

Mathias Munschauer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/547280/publications.pdf>

Version: 2024-02-01

25
papers

13,050
citations

516710

16
h-index

610901

24
g-index

31
all docs

31
docs citations

31
times ranked

19489
citing authors

#	ARTICLE	IF	CITATIONS
1	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546.	1.4	14
2	Protective immune trajectories in early viral containment of non-pneumonic SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, 1018.	12.8	16
3	The SARS-CoV-2 RNA-protein interactome in infected human cells. <i>Nature Microbiology</i> , 2021, 6, 339-353.	13.3	245
4	The lncRNA lincNMR regulates nucleotide metabolism via a YBX1 - RRM2 axis in cancer. <i>Nature Communications</i> , 2020, 11, 3214.	12.8	96
5	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. <i>Nature Genetics</i> , 2020, 52, 138-145.	21.4	73
6	Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. <i>Genes and Development</i> , 2019, 33, 1673-1687.	5.9	13
7	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	28.9	296
8	Nuclear lncRNA stabilization in the host response to bacterial infection. <i>EMBO Journal</i> , 2018, 37, .	7.8	12
9	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. <i>Nature</i> , 2018, 561, 132-136.	27.8	303
10	New insights into the cellular temporal response to proteostatic stress. <i>ELife</i> , 2018, 7, .	6.0	47
11	Developmentally faithful and effective human erythropoiesis in immunodeficient and <i>Kit</i> mutant mice. <i>American Journal of Hematology</i> , 2017, 92, E513-E519.	4.1	20
12	Systematic mapping of functional enhancer-promoter connections with CRISPR interference. <i>Science</i> , 2016, 354, 769-773.	12.6	512
13	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. <i>Biomolecules</i> , 2015, 5, 1441-1466.	4.0	26
14	Exploring the Sequence Space Contacted by the Ensemble of RNA-Binding Proteins. <i>Springer Theses</i> , 2015, , 61-72.	0.1	0
15	Revealing Cell-Type Specific Differences in Protein Occupancy on RNA. <i>Springer Theses</i> , 2015, , 73-88.	0.1	0
16	Mapping Regulatory Interactions of the RNA-Binding Protein LIN28B. <i>Springer Theses</i> , 2015, , 49-60.	0.1	0
17	Differential protein occupancy profiling of the mRNA transcriptome. <i>Genome Biology</i> , 2014, 15, R15.	9.6	72
18	High-resolution profiling of protein occupancy on polyadenylated RNA transcripts. <i>Methods</i> , 2014, 65, 302-309.	3.8	9

#	ARTICLE	IF	CITATIONS
19	MOV10 Is a 5' to 3' RNA Helicase Contributing to UPF1 mRNA Target Degradation by Translocation along 3' UTRs. <i>Molecular Cell</i> , 2014, 54, 573-585.	9.7	159
20	Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013, 495, 333-338.	27.8	6,474
21	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013, 10, 1146-1159.	3.1	76
22	FMRP targets distinct mRNA sequence elements to regulate protein expression. <i>Nature</i> , 2012, 492, 382-386.	27.8	656
23	The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. <i>Molecular Cell</i> , 2012, 46, 674-690.	9.7	1,077
24	PAR-CLIP - A Method to Identify Transcriptome-wide the Binding Sites of RNA Binding Proteins. <i>Journal of Visualized Experiments</i> , 2010, , .	0.3	220
25	Transcriptome-wide Identification of RNA-Binding Protein and MicroRNA Target Sites by PAR-CLIP. <i>Cell</i> , 2010, 141, 129-141.	28.9	2,604