David P Bartel

List of Publications by Year
in descending order

139 papers	164,622 citations	2832 97 h-index	12272 138 g-index
156 all docs	156 docs citations	156 times ranked	112509 citing authors

#	Article	IF	Citations
1	MicroRNA 3â€²-compensatory pairing occurs through two binding modes, with affinity shaped by nucleotide identity and position. ELife, 2022, 11, .	2.8	26
2	The interplay between translational efficiency, poly(A) tails, microRNAs, and neuronal activation. Rna, 2022, 28, 808-831.	1.6	2
3	Ago2 protects <i>Drosophila</i> siRNAs and microRNAs from target-directed degradation, even in the absence of 2â€²-<i>O</i>-methylation. Rna, 2021, 27, 710-724.	1.6	17
4	The molecular basis of coupling between poly(A)-tail length and translational efficiency. ELife, 2021, 10, .	2.8	62
5	Degradation of host translational machinery drives tRNA acquisition in viruses. Cell Systems, 2021, 12, 771-779.e5.	2.9	32
6	MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs. Molecular Cell, 2020, 77, 775-785.e8.	4.5	33
7	The Dynamics of Cytoplasmic mRNA Metabolism. Molecular Cell, 2020, 77, 786-799.e10.	4.5	106
8	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.	3.3	53
9	Xrn1p acts at multiple steps in the budding-yeast RNAi pathway to enhance the efficiency of silencing. Nucleic Acids Research, 2020, 48, 7404-7420.	6.5	3
10	The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. Science, 2020, 370, .	6.0	138
11	MicroRNA Clustering Assists Processing of Suboptimal MicroRNA Hairpins through the Action of the ERH Protein. Molecular Cell, 2020, 78, 289-302.e6.	4.5	48
12	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.	2.4	52
13	Global analyses of the dynamics of mammalian microRNA metabolism. Genome Research, 2019, 29, 1777-1790.	2.4	89
14	The biochemical basis of microRNA targeting efficacy. Science, 2019, 366, .	6.0	631
15	Excised linear introns regulate growth in yeast. Nature, 2019, 565, 606-611.	13.7	118
16	New CRISPR Mutagenesis Strategies Reveal Variation in Repair Mechanisms among Fungi. MSphere, 2018, 3, .	1.3	87
17	Metazoan MicroRNAs. Cell, 2018, 173, 20-51.	13.5	2,775
18	Genetic dissection of the miR-200â€“Zeb1 axis reveals its importance in tumor differentiation and invasion. Nature Communications, 2018, 9, 4671.	5.8	111

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19	Predicting microRNA targeting efficacy in Drosophila. Genome Biology, 2018, 19, 152.	3.8	91
20	A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain. Cell, 2018, 174, 350-362.e17.	13.5	485
21	Widespread Influence of 3â€²-End Structures on Mammalian mRNA Processing and Stability. Cell, 2017, 169, 905-917.e11.	13.5	123
22	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. Nucleic Acids Research, 2017, 45, W534-W538.	6.5	91
23	A Seed Mismatch Enhances Argonaute2-Catalyzed Cleavage and Partially Rescues Severely Impaired Cleavage Found in Fish. Molecular Cell, 2017, 68, 1095-1107.e5.	4.5	35
24	The influence of microRNAs and poly(A) tail length on endogenous mRNAâ€"protein complexes. Genome Biology, 2017, 18, 211.	3.8	46
25	RNA G-quadruplexes are globally unfolded in eukaryotic cells and depleted in bacteria. Science, 2016, 353, .	6.0	375
26	Impact of MicroRNA Levels, Target-Site Complementarity, and Cooperativity on Competing Endogenous RNA-Regulated Gene Expression. Molecular Cell, 2016, 64, 565-579.	4.5	300
27	Improved Ribosome-Footprint and mRNA Measurements Provide Insights into Dynamics and Regulation of Yeast Translation. Cell Reports, 2016, 14, 1787-1799.	2.9	330
28	mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos. ELife, 2016, 5, .	2.8	132
29	Predicting effective microRNA target sites in mammalian mRNAs. ELife, 2015, 4, .	2.8	5,779
30	Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. Nucleic Acids Research, 2015, 43, 5052-5064.	6.5	73
31	Principles of Long Noncoding RNA Evolution Derived from Direct Comparison of Transcriptomes in 17 Species. Cell Reports, 2015, 11, 1110-1122.	2.9	565
32	The Menu of Features that Define Primary MicroRNAs and Enable De Novo Design of MicroRNA Genes. Molecular Cell, 2015, 60, 131-145.	4.5	172
33	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.	3.3	60
34	Global Analyses of the Effect of Different Cellular Contexts on MicroRNA Targeting. Molecular Cell, 2014, 53, 1031-1043.	4.5	276
35	Assessing the ceRNA Hypothesis with Quantitative Measurements of miRNA and Target Abundance. Molecular Cell, 2014, 54, 766-776.	4.5	579
36	Poly(A)-tail profiling reveals an embryonic switch in translational control. Nature, 2014, 508, 66-71.	13.7	542

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37	Expanded identification and characterization of mammalian circular RNAs. Genome Biology, 2014, 15, 409.	3.8	1,361
38	mRNA Destabilization Is the Dominant Effect of Mammalian MicroRNAs by the Time Substantial Repression Ensues. Molecular Cell, 2014, 56, 104-115.	4.5	424
39	Widespread Changes in the Posttranscriptional Landscape at the Drosophila Oocyte-to-Embryo Transition. Cell Reports, 2014, 7, 1495-1508.	2.9	114
40	Beyond Secondary Structure: Primary-Sequence Determinants License Pri-miRNA Hairpins for Processing. Cell, 2013, 152, 844-858.	13.5	373
41	Stalled Spliceosomes Are a Signal for RNAi-Mediated Genome Defense. Cell, 2013, 152, 957-968.	13.5	173
42	lincRNAs: Genomics, Evolution, and Mechanisms. Cell, 2013, 154, 26-46.	13.5	2,337
43	3â€² UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. Genome Research, 2013, 23, 2078-2090.	2.4	186
44	Extensive alternative polyadenylation during zebrafish development. Genome Research, 2012, 22, 2054-2066.	2.4	305
45	<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.	3.3	47
46	Structure of yeast Argonaute with guide RNA. Nature, 2012, 486, 368-374.	13.7	314
47	The structural basis of RNA-catalyzed RNA polymerization. Nature Structural and Molecular Biology, 2011, 18, 1036-1042.	3.6	41
48	The Inside-Out Mechanism of Dicers from Budding Yeasts. Cell, 2011, 146, 262-276.	13.5	59
49	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. Cell, 2011, 147, 1537-1550.	13.5	1,072
50	Compatibility with Killer Explains the Rise of RNAi-Deficient Fungi. Science, 2011, 333, 1592-1592.	6.0	194
51	MicroRNA Destabilization Enables Dynamic Regulation of the miR-16 Family in Response to Cell-Cycle Changes. Molecular Cell, 2011, 43, 993-1004.	4.5	171
52	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.	3.6	803
53	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. Nature Structural and Molecular Biology, 2011, 18, 100-106.	3.6	75
54	Formation, regulation and evolution of Caenorhabditis elegans 3â€²UTRs. Nature, 2011, 469, 97-101.	13.7	432

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55	Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. Genome Research, 2011, 21, 1395-1403.	2.4	123
56	Mammalian microRNAs predominantly act to decrease target mRNA levels. Nature, 2010, 466, 835-840.	13.7	3,513
57	MicroRNAs prevent precocious gene expression and enable pattern formation during plant embryogenesis. Genes and Development, 2010, 24, 2678-2692.	2.7	322
58	Mammalian microRNAs: experimental evaluation of novel and previously annotated genes. Genes and Development, 2010, 24, 992-1009.	2.7	706
59	Expanding the MicroRNA Targeting Code: Functional Sites with Centered Pairing. Molecular Cell, 2010, 38, 789-802.	4.5	534
60	Most mammalian mRNAs are conserved targets of microRNAs. Genome Research, 2009, 19, 92-105.	2.4	7,226
61	A class I ligase ribozyme with reduced Mg²⁺ dependence: Selection, sequence analysis, and identification of functional tertiary interactions. Rna, 2009, 15, 2129-2146.	1.6	18
62	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.	3.3	80
63	Coherent but overlapping expression of microRNAs and their targets during vertebrate development. Genes and Development, 2009, 23, 466-481.	2.7	98
64	MicroRNAs: Target Recognition and Regulatory Functions. Cell, 2009, 136, 215-233.	13.5	17,802
65	Widespread Shortening of 3â€²UTRs by Alternative Cleavage and Polyadenylation Activates Oncogenes in Cancer Cells. Cell, 2009, 138, 673-684.	13.5	1,427
66	Crystal Structure of the Catalytic Core of an RNA-Polymerase Ribozyme. Science, 2009, 326, 1271-1275.	6.0	120
67	Allelic imbalance sequencing reveals that single-nucleotide polymorphisms frequently alter microRNA-directed repression. Nature Biotechnology, 2009, 27, 472-477.	9.4	60
68	RNAi in Budding Yeast. Science, 2009, 326, 544-550.	6.0	480
69	Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. Genes and Development, 2008, 22, 2773-2785.	2.7	739
70	The impact of microRNAs on protein output. Nature, 2008, 455, 64-71.	13.7	3,270
71	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. Nature, 2008, 455, 1193-1197.	13.7	630
72	TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the Schizosaccharomyces pombe siRNA pathway. Nature Structural and Molecular Biology, 2008, 15, 1015-1023.	3.6	173

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73	Endogenous siRNA and miRNA Targets Identified by Sequencing of the Arabidopsis Degradome. Current Biology, 2008, 18, 758-762.	1.8	749
74	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. Cell, 2008, 134, 521-533.	13.5	1,332
75	MicroRNAs in the Hox network: an apparent link to posterior prevalence. Nature Reviews Genetics, 2008, 9, 789-796.	7.7	167
76	A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. Genes and Development, 2008, 22, 8-13.	2.7	205
77	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.	3.3	562
78	Common Functions for Diverse Small RNAs of Land Plants. Plant Cell, 2007, 19, 1750-1769.	3.1	387
79	Most Caenorhabditis elegans microRNAs Are Individually Not Essential for Development or Viability. PLoS Genetics, 2007, 3, e215.	1.5	412
80	MicroRNA Targeting Specificity in Mammals: Determinants beyond Seed Pairing. Molecular Cell, 2007, 27, 91-105.	4.5	3,386
81	Disrupting the Pairing Between let-7 and Hmga2 Enhances Oncogenic Transformation. Science, 2007, 315, 1576-1579.	6.0	1,060
82	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of <i>Drosophila</i> microRNAs. Genome Research, 2007, 17, 1850-1864.	2.4	540
83	Intronic microRNA precursors that bypass Drosha processing. Nature, 2007, 448, 83-86.	13.7	1,365
84	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573
85	A diverse and evolutionarily fluid set of microRNAs in Arabidopsis thaliana. Genes and Development, 2006, 20, 3407-3425.	2.7	1,208
86	A Two-Hit Trigger for siRNA Biogenesis in Plants. Cell, 2006, 127, 565-577.	13.5	599
87	Large-Scale Sequencing Reveals 21U-RNAs and Additional MicroRNAs and Endogenous siRNAs in C. elegans. Cell, 2006, 127, 1193-1207.	13.5	892
88	AGO1 Homeostasis Entails Coexpression of MIR168 and AGO1 and Preferential Stabilization of miR168 by AGO1. Molecular Cell, 2006, 22, 129-136.	4.5	330
89	MicroRNAs AND THEIR REGULATORY ROLES IN PLANTS. Annual Review of Plant Biology, 2006, 57, 19-53.	8.6	2,418
90	Antiquity of MicroRNAs and Their Targets in Land Plants. Plant Cell, 2005, 17, 1658-1673.	3.1	522

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91	The Widespread Impact of Mammalian MicroRNAs on mRNA Repression and Evolution. Science, 2005, 310, 1817-1821.	6.0	1,382
92	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. Nature, 2005, 433, 769-773.	13.7	4,435
93	The microRNA miR-196 acts upstream of Hoxb8 and Shh in limb development. Nature, 2005, 438, 671-674.	13.7	365
94	Partially Redundant Functions of Arabidopsis DICER-like Enzymes and a Role for DCL4 in Producing trans-Acting siRNAs. Current Biology, 2005, 15, 1494-1500.	1.8	545
95	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.	3.1	805
96	New ligase-derived RNA polymerase ribozymes. Rna, 2005, 11, 1173-1180.	1.6	52
97	Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes. Rna, 2005, 11, 241-247.	1.6	1,253
98	MicroRNAs Regulate Brain Morphogenesis in Zebrafish. Science, 2005, 308, 833-838.	6.0	1,209
99	Conserved Seed Pairing, Often Flanked by Adenosines, Indicates that Thousands of Human Genes are MicroRNA Targets. Cell, 2005, 120, 15-20.	13.5	10,880
100	Passenger-Strand Cleavage Facilitates Assembly of siRNA into Ago2-Containing RNAi Enzyme Complexes. Cell, 2005, 123, 607-620.	13.5	991
101	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.	3.1	456
102	Regulatory Mutations of mir-48, a C. elegans let-7 Family MicroRNA, Cause Developmental Timing Defects. Developmental Cell, 2005, 9, 415-422.	3.1	92
103	Most Caenorhabditis elegans microRNAs are individually not essential for development or viability. PLoS Genetics, 2005, preprint, e215.	1.5	0
104	Patterns of flanking sequence conservation and a characteristic upstream motif for microRNA gene identification. Rna, 2004, 10, 1309-1322.	1.6	160
105	The three-dimensional architecture of the class I ligase ribozyme. Rna, 2004, 10, 176-184.	1.6	43
106	Micromanagers of gene expression: the potentially widespread influence of metazoan microRNAs. Nature Reviews Genetics, 2004, 5, 396-400.	7.7	1,289
107	MicroRNA control of PHABULOSA in leaf development: importance of pairing to the microRNA 5â€² region. EMBO Journal, 2004, 23, 3356-3364.	3.5	630
108	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.	1.8	617

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109	MicroRNAs Modulate Hematopoietic Lineage Differentiation. Science, 2004, 303, 83-86.	6.0	3,025
110	MicroRNA-Directed Cleavage of HOXB8 mRNA. Science, 2004, 304, 594-596.	6.0	1,596
111	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.	2.7	868
112	Computational Identification of Plant MicroRNAs and Their Targets, Including a Stress-Induced miRNA. Molecular Cell, 2004, 14, 787-799.	4.5	2,097
113	Endogenous trans-Acting siRNAs Regulate the Accumulation of Arabidopsis mRNAs. Molecular Cell, 2004, 16, 69-79.	4.5	742
114	MicroRNAs. Cell, 2004, 116, 281-297.	13.5	32,446
115	Substrate 2â€²-Hydroxyl Groups Required for Ribozyme-Catalyzed Polymerization. Chemistry and Biology, 2003, 10, 799-806.	6.2	25
116	Vertebrate MicroRNA Genes. Science, 2003, 299, 1540-1540.	6.0	1,035
117	A biochemical framework for RNA silencing in plants. Genes and Development, 2003, 17, 49-63.	2.7	832
118	Processivity of Ribozyme-Catalyzed RNA Polymerizationâ€. Biochemistry, 2003, 42, 8748-8755.	1.2	56
119	A uniform system for microRNA annotation. Rna, 2003, 9, 277-279.	1.6	1,620
120	Prediction of Mammalian MicroRNA Targets. Cell, 2003, 115, 787-798.	13.5	4,682
121	MicroRNAs: At the Root of Plant Development?. Plant Physiology, 2003, 132, 709-717.	2.3	389
122	The microRNAs of Caenorhabditis elegans. Genes and Development, 2003, 17, 991-1008.	2.7	1,081
123	MicroRNAs in plants. Genes and Development, 2002, 16, 1616-1626.	2.7	1,797
124	Metal Ion Requirements for Structure and Catalysis of an RNA Ligase Ribozymeâ€. Biochemistry, 2002, 41, 8103-8112.	1.2	38
125	Prediction of Plant MicroRNA Targets. Cell, 2002, 110, 513-520.	13.5	2,088
126	Small RNAs Correspond to Centromere Heterochromatic Repeats. Science, 2002, 297, 1831-1831.	6.0	423

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127	RNA-Catalyzed RNA Polymerization: Accurate and General RNA-Templated Primer Extension. Science, 2001, 292, 1319-1325.	6.0	680
128	A ribozyme selected from variants of U6 snRNA promotes 2â€²,5â€²-branch formation. Rna, 2001, 7, 29-43.	1.6	16
129	The hammerhead cleavage reaction in monovalent cations. Rna, 2001, 7, 546-552.	1.6	127
130	An Abundant Class of Tiny RNAs with Probable Regulatory Roles in Caenorhabditis elegans. Science, 2001, 294, 858-862.	6.0	3,041
131	RNAi. Cell, 2000, 101, 25-33.	13.5	2,421
132	One Sequence, Two Ribozymes: Implications for the Emergence of New Ribozyme Folds. Science, 2000, 289, 448-452.	6.0	340
133	Kinetic Framework for Ligation by an Efficient RNA Ligase Ribozymeâ€. Biochemistry, 2000, 39, 3115-3123.	1.2	55
134	Recognition of Nucleoside Triphosphates during RNA-Catalyzed Primer Extensionâ€. Biochemistry, 2000, 39, 15556-15562.	1.2	17
135	The PUMILIOâ ̂'RNA Interaction:â€‰ A Single RNA-Binding Domain Monomer Recognizes a Bipartite Target Sequence. Biochemistry, 1999, 38, 596-604.	1.2	86
136	RNA-catalysed nucleotide synthesis. Nature, 1998, 395, 260-263.	13.7	280
137	RNA-catalysed RNA polymerization using nucleoside triphosphates. Nature, 1996, 382, 373-376.	13.7	242
138	The secondary structure and sequence optimization of an RNA ligase ribozyme. Nucleic Acids Research, 1995, 23, 3231-3238.	6.5	123
139	Reverse transcriptase reads through a 2â€²â€“5â€² linkage and a 2â€²-thiphosphate in a template. Nucleic Acids Research, 1995, 23, 2811-2814.	6.5	70