

# Jernej Ule

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3569699/publications.pdf>

Version: 2024-02-01

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	HITS-CLIP yields genome-wide insights into brain alternative RNA processing. <i>Nature</i> , 2008, 456, 464-469.	13.7	1,245
2	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 909-915.	3.6	1,026
3	CLIP Identifies Nova-Regulated RNA Networks in the Brain. <i>Science</i> , 2003, 302, 1212-1215.	6.0	984
4	Characterizing the RNA targets and position-dependent splicing regulation by TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 452-458.	7.1	956
5	CLIP: A method for identifying proteinâ€“RNA interaction sites in living cells. <i>Methods</i> , 2005, 37, 376-386.	1.9	509
6	TDP-43 regulates its mRNA levels through a negative feedback loop. <i>EMBO Journal</i> , 2011, 30, 277-288.	3.5	492
7	Aberrant methylation of t<scp>RNA</scp>s links cellular stress to neuroâ€“developmental disorders. <i>EMBO Journal</i> , 2014, 33, 2020-2039.	3.5	490
8	Proteinâ€“RNA interactions: new genomic technologies and perspectives. <i>Nature Reviews Genetics</i> , 2012, 13, 77-83.	7.7	482
9	An RNA map predicting Nova-dependent splicing regulation. <i>Nature</i> , 2006, 444, 580-586.	13.7	477
10	NSun2-Mediated Cytosine-5 Methylation of Vault Noncoding RNA Determines Its Processing into Regulatory Small RNAs. <i>Cell Reports</i> , 2013, 4, 255-261.	2.9	448
11	Nova regulates brain-specific splicing to shape the synapse. <i>Nature Genetics</i> , 2005, 37, 844-852.	9.4	447
12	Alternative Splicing Regulatory Networks: Functions, Mechanisms, and Evolution. <i>Molecular Cell</i> , 2019, 76, 329-345.	4.5	446
13	Hexanucleotide Repeats in ALS/FTD Form Length-Dependent RNA Foci, Sequester RNA Binding Proteins, and Are Neurotoxic. <i>Cell Reports</i> , 2013, 5, 1178-1186.	2.9	419
14	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. <i>Cell</i> , 2013, 152, 453-466.	13.5	398
15	The Cyclin K/Cdk12 complex maintains genomic stability via regulation of expression of DNA damage response genes. <i>Genes and Development</i> , 2011, 25, 2158-2172.	2.7	387
16	iCLIP: Proteinâ€“RNA interactions at nucleotide resolution. <i>Methods</i> , 2014, 65, 274-287.	1.9	366
17	Major Shifts in Glial Regional Identity Are a Transcriptional Hallmark of Human Brain Aging. <i>Cell Reports</i> , 2017, 18, 557-570.	2.9	326
18	Psp1/Ledgf p52 Binds Methylated Histone H3K36 and Splicing Factors and Contributes to the Regulation of Alternative Splicing. <i>PLoS Genetics</i> , 2012, 8, e1002717.	1.5	296

#	ARTICLE	IF	CITATIONS
19	Molecular basis of UG-rich RNA recognition by the human splicing factor TDP-43. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1443-1449.	3.6	293
20	The SMAD2/3 interactome reveals that TGF $\beta$ 2 controls m6A mRNA methylation in pluripotency. <i>Nature</i> , 2018, 555, 256-259.	13.7	283
21	hiCLIP reveals the in vivo atlas of mRNA secondary structures recognized by Staufen 1. <i>Nature</i> , 2015, 519, 491-494.	13.7	248
22	Advances in CLIP Technologies for Studies of Protein-RNA Interactions. <i>Molecular Cell</i> , 2018, 69, 354-369.	4.5	239
23	Widespread binding of FUS along nascent RNA regulates alternative splicing in the brain. <i>Scientific Reports</i> , 2012, 2, 603.	1.6	231
24	Lessons from non-canonical splicing. <i>Nature Reviews Genetics</i> , 2016, 17, 407-421.	7.7	230
25	The RNA-binding landscapes of two SR proteins reveal unique functions and binding to diverse RNA classes. <i>Genome Biology</i> , 2012, 13, R17.	13.9	229
26	Understanding splicing regulation through RNA splicing maps. <i>Trends in Genetics</i> , 2011, 27, 89-97.	2.9	228
27	iCLIP Predicts the Dual Splicing Effects of TIA-RNA Interactions. <i>PLoS Biology</i> , 2010, 8, e1000530.	2.6	226
28	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. <i>Genome Research</i> , 2011, 21, 1572-1582.	2.4	199
29	Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions. <i>Genome Biology</i> , 2012, 13, R67.	13.9	195
30	CPSF30 and Wdr33 directly bind to AAUAAA in mammalian mRNA 3' processing. <i>Genes and Development</i> , 2014, 28, 2370-2380.	2.7	193
31	The interaction of PRC2 with RNA or chromatin is mutually antagonistic. <i>Genome Research</i> , 2016, 26, 896-907.	2.4	191
32	Neuronal Elav-like (Hu) Proteins Regulate RNA Splicing and Abundance to Control Glutamate Levels and Neuronal Excitability. <i>Neuron</i> , 2012, 75, 1067-1080.	3.8	190
33	TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UNC13A. <i>Nature</i> , 2022, 603, 131-137.	13.7	188
34	iCLIP - Transcriptome-wide Mapping of Protein-RNA Interactions with Individual Nucleotide Resolution. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	168
35	RNA modifications detection by comparative Nanopore direct RNA sequencing. <i>Nature Communications</i> , 2021, 12, 7198.	5.8	163
36	RNA binding proteins and the regulation of neuronal synaptic plasticity. <i>Current Opinion in Neurobiology</i> , 2006, 16, 102-110.	2.0	161

#	ARTICLE	IF	CITATIONS
37	CLIP and complementary methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	152
38	Progressive Motor Neuron Pathology and the Role of Astrocytes in a Human Stem Cell Model of VCP-Related ALS. <i>Cell Reports</i> , 2017, 19, 1739-1749.	2.9	146
39	HIF-driven SF3B1 induces KHK-C to enforce fructolysis and heart disease. <i>Nature</i> , 2015, 522, 444-449.	13.7	144
40	Common Molecular Pathways Mediate Long-Term Potentiation of Synaptic Excitation and Slow Synaptic Inhibition. <i>Cell</i> , 2005, 123, 105-118.	13.5	140
41	Widespread FUS mislocalization is a molecular hallmark of amyotrophic lateral sclerosis. <i>Brain</i> , 2019, 142, 2572-2580.	3.7	135
42	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. <i>Molecular Cell</i> , 2014, 56, 90-103.	4.5	131
43	Recursive splicing in long vertebrate genes. <i>Nature</i> , 2015, 521, 371-375.	13.7	128
44	The RNA-binding protein HuR is essential for the B cell antibody response. <i>Nature Immunology</i> , 2015, 16, 415-425.	7.0	125
45	Nuclear matrix protein Matrin3 regulates alternative splicing and forms overlapping regulatory networks with <scp>PTB</scp>. <i>EMBO Journal</i> , 2015, 34, 653-668.	3.5	124
46	Regulation of cyclin-dependent kinase 5 and casein kinase 1 by metabotropic glutamate receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 11062-11068.	3.3	121
47	Heteromeric RNP Assembly at LINEs Controls Lineage-Specific RNA Processing. <i>Cell</i> , 2018, 174, 1067-1081.e17.	13.5	121
48	TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. <i>Cell</i> , 2021, 184, 4680-4696.e22.	13.5	121
49	Intron retention and nuclear loss of SFPQ are molecular hallmarks of ALS. <i>Nature Communications</i> , 2018, 9, 2010.	5.8	116
50	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. <i>Bioinformatics</i> , 2016, 32, 1527-1535.	1.8	108
51	CELF4 Regulates Translation and Local Abundance of a Vast Set of mRNAs, Including Genes Associated with Regulation of Synaptic Function. <i>PLoS Genetics</i> , 2012, 8, e1003067.	1.5	106
52	Rbfox2-Coordinated Alternative Splicing of Mef2d and Rock2 Controls Myoblast Fusion during Myogenesis. <i>Molecular Cell</i> , 2014, 55, 592-603.	4.5	104
53	Cytotoxic T-cells mediate exercise-induced reductions in tumor growth. <i>ELife</i> , 2020, 9, .	2.8	93
54	Selective inhibition of microRNA accessibility by RBM38 is required for p53 activity. <i>Nature Communications</i> , 2011, 2, 513.	5.8	91

#	ARTICLE	IF	CITATIONS
55	Regulation of alternative splicing by the circadian clock and food related cues. <i>Genome Biology</i> , 2012, 13, R54.	13.9	89
56	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	4.5	88
57	Promiscuous RNA Binding Ensures Effective Encapsidation of APOBEC3 Proteins by HIV-1. <i>PLoS Pathogens</i> , 2015, 11, e1004609.	2.1	86
58	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , 2019, 74, 951-965.e13.	4.5	85
59	Phosphorylation of Protein Phosphatase Inhibitor-1 by Cdk5. <i>Journal of Biological Chemistry</i> , 2001, 276, 14490-14497.	1.6	83
60	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. <i>Cell Reports</i> , 2017, 19, 1056-1067.	2.9	83
61	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. <i>RNA Biology</i> , 2014, 11, 146-155.	1.5	82
62	Regulation of constitutive and alternative mRNA splicing across the human transcriptome by PRPF8 is determined by 5' splice site strength. <i>Genome Biology</i> , 2015, 16, 201.	3.8	81
63	CLIP: Construction of cDNA libraries for high-throughput sequencing from RNAs cross-linked to proteins in vivo. <i>Methods</i> , 2009, 48, 287-293.	1.9	79
64	3' UTR Length and Messenger Ribonucleoprotein Composition Determine Endocleavage Efficiencies at Termination Codons. <i>Cell Reports</i> , 2014, 9, 555-568.	2.9	78
65	Evolution of Nova-Dependent Splicing Regulation in the Brain. <i>PLoS Genetics</i> , 2007, 3, e173.	1.5	76
66	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. <i>Molecular Cell</i> , 2018, 72, 496-509.e9.	4.5	75
67	Insights into the design and interpretation of iCLIP experiments. <i>Genome Biology</i> , 2017, 18, 7.	3.8	73
68	P-TEFb Activation by RBM7 Shapes a Pro-survival Transcriptional Response to Genotoxic Stress. <i>Molecular Cell</i> , 2019, 74, 254-267.e10.	4.5	73
69	A retained intron in the 3' UTR of <i>Calm3</i> mRNA mediates its Staufen2-dependent localization to neuronal dendrites. <i>EMBO Reports</i> , 2017, 18, 1762-1774.	2.0	58
70	The neuronal splicing factor Nova co-localizes with target RNAs in the dendrite. <i>Frontiers in Neural Circuits</i> , 2010, 4, 5.	1.4	57
71	Splicing repression allows the gradual emergence of new Alu-exons in primate evolution. <i>ELife</i> , 2016, 5, .	2.8	57
72	Regulatory feedback from nascent RNA to chromatin and transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 331-337.	16.1	56

#	ARTICLE	IF	CITATIONS
73	Requirement of Heterogeneous Nuclear Ribonucleoprotein C for BRCA Gene Expression and Homologous Recombination. <i>PLoS ONE</i> , 2013, 8, e61368.	1.1	56
74	RNA-Binding Protein Musashi1 Is a Central Regulator of Adhesion Pathways in Glioblastoma. <i>Molecular and Cellular Biology</i> , 2015, 35, 2965-2978.	1.1	51
75	Data Science Issues in Studying Protein-RNA Interactions with CLIP Technologies. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 235-261.	2.8	51
76	The Future of Cross-Linking and Immunoprecipitation (CLIP). <i>Cold Spring Harbor Perspectives in Biology</i> , 2018, 10, a032243.	2.3	51
77	Subcellular mRNA Localization Regulates Ribosome Biogenesis in Migrating Cells. <i>Developmental Cell</i> , 2020, 55, 298-313.e10.	3.1	50
78	RNA motifs: prediction of multivalent RNA motifs that control alternative splicing. <i>Genome Biology</i> , 2014, 15, R20.	13.9	49
79	The RNA-Binding Protein Rrm4 is Essential for Efficient Secretion of Endochitinase Cts1. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011213.	2.5	48
80	Tia1 dependent regulation of mRNA subcellular location and translation controls p53 expression in B cells. <i>Nature Communications</i> , 2017, 8, 530.	5.8	48
81	FICC-Seq: a method for enzyme-specified profiling of methyl-5-uridine in cellular RNA. <i>Nucleic Acids Research</i> , 2019, 47, e113-e113.	6.5	48
82	The alternative splicing program of differentiated smooth muscle cells involves concerted non-productive splicing of post-transcriptional regulators. <i>Nucleic Acids Research</i> , 2016, 44, 8933-8950.	6.5	47
83	Perturbation of Chromatin Structure Globally Affects Localization and Recruitment of Splicing Factors. <i>PLoS ONE</i> , 2012, 7, e48084.	1.1	44
84	Cholinergic Surveillance over Hippocampal RNA Metabolism and Alzheimer's-Like Pathology. <i>Cerebral Cortex</i> , 2017, 27, bhw177.	1.6	42
85	Sequential inverse dysregulation of the RNA helicases DDX3X and DDX3Y facilitates MYC-driven lymphomagenesis. <i>Molecular Cell</i> , 2021, 81, 4059-4075.e11.	4.5	42
86	SRSF3 maintains transcriptome integrity in oocytes by regulation of alternative splicing and transposable elements. <i>Cell Discovery</i> , 2018, 4, 33.	3.1	40
87	The key protein of endosomal mRNP transport Rrm4 binds translational landmark sites of cargo mRNAs. <i>EMBO Reports</i> , 2019, 20, .	2.0	38
88	Acute depletion of METTL3 implicates N <sup>6</sup> -methyladenosine in alternative intron/exon inclusion in the nascent transcriptome. <i>Genome Research</i> , 2021, 31, 1395-1408.	2.4	37
89	Ribonucleoprotein complexes in neurologic diseases. <i>Current Opinion in Neurobiology</i> , 2008, 18, 516-523.	2.0	36
90	Alu elements: at the crossroads between disease and evolution. <i>Biochemical Society Transactions</i> , 2013, 41, 1532-1535.	1.6	36

#	ARTICLE	IF	CITATIONS
91	Control of a neuronal morphology program by an RNA-binding zinc finger protein, Unkempt. <i>Genes and Development</i> , 2015, 29, 501-512.	2.7	35
92	Aberrant sodium channel activity in the complex seizure disorder of <i>Celf4</i> mutant mice. <i>Journal of Physiology</i> , 2013, 591, 241-255.	1.3	33
93	'Oming in on RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 401.	13.9	32
94	Intergenic <i>Alu</i> exonisation facilitates the evolution of tissue-specific transcript ends. <i>Nucleic Acids Research</i> , 2015, 43, gkv956.	6.5	31
95	CLIPing the brain: Studies of protein-RNA interactions important for neurodegenerative disorders. <i>Molecular and Cellular Neurosciences</i> , 2013, 56, 429-435.	1.0	30
96	Charting DENR-dependent translation reinitiation uncovers predictive uORF features and links to circadian timekeeping via Clock. <i>Nucleic Acids Research</i> , 2019, 47, 5193-5209.	6.5	30
97	Splicing changes in SMA mouse motoneurons and SMN-depleted neuroblastoma cells: Evidence for involvement of splicing regulatory proteins. <i>RNA Biology</i> , 2014, 11, 1430-1446.	1.5	29
98	CDK11 is required for transcription of replication-dependent histone genes. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 500-510.	3.6	29
99	MIR-NATs repress MAPT translation and aid proteostasis in neurodegeneration. <i>Nature</i> , 2021, 594, 117-123.	13.7	29
100	Transcript-specific characteristics determine the contribution of endo- and exonucleolytic decay pathways during the degradation of nonsense-mediated decay substrates. <i>Rna</i> , 2017, 23, 1224-1236.	1.6	26
101	A systems view of spliceosomal assembly and branchpoints with iCLIP. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 930-940.	3.6	26
102	iCLIP identifies novel roles for SAFB1 in regulating RNA processing and neuronal function. <i>BMC Biology</i> , 2015, 13, 111.	1.7	23
103	Using hiCLIP to identify RNA duplexes that interact with a specific RNA-binding protein. <i>Nature Protocols</i> , 2017, 12, 611-637.	5.5	21
104	Functional and Mechanistic Insights From Genome-Wide Studies of Splicing Regulation in the Brain. <i>Advances in Experimental Medicine and Biology</i> , 2007, 623, 148-160.	0.8	20
105	Matrin3: connecting gene expression with the nuclear matrix. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 303-315.	3.2	18
106	Positioning Europe for the EPITRANSCRIPTOMICS challenge. <i>RNA Biology</i> , 2018, 15, 1-3.	1.5	18
107	Differential Binding of Mitochondrial Transcripts by MRB8170 and MRB4160 Regulates Distinct Editing Fates of Mitochondrial mRNA in Trypanosomes. <i>MBio</i> , 2017, 8, .	1.8	17
108	How Do You Identify m6 A Methylation in Transcriptomes at High Resolution? A Comparison of Recent Datasets. <i>Frontiers in Genetics</i> , 2020, 11, 398.	1.1	17

#	ARTICLE	IF	CITATIONS
109	Illustrating the Epitranscriptome at Nucleotide Resolution Using Methylation-iCLIP (miCLIP). <i>Methods in Molecular Biology</i> , 2017, 1562, 91-106.	0.4	15
110	The Transcriptome-wide Landscape and Modalities of EJC Binding in Adult <i>Drosophila</i> . <i>Cell Reports</i> , 2019, 28, 1219-1236.e11.	2.9	15
111	What, where, and when: the importance of post-transcriptional regulation in the brain. <i>Frontiers in Neuroscience</i> , 2013, 7, 192.	1.4	15
112	Genomic Accumulation of Retrotransposons Was Facilitated by Repressive RNA-Binding Proteins: A Hypothesis. <i>BioEssays</i> , 2019, 41, e1800132.	1.2	13
113	Intergenic RNA mainly derives from nascent transcripts of known genes. <i>Genome Biology</i> , 2021, 22, 136.	3.8	13
114	Ultraplex: A rapid, flexible, all-in-one fastq demultiplexer. <i>Wellcome Open Research</i> , 2021, 6, 141.	0.9	11
115	Chromatin-contact atlas reveals disorder-mediated protein interactions and moonlighting chromatin-associated RBPs. <i>Nucleic Acids Research</i> , 2021, 49, 13092-13107.	6.5	9
116	High-throughput sequencing methods to study neuronal RNA-protein interactions. <i>Biochemical Society Transactions</i> , 2009, 37, 1278-1280.	1.6	8
117	Cholinergic regulation of striatal Nova mRNAs. <i>Neuroscience</i> , 2010, 169, 619-627.	1.1	8
118	psiCLIP reveals dynamic RNA binding by DEAH-box helicases before and after exon ligation. <i>Nature Communications</i> , 2021, 12, 1488.	5.8	8
119	A genetically-encoded crosslinker screen identifies SERBP1 as a PKC $\mu$ substrate influencing translation and cell division. <i>Nature Communications</i> , 2021, 12, 6934.	5.8	7
120	Identifying ribosome heterogeneity using ribosome profiling. <i>Nucleic Acids Research</i> , 2022, 50, e95-e95.	6.5	7
121	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	13.9	6
122	RGS4 RNA Secondary Structure Mediates Staufen2 RNP Assembly in Neurons. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13021.	1.8	5
123	The greatest catch: big game fishing for mRNA-bound proteins. <i>Genome Biology</i> , 2012, 13, 163.	13.9	4
124	Using human pluripotent stem cells to study post-transcriptional mechanisms of neurodegenerative diseases. <i>Brain Research</i> , 2012, 1462, 129-138.	1.1	4
125	Open access, open data and peer review. <i>Genome Biology</i> , 2020, 21, 86.	3.8	4
126	Metabolic turnover and dynamics of modified ribonucleosides by $^{13}\text{C}$ labeling. <i>Journal of Biological Chemistry</i> , 2021, 297, 101294.	1.6	3



#	ARTICLE	IF	CITATIONS
127	Cross-Regulation Between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. SSRN Electronic Journal, 0, , .	0.4	2
128	Sequential Inverse Dysregulation of the RNA Helicases DDX3X and DDX3Y Facilitates MYC-Driven Lymphomagenesis. SSRN Electronic Journal, 0, , .	0.4	2
129	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
130	The origin of neural microexons. Nature Ecology and Evolution, 2019, 3, 526-527.	3.4	1
131	Proteinâ€™RNA interactions: new genomic technologies and perspectives. , 0, .		1
132	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
133	[S18]: RNA regulation and modular control of the neuronal synapse. International Journal of Developmental Neuroscience, 2006, 24, 479-479.	0.7	0
134	Jernej Ule: An RNA runaway success. Journal of Cell Biology, 2008, 180, 448-449.	2.3	0
135	No way out: when <scp>RNA</scp> elements promote nuclear retention. EMBO Journal, 2018, 37, .	3.5	0
136	Identification of HuR-specific RNA interactome in TGF-ÅŸ1-activated fibroblasts in response to cigarette smoke. , 2021, , .		0