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List of Publications by Year
in descending order

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59 papers	5,356 citations	136950 32 h-index	155660 55 g-index

67 all docs	67 docs citations	67 times ranked	6471 citing authors

#	Article	IF	Citations
1	Enhancing Open Modification Searches via a Combined Approach Facilitated by Ursgal. Journal of Proteome Research, 2021, 20, 1986-1996.	3.7	8
2	Human METTL18 is a histidine-specific methyltransferase that targets RPL3 and affects ribosome biogenesis and function. Nucleic Acids Research, 2021, 49, 3185-3203.	14.5	34
3	SMITERâ€"A Python Library for the Simulation of LC-MS/MS Experiments. Genes, 2021, 12, 396.	2.4	6
4	Humans and other commonly used model organisms are resistant to cycloheximide-mediated biases in ribosome profiling experiments. Nature Communications, 2021, 12, 5094.	12.8	21
5	Analysis of codon-specific translation by ribosome profiling. Methods in Enzymology, 2021, 658, 191-223.	1.0	3
6	Urm1: A Non-Canonical UBL. Biomolecules, 2021, 11, 139.	4.0	7
7	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. Nucleic Acids Research, 2020, 48, 830-846.	14.5	88
8	Editorial: Microbial Regulation of Translation. Frontiers in Genetics, 2020, 11, 616946.	2.3	0
9	Wnt/Beta-catenin/Esrrb signalling controls the tissue-scale reorganization and maintenance of the pluripotent lineage during murine embryonic diapause. Nature Communications, 2020, 11, 5499.	12.8	35
10	Modulation of Escherichia coli Translation by the Specific Inactivation of tRNAGly Under Oxidative Stress. Frontiers in Genetics, 2020, 11, 856.	2.3	14
11	PDCD4 controls the G1/S-phase transition in a telomerase-immortalized epithelial cell line and affects the expression level and translation of multiple mRNAs. Scientific Reports, 2020, 10, 2758.	3.3	9
12	Molecular basis for the bifunctional Uba4â€"Urm1 sulfurâ€relay system in <scp>tRNA</scp> thiolation and ubiquitinâ€like conjugation. EMBO Journal, 2020, 39, e105087.	7.8	17
13	A fully automated high-throughput workflow for 3D-based chemical screening in human midbrain organoids. ELife, 2020, 9, .	6.0	117
14	Absolute Quantifizierung nichtâ€kodierender RNAâ€Spezies mittels Mikroskalaâ€Thermophorese. Angewandte Chemie, 2019, 131, 9666-9670.	2.0	0
15	Translational offsetting as a mode of estrogen receptor Î±â€dependent regulation of geneÂexpression. EMBO Journal, 2019, 38, e101323.	7.8	33
16	Matching tRNA modifications in humans to their known and predicted enzymes. Nucleic Acids Research, 2019, 47, 2143-2159.	14.5	116
17	The epitranscriptome in translation regulation: <scp>mRNA</scp> and <scp>tRNA</scp> modifications as the two sides of the same coin?. FEBS Letters, 2019, 593, 1483-1493.	2.8	32
18	The exonuclease Xrn1 activates transcription and translation of mRNAs encoding membrane proteins. Nature Communications, 2019, 10, 1298.	12.8	36

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19	Absolute Quantification of Noncoding RNA by Microscale Thermophoresis. Angewandte Chemie - International Edition, 2019, 58, 9565-9569.	13.8	29
20	Enzymatic or In Vivo Installation of Propargyl Groups in Combination with Click Chemistry for the Enrichment and Detection of Methyltransferase Target Sites in RNA. Angewandte Chemie - International Edition, 2018, 57, 6342-6346.	13.8	82
21	Enzymatischer oder In-vivo-Einbau von Propargylgruppen in Kombination mit Klick-Chemie zur Anreicherung und Detektion von Methyltransferase-Zielsequenzen in RNA. Angewandte Chemie, 2018, 130, 6451-6455.	2.0	19
22	pymzML v2.0: introducing a highly compressed and seekable gzip format. Bioinformatics, 2018, 34, 2513-2514.	4.1	56
23	Interaction between theCaenorhabditis eleganscentriolar protein SAS-5 and microtubules facilitates organelle assembly. Molecular Biology of the Cell, 2018, 29, 722-735.	2.1	8
24	Diversity of foliar endophytic ascomycetes in the endemic Corsican pine forests. Fungal Ecology, 2018, 36, 128-140.	1.6	14
25	Differential Requirement for Translation Initiation Factor Pathways during Ecdysone-Dependent Neuronal Remodeling in Drosophila. Cell Reports, 2018, 24, 2287-2299.e4.	6.4	32
26	Dynamic Regulation of tRNA Modifications in Cancer. , 2018, , 163-186.		10
27	Nano LC-MS using capillary columns enables accurate quantification of modified ribonucleosides at low femtomol levels. Rna, 2018, 24, 1403-1417.	3.5	42
28	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. Nature Communications, 2018, 9, 3411.	12.8	81
29	The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. Nucleic Acids Research, 2018, 46, 5171-5181.	14.5	25
30	Innentitelbild: Enzymatischer oder Inâ€vivoâ€Einbau von Propargylgruppen in Kombination mit Klickâ€Chemie zur Anreicherung und Detektion von Methyltransferaseâ€Zielsequenzen in RNA (Angew. Chem. 21/2018). Angewandte Chemie, 2018, 130, 6064-6064.	2.0	0
31	Codon-specific translation reprogramming promotes resistance to targeted therapy. Nature, 2018, 558, 605-609.	27.8	177
32	Wobble uridine modificationsâ€“a reason to live, a reason to die?!. RNA Biology, 2017, 14, 1209-1222.	3.1	81
33	The novel lysine specific methyltransferase METTL21B affects mRNA translation through inducible and dynamic methylation of Lys-165 in human eukaryotic elongation factor 1 alpha (eEF1A). Nucleic Acids Research, 2017, 45, gkx002.	14.5	64
34	Methylation of human eukaryotic elongation factor alpha (eEF1A) by a member of a novel protein lysine methyltransferase family modulates mRNA translation. Nucleic Acids Research, 2017, 45, 8239-8254.	14.5	44
35	The Gcn4 transcription factor reduces protein synthesis capacity and extends yeast lifespan. Nature Communications, 2017, 8, 457.	12.8	83
36	pyQms enables universal and accurate quantification of mass spectrometry data. Molecular and Cellular Proteomics, 2017, 16, 1736-1745.	3.8	35

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37	Mutations in KEOPS-complex genes cause nephrotic syndrome with primary microcephaly. Nature Genetics, 2017, 49, 1529-1538.	21.4	164
38	A novel translational control mechanism involving RNA structures within coding sequences. Genome Research, 2017, 27, 95-106.	5.5	48
39	Elp3 links tRNA modification to IRES-dependent translation of LEF1 to sustain metastasis in breast cancer. Journal of Experimental Medicine, 2016, 213, 2503-2523.	8.5	128
40	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. Plant Physiology, 2016, 172, pp.00261.2016.	4.8	35
41	Dual randomization of oligonucleotides to reduce the bias in ribosome-profiling libraries. Methods, 2016, 107, 89-97.	3.8	50
42	Repulsive cues combined with physical barriers and cellâ€“cell adhesion determine progenitor cell positioning during organogenesis. Nature Communications, 2016, 7, 11288.	12.8	38
43	Stepwise Clearance of Repressive Roadblocks Drives Cardiac Induction in Human ESCs. Cell Stem Cell, 2016, 18, 341-353.	11.1	89
44	Optimization of Codon Translation Rates via tRNA Modifications Maintains Proteome Integrity. Cell, 2015, 161, 1606-1618.	28.9	427
45	A Dynamic Unfolded Protein Response Contributes to the Control of Cortical Neurogenesis. Developmental Cell, 2015, 35, 553-567.	7.0	169
46	An evolutionary approach uncovers a diverse response of tRNA 2-thiolation to elevated temperatures in yeast. Rna, 2015, 21, 202-212.	3.5	67
47	Structures to the people!. ELife, 2015, 4, e09249.	6.0	0
48	Modify or die? - RNA modification defects in metazoans. RNA Biology, 2014, 11, 1555-1567.	3.1	65
49	Modification of tRNALysUUU by Elongator Is Essential for Efficient Translation of Stress mRNAs. PLoS Genetics, 2013, 9, e1003647.	3.5	115
50	miR-31 Functions as a Negative Regulator of Lymphatic Vascular Lineage-Specific Differentiation In Vitro and Vascular Development In Vivo. Molecular and Cellular Biology, 2010, 30, 3620-3634.	2.3	102
51	Ubiquitin-related modifier Urm1 acts as a sulphur carrier in thiolation of eukaryotic transfer RNA. Nature, 2009, 458, 228-232.	27.8	245
52	Urm1 at the crossroad of modifications. EMBO Reports, 2008, 9, 1196-1202.	4.5	53
53	Regulated HsSAS-6 Levels Ensure Formation of a Single Procentriole per Centriole during the Centrosome Duplication Cycle. Developmental Cell, 2007, 13, 203-213.	7.0	305
54	SAS-6 defines a protein family required for centrosome duplication in C. elegans and in human cells. Nature Cell Biology, 2005, 7, 115-125.	10.3	362

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55	Centrosome Duplication and Nematodes: Recent Insights from an Old Relationship. Developmental Cell, 2005, 9, 317-325.	7.0	48
56	Centriolar SAS-5 is required for centrosome duplication in C. elegans. Nature Cell Biology, 2004, 6, 656-664.	10.3	156
57	SAS-4 Is Essential for Centrosome Duplication in C. elegans and Is Recruited to Daughter Centrioles Once per Cell Cycle. Developmental Cell, 2003, 4, 431-439.	7.0	208
58	Functional genomic analysis of cell division in C. elegans using RNAi of genes on chromosome III. Nature, 2000, 408, 331-336.	27.8	854
59	Synergism with the Coactivator OBF-1 (OCA-B, BOB-1) Is Mediated by a Specific POU Dimer Configuration. Cell, 2000, 103, 853-864.	28.9	134