Igor Ulitsky

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

92 papers	9,786 citations	41 h-index	98 g-index
112 ext. papers	12,214 ext. citations	15.4 avg, IF	7.01 L-index

#	Paper	IF	Citations
92	Discovering functional motifs in long noncoding RNAs.. *Wiley Interdisciplinary Reviews RNA*, **2022**, e1708	9.3	0
91	Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors.. *Cell Reports*, **2022**, 38, 110418	10.6	0
90	Unique features of transcription termination and initiation at closely spaced tandem human genes.. *Molecular Systems Biology*, **2022**, 18, e10682	12.2	
89	Context-specific effects of sequence elements on subcellular localization of linear and circular RNAs.. *Nature Communications*, **2022**, 13, 2481	17.4	2
88	Substoichiometric action of long noncoding RNAs.. *Nature Cell Biology*, **2022**, 24, 608-615	23.4	0
87	Identification and characterization of key long non-coding RNAs in the mouse cochlea. *RNA Biology*, **2021**, 18, 1160-1169	4.8	1
86	Inefficient splicing curbs noncoding RNA transcription. *Nature Structural and Molecular Biology*, **2021**, 28, 327-328	17.6	
85	The evolutionarily conserved long non-coding RNA LINC00261 drives neuroendocrine prostate cancer proliferation and metastasis via distinct nuclear and cytoplasmic mechanisms. *Molecular Oncology*, **2021**, 15, 1921-1941	7.9	9
84	MIR503HG Loss Promotes Endothelial-to-Mesenchymal Transition in Vascular Disease. *Circulation Research*, **2021**, 128, 1173-1190	15.7	7
83	High-resolution mapping of function and protein binding in an RNA nuclear enrichment sequence. *EMBO Journal*, **2021**, 40, e106357	13	5
82	SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. *Nature*, **2021**, 594, 240-245	50.4	57
81	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	6	1
80	SCIRT lncRNA Restrains Tumorigenesis by Opposing Transcriptional Programs of Tumor-Initiating Cells. *Cancer Research*, **2021**, 81, 580-593	10.1	7
79	Therapy based on functional RNA elements. *Science*, **2021**, 373, 623-624	33.3	3
78	Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. *Genome Biology*, **2021**, 22, 29	18.3	8
77	Gene Architecture and Sequence Composition Underpin Selective Dependency of Nuclear Export of Long RNAs on NXF1 and the TREX Complex. *Molecular Cell*, **2020**, 79, 251-267.e6	17.6	32
76	A guide to naming human non-coding RNA genes. *EMBO Journal*, **2020**, 39, e103777	13	39

(2018-2020)

75	Regulation of neuronal commitment in mouse embryonic stem cells by the Reno1/Bahcc1 locus. *EMBO Reports*, **2020**, 21, e51264	6.5	1
74	A MAFG-lncRNA axis links systemic nutrient abundance to hepatic glucose metabolism. *Nature Communications*, **2020**, 11, 644	17.4	14
73	Regulation of gene expression by cis-acting long non-coding RNAs. *Nature Reviews Genetics*, **2020**, 21, 102-117	30.1	216
72	Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Research*, **2020**, 30, 1060-1072	9.7	41
71	Targeting purine synthesis in ASS1-expressing tumors enhances the response to immune checkpoint inhibitors.. *Nature Cancer*, **2020**, 1, 894-908	15.4	13
70	Transcription Dynamics Regulate Poly(A) Tails and Expression of the RNA Degradation Machinery to Balance mRNA Levels. *Molecular Cell*, **2020**, 78, 434-444.e5	17.6	18
69	Endothelial function and dysfunction in the cardiovascular system: the long non-coding road. *Cardiovascular Research*, **2019**, 115, 1692-1704	9.9	24
68	Predictive models of subcellular localization of long RNAs. *Rna*, **2019**, 25, 557-572	5.8	33
67	The EXPANDER Integrated Platform for Transcriptome Analysis. *Journal of Molecular Biology*, **2019**, 431, 2398-2406	6.5	13
66	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. *Circulation Research*, **2019**, 125, 535-551	15.7	50
65	Regulation of CHD2 expression by the Chaserr long noncoding RNA gene is essential for viability. *Nature Communications*, **2019**, 10, 5092	17.4	29
64	Aging well with. *ELife*, **2019**, 8,	8.9	4
63	Long Noncoding RNAs in Development and Regeneration of the Neural Lineage. *Cold Spring Harbor Symposia on Quantitative Biology*, **2019**, 84, 165-177	3.9	3
62	In-cell identification and measurement of RNA-protein interactions. *Nature Communications*, **2019**, 10, 5317	17.4	23
61	Alternative 3′UTRs direct localization of functionally diverse protein isoforms in neuronal compartments. *Nucleic Acids Research*, **2019**, 47, 2560-2573	20.1	56
60	SAM68 is required for regulation of Pumilio by the NORAD long noncoding RNA. *Genes and Development*, **2018**, 32, 70-78	12.6	41
59	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells. *Nature*, **2018**, 555, 107-111	50.4	169
58	Interactions between short and long noncoding RNAs. *FEBS Letters*, **2018**, 592, 2874-2883	3.8	64

57	Altered p53 functionality in cancer-associated fibroblasts contributes to their cancer-supporting features. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 6410-6415	11.5	49
56	Production of Spliced Long Noncoding RNAs Specifies Regions with Increased Enhancer Activity. *Cell Systems*, **2018**, 7, 537-547.e3	10.6	36
55	Predicting microRNA targeting efficacy in Drosophila. *Genome Biology*, **2018**, 19, 152	18.3	41
54	Regulation of Neuroregeneration by Long Noncoding RNAs. *Molecular Cell*, **2018**, 72, 553-567.e5	17.6	42
53	Efficient and Accurate Translation Initiation Directed by TISU Involves RPS3 and RPS10e Binding and Differential Eukaryotic Initiation Factor 1A Regulation. *Molecular and Cellular Biology*, **2017**, 37,	4.8	25
52	A subset of conserved mammalian long non-coding RNAs are fossils of ancestral protein-coding genes. *Genome Biology*, **2017**, 18, 162	18.3	41
51	The human lncRNA LINC-PINT inhibits tumor cell invasion through a highly conserved sequence element. *Genome Biology*, **2017**, 18, 202	18.3	122
50	Analysis of blood-based gene expression in idiopathic Parkinson disease. *Neurology*, **2017**, 89, 1676-1683	6.5	59
49	Genome-wide identification and expression profiling of long non-coding RNAs in auditory and vestibular systems. *Scientific Reports*, **2017**, 7, 8637	4.9	13
48	Cap-proximal nucleotides via differential eIF4E binding and alternative promoter usage mediate translational response to energy stress. *ELife*, **2017**, 6,	8.9	48
47	Methods for distinguishing between protein-coding and long noncoding RNAs and the elusive biological purpose of translation of long noncoding RNAs. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2016**, 1859, 31-40	6	60
46	Evolution to the rescue: using comparative genomics to understand long non-coding RNAs. *Nature Reviews Genetics*, **2016**, 17, 601-14	30.1	336
45	The functions of long noncoding RNAs in development and stem cells. *Development (Cambridge)*, **2016**, 143, 3882-3894	6.6	143
44	Circular RNAs are long-lived and display only minimal early alterations in response to a growth factor. *Nucleic Acids Research*, **2016**, 44, 1370-83	20.1	289
43	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells. *Nature Communications*, **2016**, 7, 12209	17.4	138
42	LIMT is a novel metastasis inhibiting lncRNA suppressed by EGF and downregulated in aggressive breast cancer. *EMBO Molecular Medicine*, **2016**, 8, 1052-64	12	66
41	Principles of long noncoding RNA evolution derived from direct comparison of transcriptomes in 17 species. *Cell Reports*, **2015**, 11, 1110-22	10.6	377
40	Recurrent inactivating RASA2 mutations in melanoma. *Nature Genetics*, **2015**, 47, 1408-10	36.3	73

39	Diversion of aspartate in ASS1-deficient tumours fosters de novo pyrimidine synthesis. *Nature*, **2015**, 527, 379-383	50.4	179
38	Nuclear Retention of mRNA in Mammalian Tissues. *Cell Reports*, **2015**, 13, 2653-62	10.6	157
37	Beyond secondary structure: primary-sequence determinants license pri-miRNA hairpins for processing. *Cell*, **2013**, 152, 844-58	56.2	281
36	lincRNAs: genomics, evolution, and mechanisms. *Cell*, **2013**, 154, 26-46	56.2	1841
35	Extensive alternative polyadenylation during zebrafish development. *Genome Research*, **2012**, 22, 2054-66	9.7	220
34	Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. *Cell*, **2011**, 147, 1537-50	56.2	882
33	Dynamic changes in the copy number of pluripotency and cell proliferation genes in human ESCs and iPSCs during reprogramming and time in culture. *Cell Stem Cell*, **2011**, 8, 106-18	18	700
32	SPIKE: a database of highly curated human signaling pathways. *Nucleic Acids Research*, **2011**, 39, D793-9	20.1	59
31	Integration of transcriptomics, proteomics, and microRNA analyses reveals novel microRNA regulation of targets in the mammalian inner ear. *PLoS ONE*, **2011**, 6, e18195	3.7	67
30	A point mutation in translation initiation factor eIF2B leads to function--and time-specific changes in brain gene expression. *PLoS ONE*, **2011**, 6, e26992	3.7	11
29	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. *Nature Structural and Molecular Biology*, **2010**, 17, 901-8	17.6	79
28	Expander: from expression microarrays to networks and functions. *Nature Protocols*, **2010**, 5, 303-22	18.8	165
27	Towards computational prediction of microRNA function and activity. *Nucleic Acids Research*, **2010**, 38, e160	20.1	75
26	Propagation of human embryonic and induced pluripotent stem cells in an indirect co-culture system. *Biochemical and Biophysical Research Communications*, **2010**, 393, 211-6	3.4	13
25	Different sets of QTLs influence fitness variation in yeast. *Molecular Systems Biology*, **2010**, 6, 346	12.2	21
24	DEGAS: de novo discovery of dysregulated pathways in human diseases. *PLoS ONE*, **2010**, 5, e13367	3.7	94
23	Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences. *Lecture Notes in Computer Science*, **2010**, 578-579	0.9	
22	Identifying functional modules using expression profiles and confidence-scored protein interactions. *Bioinformatics*, **2009**, 25, 1158-64	7.2	93

21	Allegro: analyzing expression and sequence in concert to discover regulatory programs. *Nucleic Acids Research*, **2009**, 37, 1566-79	20.1	36
20	Towards accurate imputation of quantitative genetic interactions. *Genome Biology*, **2009**, 10, R140	18.3	19
19	SPIKE--a database, visualization and analysis tool of cellular signaling pathways. *BMC Bioinformatics*, **2008**, 9, 110	3.6	48
18	MetaReg: a platform for modeling, analysis and visualization of biological systems using large-scale experimental data. *Genome Biology*, **2008**, 9, R1	18.3	15
17	Regulatory networks define phenotypic classes of human stem cell lines. *Nature*, **2008**, 455, 401-5	50.4	283
16	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. *Molecular Systems Biology*, **2008**, 4, 209	12.2	59
15	Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence. *Stem Cells*, **2008**, 26, 1506-16	5.8	184
14	DETECTING PATHWAYS TRANSCRIPTIONALLY CORRELATED WITH CLINICAL PARAMETERS **2008**,		2
13	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles **2008**, 347-359		34
12	Detecting pathways transcriptionally correlated with clinical parameters. *Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference*, **2008**, 7, 249-58		5
11	Network-based prediction of protein function. *Molecular Systems Biology*, **2007**, 3, 88	12.2	743
10	Identification of functional modules using network topology and high-throughput data. *BMC Systems Biology*, **2007**, 1, 8	3.5	229
9	The average common substring approach to phylogenomic reconstruction. *Journal of Computational Biology*, **2006**, 13, 336-50	1.7	153
8	Structural features within the NORAD long noncoding RNA underlie efficient repression of Pumilio activity		1
7	Massively parallel identification of zipcodes in primary cortical neurons		2
6	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells		1
5	High-Resolution Dissection of Conducive Reprogramming Trajectory to Ground State Pluripotency		3
4	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells		2

LIST OF PUBLICATIONS

3	SARS-CoV-2 utilizes a multipronged strategy to suppress host protein synthesis	2
2	Regulation of CHD2 expression by the Chaserr long noncoding RNA is essential for viability	1
1	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping	6