Markus Landthaler

List of Publications by Citations

101 papers	21,790 citations	46 h-index	117 g-index
117 ext. papers	26,673 ext. citations	15.7 avg, IF	6.24 L-index

#	Paper	IF	Citations
101	Circular RNAs are a large class of animal RNAs with regulatory potency. *Nature*, **2013**, 495, 333-8	50.4	4603
100	A mammalian microRNA expression atlas based on small RNA library sequencing. *Cell*, **2007**, 129, 1401-14	56.2	3005
99	Transcriptome-wide identification of RNA-binding protein and microRNA target sites by PAR-CLIP. *Cell*, **2010**, 141, 129-41	56.2	2161
98	Human Argonaute2 mediates RNA cleavage targeted by miRNAs and siRNAs. *Molecular Cell*, **2004**, 15, 185-97	17.6	1465
97	Translation of CircRNAs. *Molecular Cell*, **2017**, 66, 9-21.e7	17.6	945
96	The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts. *Molecular Cell*, **2012**, 46, 674-90	17.6	833
95	Endogenous MHC class II processing of a viral nuclear antigen after autophagy. *Science*, **2005**, 307, 593-6	33.3	702
94	The human DiGeorge syndrome critical region gene 8 and Its D. melanogaster homolog are required for miRNA biogenesis. *Current Biology*, **2004**, 14, 2162-7	6.3	678
93	Analysis of intron sequences reveals hallmarks of circular RNA biogenesis in animals. *Cell Reports*, **2015**, 10, 170-7	10.6	643
92	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. *Cell*, **2020**, 182, 1419-1440.e23	56.2	558
91	Transcriptome-wide analysis of regulatory interactions of the RNA-binding protein HuR. *Molecular Cell*, **2011**, 43, 340-52	17.6	513
90	Cellular cofactors affecting hepatitis C virus infection and replication. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12884-9	11.5	478
89	Sequence-specific inhibition of microRNA- and siRNA-induced RNA silencing. *Rna*, **2004**, 10, 544-50	5.8	477
88	Identification of novel argonaute-associated proteins. *Current Biology*, **2005**, 15, 2149-55	6.3	425
87	Molecular characterization of human Argonaute-containing ribonucleoprotein complexes and their bound target mRNAs. *Rna*, **2008**, 14, 2580-96	5.8	283
86	Regnase-1 and Roquin Regulate a Common Element in Inflammatory mRNAs by Spatiotemporally Distinct Mechanisms. *Cell*, **2015**, 161, 1058-1073	56.2	227
85	Detecting actively translated open reading frames in ribosome profiling data. *Nature Methods*, **2016**, 13, 165-70	21.6	225

84	The Translational Landscape of the Human Heart. *Cell*, **2019**, 178, 242-260.e29	56.2	210
83	DGCR8-dependent microRNA biogenesis is essential for skin development. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 498-502	11.5	190
82	FOXO1 is an essential regulator of pluripotency in human embryonic stem cells. *Nature Cell Biology*, **2011**, 13, 1092-9	23.4	180
81	PAR-CliP--a method to identify transcriptome-wide the binding sites of RNA binding proteins. *Journal of Visualized Experiments*, **2010**,	1.6	169
80	doRiNA: a database of RNA interactions in post-transcriptional regulation. *Nucleic Acids Research*, **2012**, 40, D180-6	20.1	151
79	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. *Journal of Clinical Investigation*, **2014**, 124, 3419-30	15.9	129
78	MOV10 Is a 5Sto 3SRNA helicase contributing to UPF1 mRNA target degradation by translocation along 3SUTRs. *Molecular Cell*, **2014**, 54, 573-85	17.6	119
77	Cold-induced RNA-binding proteins regulate circadian gene expression by controlling alternative polyadenylation. *Scientific Reports*, **2013**, 3, 2054	4.9	109
76	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. *Immunity*, **2020**, 53, 1296-1314.e9	32.3	109
75	DoRiNA 2.0--upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. *Nucleic Acids Research*, **2015**, 43, D160-7	20.1	97
74	Swarm Learning for decentralized and confidential clinical machine learning. *Nature*, **2021**, 594, 265-270	50.4	89
73	DNA binding and cleavage by the HNH homing endonuclease I-HmuI. *Journal of Molecular Biology*, **2004**, 342, 43-56	6.5	88
72	A variety of dicer substrates in human and C. elegans. *Cell*, **2014**, 159, 1153-1167	56.2	80
71	Relative contribution of sequence and structure features to the mRNA binding of Argonaute/EIF2C-miRNA complexes and the degradation of miRNA targets. *Genome Research*, **2009**, 19, 2009-20	9.7	77
70	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-**B** pathway. *Nature Communications*, **2015**, 6, 7367	17.4	74
69	The Lupus Autoantigen La Prevents Mis-channeling of tRNA Fragments into the Human MicroRNA Pathway. *Molecular Cell*, **2016**, 63, 110-24	17.6	73
68	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. *IScience*, **2021**, 24, 102151	6.1	72
67	PAR-CLIP (Photoactivatable Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation): a step-by-step protocol to the transcriptome-wide identification of binding sites of RNA-binding proteins. *Methods in Enzymology*, **2014**, 539, 113-61	1.7	68

66	Integrative analysis revealed the molecular mechanism underlying RBM10-mediated splicing regulation. *EMBO Molecular Medicine*, **2013**, 5, 1431-42	12	67
65	Unexpected abundance of self-splicing introns in the genome of bacteriophage Twort: introns in multiple genes, a single gene with three introns, and exon skipping by group I ribozymes. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 7005-10	11.5	67
64	Quantitative interaction proteomics of neurodegenerative disease proteins. *Cell Reports*, **2015**, 11, 1134-46	8.6	62
63	The mRNA-bound proteome of the early fly embryo. *Genome Research*, **2016**, 26, 1000-9	9.7	54
62	Intronless homing: site-specific endonuclease SegF of bacteriophage T4 mediates localized marker exclusion analogous to homing endonucleases of group I introns. *Genes and Development*, **2002**, 16, 351-62	12.6	54
61	Transcriptome-wide analysis of protein-RNA interactions using high-throughput sequencing. *Seminars in Cell and Developmental Biology*, **2012**, 23, 206-12	7.5	53
60	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. *Nature Communications*, **2021**, 12, 3818	17.4	53
59	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. *Nature Communications*, **2019**, 10, 4878	17.4	51
58	Retrotransposition strategies of the Lactococcus lactis Ll.LtrB group II intron are dictated by host identity and cellular environment. *Molecular Microbiology*, **2005**, 56, 509-24	4.1	48
57	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. *RNA Biology*, **2013**, 10, 1146-59	4.8	47
56	Two self-splicing group I introns in the ribonucleotide reductase large subunit gene of Staphylococcus aureus phage Twort. *Nucleic Acids Research*, **2002**, 30, 1935-43	20.1	47
55	Phosphorylation of the Ribosomal Protein RPL12/uL11 Affects Translation during Mitosis. *Molecular Cell*, **2018**, 72, 84-98.e9	17.6	45
54	Differential protein occupancy profiling of the mRNA transcriptome. *Genome Biology*, **2014**, 15, R15	18.3	44
53	JACUSA: site-specific identification of RNA editing events from replicate sequencing data. *BMC Bioinformatics*, **2017**, 18, 7	3.6	43
52	Codon bias confers stability to human mRNAs. *EMBO Reports*, **2019**, 20, e48220	6.5	43
51	Virus-induced senescence is a driver and therapeutic target in COVID-19. *Nature*, **2021**, 599, 283-289	50.4	38
50	Mutant FUS and ELAVL4 (HuD) Aberrant Crosstalk in Amyotrophic Lateral Sclerosis. *Cell Reports*, **2019**, 27, 3818-3831.e5	10.6	35
49	The nicking homing endonuclease I-BasI is encoded by a group I intron in the DNA polymerase gene of the Bacillus thuringiensis phage Bastille. *Nucleic Acids Research*, **2003**, 31, 3071-7	20.1	35

48	DDX54 regulates transcriptome dynamics during DNA damage response. *Genome Research*, **2017**, 27, 1344-1359	9.7	32
47	Early IFN- signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. *Immunity*, **2021**, 54, 2650-2669.e14	32.3	31
46	Mu opioid receptor knockdown in the substantia nigra/ventral tegmental area by synthetic small interfering RNA blocks the rewarding and locomotor effects of heroin. *Neuroscience*, **2009**, 158, 474-83	3.9	29
45	LARP4B is an AU-rich sequence associated factor that promotes mRNA accumulation and translation. *Rna*, **2015**, 21, 1294-305	5.8	28
44	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. *Nature Communications*, **2014**, 5, 5701	17.4	27
43	Group I intron homing in Bacillus phages SPO1 and SP82: a gene conversion event initiated by a nicking homing endonuclease. *Journal of Bacteriology*, **2004**, 186, 4307-14	3.5	27
42	Loss of macp Ribosomal RNA Modification Is a Major Feature of Cancer. *Cell Reports*, **2020**, 31, 107611	10.6	26
41	An immediate-late gene expression module decodes ERK signal duration. *Molecular Systems Biology* , **2017**, 13, 928	12.2	25
40	New insights into the cellular temporal response to proteostatic stress. *ELife*, **2018**, 7,	8.9	25
39	Mechanism of Virus Attenuation by Codon Pair Deoptimization. *Cell Reports*, **2020**, 31, 107586	10.6	24
38	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. *Genome Biology*, **2017**, 18, 209	18.3	24
37	Integrative functional genomics decodes herpes simplex virus 1. *Nature Communications*, **2020**, 11, 2038	17.4	23
36	I-BasI and I-HmuI: two phage intron-encoded endonucleases with homologous DNA recognition sequences but distinct DNA specificities. *Journal of Molecular Biology*, **2006**, 358, 1137-51	6.5	22
35	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis.. *Cell*, **2021**, 184, 6243-6261.e27	39.6	22
34	Rapid creation of stable mammalian cell lines for regulated expression of proteins using the Gateway recombination cloning technology and Flp-In T-REx lines. *Methods in Enzymology*, **2013**, 529, 99-124	1.7	20
33	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. *Biomolecules*, **2015**, 5, 1441-66	5.9	20
32	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. *Nucleic Acids Research*, **2020**, 48, 2518-2530	20.1	18
31	SiRNA-mediated selective inhibition of mutant keratin mRNAs responsible for the skin disorder pachyonychia congenita. *Annals of the New York Academy of Sciences*, **2006**, 1082, 56-61	6.5	17

30	Eyes on Translation. *Molecular Cell*, **2016**, 63, 918-25	17.6	16
29	4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. *Cell Reports*, **2020**, 33, 108262	10.6	15
28	DDX3 depletion represses translation of mRNAs with complex 5SUTRs. *Nucleic Acids Research*, **2021**, 49, 5336-5350	20.1	11
27	Fluorescence cross-correlation spectroscopy reveals mechanistic insights into the effect of 2SO-methyl modified siRNAs in living cells. *Biophysical Journal*, **2011**, 100, 2981-90	2.9	10
26	Complement activation induces excessive T cell cytotoxicity in severe COVID-19.. *Cell*, **2021**,	56.2	9
25	Transcriptome-wide Identification of RNA-binding Protein Binding Sites Using Photoactivatable-Ribonucleoside-Enhanced Crosslinking Immunoprecipitation (PAR-CLIP). *Current Protocols in Molecular Biology*, **2017**, 118, 27.6.1-27.6.19	2.9	8
24	The Zinc Finger Antiviral Protein ZAP Restricts Human Cytomegalovirus and Selectively Binds and Destabilizes Viral / Transcripts. *MBio*, **2021**, 12,	7.8	8
23	Protein Synthesis in the Developing Neocortex at Near-Atomic Resolution Reveals Ebp1-Mediated Neuronal Proteostasis at the 60S Tunnel Exit. *Molecular Cell*, **2021**, 81, 304-322.e16	17.6	8
22	Temporal omics analysis in Syrian hamsters unravel cellular effector responses to moderate COVID-19. *Nature Communications*, **2021**, 12, 4869	17.4	8
21	Expanding the map of protein-RNA interaction sites via cell fusion followed by PAR-CLIP. *RNA Biology*, **2018**, 15, 359-368	4.8	7
20	Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. *Genes and Development*, **2019**, 33, 1673-1687	12.6	7
19	High-resolution profiling of protein occupancy on polyadenylated RNA transcripts. *Methods*, **2014**, 65, 302-9	4.6	7
18	Spatio-temporal mRNA tracking in the early zebrafish embryo. *Nature Communications*, **2021**, 12, 3358	17.4	7
17	Mitogen-activated protein kinase activity drives cell trajectories in colorectal cancer. *EMBO Molecular Medicine*, **2021**, 13, e14123	12	7
16	mRNA interactome capture in mammalian cells. *Methods*, **2017**, 126, 38-43	4.6	6
15	An arrayed RNA interference genome-wide screen identifies candidate genes involved in the MicroRNA 21 biogenesis pathway. *Assay and Drug Development Technologies*, **2013**, 11, 191-205	2.1	6
14	Longitudinal omics in Syrian hamsters integrated with human data unravel complexity of moderate immune responses to SARS-CoV-2		5
13	Chaperones get RISC loaded. *Molecular Cell*, **2010**, 39, 161-2	17.6	4

List of Publications

12	DDX3 depletion represses translation of mRNAs with complex 5? UTRs		2
11	Herpesviral induction of germline transcription factor DUX4 is critical for viral gene expression		2
10	CRNKL1 Is a Highly Selective Regulator of Intron-Retaining HIV-1 and Cellular mRNAs. *MBio*, **2021**, 12,	7.8	2
9	Transcriptome-Wide Identification of Protein Binding Sites on RNA by PAR-CLIP (Photoactivatable-Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation) **2014**, 877-898		1
8	Systematic Detection of Poly(A) RNA-Interacting Proteins and Their Differential Binding. *Methods in Molecular Biology*, **2018**, 1649, 405-417	1.4	1
7	HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins.. *Nature Communications*, **2022**, 13, 2727	17.4	1
6	Engineering, decoding and systems-level characterization of chimpanzee cytomegalovirus.. *PLoS Pathogens*, **2022**, 18, e1010193	7.6	0
5	Integrated multi-omics analysis of RB-loss identifies widespread cellular programming and synthetic weaknesses. *Communications Biology*, **2021**, 4, 977	6.7	0
4	In Vitro Kinase-to-Phosphosite Database (iKiP-DB) Predicts Kinase Activity in Phosphoproteomic Datasets. *Journal of Proteome Research*, **2022**, 21, 1575-1587	5.6	0
3	Rattus norvegicus BN/SHR liver and heart left ventricle ribosomal RNA depleted directional RNA sequencing. *BMC Research Notes*, **2017**, 10, 395	2.3	
2	Mechanisms of small RNA mediated mammalian gene silencing. *FASEB Journal*, **2007**, 21, A149	0.9	
1	Transcriptome-wide Identification of the mRNA target sites of the Fragile-X Mental Retardation Proteins. *FASEB Journal*, **2009**, 23, 666.2	0.9	