

Igor Ulitsky

List of Publications by Citations

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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	lincRNAs: genomics, evolution, and mechanisms. <i>Cell</i> , 2013 , 154, 26-46	56.2	1841
91	Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. <i>Cell</i> , 2011 , 147, 1537-50	56.2	882
90	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007 , 3, 88	12.2	743
89	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, 106-18	18	700
88	Principles of long noncoding RNA evolution derived from direct comparison of transcriptomes in 17 species. <i>Cell Reports</i> , 2015 , 11, 1110-22	10.6	377
87	Evolution to the rescue: using comparative genomics to understand long non-coding RNAs. <i>Nature Reviews Genetics</i> , 2016 , 17, 601-14	30.1	336
86	Circular RNAs are long-lived and display only minimal early alterations in response to a growth factor. <i>Nucleic Acids Research</i> , 2016 , 44, 1370-83	20.1	289
85	Regulatory networks define phenotypic classes of human stem cell lines. <i>Nature</i> , 2008 , 455, 401-5	50.4	283
84	Beyond secondary structure: primary-sequence determinants license pri-miRNA hairpins for processing. <i>Cell</i> , 2013 , 152, 844-58	56.2	281
83	Identification of functional modules using network topology and high-throughput data. <i>BMC Systems Biology</i> , 2007 , 1, 8	3.5	229
82	Extensive alternative polyadenylation during zebrafish development. <i>Genome Research</i> , 2012 , 22, 2054-667	6.7	220
81	Regulation of gene expression by cis-acting long non-coding RNAs. <i>Nature Reviews Genetics</i> , 2020 , 21, 102-117	30.1	216
80	Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence. <i>Stem Cells</i> , 2008 , 26, 1506-16	5.8	184
79	Diversion of aspartate in ASS1-deficient tumours fosters de novo pyrimidine synthesis. <i>Nature</i> , 2015 , 527, 379-383	50.4	179
78	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells. <i>Nature</i> , 2018 , 555, 107-111	50.4	169
77	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010 , 5, 303-22	18.8	165
76	Nuclear Retention of mRNA in Mammalian Tissues. <i>Cell Reports</i> , 2015 , 13, 2653-62	10.6	157

75	The average common substrating approach to phylogenomic reconstruction. <i>Journal of Computational Biology</i> , 2006 , 13, 336-50	1.7	153
74	The functions of long noncoding RNAs in development and stem cells. <i>Development (Cambridge)</i> , 2016 , 143, 3882-3894	6.6	143
73	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells. <i>Nature Communications</i> , 2016 , 7, 12209	17.4	138
72	The human lncRNA LINC-PINT inhibits tumor cell invasion through a highly conserved sequence element. <i>Genome Biology</i> , 2017 , 18, 202	18.3	122
71	DEGAS: de novo discovery of dysregulated pathways in human diseases. <i>PLoS ONE</i> , 2010 , 5, e13367	3.7	94
70	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , 2009 , 25, 1158-64	7.2	93
69	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, 901-8	17.6	79
68	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , 2010 , 38, e160	20.1	75
67	Recurrent inactivating RASA2 mutations in melanoma. <i>Nature Genetics</i> , 2015 , 47, 1408-10	36.3	73
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	3.7	67
65	LIMT is a novel metastasis inhibiting lncRNA suppressed by EGF and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016 , 8, 1052-64	12	66
64	Interactions between short and long noncoding RNAs. <i>FEBS Letters</i> , 2018 , 592, 2874-2883	3.8	64
63	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	6	60
62	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017 , 89, 1676-1683	36.5	59
61	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011 , 39, D793-9	20.1	59
60	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , 2008 , 4, 209	12.2	59
59	SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. <i>Nature</i> , 2021 , 594, 240-245	50.4	57
58	Alternative 3UTRs direct localization of functionally diverse protein isoforms in neuronal compartments. <i>Nucleic Acids Research</i> , 2019 , 47, 2560-2573	20.1	56

57	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	15.7	50
56	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	11.5	49
55	SPIKE--a database, visualization and analysis tool of cellular signaling pathways. <i>BMC Bioinformatics</i> , 2008 , 9, 110	3.6	48
54	Cap-proximal nucleotides via differential eIF4E binding and alternative promoter usage mediate translational response to energy stress. <i>ELife</i> , 2017 , 6,	8.9	48
53	Regulation of Neuroregeneration by Long Noncoding RNAs. <i>Molecular Cell</i> , 2018 , 72, 553-567.e5	17.6	42
52	A subset of conserved mammalian long non-coding RNAs are fossils of ancestral protein-coding genes. <i>Genome Biology</i> , 2017 , 18, 162	18.3	41
51	SAM68 is required for regulation of Pumilio by the NORAD long noncoding RNA. <i>Genes and Development</i> , 2018 , 32, 70-78	12.6	41
50	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
49	Predicting microRNA targeting efficacy in Drosophila. <i>Genome Biology</i> , 2018 , 19, 152	18.3	41
48	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020 , 39, e103777	13	39
47	Allegro: analyzing expression and sequence in concert to discover regulatory programs. <i>Nucleic Acids Research</i> , 2009 , 37, 1566-79	20.1	36
46	Production of Spliced Long Noncoding RNAs Specifies Regions with Increased Enhancer Activity. <i>Cell Systems</i> , 2018 , 7, 537-547.e3	10.6	36
45	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles 2008 , 347-359		34
44	Predictive models of subcellular localization of long RNAs. <i>Rna</i> , 2019 , 25, 557-572	5.8	33
43	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	17.6	32
42	Regulation of CHD2 expression by the Chaserr long noncoding RNA gene is essential for viability. <i>Nature Communications</i> , 2019 , 10, 5092	17.4	29
41	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,	4.8	25
40	Endothelial function and dysfunction in the cardiovascular system: the long non-coding road. <i>Cardiovascular Research</i> , 2019 , 115, 1692-1704	9.9	24

39	In-cell identification and measurement of RNA-protein interactions. <i>Nature Communications</i> , 2019 , 10, 5317	17.4	23
38	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , 2010 , 6, 346	12.2	21
37	Towards accurate imputation of quantitative genetic interactions. <i>Genome Biology</i> , 2009 , 10, R140	18.3	19
36	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	17.6	18
35	MetaReg: a platform for modeling, analysis and visualization of biological systems using large-scale experimental data. <i>Genome Biology</i> , 2008 , 9, R1	18.3	15
34	A MAFG-lncRNA axis links systemic nutrient abundance to hepatic glucose metabolism. <i>Nature Communications</i> , 2020 , 11, 644	17.4	14
33	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019 , 431, 2398-2406	6.5	13
32	Genome-wide identification and expression profiling of long non-coding RNAs in auditory and vestibular systems. <i>Scientific Reports</i> , 2017 , 7, 8637	4.9	13
31	Propagation of human embryonic and induced pluripotent stem cells in an indirect co-culture system. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 393, 211-6	3.4	13
30	Targeting purine synthesis in ASS1-expressing tumors enhances the response to immune checkpoint inhibitors.. <i>Nature Cancer</i> , 2020 , 1, 894-908	15.4	13
29	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	3.7	11
28	The evolutionarily conserved long non-coding RNA LINC00261 drives neuroendocrine prostate cancer proliferation and metastasis via distinct nuclear and cytoplasmic mechanisms. <i>Molecular Oncology</i> , 2021 , 15, 1921-1941	7.9	9
27	Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. <i>Genome Biology</i> , 2021 , 22, 29	18.3	8
26	MIR503HG Loss Promotes Endothelial-to-Mesenchymal Transition in Vascular Disease. <i>Circulation Research</i> , 2021 , 128, 1173-1190	15.7	7
25	SCIRT lncRNA Restrains Tumorigenesis by Opposing Transcriptional Programs of Tumor-Initiating Cells. <i>Cancer Research</i> , 2021 , 81, 580-593	10.1	7
24	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
23	High-resolution mapping of function and protein binding in an RNA nuclear enrichment sequence. <i>EMBO Journal</i> , 2021 , 40, e106357	13	5
22	Detecting pathways transcriptionally correlated with clinical parameters. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 249-58		5

21	Aging well with. <i>ELife</i> , 2019 , 8,	8.9	4
20	High-Resolution Dissection of Conductive Reprogramming Trajectory to Ground State Pluripotency		3
19	Long Noncoding RNAs in Development and Regeneration of the Neural Lineage. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019 , 84, 165-177	3.9	3
18	Therapy based on functional RNA elements. <i>Science</i> , 2021 , 373, 623-624	33.3	3
17	DETECTING PATHWAYS TRANSCRIPTIONALLY CORRELATED WITH CLINICAL PARAMETERS 2008 ,		2
16	Massively parallel identification of zipcodes in primary cortical neurons		2
15	Sequences enriched in Alu repeats drive nuclear localization of long RNAs in human cells		2
14	SARS-CoV-2 utilizes a multipronged strategy to suppress host protein synthesis		2
13	Context-specific effects of sequence elements on subcellular localization of linear and circular RNAs.. <i>Nature Communications</i> , 2022 , 13, 2481	17.4	2
12	Identification and characterization of key long non-coding RNAs in the mouse cochlea. <i>RNA Biology</i> , 2021 , 18, 1160-1169	4.8	1
11	Structural features within the NORAD long noncoding RNA underlie efficient repression of Pumilio activity		1
10	Regulation of neuronal commitment in mouse embryonic stem cells by the Reno1/Bahcc1 locus. <i>EMBO Reports</i> , 2020 , 21, e51264	6.5	1
9	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells		1
8	Regulation of CHD2 expression by the Chaserr long noncoding RNA is essential for viability		1
7	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	6	1
6	Discovering functional motifs in long noncoding RNAs.. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022 , e1708	9.3	0
5	Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors.. <i>Cell Reports</i> , 2022 , 38, 110418	10.6	0
4	Substoichiometric action of long noncoding RNAs.. <i>Nature Cell Biology</i> , 2022 , 24, 608-615	23.4	0

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| 3 | Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences. <i>Lecture Notes in Computer Science</i> , 2010 , 578-579 | 0.9 |
| 2 | Inefficient splicing curbs noncoding RNA transcription. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 327-328 | 17.6 |
| 1 | Unique features of transcription termination and initiation at closely spaced tandem human genes.. <i>Molecular Systems Biology</i> , 2022 , 18, e10682 | 12.2 |