Jernej Ule

List of Publications by Year
in descending order

136 papers	19,174 citations	17405 63 h-index	13727 129 g-index
175 all docs	175 docs citations	175 times ranked	21126 citing authors

#	Article	IF	Citations
1	TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UNC13A. Nature, 2022, 603, 131-137.	13.7	188
2	U1A is a positive regulator of the expression of heterologous and cellular genes involved in cell proliferation and migration. Molecular Therapy - Nucleic Acids, 2022, 28, 831-846.	2.3	1
3	Identifying ribosome heterogeneity using ribosome profiling. Nucleic Acids Research, 2022, 50, e95-e95.	6.5	7
4	psiCLIP reveals dynamic RNA binding by DEAH-box helicases before and after exon ligation. Nature Communications, 2021, 12, 1488.	5.8	8
5	CLIP and complementary methods. Nature Reviews Methods Primers, 2021, 1, .	11.8	152
6	Intergenic RNA mainly derives from nascent transcripts of known genes. Genome Biology, 2021, 22, 136.	3.8	13
7	MIR-NATs repress MAPT translation and aid proteostasis in neurodegeneration. Nature, 2021, 594, 117-123.	13.7	29
8	Acute depletion of METTL3 implicates N⁶-methyladenosine in alternative intron/exon inclusion in the nascent transcriptome. Genome Research, 2021, 31, 1395-1408.	2.4	37
9	Ultraplex: A rapid, flexible, all-in-one fastq demultiplexer. Wellcome Open Research, 2021, 6, 141.	0.9	11
10	Sequential inverse dysregulation of the RNA helicases DDX3X and DDX3Y facilitates MYC-driven lymphomagenesis. Molecular Cell, 2021, 81, 4059-4075.e11.	4.5	42
11	TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. Cell, 2021, 184, 4680-4696.e22.	13.5	121
12	Metabolic turnover and dynamics of modified ribonucleosides by 13C labeling. Journal of Biological Chemistry, 2021, 297, 101294.	1.6	3
13	Identification of HuR-specific RNA interactome in TGF-ÃŸ1-activated fibroblasts in response to cigarette smoke. , 2021, , .		0
14	A genetically-encoded crosslinker screen identifies SERBP1 as a PKCÎµ substrate influencing translation and cell division. Nature Communications, 2021, 12, 6934.	5.8	7
15	RGS4 RNA Secondary Structure Mediates Staufen2 RNP Assembly in Neurons. International Journal of Molecular Sciences, 2021, 22, 13021.	1.8	5
16	RNA modifications detection by comparative Nanopore direct RNA sequencing. Nature Communications, 2021, 12, 7198.	5.8	163
17	Chromatin-contact atlas reveals disorder-mediated protein interactions and moonlighting chromatin-associated RBPs. Nucleic Acids Research, 2021, 49, 13092-13107.	6.5	9
18	Subcellular mRNA Localization Regulates Ribosome Biogenesis in Migrating Cells. Developmental Cell, 2020, 55, 298-313.e10.	3.1	50

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19	CDK11 is required for transcription of replication-dependent histone genes. Nature Structural and Molecular Biology, 2020, 27, 500-510.	3.6	29
20	Open access, open data and peer review. Genome Biology, 2020, 21, 86.	3.8	4
21	How Do You Identify m6 A Methylation in Transcriptomes at High Resolution? A Comparison of Recent Datasets. Frontiers in Genetics, 2020, 11, 398.	1.1	17
22	Cytotoxic T-cells mediate exercise-induced reductions in tumor growth. ELife, 2020, 9, .	2.8	93
23	The Transcriptome-wide Landscape and Modalities of EJC Binding in Adult Drosophila. Cell Reports, 2019, 28, 1219-1236.e11.	2.9	15
24	Widespread FUS mislocalization is a molecular hallmark of amyotrophic lateral sclerosis. Brain, 2019, 142, 2572-2580.	3.7	135
25	FICC-Seq: a method for enzyme-specified profiling of methyl-5-uridine in cellular RNA. Nucleic Acids Research, 2019, 47, e113-e113.	6.5	48
26	Alternative Splicing Regulatory Networks: Functions, Mechanisms, and Evolution. Molecular Cell, 2019, 76, 329-345.	4.5	446
27	A systems view of spliceosomal assembly and branchpoints with iCLIP. Nature Structural and Molecular Biology, 2019, 26, 930-940.	3.6	26
28	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. Molecular Cell, 2019, 74, 951-965.e13.	4.5	85
29	Charting DENR-dependent translation reinitiation uncovers predictive uORF features and links to circadian timekeeping via Clock. Nucleic Acids Research, 2019, 47, 5193-5209.	6.5	30
30	The origin of neural microexons. Nature Ecology and Evolution, 2019, 3, 526-527.	3.4	1
31	P-TEFb Activation by RBM7 Shapes a Pro-survival Transcriptional Response to Genotoxic Stress. Molecular Cell, 2019, 74, 254-267.e10.	4.5	73
32	Genomic Accumulation of Retrotransposons Was Facilitated by Repressive RNAâ€Binding Proteins: A Hypothesis. BioEssays, 2019, 41, e1800132.	1.2	13
33	The key protein of endosomal mRNP transport Rrm4 binds translational landmark sites of cargo mRNAs. EMBO Reports, 2019, 20, .	2.0	38
34	The SMAD2/3 interactome reveals that TGFÎ² controls m6A mRNA methylation in pluripotency. Nature, 2018, 555, 256-259.	13.7	283
35	No way out: when <scp>RNA</scp> elements promote nuclear retention. EMBO Journal, 2018, 37, .	3.5	0
36	Positioning Europe for the EPITRANSCRIPTOMICS challenge. RNA Biology, 2018, 15, 1-3.	1.5	18

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37	Advances in CLIP Technologies for Studies of Protein-RNA Interactions. Molecular Cell, 2018, 69, 354-369.	4.5	239
38	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. Molecular Cell, 2018, 72, 496-509.e9.	4.5	75
39	Data Science Issues in Studying Proteinâ€“RNA Interactions with CLIP Technologies. Annual Review of Biomedical Data Science, 2018, 1, 235-261.	2.8	51
40	Intron retention and nuclear loss of SFPQ are molecular hallmarks of ALS. Nature Communications, 2018, 9, 2010.	5.8	116
41	SRSF3 maintains transcriptome integrity in oocytes by regulation of alternative splicing and transposable elements. Cell Discovery, 2018, 4, 33.	3.1	40
42	Heteromeric RNP Assembly at LINEs Controls Lineage-Specific RNA Processing. Cell, 2018, 174, 1067-1081.e17.	13.5	121
43	The Future of Cross-Linking and Immunoprecipitation (CLIP). Cold Spring Harbor Perspectives in Biology, 2018, 10, a032243.	2.3	51
44	â€˜Readâ€“through markingâ€™ reveals differential nucleotide composition of read-through and truncated cDNAs in iCLIP. Wellcome Open Research, 2018, 3, 77.	0.9	2
45	Cholinergic Surveillance over Hippocampal RNA Metabolism and Alzheimer's-Like Pathology. Cerebral Cortex, 2017, 27, bhw177.	1.6	42
46	Major Shifts in Glial Regional Identity Are a Transcriptional Hallmark of Human Brain Aging. Cell Reports, 2017, 18, 557-570.	2.9	326
47	Using hiCLIP to identify RNA duplexes that interact with a specific RNA-binding protein. Nature Protocols, 2017, 12, 611-637.	5.5	21
48	Insights into the design and interpretation of iCLIP experiments. Genome Biology, 2017, 18, 7.	3.8	73
49	Regulatory feedback from nascent RNA to chromatin and transcription. Nature Reviews Molecular Cell Biology, 2017, 18, 331-337.	16.1	56
50	Transcript-specific characteristics determine the contribution of endo- and exonucleolytic decay pathways during the degradation of nonsense-mediated decay substrates. Rna, 2017, 23, 1224-1236.	1.6	26
51	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. Cell Reports, 2017, 19, 1056-1067.	2.9	83
52	Progressive Motor Neuron Pathology and the Role of Astrocytes in a Human Stem Cell Model of VCP-Related ALS. Cell Reports, 2017, 19, 1739-1749.	2.9	146
53	Illustrating the Epitranscriptome at Nucleotide Resolution Using Methylation-iCLIP (miCLIP). Methods in Molecular Biology, 2017, 1562, 91-106.	0.4	15
54	Differential Binding of Mitochondrial Transcripts by MRB8170 and MRB4160 Regulates Distinct Editing Fates of Mitochondrial mRNA in Trypanosomes. MBio, 2017, 8, .	1.8	17

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55	Tia1 dependent regulation of mRNA subcellular location and translation controls p53 expression in B cells. Nature Communications, 2017, 8, 530.	5.8	48
56	A retained intron in the 3â€²â€•<scp>UTR</scp> of Calm3 <scp>mRNA</scp> mediates its Staufen2â€•and activityâ€dependent localization to neuronal dendrites. EMBO Reports, 2017, 18, 1762-1774.	2.0	58
57	Splicing repression allows the gradual emergence of new Alu-exons in primate evolution. ELife, 2016, 5, .	2.8	57
58	The alternative splicing program of differentiated smooth muscle cells involves concerted non-productive splicing of post-transcriptional regulators. Nucleic Acids Research, 2016, 44, 8933-8950.	6.5	47
59	Matrin3: connecting gene expression with the nuclear matrix. Wiley Interdisciplinary Reviews RNA, 2016, 7, 303-315.	3.2	18
60	The interaction of PRC2 with RNA or chromatin is mutually antagonistic. Genome Research, 2016, 26, 896-907.	2.4	191
61	Lessons from non-canonical splicing. Nature Reviews Genetics, 2016, 17, 407-421.	7.7	230
62	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. Bioinformatics, 2016, 32, 1527-1535.	1.8	108
63	iCLIP identifies novel roles for SAFB1 in regulating RNA processing and neuronal function. BMC Biology, 2015, 13, 111.	1.7	23
64	IntergenicAluexonisation facilitates the evolution of tissue-specific transcript ends. Nucleic Acids Research, 2015, 43, gkv956.	6.5	31
65	Nuclear matrix protein Matrin3 regulates alternative splicing and forms overlapping regulatory networks with <scp>PTB</scp>. EMBO Journal, 2015, 34, 653-668.	3.5	124
66	The RNA-binding protein HuR is essential for the B cell antibody response. Nature Immunology, 2015, 16, 415-425.	7.0	125
67	Control of a neuronal morphology program by an RNA-binding zinc finger protein, Unkempt. Genes and Development, 2015, 29, 501-512.	2.7	35
68	HIF-driven SF3B1 induces KHK-C to enforce fructolysis and heart disease. Nature, 2015, 522, 444-449.	13.7	144
69	RNA-Binding Protein Musashi1 Is a Central Regulator of Adhesion Pathways in Glioblastoma. Molecular and Cellular Biology, 2015, 35, 2965-2978.	1.1	51
70	Promiscuous RNA Binding Ensures Effective Encapsidation of APOBEC3 Proteins by HIV-1. PLoS Pathogens, 2015, 11, e1004609.	2.1	86
71	Recursive splicing in long vertebrate genes. Nature, 2015, 521, 371-375.	13.7	128
72	hiCLIP reveals the in vivo atlas of mRNA secondary structures recognized by Staufen 1. Nature, 2015, 519, 491-494.	13.7	248

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73	Regulation of constitutive and alternative mRNA splicing across the human transcriptome by PRPF8 is determined by 5â€² splice site strength. Genome Biology, 2015, 16, 201.	3.8	81
74	3â€² UTR Length and Messenger Ribonucleoprotein Composition Determine Endocleavage Efficiencies at Termination Codons. Cell Reports, 2014, 9, 555-568.	2.9	78
75	Splicing changes in SMA mouse motoneurons and SMN-depleted neuroblastoma cells: Evidence for involvement of splicing regulatory proteins. RNA Biology, 2014, 11, 1430-1446.	1.5	29
76	CPSF30 and Wdr33 directly bind to AAUAAA in mammalian mRNA 3â€² processing. Genes and Development, 2014, 28, 2370-2380.	2.7	193
77	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. RNA Biology, 2014, 11, 146-155.	1.5	82
78	'Oming in on RNAâ€“protein interactions. Genome Biology, 2014, 15, 401.	13.9	32
79	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. Molecular Cell, 2014, 56, 389-399.	4.5	88
80	Aberrant methylation of t<scp>RNA</scp>s links cellular stress to neuroâ€developmental disorders. EMBO Journal, 2014, 33, 2020-2039.	3.5	490
81	Rbfox2-Coordinated Alternative Splicing of Mef2d and Rock2 Controls Myoblast Fusion during Myogenesis. Molecular Cell, 2014, 55, 592-603.	4.5	104
82	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. Molecular Cell, 2014, 56, 90-103.	4.5	131
83	RNAmotifs: prediction of multivalent RNA motifs that control alternative splicing. Genome Biology, 2014, 15, R20.	13.9	49
84	iCLIP: Proteinâ€“RNA interactions at nucleotide resolution. Methods, 2014, 65, 274-287.	1.9	366
85	Hexanucleotide Repeats in ALS/FTD Form Length-Dependent RNA Foci, Sequester RNA Binding Proteins, and Are Neurotoxic. Cell Reports, 2013, 5, 1178-1186.	2.9	419
86	Sixty years of genome biology. Genome Biology, 2013, 14, 113.	13.9	6
87	NSun2-Mediated Cytosine-5 Methylation of Vault Noncoding RNA Determines Its Processing into Regulatory Small RNAs. Cell Reports, 2013, 4, 255-261.	2.9	448
88	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. Cell, 2013, 152, 453-466.	13.5	398
89	Aberrant sodium channel activity in the complex seizure disorder of Celf4 mutant mice. Journal of Physiology, 2013, 591, 241-255.	1.3	33
90	CLIPing the brain: Studies of proteinâ€“RNA interactions important for neurodegenerative disorders. Molecular and Cellular Neurosciences, 2013, 56, 429-435.	1.0	30

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91	Molecular basis of UG-rich RNA recognition by the human splicing factor TDP-43. Nature Structural and Molecular Biology, 2013, 20, 1443-1449.	3.6	293
92	Alu elements: at the crossroads between disease and evolution. Biochemical Society Transactions, 2013, 41, 1532-1535.	1.6	36
93	Requirement of Heterogeneous Nuclear Ribonucleoprotein C for BRCA Gene Expression and Homologous Recombination. PLoS ONE, 2013, 8, e61368.	1.1	56
94	What, where, and when: the importance of post-transcriptional regulation in the brain. Frontiers in Neuroscience, 2013, 7, 192.	1.4	15
95	CELF4 Regulates Translation and Local Abundance of a Vast Set of mRNAs, Including Genes Associated with Regulation of Synaptic Function. PLoS Genetics, 2012, 8, e1003067.	1.5	106
96	Psip1/Ledgf p52 Binds Methylated Histone H3K36 and Splicing Factors and Contributes to the Regulation of Alternative Splicing. PLoS Genetics, 2012, 8, e1002717.	1.5	296
97	Regulation of alternative splicing by the circadian clock and food related cues. Genome Biology, 2012, 13, R54.	13.9	89
98	The greatest catch: big game fishing for mRNA-bound proteins. Genome Biology, 2012, 13, 163.	13.9	4
99	Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions. Genome Biology, 2012, 13, R67.	13.9	195
100	Neuronal Elav-like (Hu) Proteins Regulate RNA Splicing and Abundance to Control Glutamate Levels and Neuronal Excitability. Neuron, 2012, 75, 1067-1080.	3.8	190
101	Widespread binding of FUS along nascent RNA regulates alternative splicing in the brain. Scientific Reports, 2012, 2, 603.	1.6	231
102	Perturbation of Chromatin Structure Globally Affects Localization and Recruitment of Splicing Factors. PLoS ONE, 2012, 7, e48084.	1.1	44
103	The RNA-binding landscapes of two SR proteins reveal unique functions and binding to diverse RNA classes. Genome Biology, 2012, 13, R17.	13.9	229
104	Proteinâ€“RNA interactions: new genomic technologies and perspectives. Nature Reviews Genetics, 2012, 13, 77-83.	7.7	482
105	Using human pluripotent stem cells to study post-transcriptional mechanisms of neurodegenerative diseases. Brain Research, 2012, 1462, 129-138.	1.1	4
106	Selective inhibition of microRNA accessibility by RBM38 is required for p53 activity. Nature Communications, 2011, 2, 513.	5.8	91
107	iCLIP - Transcriptome-wide Mapping of Protein-RNA Interactions with Individual Nucleotide Resolution. Journal of Visualized Experiments, 2011, , .	0.2	168
108	Characterizing the RNA targets and position-dependent splicing regulation by TDP-43. Nature Neuroscience, 2011, 14, 452-458.	7.1	956

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109	TDP-43 regulates its mRNA levels through a negative feedback loop. EMBO Journal, 2011, 30, 277-288.	3.5	492
110	Understanding splicing regulation through RNA splicing maps. Trends in Genetics, 2011, 27, 89-97.	2.9	228
111	The RNA-Binding Protein Rrm4 is Essential for Efficient Secretion of Endochitinase Cts1. Molecular and Cellular Proteomics, 2011, 10, M111.011213.	2.5	48
112	The Cyclin K/Cdk12 complex maintains genomic stability via regulation of expression of DNA damage response genes. Genes and Development, 2011, 25, 2158-2172.	2.7	387
113	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. Genome Research, 2011, 21, 1572-1582.	2.4	199
114	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution. Nature Structural and Molecular Biology, 2010, 17, 909-915.	3.6	1,026
115	The neuronal splicing factor Nova co-localizes with target RNAs in the dendrite. Frontiers in Neural Circuits, 2010, 4, 5.	1.4	57
116	iCLIP Predicts the Dual Splicing Effects of TIA-RNA Interactions. PLoS Biology, 2010, 8, e1000530.	2.6	226
117	Cholinergic regulation of striatal Nova mRNAs. Neuroscience, 2010, 169, 619-627.	1.1	8
118	CLIP: Construction of cDNA libraries for high-throughput sequencing from RNAs cross-linked to proteins in vivo. Methods, 2009, 48, 287-293.	1.9	79
119	High-throughput sequencing methods to study neuronal RNAâ€“protein interactions. Biochemical Society Transactions, 2009, 37, 1278-1280.	1.6	8
120	HITS-CLIP yields genome-wide insights into brain alternative RNA processing. Nature, 2008, 456, 464-469.	13.7	1,245
121	Ribonucleoprotein complexes in neurologic diseases. Current Opinion in Neurobiology, 2008, 18, 516-523.	2.0	36
122	Jernej Ule: An RNA runaway success. Journal of Cell Biology, 2008, 180, 448-449.	2.3	0
123	Evolution of Nova-Dependent Splicing Regulation in the Brain. PLoS Genetics, 2007, 3, e173.	1.5	76
124	Functional and Mechanistic Insights From Genome-Wide Studies of Splicing Regulation in the Brain. Advances in Experimental Medicine and Biology, 2007, 623, 148-160.	0.8	20
125	[S18]: RNA regulation and modular control of the neuronal synapse. International Journal of Developmental Neuroscience, 2006, 24, 479-479.	0.7	0
126	An RNA map predicting Nova-dependent splicing regulation. Nature, 2006, 444, 580-586.	13.7	477

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127	RNA binding proteins and the regulation of neuronal synaptic plasticity. Current Opinion in Neurobiology, 2006, 16, 102-110.	2.0	161
128	Nova regulates brain-specific splicing to shape the synapse. Nature Genetics, 2005, 37, 844-852.	9.4	447
129	Common Molecular Pathways Mediate Long-Term Potentiation of Synaptic Excitation and Slow Synaptic Inhibition. Cell, 2005, 123, 105-118.	13.5	140
130	CLIP: A method for identifying proteinâ€“RNA interaction sites in living cells. Methods, 2005, 37, 376-386.	1.9	509
131	CLIP Identifies Nova-Regulated RNA Networks in the Brain. Science, 2003, 302, 1212-1215.	6.0	984
132	Regulation of cyclin-dependent kinase 5 and casein kinase 1 by metabotropic glutamate receptors. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11062-11068.	3.3	121
133	Phosphorylation of Protein Phosphatase Inhibitor-1 by Cdk5. Journal of Biological Chemistry, 2001, 276, 14490-14497.	1.6	83
134	Proteinâ€“RNA interactions: new genomic technologies and perspectives. , 0, .		1
135	Cross-Regulation Between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. SSRN Electronic Journal, 0, , .	0.4	2
136	Sequential Inverse Dysregulation of the RNA Helicases DDX3X and DDX3Y Facilitates MYC-Driven Lymphomagenesis. SSRN Electronic Journal, 0, , .	0.4	2