

David P Bartel

List of Publications by Citations

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

147
papers

138,328
citations

94
h-index

155
g-index

155
ext. papers

154,208
ext. citations

23.8
avg, IF

9.47
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 147 | MicroRNAs: genomics, biogenesis, mechanism, and function. <i>Cell</i> , 2004 , 116, 281-97 | 56.2 | 28094 |
| 146 | MicroRNAs: target recognition and regulatory functions. <i>Cell</i> , 2009 , 136, 215-33 | 56.2 | 15104 |
| 145 | Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. <i>Cell</i> , 2005 , 120, 15-20 | 56.2 | 9564 |
| 144 | Most mammalian mRNAs are conserved targets of microRNAs. <i>Genome Research</i> , 2009 , 19, 92-105 | 9.7 | 5919 |
| 143 | Prediction of mammalian microRNA targets. <i>Cell</i> , 2003 , 115, 787-98 | 56.2 | 4144 |
| 142 | Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. <i>Nature</i> , 2005 , 433, 769-73 | 50.4 | 3967 |
| 141 | Predicting effective microRNA target sites in mammalian mRNAs. <i>ELife</i> , 2015 , 4, | 8.9 | 3825 |
| 140 | Mammalian microRNAs predominantly act to decrease target mRNA levels. <i>Nature</i> , 2010 , 466, 835-40 | 50.4 | 3074 |
| 139 | MicroRNA targeting specificity in mammals: determinants beyond seed pairing. <i>Molecular Cell</i> , 2007 , 27, 91-105 | 17.6 | 2989 |
| 138 | The impact of microRNAs on protein output. <i>Nature</i> , 2008 , 455, 64-71 | 50.4 | 2911 |
| 137 | MicroRNAs modulate hematopoietic lineage differentiation. <i>Science</i> , 2004 , 303, 83-6 | 33.3 | 2736 |
| 136 | An abundant class of tiny RNAs with probable regulatory roles in <i>Caenorhabditis elegans</i> . <i>Science</i> , 2001 , 294, 858-62 | 33.3 | 2719 |
| 135 | RNAi: double-stranded RNA directs the ATP-dependent cleavage of mRNA at 21 to 23 nucleotide intervals. <i>Cell</i> , 2000 , 101, 25-33 | 56.2 | 2137 |
| 134 | MicroRNAs and their regulatory roles in plants. <i>Annual Review of Plant Biology</i> , 2006 , 57, 19-53 | 30.7 | 2102 |
| 133 | lincRNAs: genomics, evolution, and mechanisms. <i>Cell</i> , 2013 , 154, 26-46 | 56.2 | 1841 |
| 132 | Computational identification of plant microRNAs and their targets, including a stress-induced miRNA. <i>Molecular Cell</i> , 2004 , 14, 787-99 | 17.6 | 1839 |
| 131 | Prediction of plant microRNA targets. <i>Cell</i> , 2002 , 110, 513-20 | 56.2 | 1809 |

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|-----|--|------|------|
| 130 | MicroRNAs in plants. <i>Genes and Development</i> , 2002 , 16, 1616-26 | 12.6 | 1607 |
| 129 | Metazoan MicroRNAs. <i>Cell</i> , 2018 , 173, 20-51 | 56.2 | 1506 |
| 128 | MicroRNA-directed cleavage of HOXB8 mRNA. <i>Science</i> , 2004 , 304, 594-6 | 33.3 | 1428 |
| 127 | A uniform system for microRNA annotation. <i>Rna</i> , 2003 , 9, 277-9 | 5.8 | 1332 |
| 126 | The widespread impact of mammalian MicroRNAs on mRNA repression and evolution. <i>Science</i> , 2005 , 310, 1817-21 | 33.3 | 1249 |
| 125 | Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. <i>Cell</i> , 2008 , 134, 521-33 | 56.2 | 1228 |
| 124 | Micromanagers of gene expression: the potentially widespread influence of metazoan microRNAs. <i>Nature Reviews Genetics</i> , 2004 , 5, 396-400 | 30.1 | 1141 |
| 123 | Intronic microRNA precursors that bypass Drosha processing. <i>Nature</i> , 2007 , 448, 83-6 | 50.4 | 1138 |
| 122 | Widespread shortening of 3'UTRs by alternative cleavage and polyadenylation activates oncogenes in cancer cells. <i>Cell</i> , 2009 , 138, 673-84 | 56.2 | 1129 |
| 121 | Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes. <i>Rna</i> , 2005 , 11, 241-7 | 5.8 | 1109 |
| 120 | MicroRNAs regulate brain morphogenesis in zebrafish. <i>Science</i> , 2005 , 308, 833-8 | 33.3 | 1080 |
| 119 | A diverse and evolutionarily fluid set of microRNAs in <i>Arabidopsis thaliana</i> . <i>Genes and Development</i> , 2006 , 20, 3407-25 | 12.6 | 1058 |
| 118 | Expanded identification and characterization of mammalian circular RNAs. <i>Genome Biology</i> , 2014 , 15, 409 | 18.3 | 1039 |
| 117 | Disrupting the pairing between let-7 and Hmga2 enhances oncogenic transformation. <i>Science</i> , 2007 , 315, 1576-9 | 33.3 | 960 |
| 116 | The microRNAs of <i>Caenorhabditis elegans</i> . <i>Genes and Development</i> , 2003 , 17, 991-1008 | 12.6 | 926 |
| 115 | Vertebrate microRNA genes. <i>Science</i> , 2003 , 299, 1540 | 33.3 | 899 |
| 114 | Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. <i>Cell</i> , 2011 , 147, 1537-50 | 56.2 | 882 |
| 113 | Passenger-strand cleavage facilitates assembly of siRNA into Ago2-containing RNAi enzyme complexes. <i>Cell</i> , 2005 , 123, 607-20 | 56.2 | 880 |

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|-----|---|------|-----|
| 112 | Large-scale sequencing reveals 21U-RNAs and additional microRNAs and endogenous siRNAs in <i>C. elegans</i> . <i>Cell</i> , 2006 , 127, 1193-207 | 56.2 | 774 |
| 111 | A biochemical framework for RNA silencing in plants. <i>Genes and Development</i> , 2003 , 17, 49-63 | 12.6 | 738 |
| 110 | The action of ARGONAUTE1 in the miRNA pathway and its regulation by the miRNA pathway are crucial for plant development. <i>Genes and Development</i> , 2004 , 18, 1187-97 | 12.6 | 719 |
| 109 | Weak seed-pairing stability and high target-site abundance decrease the proficiency of <i>Isy-6</i> and other microRNAs. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1139-46 | 17.6 | 701 |
| 108 | MicroRNA-directed regulation of Arabidopsis AUXIN RESPONSE FACTOR17 is essential for proper development and modulates expression of early auxin response genes. <i>Plant Cell</i> , 2005 , 17, 1360-75 | 11.6 | 682 |
| 107 | Endogenous trans-acting siRNAs regulate the accumulation of Arabidopsis mRNAs. <i>Molecular Cell</i> , 2004 , 16, 69-79 | 17.6 | 671 |
| 106 | Mammalian microRNAs: experimental evaluation of novel and previously annotated genes. <i>Genes and Development</i> , 2010 , 24, 992-1009 | 12.6 | 610 |
| 105 | Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. <i>Genes and Development</i> , 2008 , 22, 2773-85 | 12.6 | 606 |
| 104 | Endogenous siRNA and miRNA targets identified by sequencing of the Arabidopsis degradome. <i>Current Biology</i> , 2008 , 18, 758-762 | 6.3 | 597 |
| 103 | MicroRNA regulation of NAC-domain targets is required for proper formation and separation of adjacent embryonic, vegetative, and floral organs. <i>Current Biology</i> , 2004 , 14, 1035-46 | 6.3 | 540 |
| 102 | MicroRNA control of PHABULOSA in leaf development: importance of pairing to the microRNA 5'U region. <i>EMBO Journal</i> , 2004 , 23, 3356-64 | 13 | 538 |
| 101 | RNA-catalyzed RNA polymerization: accurate and general RNA-templated primer extension. <i>Science</i> , 2001 , 292, 1319-25 | 33.3 | 523 |
| 100 | Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. <i>Nature</i> , 2008 , 455, 1193-7 | 50.4 | 522 |
| 99 | A two-hit trigger for siRNA biogenesis in plants. <i>Cell</i> , 2006 , 127, 565-77 | 56.2 | 517 |
| 98 | Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007 , 450, 219-32 | 50.4 | 506 |
| 97 | miR-150, a microRNA expressed in mature B and T cells, blocks early B cell development when expressed prematurely. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7080-5 | 11.5 | 505 |
| 96 | Partially redundant functions of Arabidopsis DICER-like enzymes and a role for DCL4 in producing trans-acting siRNAs. <i>Current Biology</i> , 2005 , 15, 1494-500 | 6.3 | 480 |
| 95 | Expanding the microRNA targeting code: functional sites with centered pairing. <i>Molecular Cell</i> , 2010 , 38, 789-802 | 17.6 | 466 |

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|----|---|------|-----|
| 94 | Evolution, biogenesis, expression, and target predictions of a substantially expanded set of <i>Drosophila</i> microRNAs. <i>Genome Research</i> , 2007 , 17, 1850-64 | 9.7 | 462 |
| 93 | Antiquity of microRNAs and their targets in land plants. <i>Plant Cell</i> , 2005 , 17, 1658-73 | 11.6 | 461 |
| 92 | Assessing the ceRNA hypothesis with quantitative measurements of miRNA and target abundance. <i>Molecular Cell</i> , 2014 , 54, 766-76 | 17.6 | 451 |
| 91 | RNAi in budding yeast. <i>Science</i> , 2009 , 326, 544-550 | 33.3 | 398 |
| 90 | Poly(A)-tail profiling reveals an embryonic switch in translational control. <i>Nature</i> , 2014 , 508, 66-71 | 50.4 | 397 |
| 89 | The let-7 MicroRNA family members mir-48, mir-84, and mir-241 function together to regulate developmental timing in <i>Caenorhabditis elegans</i> . <i>Developmental Cell</i> , 2005 , 9, 403-14 | 10.2 | 379 |
| 88 | Principles of long noncoding RNA evolution derived from direct comparison of transcriptomes in 17 species. <i>Cell Reports</i> , 2015 , 11, 1110-22 | 10.6 | 377 |
| 87 | Most <i>Caenorhabditis elegans</i> microRNAs are individually not essential for development or viability. <i>PLoS Genetics</i> , 2007 , 3, e215 | 6 | 368 |
| 86 | Small RNAs correspond to centromere heterochromatic repeats. <i>Science</i> , 2002 , 297, 1831 | 33.3 | 368 |
| 85 | MicroRNAs: at the root of plant development?. <i>Plant Physiology</i> , 2003 , 132, 709-17 | 6.6 | 354 |
| 84 | Formation, regulation and evolution of <i>Caenorhabditis elegans</i> 3ΨTRs. <i>Nature</i> , 2011 , 469, 97-101 | 50.4 | 353 |
| 83 | The microRNA miR-196 acts upstream of Hoxb8 and Shh in limb development. <i>Nature</i> , 2005 , 438, 671-4 | 50.4 | 343 |
| 82 | Common functions for diverse small RNAs of land plants. <i>Plant Cell</i> , 2007 , 19, 1750-69 | 11.6 | 340 |
| 81 | mRNA destabilization is the dominant effect of mammalian microRNAs by the time substantial repression ensues. <i>Molecular Cell</i> , 2014 , 56, 104-15 | 17.6 | 317 |
| 80 | A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain. <i>Cell</i> , 2018 , 174, 350-362.e17 | 56.2 | 309 |
| 79 | One sequence, two ribozymes: implications for the emergence of new ribozyme folds. <i>Science</i> , 2000 , 289, 448-52 | 33.3 | 296 |
| 78 | Beyond secondary structure: primary-sequence determinants license pri-miRNA hairpins for processing. <i>Cell</i> , 2013 , 152, 844-58 | 56.2 | 281 |
| 77 | AGO1 homeostasis entails coexpression of MIR168 and AGO1 and preferential stabilization of miR168 by AGO1. <i>Molecular Cell</i> , 2006 , 22, 129-36 | 17.6 | 272 |

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|----|---|------|-----|
| 76 | MicroRNAs prevent precocious gene expression and enable pattern formation during plant embryogenesis. <i>Genes and Development</i> , 2010 , 24, 2678-92 | 12.6 | 266 |
| 75 | RNA G-quadruplexes are globally unfolded in eukaryotic cells and depleted in bacteria. <i>Science</i> , 2016 , 353, | 33.3 | 247 |
| 74 | Improved Ribosome-Footprint and mRNA Measurements Provide Insights into Dynamics and Regulation of Yeast Translation. <i>Cell Reports</i> , 2016 , 14, 1787-1799 | 10.6 | 237 |
| 73 | RNA-catalysed nucleotide synthesis. <i>Nature</i> , 1998 , 395, 260-3 | 50.4 | 237 |
| 72 | Structure of yeast Argonaute with guide RNA. <i>Nature</i> , 2012 , 486, 368-74 | 50.4 | 226 |
| 71 | Extensive alternative polyadenylation during zebrafish development. <i>Genome Research</i> , 2012 , 22, 2054-667 | 66.7 | 220 |
| 70 | Impact of MicroRNA Levels, Target-Site Complementarity, and Cooperativity on Competing Endogenous RNA-Regulated Gene Expression. <i>Molecular Cell</i> , 2016 , 64, 565-579 | 17.6 | 207 |
| 69 | Global analyses of the effect of different cellular contexts on microRNA targeting. <i>Molecular Cell</i> , 2014 , 53, 1031-1043 | 17.6 | 205 |
| 68 | RNA-catalysed RNA polymerization using nucleoside triphosphates. <i>Nature</i> , 1996 , 382, 373-6 | 50.4 | 197 |
| 67 | A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. <i>Genes and Development</i> , 2008 , 22, 8-13 | 12.6 | 188 |
| 66 | Compatibility with killer explains the rise of RNAi-deficient fungi. <i>Science</i> , 2011 , 333, 1592 | 33.3 | 164 |
| 65 | The biochemical basis of microRNA targeting efficacy. <i>Science</i> , 2019 , 366, | 33.3 | 160 |
| 64 | TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the <i>Schizosaccharomyces pombe</i> siRNA pathway. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1015-23 | 17.6 | 151 |
| 63 | MicroRNAs in the Hox network: an apparent link to posterior prevalence. <i>Nature Reviews Genetics</i> , 2008 , 9, 789-96 | 30.1 | 151 |
| 62 | MicroRNA destabilization enables dynamic regulation of the miR-16 family in response to cell-cycle changes. <i>Molecular Cell</i> , 2011 , 43, 993-1004 | 17.6 | 141 |
| 61 | Patterns of flanking sequence conservation and a characteristic upstream motif for microRNA gene identification. <i>Rna</i> , 2004 , 10, 1309-22 | 5.8 | 138 |
| 60 | Stalled spliceosomes are a signal for RNAi-mediated genome defense. <i>Cell</i> , 2013 , 152, 957-68 | 56.2 | 124 |
| 59 | 3'UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. <i>Genome Research</i> , 2013 , 23, 2078-90 | 9.7 | 123 |

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|----|---|------|-----|
| 58 | The hammerhead cleavage reaction in monovalent cations. <i>Rna</i> , 2001 , 7, 546-52 | 5.8 | 118 |
| 57 | The Menu of Features that Define Primary MicroRNAs and Enable De Novo Design of MicroRNA Genes. <i>Molecular Cell</i> , 2015 , 60, 131-45 | 17.6 | 111 |
| 56 | The secondary structure and sequence optimization of an RNA ligase ribozyme. <i>Nucleic Acids Research</i> , 1995 , 23, 3231-8 | 20.1 | 111 |
| 55 | Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. <i>Genome Research</i> , 2011 , 21, 1395-403 | 9.7 | 102 |
| 54 | Crystal structure of the catalytic core of an RNA-polymerase ribozyme. <i>Science</i> , 2009 , 326, 1271-5 | 33.3 | 95 |
| 53 | Coherent but overlapping expression of microRNAs and their targets during vertebrate development. <i>Genes and Development</i> , 2009 , 23, 466-81 | 12.6 | 89 |
| 52 | mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos. <i>ELife</i> , 2016 , 5, | 8.9 | 86 |
| 51 | Regulatory mutations of mir-48, a C. elegans let-7 family MicroRNA, cause developmental timing defects. <i>Developmental Cell</i> , 2005 , 9, 415-22 | 10.2 | 84 |
| 50 | Widespread changes in the posttranscriptional landscape at the Drosophila oocyte-to-embryo transition. <i>Cell Reports</i> , 2014 , 7, 1495-1508 | 10.6 | 81 |
| 49 | The PUMILIO-RNA interaction: a single RNA-binding domain monomer recognizes a bipartite target sequence. <i>Biochemistry</i> , 1999 , 38, 596-604 | 3.2 | 78 |
| 48 | In ovo application of antagomiRs indicates a role for miR-196 in patterning the chick axial skeleton through Hox gene regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 18610-5 | 11.5 | 74 |
| 47 | Widespread Influence of 3'UTR Structures on Mammalian mRNA Processing and Stability. <i>Cell</i> , 2017 , 169, 905-917.e11 | 56.2 | 69 |
| 46 | Reverse transcriptase reads through a 2'5' linkage and a 2' thiophosphate in a template. <i>Nucleic Acids Research</i> , 1995 , 23, 2811-4 | 20.1 | 65 |
| 45 | Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. <i>Nucleic Acids Research</i> , 2015 , 43, 5052-64 | 20.1 | 62 |
| 44 | Excised linear introns regulate growth in yeast. <i>Nature</i> , 2019 , 565, 606-611 | 50.4 | 62 |
| 43 | The inside-out mechanism of Dicers from budding yeasts. <i>Cell</i> , 2011 , 146, 262-76 | 56.2 | 57 |
| 42 | Allelic imbalance sequencing reveals that single-nucleotide polymorphisms frequently alter microRNA-directed repression. <i>Nature Biotechnology</i> , 2009 , 27, 472-7 | 44.5 | 57 |
| 41 | Genetic dissection of the miR-200-Zeb1 axis reveals its importance in tumor differentiation and invasion. <i>Nature Communications</i> , 2018 , 9, 4671 | 17.4 | 57 |

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|----|---|------|----|
| 40 | A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 100-6 | 17.6 | 56 |
| 39 | Kinetic framework for ligation by an efficient RNA ligase ribozyme. <i>Biochemistry</i> , 2000 , 39, 3115-23 | 3.2 | 51 |
| 38 | Processivity of ribozyme-catalyzed RNA polymerization. <i>Biochemistry</i> , 2003 , 42, 8748-55 | 3.2 | 49 |
| 37 | kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. <i>Nucleic Acids Research</i> , 2017 , 45, W534-W538 | 20.1 | 47 |
| 36 | The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. <i>Science</i> , 2020 , 370, | 33.3 | 47 |
| 35 | New CRISPR Mutagenesis Strategies Reveal Variation in Repair Mechanisms among Fungi. <i>MSphere</i> , 2018 , 3, | 5 | 44 |
| 34 | Author response: Predicting effective microRNA target sites in mammalian mRNAs 2015 , | | 44 |
| 33 | <i>Candida albicans</i> Dicer (CaDcr1) is required for efficient ribosomal and spliceosomal RNA maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 523-8 | 11.5 | 43 |
| 32 | New ligase-derived RNA polymerase ribozymes. <i>Rna</i> , 2005 , 11, 1173-80 | 5.8 | 43 |
| 31 | Predicting microRNA targeting efficacy in <i>Drosophila</i> . <i>Genome Biology</i> , 2018 , 19, 152 | 18.3 | 41 |
| 30 | Independent regulation of vertebral number and vertebral identity by microRNA-196 paralogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4884-93 | 11.5 | 40 |
| 29 | The three-dimensional architecture of the class I ligase ribozyme. <i>Rna</i> , 2004 , 10, 176-84 | 5.8 | 36 |
| 28 | Global analyses of the dynamics of mammalian microRNA metabolism. <i>Genome Research</i> , 2019 , 29, 1777-1790 | 17.9 | 34 |
| 27 | Metal ion requirements for structure and catalysis of an RNA ligase ribozyme. <i>Biochemistry</i> , 2002 , 41, 8103-12 | 3.2 | 34 |
| 26 | The Dynamics of Cytoplasmic mRNA Metabolism. <i>Molecular Cell</i> , 2020 , 77, 786-799.e10 | 17.6 | 33 |
| 25 | The structural basis of RNA-catalyzed RNA polymerization. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1036-42 | 17.6 | 32 |
| 24 | The influence of microRNAs and poly(A) tail length on endogenous mRNA-protein complexes. <i>Genome Biology</i> , 2017 , 18, 211 | 18.3 | 28 |
| 23 | The biochemical basis for the cooperative action of microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 17764-17774 | 11.5 | 23 |

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|----|--|------|----|
| 22 | Substrate 2′-hydroxyl groups required for ribozyme-catalyzed polymerization. <i>Chemistry and Biology</i> , 2003 , 10, 799-806 | | 22 |
| 21 | Early genome activation in is extensive with an initial tendency for aborted transcripts and retained introns. <i>Genome Research</i> , 2019 , 29, 1188-1197 | 9.7 | 19 |
| 20 | A Seed Mismatch Enhances Argonaute2-Catalyzed Cleavage and Partially Rescues Severely Impaired Cleavage Found in Fish. <i>Molecular Cell</i> , 2017 , 68, 1095-1107.e5 | 17.6 | 17 |
| 19 | A class I ligase ribozyme with reduced Mg ²⁺ dependence: Selection, sequence analysis, and identification of functional tertiary interactions. <i>Rna</i> , 2009 , 15, 2129-46 | 5.8 | 17 |
| 18 | Recognition of nucleoside triphosphates during RNA-catalyzed primer extension. <i>Biochemistry</i> , 2000 , 39, 15556-62 | 3.2 | 16 |
| 17 | A ribozyme selected from variants of U6 snRNA promotes 2′,5′-branch formation. <i>Rna</i> , 2001 , 7, 29-43 | 5.8 | 16 |
| 16 | MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs. <i>Molecular Cell</i> , 2020 , 77, 775-785.e8 | 17.6 | 15 |
| 15 | MicroRNA Clustering Assists Processing of Suboptimal MicroRNA Hairpins through the Action of the ERH Protein. <i>Molecular Cell</i> , 2020 , 78, 289-302.e6 | 17.6 | 15 |
| 14 | The molecular basis of coupling between poly(A)-tail length and translational efficiency. <i>ELife</i> , 2021 , 10, | 8.9 | 9 |
| 13 | Degradation of host translational machinery drives tRNA acquisition in viruses. <i>Cell Systems</i> , 2021 , 12, 771-779.e5 | 10.6 | 6 |
| 12 | MicroRNA 3′-compensatory pairing occurs through two binding modes, with affinity shaped by nucleotide identity and position.. <i>ELife</i> , 2022 , 11, | 8.9 | 4 |
| 11 | The biochemical basis of microRNA targeting efficacy | | 3 |
| 10 | The Dynamics of Cytoplasmic mRNA Metabolism | | 3 |
| 9 | Xrn1p acts at multiple steps in the budding-yeast RNAi pathway to enhance the efficiency of silencing. <i>Nucleic Acids Research</i> , 2020 , 48, 7404-7420 | 20.1 | 3 |
| 8 | Author response: mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos 2016 , | | 2 |
| 7 | MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs | | 2 |
| 6 | Ago2 protects siRNAs and microRNAs from target-directed degradation, even in the absence of 2′-methylation. <i>Rna</i> , 2021 , 27, 710-724 | 5.8 | 2 |
| 5 | Xrn1p Acts at Multiple Steps in the Budding-Yeast RNAi Pathway to Enhance the Efficiency of Silencing | | 1 |

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| 4 | A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain | 1 |
| 3 | kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences | 1 |
| 2 | Pairing to the microRNA 3' region occurs through two alternative binding modes, with affinity shaped by nucleotide identity as well as pairing position | 1 |
| 1 | Most <i>Caenorhabditis elegans</i> microRNAs are individually not essential for development or viability. <i>PLoS Genetics</i> , 2005, preprint, e215 | 6 |