

Uwe Ohler

List of Publications by Year in descending order

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77
papers

8,738
citations

87401

40
h-index

93651

72
g-index

96
all docs

96
docs citations

96
times ranked

15095
citing authors

#	ARTICLE	IF	CITATIONS
1	SLM2 Is A Novel Cardiac Splicing Factor Involved in Heart Failure due to Dilated Cardiomyopathy. Genomics, Proteomics and Bioinformatics, 2022, 20, 129-146.	3.0	4
2	Intricacies of single-cell multi-omics data integration. Trends in Genetics, 2022, 38, 128-139.	2.9	25
3	Single-cell-resolved dynamics of chromatin architecture delineate cell and regulatory states in zebrafish embryos. Cell Genomics, 2022, 2, 100083.	3.0	8
4	Deep learning for prediction of population health costs. BMC Medical Informatics and Decision Making, 2022, 22, 32.	1.5	6
5	A single-cell Arabidopsis root atlas reveals developmental trajectories in wild-type and cell identity mutants. Developmental Cell, 2022, 57, 543-560.e9.	3.1	106
6	Simultaneous dimensionality reduction and integration for single-cell ATAC-seq data using deep learning. Nature Machine Intelligence, 2022, 4, 162-168.	8.3	15
7	The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes. Cell Reports, 2022, 38, 110524.	2.9	7
8	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	9.4	26
9	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
10	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.	4.5	27
11	Genome-Wide Analysis of Actively Translated Open Reading Frames Using RiboTaper/ORFquant. Methods in Molecular Biology, 2021, 2252, 331-346.	0.4	4
12	Inferring time series chromatin states for promoter-enhancer pairs based on Hi-C data. BMC Genomics, 2021, 22, 84.	1.2	3
13	Spatio-temporal mRNA tracking in the early zebrafish embryo. Nature Communications, 2021, 12, 3358.	5.8	25
14	Ythdf is a N6-methyladenosine reader that modulates Fmr1 target mRNA selection and restricts axonal growth in <i>Drosophila</i> . EMBO Journal, 2021, 40, e104975.	3.5	56
15	How to find genomic regions relevant for gene regulation. Medizinische Genetik, 2021, 33, 157-165.	0.1	0
16	Towards a deeper annotation of human lncRNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194385.	0.9	12
17	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. Molecular Cell, 2020, 77, 352-367.e8.	4.5	48
18	Deep learning for genomics using Janggu. Nature Communications, 2020, 11, 3488.	5.8	47

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19	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. <i>Developmental Cell</i> , 2020, 55, 648-664.e9.	3.1	47
20	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. <i>Nature Communications</i> , 2020, 11, 1293.	5.8	196
21	Quantification of translation uncovers the functions of the alternative transcriptome. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 717-725.	3.6	35
22	Deep neural networks for interpreting RNA-binding protein target preferences. <i>Genome Research</i> , 2020, 30, 214-226.	2.4	77
23	The Translational Landscape of the Human Heart. <i>Cell</i> , 2019, 178, 242-260.e29.	13.5	407
24	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. <i>Nature Communications</i> , 2019, 10, 990.	5.8	168
25	Global identification of functional microRNA-mRNA interactions in <i>Drosophila</i> . <i>Nature Communications</i> , 2019, 10, 1626.	5.8	35
26	Reproducible inference of transcription factor footprints in ATAC-seq and DNase-seq datasets using protocol-specific bias modeling. <i>Genome Biology</i> , 2019, 20, 42.	3.8	73
27	Deciphering human ribonucleoprotein regulatory networks. <i>Nucleic Acids Research</i> , 2019, 47, 570-581.	6.5	54
28	Redundant regulation. <i>Nature Ecology and Evolution</i> , 2018, 2, 418-419.	3.4	0
29	Finding RNA structure in the unstructured RBPome. <i>BMC Genomics</i> , 2018, 19, 154.	1.2	7
30	omniCLIP: probabilistic identification of protein-RNA interactions from CLIP-seq data. <i>Genome Biology</i> , 2018, 19, 183.	3.8	19
31	Determinants of promoter and enhancer transcription directionality in metazoans. <i>Nature Communications</i> , 2018, 9, 4472.	5.8	22
32	Ectopic Transplastomic Expression of a Synthetic MatK Gene Leads to Cotyledon-Specific Leaf Variegation. <i>Frontiers in Plant Science</i> , 2018, 9, 1453.	1.7	14
33	SSMART: sequence-structure motif identification for RNA-binding proteins. <i>Bioinformatics</i> , 2018, 34, 3990-3998.	1.8	21
34	RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. <i>Nucleic Acids Research</i> , 2017, 45, e91-e91.	6.5	23
35	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. <i>Journal of Biotechnology</i> , 2017, 261, 76-84.	1.9	21
36	DDX54 regulates transcriptome dynamics during DNA damage response. <i>Genome Research</i> , 2017, 27, 1344-1359.	2.4	46

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37	A Multi-step Transcriptional and Chromatin State Cascade Underlies Motor Neuron Programming from Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 205-217.e8.	5.2	86
38	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017, 8, 583.	5.8	176
39	Beyond Read-Counts: Ribo-seq Data Analysis to Understand the Functions of the Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 728-744.	2.9	101
40	Integrative classification of human coding and noncoding genes through RNA metabolism profiles. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 86-96.	3.6	157
41	McEnhancer: predicting gene expression via semi-supervised assignment of enhancers to target genes. <i>Genome Biology</i> , 2017, 18, 199.	3.8	27
42	Divergent transcription and epigenetic directionality of human promoters. <i>FEBS Journal</i> , 2016, 283, 4214-4222.	2.2	22
43	CSEQ-SIMULATOR: A DATA SIMULATOR FOR CLIP-SEQ EXPERIMENTS. , 2016, , .		7
44	The mRNA-bound proteome of the early fly embryo. <i>Genome Research</i> , 2016, 26, 1000-1009.	2.4	66
45	High-Resolution Expression Map of the Arabidopsis Root Reveals Alternative Splicing and lincRNA Regulation. <i>Developmental Cell</i> , 2016, 39, 508-522.	3.1	245
46	Super-resolution ribosome profiling reveals unannotated translation events in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7126-E7135.	3.3	222
47	Detecting actively translated open reading frames in ribosome profiling data. <i>Nature Methods</i> , 2016, 13, 165-170.	9.0	368
48	Identifying RBP Targets with RIP-seq. <i>Methods in Molecular Biology</i> , 2016, 1358, 141-152.	0.4	9
49	CSEQ-SIMULATOR: A DATA SIMULATOR FOR CLIP-SEQ EXPERIMENTS. <i>Pacific Symposium on Biocomputing</i> Pacific Symposium on Biocomputing, 2016, 21, 433-44.	0.7	6
50	Regnase-1 and Roquin Regulate a Common Element in Inflammatory mRNAs by Spatiotemporally Distinct Mechanisms. <i>Cell</i> , 2015, 161, 1058-1073.	13.5	296
51	Human Promoters Are Intrinsically Directional. <i>Molecular Cell</i> , 2015, 57, 674-684.	4.5	115
52	Transcriptional control of tissue formation throughout root development. <i>Science</i> , 2015, 350, 426-430.	6.0	128
53	Perspectives on Unidirectional versus Divergent Transcription. <i>Molecular Cell</i> , 2015, 60, 348-349.	4.5	19
54	JAMM: a peak finder for joint analysis of NGS replicates. <i>Bioinformatics</i> , 2015, 31, 48-55.	1.8	57

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55	Explicit DNase sequence bias modeling enables high-resolution transcription factor footprint detection. <i>Nucleic Acids Research</i> , 2014, 42, 11865-11878.	6.5	73
56	COUGERâ€”co-factors associated with uniquely-bound genomic regions. <i>Nucleic Acids Research</i> , 2014, 42, W461-W467.	6.5	0
57	Improved transcript isoform discovery using ORF graphs. <i>Bioinformatics</i> , 2014, 30, 1958-1964.	1.8	5
58	Identification of the RNA recognition element of the RBPMS family of RNA-binding proteins and their transcriptome-wide mRNA targets. <i>Rna</i> , 2014, 20, 1090-1102.	1.6	64
59	Paired-End Analysis of Transcription Start Sites in <i>Arabidopsis</i> Reveals Plant-Specific Promoter Signatures. <i>Plant Cell</i> , 2014, 26, 2746-2760.	3.1	112
60	Global target mRNA specification and regulation by the RNA-binding protein ZFP36. <i>Genome Biology</i> , 2014, 15, R12.	13.9	141
61	Using machine learning to identify disease-relevant regulatory RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15516-15517.	3.3	0
62	MicroRNA target site identification by integrating sequence and binding information. <i>Nature Methods</i> , 2013, 10, 630-633.	9.0	56
63	The protein expression landscape of the <i>Arabidopsis</i> root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6811-6818.	3.3	140
64	FMRP targets distinct mRNA sequence elements to regulate protein expression. <i>Nature</i> , 2012, 492, 382-386.	13.7	656
65	Predicting cell-typeâ€”specific gene expression from regions of open chromatin. <i>Genome Research</i> , 2012, 22, 1711-1722.	2.4	227
66	PARalyzer: definition of RNA binding sites from PAR-CLIP short-read sequence data. <i>Genome Biology</i> , 2011, 12, R79.	13.9	332
67	Integrative Regulatory Mapping Indicates that the RNA-Binding Protein HuR Couples Pre-mRNA Processing and mRNA Stability. <i>Molecular Cell</i> , 2011, 43, 327-339.	4.5	605
68	Transcription Initiation Patterns Indicate Divergent Strategies for Gene Regulation at the Chromatin Level. <i>PLoS Genetics</i> , 2011, 7, e1001274.	1.5	124
69	A paired-end sequencing strategy to map the complex landscape of transcription initiation. <i>Nature Methods</i> , 2010, 7, 521-527.	9.0	153
70	Promoting developmental transcription. <i>Development (Cambridge)</i> , 2010, 137, 15-26.	1.2	73
71	Evidence-ranked motif identification. <i>Genome Biology</i> , 2010, 11, R19.	13.9	77
72	A transcription factor affinity-based code for mammalian transcription initiation. <i>Genome Research</i> , 2009, 19, 644-656.	2.4	54

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73	Motif composition, conservation and condition-specificity of single and alternative transcription start sites in the Drosophila genome. <i>Genome Biology</i> , 2009, 10, R73.	13.9	86
74	A High-Resolution Root Spatiotemporal Map Reveals Dominant Expression Patterns. <i>Science</i> , 2007, 318, 801-806.	6.0	1,048
75	Spatial preferences of microRNA targets in 3' untranslated regions. <i>BMC Genomics</i> , 2007, 8, 152.	1.2	103
76	Transcriptional and posttranscriptional regulation of transcription factor expression in Arabidopsis roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6055-6060.	3.3	257
77	Computational analysis of core promoters in the Drosophila genome. <i>Genome Biology</i> , 2002, 3, research0087.1.	13.9	374