

Andrzej Dziembowski

List of Publications by Year in descending order

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99
papers

7,043
citations

81434

41
h-index

73587

79
g-index

108
all docs

108
docs citations

108
times ranked

9136
citing authors

#	ARTICLE	IF	CITATIONS
1	Measuring the tail: Methods for poly(A) tail profiling. Wiley Interdisciplinary Reviews RNA, 2023, 14, .	3.2	16
2	A long noncoding RNA promotes parasite differentiation in African trypanosomes. Science Advances, 2022, 8, .	4.7	12
3	Functions and mechanisms of <scp>RNA</scp> tailing by metazoan terminal nucleotidyltransferases. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1622.	3.2	30
4	The TUTase URT1 connects decapping activators and prevents the accumulation of excessively deadenylated mRNAs to avoid siRNA biogenesis. Nature Communications, 2021, 12, 1298.	5.8	32
5	Cytoplasmic polyadenylation by TENT5A is required for proper bone formation. Cell Reports, 2021, 35, 109015.	2.9	24
6	Three-layered control of mRNA poly(A) tail synthesis in <i>Saccharomyces cerevisiae</i>. Genes and Development, 2021, 35, 1290-1303.	2.7	10
7	Global view on the metabolism of RNA poly(A) tails in yeast <i>Saccharomyces cerevisiae</i> . Nature Communications, 2021, 12, 4951.	5.8	40
8	Landscape of functional interactions of human processive ribonucleases revealed by high-throughput siRNA screenings. IScience, 2021, 24, 103036.	1.9	6
9	Reproducible and efficient new method of RNA 3' end labelling by CutA nucleotidyltransferase-mediated CC-tailing. RNA Biology, 2021, , 1-17.	1.5	0
10	Structure and mechanism of CutA, RNA nucleotidyl transferase with an unusual preference for cytosine. Nucleic Acids Research, 2020, 48, 9387-9405.	6.5	2
11	Mitochondrial protein biogenesis in the synapse is supported by local translation. EMBO Reports, 2020, 21, e48882.	2.0	63
12	Immunoglobulin expression and the humoral immune response is regulated by the non-canonical poly(A) polymerase TENT5C. Nature Communications, 2020, 11, 2032.	5.8	34
13	Genomic Analysis of Î³-Hexachlorocyclohexane-Degrading <i>Sphingopyxis lindanitolerans</i> WS5A3p Strain in the Context of the Pangenome of <i>Sphingopyxis</i> . Genes, 2019, 10, 688.	1.0	13
14	Quantitative proteomics revealed C6orf203/MTRES1 as a factor preventing stress-induced transcription deficiency in human mitochondria. Nucleic Acids Research, 2019, 47, 7502-7517.	6.5	21
15	Proteomic and transcriptomic experiments reveal an essential role of RNA degradosome complexes in shaping the transcriptome of <i>Mycobacterium tuberculosis</i> . Nucleic Acids Research, 2019, 47, 5892-5905.	6.5	50
16	Dominant <i>ELOVL1</i> mutation causes neurological disorder with ichthyotic keratoderma, spasticity, hypomyelination and dysmorphic features. Journal of Medical Genetics, 2018, 55, 408-414.	1.5	41
17	<i>Pseudomonas laurylsulfatorans</i> sp. nov., sodium dodecyl sulfate degrading bacteria, isolated from the peaty soil of a wastewater treatment plant. Systematic and Applied Microbiology, 2018, 41, 348-354.	1.2	27
18	PlasFlow: predicting plasmid sequences in metagenomic data using genome signatures. Nucleic Acids Research, 2018, 46, e35-e35.	6.5	389

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19	Structural analysis of mtEXO mitochondrial RNA degradosome reveals tight coupling of nuclease and helicase components. <i>Nature Communications</i> , 2018, 9, 97.	5.8	23
20	<i>Pseudomonas silesiensis</i> sp. nov. strain A3T isolated from a biological pesticide sewage treatment plant and analysis of the complete genome sequence. <i>Systematic and Applied Microbiology</i> , 2018, 41, 13-22.	1.2	23
21	Terminal nucleotidyl transferases (TENTs) in mammalian RNA metabolism. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20180162.	1.8	46
22	5â€² and 3â€² modifications controlling RNA degradation: from safeguards to executioners. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20180160.	1.8	19
23	Comparative analysis of deep sequenced methanogenic communities: identification of microorganisms responsible for methane production. <i>Microbial Cell Factories</i> , 2018, 17, 197.	1.9	27
24	Controlling the mitochondrial antisense â€œ role of the SUV3-PNPase complex and its co-factor GRSF1 in mitochondrial RNA surveillance. <i>Molecular and Cellular Oncology</i> , 2018, 5, e1516452.	0.3	14
25	Elimination of O1/Aâ€²â€²A0 pre-rRNA processing by-product in human cells involves cooperative action of two nuclear exosome-associated nucleases: RRP6 and DIS3. <i>Rna</i> , 2018, 24, 1677-1692.	1.6	15
26	Genomic and Functional Characterization of Environmental Strains of SDS-Degrading <i>Pseudomonas</i> spp., Providing a Source of New Sulfatases. <i>Frontiers in Microbiology</i> , 2018, 9, 1795.	1.5	17
27	Intrinsically disordered N-terminal domain of the <i>Helicoverpa armigera</i> Ultraspiracle stabilizes the dimeric form via a scorpion-like structure. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2018, 183, 167-183.	1.2	5
28	Mitochondrial double-stranded RNA triggers antiviral signalling in humans. <i>Nature</i> , 2018, 560, 238-242.	13.7	397
29	Uridylation by TUT4/7 Restricts Retrotransposition of Human LINE-1s. <i>Cell</i> , 2018, 174, 1537-1548.e29.	13.5	74
30	Dedicated surveillance mechanism controls G-quadruplex forming non-coding RNAs in human mitochondria. <i>Nature Communications</i> , 2018, 9, 2558.	5.8	67
31	<i>Sphingopyxis lindanitolerans</i> sp. nov. strain WS5A3pT enriched from a pesticide disposal site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3935-3941.	0.8	13
32	Versatile approach for functional analysis of human proteins and efficient stable cell line generation using FLP-mediated recombination system. <i>PLoS ONE</i> , 2018, 13, e0194887.	1.1	32
33	Nucleoplasmin-like domain of FKBP39 from <i>Drosophila melanogaster</i> forms a tetramer with partly disordered tentacle-like C-terminal segments. <i>Scientific Reports</i> , 2017, 7, 40405.	1.6	7
34	DNA Ligase C and Prim-PolC participate in base excision repair in mycobacteria. <i>Nature Communications</i> , 2017, 8, 1251.	5.8	25
35	Biochemical and structural bioinformatics studies of fungal CutA nucleotidyltransferases explain their unusual specificity toward CTP and increased tendency for cytidine incorporation at the 3â€²-terminal positions of synthesized tails. <i>Rna</i> , 2017, 23, 1902-1926.	1.6	7
36	The non-canonical poly(A) polymerase FAM46C acts as an onco-suppressor in multiple myeloma. <i>Nature Communications</i> , 2017, 8, 619.	5.8	77

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37	Two novel C-terminal frameshift mutations in the β^2 -globin gene lead to rapid mRNA decay. BMC Medical Genetics, 2017, 18, 65.	2.1	5
38	Draft Genome Sequence of the Type Strain <i>Sphingopyxis wittflariensis</i> DSM 14551. Genome Announcements, 2017, 5, .	0.8	5
39	Isolation and Characterization of <i>Pseudomonas</i> spp. Strains That Efficiently Decompose Sodium Dodecyl Sulfate. Frontiers in Microbiology, 2017, 8, 1872.	1.5	28
40	Draft Genome Sequence of the Type Strain <i>Pseudomonas umsongensis</i> DSM 16611. Genome Announcements, 2017, 5, .	0.8	4
41	Draft Genome Sequence of the Type Strain <i>Sphingopyxis bauzanensis</i> DSM 22271. Genome Announcements, 2017, 5, .	0.8	4
42	Draft Genome Sequence of the Type Strain <i>Pseudomonas jessenii</i> DSM 17150. Genome Announcements, 2017, 5, .	0.8	3
43	A short splicing isoform of HBS1L links the cytoplasmic exosome and SKI complexes in humans. Nucleic Acids Research, 2016, 45, gkw862.	6.5	40
44	Perlman syndrome nuclease DIS3L2 controls cytoplasmic non-coding RNAs and provides surveillance pathway for maturing snRNAs. Nucleic Acids Research, 2016, 44, gkw649.	6.5	81
45	Cytoplasmic RNA decay pathways - Enzymes and mechanisms. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 3125-3147.	1.9	156
46	Beyond the known functions of the CCR4-NOT complex in gene expression regulatory mechanisms. BioEssays, 2016, 38, 1048-1058.	1.2	15
47	Filaggrin inhibits generation of CD1a neolipid antigens by house dust mite-derived phospholipase. Science Translational Medicine, 2016, 8, 325ra18.	5.8	77
48	The architecture of the <i>Schizosaccharomyces pombe</i> CCR4-NOT complex. Nature Communications, 2016, 7, 10433.	5.8	47
49	The Human Nuclear Exosome Targeting Complex Is Loaded onto Newly Synthesized RNA to Direct Early Ribonucleolysis. Cell Reports, 2015, 10, 178-192.	2.9	157
50	Rbs1, a New Protein Implicated in RNA Polymerase III Biogenesis in Yeast <i>Saccharomyces cerevisiae</i> . Molecular and Cellular Biology, 2015, 35, 1169-1181.	1.1	30
51	hUTP24 is essential for processing of the human rRNA precursor at site A ₁ , but not at site A ₀ . RNA Biology, 2015, 12, 1010-1029.	1.5	24
52	Mistargeted mitochondrial proteins activate a proteostatic response in the cytosol. Nature, 2015, 524, 485-488.	18.7	348
53	Characterization of the Mycobacterial Acyl-CoA Carboxylase Holo Complexes Reveals Their Functional Expansion into Amino Acid Catabolism. PLoS Pathogens, 2015, 11, e1004623.	2.1	19
54	DIS3 shapes the RNA polymerase II transcriptome in humans by degrading a variety of unwanted transcripts. Genome Research, 2015, 25, 1622-1633.	2.4	73

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55	Purification of Eukaryotic Exoribonucleases Following Heterologous Expression in Bacteria and Analysis of Their Biochemical Properties by In Vitro Enzymatic Assays. <i>Methods in Molecular Biology</i> , 2015, 1259, 417-452.	0.4	7
56	Proteins involved in the degradation of cytoplasmic mRNA in the major eukaryotic model systems. <i>RNA Biology</i> , 2014, 11, 1122-1136.	1.5	74
57	Probabilistic Approach to Predicting Substrate Specificity of Methyltransferases. <i>PLoS Computational Biology</i> , 2014, 10, e1003514.	1.5	19
58	Linear mtDNA fragments and unusual mtDNA rearrangements associated with pathological deficiency of MGME1 exonuclease. <i>Human Molecular Genetics</i> , 2014, 23, 6147-6162.	1.4	64
59	Multiple myeloma-associated hDIS3 mutations cause perturbations in cellular RNA metabolism and suggest hDIS3 PIN domain as a potential drug target. <i>Nucleic Acids Research</i> , 2014, 42, 1270-1290.	6.5	69
60	Structural and Biochemical Insights to the Role of the CCR4-NOT Complex and DDX6 ATPase in MicroRNA Repression. <i>Molecular Cell</i> , 2014, 54, 751-765.	4.5	276
61	Identification of Protein Partners in Mycobacteria Using a Single-Step Affinity Purification Method. <i>PLoS ONE</i> , 2014, 9, e91380.	1.1	20
62	U6 RNA biogenesis and disease association. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 581-592.	3.2	37
63	RNA decay machines: The exosome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 552-560.	0.9	202
64	Exonuclease hDIS3L2 specifies an exosome-independent 3' to 5' degradation pathway of human cytoplasmic mRNA. <i>EMBO Journal</i> , 2013, 32, 1855-1868.	3.5	136
65	The RNA exosome complex central channel controls both exonuclease and endonuclease Dis3 activities in vivo and in vitro. <i>Nucleic Acids Research</i> , 2013, 41, 3845-3858.	6.5	53
66	Identification of a novel human mitochondrial endo-/exonuclease Ddk1/c20orf72 necessary for maintenance of proper 7S DNA levels. <i>Nucleic Acids Research</i> , 2013, 41, 3144-3161.	6.5	41
67	Human mitochondrial RNA decay mediated by PNPase-hSuv3 complex takes place in distinct foci. <i>Nucleic Acids Research</i> , 2013, 41, 1223-1240.	6.5	160
68	A new strategy for gene targeting and functional proteomics using the DT40 cell line. <i>Nucleic Acids Research</i> , 2013, 41, e167-e167.	6.5	17
69	Architecture and nucleic acids recognition mechanism of the THO complex, an mRNP assembly factor. <i>EMBO Journal</i> , 2012, 31, 1605-1616.	3.5	79
70	<i>C16orf57</i> , a gene mutated in poikiloderma with neutropenia, encodes a putative phosphodiesterase responsible for the U6 snRNA 3' end modification. <i>Genes and Development</i> , 2012, 26, 1911-1925.	2.7	73
71	Biochemistry and Function of RNA Exosomes. <i>The Enzymes</i> , 2012, 31, 1-30.	0.7	5
72	The yeast THO complex forms a 5-subunit assembly that directly interacts with active chromatin. <i>Bioarchitecture</i> , 2012, 2, 134-137.	1.5	14

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73	The eukaryotic RNA exosome: Same scaffold but variable catalytic subunits. <i>RNA Biology</i> , 2011, 8, 61-66.	1.5	97
74	Interaction Profiling Identifies the Human Nuclear Exosome Targeting Complex. <i>Molecular Cell</i> , 2011, 43, 624-637.	4.5	355
75	Comprehensive Structural and Substrate Specificity Classification of the <i>Saccharomyces cerevisiae</i> Methyltransferase. <i>PLoS ONE</i> , 2011, 6, e23168.	1.1	50
76	Systematic Bioinformatics and Experimental Validation of Yeast Complexes Reduces the Rate of Attrition during Structural Investigations. <i>Structure</i> , 2010, 18, 1075-1082.	1.6	8
77	Mechanisms of RNA Degradation by the Eukaryotic Exosome. <i>ChemBioChem</i> , 2010, 11, 938-945.	1.3	35
78	The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. <i>EMBO Journal</i> , 2010, 29, 2342-2357.	3.5	237
79	RNA channelling by the eukaryotic exosome. <i>EMBO Reports</i> , 2010, 11, 936-942.	2.0	68
80	Novel endoribonucleases as central players in various pathways of eukaryotic RNA metabolism. <i>Rna</i> , 2010, 16, 1692-1724.	1.6	69
81	Catalytic Properties of the Eukaryotic Exosome. <i>Advances in Experimental Medicine and Biology</i> , 2010, 702, 63-78.	0.8	28
82	Catalytic properties of the eukaryotic exosome. <i>Advances in Experimental Medicine and Biology</i> , 2010, 702, 63-78.	0.8	5
83	Structure of the yeast Pml1 splicing factor and its integration into the RES complex. <i>Nucleic Acids Research</i> , 2009, 37, 129-143.	6.5	69
84	Endonucleolytic RNA cleavage by a eukaryotic exosome. <i>Nature</i> , 2008, 456, 993-996.	13.7	284
85	Structure of the Active Subunit of the Yeast Exosome Core, Rrp44: Diverse Modes of Substrate Recruitment in the RNase II Nuclease Family. <i>Molecular Cell</i> , 2008, 29, 717-728.	4.5	175
86	RNA channelling by the archaeal exosome. <i>EMBO Reports</i> , 2007, 8, 470-476.	2.0	108
87	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 15-22.	3.6	381
88	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006, 7, 605-610.	2.0	168
89	Identification of a novel human nuclear-encoded mitochondrial poly(A) polymerase. <i>Nucleic Acids Research</i> , 2004, 32, 6001-6014.	6.5	143
90	Proteomic analysis identifies a new complex required for nuclear pre-mRNA retention and splicing. <i>EMBO Journal</i> , 2004, 23, 4847-4856.	3.5	139

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91	RNA Degradation in Yeast and Human Mitochondria. Toxicology Mechanisms and Methods, 2004, 14, 53-57.	1.3	1
92	Recent developments in the analysis of protein complexes1. FEBS Letters, 2004, 556, 1-6.	1.3	82
93	Human Polynucleotide Phosphorylase, hPNPase, is Localized in Mitochondria. Journal of Molecular Biology, 2003, 329, 853-857.	2.0	78
94	The Yeast Mitochondrial Degradosome. Journal of Biological Chemistry, 2003, 278, 1603-1611.	1.6	135
95	Localisation of the human hSuv3p helicase in the mitochondrial matrix and its preferential unwinding of dsDNA. Nucleic Acids Research, 2002, 30, 5074-5086.	6.5	81
96	Genetic and Biochemical Approaches for Analysis of Mitochondrial Degradosome from Saccharomyces cerevisiae. Methods in Enzymology, 2001, 342, 367-378.	0.4	14
97	Analysis of 3' and 5' Ends of RNA by Solid-Phase S1 Nuclease Mapping. Analytical Biochemistry, 2001, 294, 87-89.	1.1	3
98	The yeast nuclear gene DSS1, which codes for a putative RNase II, is necessary for the function of the mitochondrial degradosome in processing and turnover of RNA. Molecular Genetics and Genomics, 1998, 260, 108-114.	2.4	63
99	Interaction Analysis. , 0, , 295-315.		0