

Markus Landthaler

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/2910232/markus-landthaler-publications-by-year.pdf>

Version: 2024-04-17

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	Engineering, decoding and systems-level characterization of chimpanzee cytomegalovirus.. <i>PLoS Pathogens</i> , 2022 , 18, e1010193	7.6	0
100	HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins.. <i>Nature Communications</i> , 2022 , 13, 2727	17.4	1
99	In Vitro Kinase-to-Phosphosite Database (iKiP-DB) Predicts Kinase Activity in Phosphoproteomic Datasets. <i>Journal of Proteome Research</i> , 2022 , 21, 1575-1587	5.6	0
98	Complement activation induces excessive T cell cytotoxicity in severe COVID-19.. <i>Cell</i> , 2021 ,	56.2	9
97	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis.. <i>Cell</i> , 2021 , 184, 6243-6261.e27	35.6	27
96	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>IScience</i> , 2021 , 24, 102151	6.1	72
95	DDX3 depletion represses translation of mRNAs with complex 5SUTRs. <i>Nucleic Acids Research</i> , 2021 , 49, 5336-5350	20.1	11
94	Swarm Learning for decentralized and confidential clinical machine learning. <i>Nature</i> , 2021 , 594, 265-270	50.4	89
93	The Zinc Finger Antiviral Protein ZAP Restricts Human Cytomegalovirus and Selectively Binds and Destabilizes Viral / Transcripts. <i>MBio</i> , 2021 , 12,	7.8	8
92	Spatio-temporal mRNA tracking in the early zebrafish embryo. <i>Nature Communications</i> , 2021 , 12, 3358	17.4	7
91	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. <i>Nature Communications</i> , 2021 , 12, 3818	17.4	53
90	Protein Synthesis in the Developing Neocortex at Near-Atomic Resolution Reveals Ebp1-Mediated Neuronal Proteostasis at the 60S Tunnel Exit. <i>Molecular Cell</i> , 2021 , 81, 304-322.e16	17.6	8
89	CRNKL1 Is a Highly Selective Regulator of Intron-Retaining HIV-1 and Cellular mRNAs. <i>MBio</i> , 2021 , 12,	7.8	2
88	Temporal omics analysis in Syrian hamsters unravel cellular effector responses to moderate COVID-19. <i>Nature Communications</i> , 2021 , 12, 4869	17.4	8
87	Mitogen-activated protein kinase activity drives cell trajectories in colorectal cancer. <i>EMBO Molecular Medicine</i> , 2021 , 13, e14123	12	7
86	Integrated multi-omics analysis of RB-loss identifies widespread cellular programming and synthetic weaknesses. <i>Communications Biology</i> , 2021 , 4, 977	6.7	0
85	Early IFN- β signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. <i>Immunity</i> , 2021 , 54, 2650-2669.e14	32.3	31

84	Virus-induced senescence is a driver and therapeutic target in COVID-19. <i>Nature</i> , 2021 , 599, 283-289	50.4	38
83	Mechanism of Virus Attenuation by Codon Pair Deoptimization. <i>Cell Reports</i> , 2020 , 31, 107586	10.6	24
82	Loss of macp[Ribosomal RNA Modification Is a Major Feature of Cancer. <i>Cell Reports</i> , 2020 , 31, 107611	10.6	26
81	Integrative functional genomics decodes herpes simplex virus 1. <i>Nature Communications</i> , 2020 , 11, 203817.4	17.4	23
80	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020 , 48, 2518-2530	20.1	18
79	4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. <i>Cell Reports</i> , 2020 , 33, 108262	10.6	15
78	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020 , 53, 1296-1314.e9	32.3	109
77	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020 , 182, 1419-1440.e236.2	36.2	558
76	Mutant FUS and ELAVL4 (HuD) Aberrant Crosstalk in Amyotrophic Lateral Sclerosis. <i>Cell Reports</i> , 2019 , 27, 3818-3831.e5	10.6	35
75	The Translational Landscape of the Human Heart. <i>Cell</i> , 2019 , 178, 242-260.e29	56.2	210
74	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. <i>Nature Communications</i> , 2019 , 10, 4878	17.4	51
73	Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. <i>Genes and Development</i> , 2019 , 33, 1673-1687	12.6	7
72	Codon bias confers stability to human mRNAs. <i>EMBO Reports</i> , 2019 , 20, e48220	6.5	43
71	Expanding the map of protein-RNA interaction sites via cell fusion followed by PAR-CLIP. <i>RNA Biology</i> , 2018 , 15, 359-368	4.8	7
70	New insights into the cellular temporal response to proteostatic stress. <i>ELife</i> , 2018 , 7,	8.9	25
69	Systematic Detection of Poly(A) RNA-Interacting Proteins and Their Differential Binding. <i>Methods in Molecular Biology</i> , 2018 , 1649, 405-417	1.4	1
68	Phosphorylation of the Ribosomal Protein RPL12/uL11 Affects Translation during Mitosis. <i>Molecular Cell</i> , 2018 , 72, 84-98.e9	17.6	45
67	JACUSA: site-specific identification of RNA editing events from replicate sequencing data. <i>BMC Bioinformatics</i> , 2017 , 18, 7	3.6	43

66	An immediate-late gene expression module decodes ERK signal duration. <i>Molecular Systems Biology</i> , 2017 , 13, 928	12.2	25
65	DDX54 regulates transcriptome dynamics during DNA damage response. <i>Genome Research</i> , 2017 , 27, 1344-1359	9.7	32
64	Transcriptome-wide Identification of RNA-binding Protein Binding Sites Using Photoactivatable-Ribonucleoside-Enhanced Crosslinking Immunoprecipitation (PAR-CLIP). <i>Current Protocols in Molecular Biology</i> , 2017 , 118, 27.6.1-27.6.19	2.9	8
63	Translation of CircRNAs. <i>Molecular Cell</i> , 2017 , 66, 9-21.e7	17.6	945
62	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , 2017 , 18, 209	18.3	24
61	Rattus norvegicus BN/SHR liver and heart left ventricle ribosomal RNA depleted directional RNA sequencing. <i>BMC Research Notes</i> , 2017 , 10, 395	2.3	
60	mRNA interactome capture in mammalian cells. <i>Methods</i> , 2017 , 126, 38-43	4.6	6
59	Eyes on Translation. <i>Molecular Cell</i> , 2016 , 63, 918-25	17.6	16
58	The mRNA-bound proteome of the early fly embryo. <i>Genome Research</i> , 2016 , 26, 1000-9	9.7	54
57	The Lupus Autoantigen La Prevents Mis-channeling of tRNA Fragments into the Human MicroRNA Pathway. <i>Molecular Cell</i> , 2016 , 63, 110-24	17.6	73
56	Detecting actively translated open reading frames in ribosome profiling data. <i>Nature Methods</i> , 2016 , 13, 165-70	21.6	225
55	Quantitative interaction proteomics of neurodegenerative disease proteins. <i>Cell Reports</i> , 2015 , 11, 1134-1146	11.6	62
54	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- κ B pathway. <i>Nature Communications</i> , 2015 , 6, 7367	17.4	74
53	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. <i>Biomolecules</i> , 2015 , 5, 1441-66	5.9	20
52	Regnase-1 and Roquin Regulate a Common Element in Inflammatory mRNAs by Spatiotemporally Distinct Mechanisms. <i>Cell</i> , 2015 , 161, 1058-1073	56.2	227
51	LARP4B is an AU-rich sequence associated factor that promotes mRNA accumulation and translation. <i>Rna</i> , 2015 , 21, 1294-305	5.8	28
50	Analysis of intron sequences reveals hallmarks of circular RNA biogenesis in animals. <i>Cell Reports</i> , 2015 , 10, 170-7	10.6	643
49	DoRiNA 2.0--upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2015 , 43, D160-7	20.1	97

48	High-resolution profiling of protein occupancy on polyadenylated RNA transcripts. <i>Methods</i> , 2014 , 65, 302-9	4.6	7
47	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. <i>Methods in Enzymology</i> , 2014 , 539, 113-61	1.7	68
46	A variety of dicer substrates in human and <i>C. elegans</i> . <i>Cell</i> , 2014 , 159, 1153-1167	56.2	80
45	Transcriptome-Wide Identification of Protein Binding Sites on RNA by PAR-CLIP (Photoactivatable-Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation) 2014 , 877-898		1
44	MOV10 Is a 5Sto 3SRNA helicase contributing to UPF1 mRNA target degradation by translocation along 3SUTRs. <i>Molecular Cell</i> , 2014 , 54, 573-85	17.6	119
43	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. <i>Nature Communications</i> , 2014 , 5, 5701	17.4	27
42	Differential protein occupancy profiling of the mRNA transcriptome. <i>Genome Biology</i> , 2014 , 15, R15	18.3	44
41	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014 , 124, 3419-30	15.9	129
40	Integrative analysis revealed the molecular mechanism underlying RBM10-mediated splicing regulation. <i>EMBO Molecular Medicine</i> , 2013 , 5, 1431-42	12	67
39	Rapid creation of stable mammalian cell lines for regulated expression of proteins using the Gateway [®] recombination cloning technology and FLP-In T-REx [®] lines. <i>Methods in Enzymology</i> , 2013 , 529, 99-124	1.7	20
38	Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013 , 495, 333-8	50.4	4603
37	An arrayed RNA interference genome-wide screen identifies candidate genes involved in the MicroRNA 21 biogenesis pathway. <i>Assay and Drug Development Technologies</i> , 2013 , 11, 191-205	2.1	6
36	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013 , 10, 1146-59	4.8	47
35	Cold-induced RNA-binding proteins regulate circadian gene expression by controlling alternative polyadenylation. <i>Scientific Reports</i> , 2013 , 3, 2054	4.9	109
34	Transcriptome-wide analysis of protein-RNA interactions using high-throughput sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012 , 23, 206-12	7.5	53
33	The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts. <i>Molecular Cell</i> , 2012 , 46, 674-90	17.6	833
32	doRiNA: a database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2012 , 40, D180-6	20.1	151
31	Fluorescence cross-correlation spectroscopy reveals mechanistic insights into the effect of 2SO-methyl modified siRNAs in living cells. <i>Biophysical Journal</i> , 2011 , 100, 2981-90	2.9	10

30	Transcriptome-wide analysis of regulatory interactions of the RNA-binding protein HuR. <i>Molecular Cell</i> , 2011 , 43, 340-52	17.6	513
29	FOXO1 is an essential regulator of pluripotency in human embryonic stem cells. <i>Nature Cell Biology</i> , 2011 , 13, 1092-9	23.4	180
28	Chaperones get RISC loaded. <i>Molecular Cell</i> , 2010 , 39, 161-2	17.6	4
27	Transcriptome-wide identification of RNA-binding protein and microRNA target sites by PAR-CLIP. <i>Cell</i> , 2010 , 141, 129-41	56.2	2161
26	PAR-CLIP—a method to identify transcriptome-wide the binding sites of RNA binding proteins. <i>Journal of Visualized Experiments</i> , 2010 ,	1.6	169
25	Relative contribution of sequence and structure features to the mRNA binding of Argonaute/EIF2C-miRNA complexes and the degradation of miRNA targets. <i>Genome Research</i> , 2009 , 19, 2009-20	9.7	77
24	DGCR8-dependent microRNA biogenesis is essential for skin development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 498-502	11.5	190
23	Mu opioid receptor knockdown in the substantia nigra/ventral tegmental area by synthetic small interfering RNA blocks the rewarding and locomotor effects of heroin. <i>Neuroscience</i> , 2009 , 158, 474-83	3.9	29
22	Transcriptome-wide Identification of the mRNA target sites of the Fragile-X Mental Retardation Proteins. <i>FASEB Journal</i> , 2009 , 23, 666.2	0.9	
21	Molecular characterization of human Argonaute-containing ribonucleoprotein complexes and their bound target mRNAs. <i>Rna</i> , 2008 , 14, 2580-96	5.8	283
20	Cellular cofactors affecting hepatitis C virus infection and replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12884-9	11.5	478
19	A mammalian microRNA expression atlas based on small RNA library sequencing. <i>Cell</i> , 2007 , 129, 1401-14	46.2	3005
18	Mechanisms of small RNA mediated mammalian gene silencing. <i>FASEB Journal</i> , 2007 , 21, A149	0.9	
17	I-BasI and I-HmuI: two phage intron-encoded endonucleases with homologous DNA recognition sequences but distinct DNA specificities. <i>Journal of Molecular Biology</i> , 2006 , 358, 1137-51	6.5	22
16	SiRNA-mediated selective inhibition of mutant keratin mRNAs responsible for the skin disorder pachyonychia congenita. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1082, 56-61	6.5	17
15	Retrotransposition strategies of the <i>Lactococcus lactis</i> Ll.LtrB group II intron are dictated by host identity and cellular environment. <i>Molecular Microbiology</i> , 2005 , 56, 509-24	4.1	48
14	Identification of novel argonaute-associated proteins. <i>Current Biology</i> , 2005 , 15, 2149-55	6.3	425
13	Endogenous MHC class II processing of a viral nuclear antigen after autophagy. <i>Science</i> , 2005 , 307, 593-6	33.3	702

12	Group I intron homing in Bacillus phages SPO1 and SP82: a gene conversion event initiated by a nicking homing endonuclease. <i>Journal of Bacteriology</i> , 2004 , 186, 4307-14	3.5	27
11	The human DiGeorge syndrome critical region gene 8 and Its D. melanogaster homolog are required for miRNA biogenesis. <i>Current Biology</i> , 2004 , 14, 2162-7	6.3	678
10	Sequence-specific inhibition of microRNA- and siRNA-induced RNA silencing. <i>Rna</i> , 2004 , 10, 544-50	5.8	477
9	Human Argonaute2 mediates RNA cleavage targeted by miRNAs and siRNAs. <i>Molecular Cell</i> , 2004 , 15, 185-97	17.6	1465
8	DNA binding and cleavage by the HNH homing endonuclease I-Hmul. <i>Journal of Molecular Biology</i> , 2004 , 342, 43-56	6.5	88
7	The nicking homing endonuclease I-BasI is encoded by a group I intron in the DNA polymerase gene of the Bacillus thuringiensis phage Bastille. <i>Nucleic Acids Research</i> , 2003 , 31, 3071-7	20.1	35
6	Two self-splicing group I introns in the ribonucleotide reductase large subunit gene of Staphylococcus aureus phage Twort. <i>Nucleic Acids Research</i> , 2002 , 30, 1935-43	20.1	47
5	Intronless homing: site-specific endonuclease SegF of bacteriophage T4 mediates localized marker exclusion analogous to homing endonucleases of group I introns. <i>Genes and Development</i> , 2002 , 16, 351-62	12.6	54
4	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 7005-10	11.5	67
3	Longitudinal omics in Syrian hamsters integrated with human data unravel complexity of moderate immune responses to SARS-CoV-2		5
2	DDX3 depletion represses translation of mRNAs with complex 5' UTRs		2
1	Herpesviral induction of germline transcription factor DUX4 is critical for viral gene expression		2