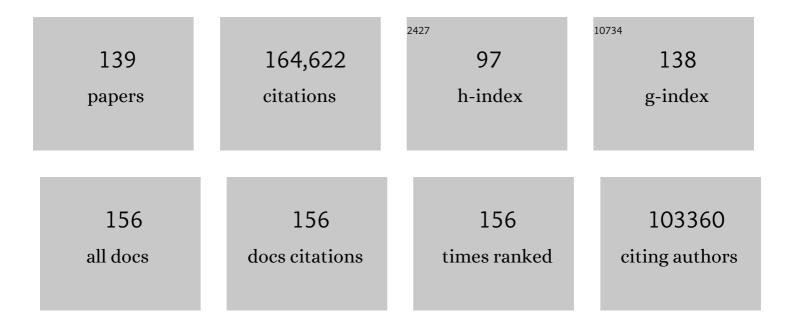
David P Bartel

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	MicroRNAs. Cell, 2004, 116, 281-297.	28.9	32,446
2	MicroRNAs: Target Recognition and Regulatory Functions. Cell, 2009, 136, 215-233.	28.9	17,802
3	Conserved Seed Pairing, Often Flanked by Adenosines, Indicates that Thousands of Human Genes are MicroRNA Targets. Cell, 2005, 120, 15-20.	28.9	10,880
4	Most mammalian mRNAs are conserved targets of microRNAs. Genome Research, 2009, 19, 92-105.	5.5	7,226
5	Predicting effective microRNA target sites in mammalian mRNAs. ELife, 2015, 4, .	6.0	5,779
6	Prediction of Mammalian MicroRNA Targets. Cell, 2003, 115, 787-798.	28.9	4,682
7	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. Nature, 2005, 433, 769-773.	27.8	4,435
8	Mammalian microRNAs predominantly act to decrease target mRNA levels. Nature, 2010, 466, 835-840.	27.8	3,513
9	MicroRNA Targeting Specificity in Mammals: Determinants beyond Seed Pairing. Molecular Cell, 2007, 27, 91-105.	9.7	3,386
10	The impact of microRNAs on protein output. Nature, 2008, 455, 64-71.	27.8	3,270
11	An Abundant Class of Tiny RNAs with Probable Regulatory Roles in <i>Caenorhabditis elegans</i> . Science, 2001, 294, 858-862.	12.6	3,041
12	MicroRNAs Modulate Hematopoietic Lineage Differentiation. Science, 2004, 303, 83-86.	12.6	3,025
13	Metazoan MicroRNAs. Cell, 2018, 173, 20-51.	28.9	2,775
14	RNAi. Cell, 2000, 101, 25-33.	28.9	2,421
15	MicroRNAs AND THEIR REGULATORY ROLES IN PLANTS. Annual Review of Plant Biology, 2006, 57, 19-53.	18.7	2,418
16	lincRNAs: Genomics, Evolution, and Mechanisms. Cell, 2013, 154, 26-46.	28.9	2,337
17	Computational Identification of Plant MicroRNAs and Their Targets, Including a Stress-Induced miRNA. Molecular Cell, 2004, 14, 787-799.	9.7	2,097
18	Prediction of Plant MicroRNA Targets. Cell, 2002, 110, 513-520.	28.9	2,088

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19	MicroRNAs in plants. Genes and Development, 2002, 16, 1616-1626.	5.9	1,797
20	A uniform system for microRNA annotation. Rna, 2003, 9, 277-279.	3.5	1,620
21	MicroRNA-Directed Cleavage of <i>HOXB8</i> mRNA. Science, 2004, 304, 594-596.	12.6	1,596
22	Widespread Shortening of 3′UTRs by Alternative Cleavage and Polyadenylation Activates Oncogenes in Cancer Cells. Cell, 2009, 138, 673-684.	28.9	1,427
23	The Widespread Impact of Mammalian MicroRNAs on mRNA Repression and Evolution. Science, 2005, 310, 1817-1821.	12.6	1,382
24	Intronic microRNA precursors that bypass Drosha processing. Nature, 2007, 448, 83-86.	27.8	1,365
25	Expanded identification and characterization of mammalian circular RNAs. Genome Biology, 2014, 15, 409.	8.8	1,361
26	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. Cell, 2008, 134, 521-533.	28.9	1,332
27	Micromanagers of gene expression: the potentially widespread influence of metazoan microRNAs. Nature Reviews Genetics, 2004, 5, 396-400.	16.3	1,289
28	Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes. Rna, 2005, 11, 241-247.	3.5	1,253
29	MicroRNAs Regulate Brain Morphogenesis in Zebrafish. Science, 2005, 308, 833-838.	12.6	1,209
30	A diverse and evolutionarily fluid set of microRNAs in Arabidopsis thaliana. Genes and Development, 2006, 20, 3407-3425.	5.9	1,208
31	The microRNAs of <i>Caenorhabditis elegans</i> . Genes and Development, 2003, 17, 991-1008.	5.9	1,081
32	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. Cell, 2011, 147, 1537-1550.	28.9	1,072
33	Disrupting the Pairing Between let-7 and Hmga2 Enhances Oncogenic Transformation. Science, 2007, 315, 1576-1579.	12.6	1,060
34	Vertebrate MicroRNA Genes. Science, 2003, 299, 1540-1540.	12.6	1,035
35	Passenger-Strand Cleavage Facilitates Assembly of siRNA into Ago2-Containing RNAi Enzyme Complexes. Cell, 2005, 123, 607-620.	28.9	991
36	Large-Scale Sequencing Reveals 21U-RNAs and Additional MicroRNAs and Endogenous siRNAs in C. elegans. Cell, 2006, 127, 1193-1207.	28.9	892

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37	The action of ARGONAUTE1 in the miRNA pathway and its regulation by the miRNA pathway are crucial for plant development. Genes and Development, 2004, 18, 1187-1197.	5.9	868
38	A biochemical framework for RNA silencing in plants. Genes and Development, 2003, 17, 49-63.	5.9	832
39	MicroRNA-Directed Regulation of Arabidopsis AUXIN RESPONSE FACTOR17 Is Essential for Proper Development and Modulates Expression of Early Auxin Response Genes. Plant Cell, 2005, 17, 1360-1375.	6.6	805
40	Weak seed-pairing stability and high target-site abundance decrease the proficiency of lsy-6 and other microRNAs. Nature Structural and Molecular Biology, 2011, 18, 1139-1146.	8.2	803
41	Endogenous siRNA and miRNA Targets Identified by Sequencing of the Arabidopsis Degradome. Current Biology, 2008, 18, 758-762.	3.9	749
42	Endogenous trans-Acting siRNAs Regulate the Accumulation of Arabidopsis mRNAs. Molecular Cell, 2004, 16, 69-79.	9.7	742
43	Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. Genes and Development, 2008, 22, 2773-2785.	5.9	739
44	Mammalian microRNAs: experimental evaluation of novel and previously annotated genes. Genes and Development, 2010, 24, 992-1009.	5.9	706
45	RNA-Catalyzed RNA Polymerization: Accurate and General RNA-Templated Primer Extension. Science, 2001, 292, 1319-1325.	12.6	680
46	The biochemical basis of microRNA targeting efficacy. Science, 2019, 366, .	12.6	631
47	MicroRNA control of PHABULOSA in leaf development: importance of pairing to the microRNA 5′ region. EMBO Journal, 2004, 23, 3356-3364.	7.8	630
48	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. Nature, 2008, 455, 1193-1197.	27.8	630
49	MicroRNA Regulation of NAC-Domain Targets Is Required for Proper Formation and Separation of Adjacent Embryonic, Vegetative, and Floral Organs. Current Biology, 2004, 14, 1035-1046.	3.9	617
50	A Two-Hit Trigger for siRNA Biogenesis in Plants. Cell, 2006, 127, 565-577.	28.9	599
51	Assessing the ceRNA Hypothesis with Quantitative Measurements of miRNA and Target Abundance. Molecular Cell, 2014, 54, 766-776.	9.7	579
52	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	27.8	573
53	Principles of Long Noncoding RNA Evolution Derived from Direct Comparison of Transcriptomes in 17 Species. Cell Reports, 2015, 11, 1110-1122.	6.4	565
54	miR-150, a microRNA expressed in mature B and T cells, blocks early B cell development when expressed prematurely. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7080-7085.	7.1	562

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55	Partially Redundant Functions of Arabidopsis DICER-like Enzymes and a Role for DCL4 in Producing trans-Acting siRNAs. Current Biology, 2005, 15, 1494-1500.	3.9	545
56	Poly(A)-tail profiling reveals an embryonic switch in translational control. Nature, 2014, 508, 66-71.	27.8	542
57	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of <i>Drosophila</i> microRNAs. Genome Research, 2007, 17, 1850-1864.	5.5	540
58	Expanding the MicroRNA Targeting Code: Functional Sites with Centered Pairing. Molecular Cell, 2010, 38, 789-802.	9.7	534
59	Antiquity of MicroRNAs and Their Targets in Land Plants. Plant Cell, 2005, 17, 1658-1673.	6.6	522
60	A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain. Cell, 2018, 174, 350-362.e17.	28.9	485
61	RNAi in Budding Yeast. Science, 2009, 326, 544-550.	12.6	480
62	The let-7 MicroRNA Family Members mir-48, mir-84, and mir-241 Function Together to Regulate Developmental Timing in Caenorhabditis elegans. Developmental Cell, 2005, 9, 403-414.	7.0	456
63	Formation, regulation and evolution of Caenorhabditis elegans 3′UTRs. Nature, 2011, 469, 97-101.	27.8	432
64	mRNA Destabilization Is the Dominant Effect of Mammalian MicroRNAs by the Time Substantial Repression Ensues. Molecular Cell, 2014, 56, 104-115.	9.7	424
65	Small RNAs Correspond to Centromere Heterochromatic Repeats. Science, 2002, 297, 1831-1831.	12.6	423
66	Most Caenorhabditis elegans microRNAs Are Individually Not Essential for Development or Viability. PLoS Genetics, 2007, 3, e215.	3.5	412
67	MicroRNAs: At the Root of Plant Development?. Plant Physiology, 2003, 132, 709-717.	4.8	389
68	Common Functions for Diverse Small RNAs of Land Plants. Plant Cell, 2007, 19, 1750-1769.	6.6	387
69	RNA G-quadruplexes are globally unfolded in eukaryotic cells and depleted in bacteria. Science, 2016, 353, .	12.6	375
70	Beyond Secondary Structure: Primary-Sequence Determinants License Pri-miRNA Hairpins for Processing. Cell, 2013, 152, 844-858.	28.9	373
71	The microRNA miR-196 acts upstream of Hoxb8 and Shh in limb development. Nature, 2005, 438, 671-674.	27.8	365
72	One Sequence, Two Ribozymes: Implications for the Emergence of New Ribozyme Folds. Science, 2000, 289, 448-452.	12.6	340

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73	AGO1 Homeostasis Entails Coexpression of MIR168 and AGO1 and Preferential Stabilization of miR168 by AGO1. Molecular Cell, 2006, 22, 129-136.	9.7	330
74	Improved Ribosome-Footprint and mRNA Measurements Provide Insights into Dynamics and Regulation of Yeast Translation. Cell Reports, 2016, 14, 1787-1799.	6.4	330
75	MicroRNAs prevent precocious gene expression and enable pattern formation during plant embryogenesis. Genes and Development, 2010, 24, 2678-2692.	5.9	322
76	Structure of yeast Argonaute with guide RNA. Nature, 2012, 486, 368-374.	27.8	314
77	Extensive alternative polyadenylation during zebrafish development. Genome Research, 2012, 22, 2054-2066.	5.5	305
78	Impact of MicroRNA Levels, Target-Site Complementarity, and Cooperativity on Competing Endogenous RNA-Regulated Gene Expression. Molecular Cell, 2016, 64, 565-579.	9.7	300
79	RNA-catalysed nucleotide synthesis. Nature, 1998, 395, 260-263.	27.8	280
80	Global Analyses of the Effect of Different Cellular Contexts on MicroRNA Targeting. Molecular Cell, 2014, 53, 1031-1043.	9.7	276
81	RNA-catalysed RNA polymerization using nucleoside triphosphates. Nature, 1996, 382, 373-376.	27.8	242
82	A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. Genes and Development, 2008, 22, 8-13.	5.9	205
83	Compatibility with Killer Explains the Rise of RNAi-Deficient Fungi. Science, 2011, 333, 1592-1592.	12.6	194
84	3′ UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. Genome Research, 2013, 23, 2078-2090.	5.5	186
85	TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the Schizosaccharomyces pombe siRNA pathway. Nature Structural and Molecular Biology, 2008, 15, 1015-1023.	8.2	173
86	Stalled Spliceosomes Are a Signal for RNAi-Mediated Genome Defense. Cell, 2013, 152, 957-968.	28.9	173
87	The Menu of Features that Define Primary MicroRNAs and Enable De Novo Design of MicroRNA Genes. Molecular Cell, 2015, 60, 131-145.	9.7	172
88	MicroRNA Destabilization Enables Dynamic Regulation of the miR-16 Family in Response to Cell-Cycle Changes. Molecular Cell, 2011, 43, 993-1004.	9.7	171
89	MicroRNAs in the Hox network: an apparent link to posterior prevalence. Nature Reviews Genetics, 2008, 9, 789-796.	16.3	167
90	Patterns of flanking sequence conservation and a characteristic upstream motif for microRNA gene identification. Rna, 2004, 10, 1309-1322.	3.5	160

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91	The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. Science, 2020, 370, .	12.6	138
92	mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos. ELife, 2016, 5, .	6.0	132
93	The hammerhead cleavage reaction in monovalent cations. Rna, 2001, 7, 546-552.	3.5	127
94	The secondary structure and sequence optimization of an RNA ligase ribozyme. Nucleic Acids Research, 1995, 23, 3231-3238.	14.5	123
95	Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. Genome Research, 2011, 21, 1395-1403.	5.5	123
96	Widespread Influence of 3′-End Structures on Mammalian mRNA Processing and Stability. Cell, 2017, 169, 905-917.e11.	28.9	123
97	Crystal Structure of the Catalytic Core of an RNA-Polymerase Ribozyme. Science, 2009, 326, 1271-1275.	12.6	120
98	Excised linear introns regulate growth in yeast. Nature, 2019, 565, 606-611.	27.8	118
99	Widespread Changes in the Posttranscriptional Landscape at the Drosophila Oocyte-to-Embryo Transition. Cell Reports, 2014, 7, 1495-1508.	6.4	114
100	Genetic dissection of the miR-200–Zeb1 axis reveals its importance in tumor differentiation and invasion. Nature Communications, 2018, 9, 4671.	12.8	111
101	The Dynamics of Cytoplasmic mRNA Metabolism. Molecular Cell, 2020, 77, 786-799.e10.	9.7	106
102	Coherent but overlapping expression of microRNAs and their targets during vertebrate development. Genes and Development, 2009, 23, 466-481.	5.9	98
103	Regulatory Mutations of mir-48, a C. elegans let-7 Family MicroRNA, Cause Developmental Timing Defects. Developmental Cell, 2005, 9, 415-422.	7.0	92
104	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. Nucleic Acids Research, 2017, 45, W534-W538.	14.5	91
105	Predicting microRNA targeting efficacy in Drosophila. Genome Biology, 2018, 19, 152.	8.8	91
106	Global analyses of the dynamics of mammalian microRNA metabolism. Genome Research, 2019, 29, 1777-1790.	5.5	89
107	New CRISPR Mutagenesis Strategies Reveal Variation in Repair Mechanisms among Fungi. MSphere, 2018, 3, .	2.9	87
108	The PUMILIOâ^'RNA Interaction:  A Single RNA-Binding Domain Monomer Recognizes a Bipartite Target Sequence. Biochemistry, 1999, 38, 596-604.	2.5	86

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109	In ovo application of antagomiRs indicates a role for miR-196 in patterning the chick axial skeleton through Hox gene regulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18610-18615.	7.1	80
110	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. Nature Structural and Molecular Biology, 2011, 18, 100-106.	8.2	75
111	Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. Nucleic Acids Research, 2015, 43, 5052-5064.	14.5	73
112	Reverse transcriptase reads through a 2′–5′ linkage and a 2′-thiphosphate in a template. Nucleic Acids Research, 1995, 23, 2811-2814.	14.5	70
113	The molecular basis of coupling between poly(A)-tail length and translational efficiency. ELife, 2021, 10, .	6.0	62
114	Allelic imbalance sequencing reveals that single-nucleotide polymorphisms frequently alter microRNA-directed repression. Nature Biotechnology, 2009, 27, 472-477.	17.5	60
115	Independent regulation of vertebral number and vertebral identity by microRNA-196 paralogs. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4884-93.	7.1	60
116	The Inside-Out Mechanism of Dicers from Budding Yeasts. Cell, 2011, 146, 262-276.	28.9	59
117	Processivity of Ribozyme-Catalyzed RNA Polymerizationâ€. Biochemistry, 2003, 42, 8748-8755.	2.5	56
118	Kinetic Framework for Ligation by an Efficient RNA Ligase Ribozymeâ€. Biochemistry, 2000, 39, 3115-3123.	2.5	55
119	The biochemical basis for the cooperative action of microRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17764-17774.	7.1	53
120	New ligase-derived RNA polymerase ribozymes. Rna, 2005, 11, 1173-1180.	3.5	52
121	Early genome activation in <i>Drosophila</i> is extensive with an initial tendency for aborted transcripts and retained introns. Genome Research, 2019, 29, 1188-1197.	5.5	52
122	MicroRNA Clustering Assists Processing of Suboptimal MicroRNA Hairpins through the Action of the ERH Protein. Molecular Cell, 2020, 78, 289-302.e6.	9.7	48
123	<i>Candida albicans</i> Dicer (CaDcr1) is required for efficient ribosomal and spliceosomal RNA maturation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 523-528.	7.1	47
124	The influence of microRNAs and poly(A) tail length on endogenous mRNA–protein complexes. Genome Biology, 2017, 18, 211.	8.8	46
125	The three-dimensional architecture of the class I ligase ribozyme. Rna, 2004, 10, 176-184.	3.5	43
126	The structural basis of RNA-catalyzed RNA polymerization. Nature Structural and Molecular Biology, 2011, 18, 1036-1042.	8.2	41

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127	Metal Ion Requirements for Structure and Catalysis of an RNA Ligase Ribozymeâ€. Biochemistry, 2002, 41, 8103-8112.	2.5	38
128	A Seed Mismatch Enhances Argonaute2-Catalyzed Cleavage and Partially Rescues Severely Impaired Cleavage Found in Fish. Molecular Cell, 2017, 68, 1095-1107.e5.	9.7	35
129	MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs. Molecular Cell, 2020, 77, 775-785.e8.	9.7	33
130	Degradation of host translational machinery drives tRNA acquisition in viruses. Cell Systems, 2021, 12, 771-779.e5.	6.2	32
131	MicroRNA $3\hat{a}\in^2$ -compensatory pairing occurs through two binding modes, with affinity shaped by nucleotide identity and position. ELife, 2022, 11, .	6.0	26
132	Substrate 2′-Hydroxyl Groups Required for Ribozyme-Catalyzed Polymerization. Chemistry and Biology, 2003, 10, 799-806.	6.0	25
133	A class I ligase ribozyme with reduced Mg ²⁺ dependence: Selection, sequence analysis, and identification of functional tertiary interactions. Rna, 2009, 15, 2129-2146.	3.5	18
134	Recognition of Nucleoside Triphosphates during RNA-Catalyzed Primer Extensionâ€. Biochemistry, 2000, 39, 15556-15562.	2.5	17
135	Ago2 protects <i>Drosophila</i> siRNAs and microRNAs from target-directed degradation, even in the absence of 2′- <i>O</i> -methylation. Rna, 2021, 27, 710-724.	3.5	17
136	A ribozyme selected from variants of U6 snRNA promotes 2′,5′-branch formation. Rna, 2001, 7, 29-43.	3.5	16
137	Xrn1p acts at multiple steps in the budding-yeast RNAi pathway to enhance the efficiency of silencing. Nucleic Acids Research, 2020, 48, 7404-7420.	14.5	3
138	The interplay between translational efficiency, poly(A) tails, microRNAs, and neuronal activation. Rna, 2022, 28, 808-831.	3.5	2
139	Most Caenorhabditis elegans microRNAs are individually not essential for development or viability. PLoS Genetics, 2005, preprint, e215.	3.5	0