 2022, 24, 608-615.	10.3	31
59	A MAFG-lncRNA axis links systemic nutrient abundance to hepatic glucose metabolism. <i>Nature Communications</i> , 2020, 11, 644.	12.8	29
60	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 346.	7.2	28
61	Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. <i>Genome Biology</i> , 2021, 22, 29.	8.8	27
62	Towards accurate imputation of quantitative genetic interactions. <i>Genome Biology</i> , 2009, 10, R140.	9.6	24
63	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	4.2	24
64	The evolutionarily conserved long non-coding RNA <i>LINC00261</i> drives neuroendocrine prostate cancer proliferation and metastasis via distinct nuclear and cytoplasmic mechanisms. <i>Molecular Oncology</i> , 2021, 15, 1921-1941.	4.6	22
65	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
66	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
67	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. <i>Genome Biology</i> , 2008, 9, R1.	9.6	18
68	SCIRT lncRNA Restrains Tumorigenesis by Opposing Transcriptional Programs of Tumor-Initiating Cells. <i>Cancer Research</i> , 2021, 81, 580-593.	0.9	18
69	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
70	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
71	Context-specific effects of sequence elements on subcellular localization of linear and circular RNAs. <i>Nature Communications</i> , 2022, 13, 2481.	12.8	13
72	Highly conserved and cis-acting lncRNAs produced from paralogous regions in the center of HOXA and HOXB clusters in the endoderm lineage. <i>PLoS Genetics</i> , 2021, 17, e1009681.	3.5	12

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73	Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors. <i>Cell Reports</i> , 2022, 38, 110418.	6.4	12
74	High-resolution mapping of function and protein binding in an RNA nuclear enrichment sequence. <i>EMBO Journal</i> , 2021, 40, e106357.	7.8	11
75	Discovering functional motifs in long noncoding RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, , e1708.	6.4	10
76	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
77	OCT4 activates a <i>Suv39h1</i> -repressive antisense lncRNA to couple histone H3 Lysine 9 methylation to pluripotency. <i>Nucleic Acids Research</i> , 2022, 50, 7367-7379.	14.5	7
78	Aging well with Norad. <i>ELife</i> , 2019, 8, .	6.0	6
79	Detecting pathways transcriptionally correlated with clinical parameters. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008, 7, 249-58.	0.4	6
80	Novel Transcript Discovery Expands the Repertoire of Pathologically-Associated, Long Non-Coding RNAs in Vascular Smooth Muscle Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1484.	4.1	5
81	Therapy based on functional RNA elements. <i>Science</i> , 2021, 373, 623-624.	12.6	5
82	Identification and characterization of key long non-coding RNAs in the mouse cochlea. <i>RNA Biology</i> , 2021, 18, 1160-1169.	3.1	4
83	DETECTING PATHWAYS TRANSCRIPTIONALLY CORRELATED WITH CLINICAL PARAMETERS. , 2008, , .		4
84	Transcriptome and chromatin alterations in social fear indicate association of MEG3 with successful extinction of fear. <i>Molecular Psychiatry</i> , 2022, 27, 4064-4076.	7.9	3
85	Unique features of transcription termination and initiation at closely spaced tandem human genes. <i>Molecular Systems Biology</i> , 2022, 18, e10682.	7.2	2
86	Unique features of transcription termination and initiation at closely spaced tandem human genes. <i>Molecular Systems Biology</i> , 2022, 18, .	7.2	2
87	Inefficient splicing curbs noncoding RNA transcription. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 327-328.	8.2	1
88	Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences. <i>Lecture Notes in Computer Science</i> , 2010, , 578-579.	1.3	0
89	The Molecular and Functional Foundations of Conductive Somatic Cell Reprogramming to Ground State Pluripotency. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0