David P Bartel

List of Publications by Year in Descending Order

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	MicroRNA 3′ compensatory pairing occurs through two binding modes, with affinity shaped by nucleotide identity and position.. *ELife*, **2022**, 11,	8.9	4
146	Ago2 protects siRNAs and microRNAs from target-directed degradation, even in the absence of 2′-methylation. *Rna*, **2021**, 27, 710-724	5.8	2
145	The molecular basis of coupling between poly(A)-tail length and translational efficiency. *ELife*, **2021**, 10,	8.9	9
144	Degradation of host translational machinery drives tRNA acquisition in viruses. *Cell Systems*, **2021**, 12, 771-779.e5	10.6	6
143	MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs. *Molecular Cell*, **2020**, 77, 775-785.e8	17.6	15
142	The Dynamics of Cytoplasmic mRNA Metabolism. *Molecular Cell*, **2020**, 77, 786-799.e10	17.6	33
141	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	11.5	23
140	Xrn1p acts at multiple steps in the budding-yeast RNAi pathway to enhance the efficiency of silencing. *Nucleic Acids Research*, **2020**, 48, 7404-7420	20.1	3
139	The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. *Science*, **2020**, 370,	33.3	47
138	MicroRNA Clustering Assists Processing of Suboptimal MicroRNA Hairpins through the Action of the ERH Protein. *Molecular Cell*, **2020**, 78, 289-302.e6	17.6	15
137	Global analyses of the dynamics of mammalian microRNA metabolism. *Genome Research*, **2019**, 29, 1777-1790	9.1	34
136	Early genome activation in is extensive with an initial tendency for aborted transcripts and retained introns. *Genome Research*, **2019**, 29, 1188-1197	9.7	19
135	The biochemical basis of microRNA targeting efficacy. *Science*, **2019**, 366,	33.3	160
134	Excised linear introns regulate growth in yeast. *Nature*, **2019**, 565, 606-611	50.4	62
133	New CRISPR Mutagenesis Strategies Reveal Variation in Repair Mechanisms among Fungi. *MSphere*, **2018**, 3,	5	44
132	Metazoan MicroRNAs. *Cell*, **2018**, 173, 20-51	56.2	1506
131	A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain. *Cell*, **2018**, 174, 350-362.e17	56.2	309

130	Genetic dissection of the miR-200-Zeb1 axis reveals its importance in tumor differentiation and invasion. *Nature Communications*, **2018**, 9, 4671	17.4	57
129	Predicting microRNA targeting efficacy in Drosophila. *Genome Biology*, **2018**, 19, 152	18.3	41
128	Widespread Influence of 3′UEnd Structures on Mammalian mRNA Processing and Stability. *Cell*, **2017**, 169, 905-917.e11	56.2	69
127	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. *Nucleic Acids Research*, **2017**, 45, W534-W538	20.1	47
126	The influence of microRNAs and poly(A) tail length on endogenous mRNA-protein complexes. *Genome Biology*, **2017**, 18, 211	18.3	28
125	A Seed Mismatch Enhances Argonaute2-Catalyzed Cleavage and Partially Rescues Severely Impaired Cleavage Found in Fish. *Molecular Cell*, **2017**, 68, 1095-1107.e5	17.6	17
124	Impact of MicroRNA Levels, Target-Site Complementarity, and Cooperativity on Competing Endogenous RNA-Regulated Gene Expression. *Molecular Cell*, **2016**, 64, 565-579	17.6	207
123	Improved Ribosome-Footprint and mRNA Measurements Provide Insights into Dynamics and Regulation of Yeast Translation. *Cell Reports*, **2016**, 14, 1787-1799	10.6	237
122	mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos. *ELife*, **2016**, 5,	8.9	86
121	Author response: mRNA poly(A)-tail changes specified by deadenylation broadly reshape translation in Drosophila oocytes and early embryos **2016**,		2
120	RNA G-quadruplexes are globally unfolded in eukaryotic cells and depleted in bacteria. *Science*, **2016**, 353,	33.3	247
119	Principles of long noncoding RNA evolution derived from direct comparison of transcriptomes in 17 species. *Cell Reports*, **2015**, 11, 1110-22	10.6	377
118	The Menu of Features that Define Primary MicroRNAs and Enable De Novo Design of MicroRNA Genes. *Molecular Cell*, **2015**, 60, 131-45	17.6	111
117	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	11.5	40
116	Predicting effective microRNA target sites in mammalian mRNAs. *ELife*, **2015**, 4,	8.9	3825
115	Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. *Nucleic Acids Research*, **2015**, 43, 5052-64	20.1	62
114	Author response: Predicting effective microRNA target sites in mammalian mRNAs **2015**,		44
113	Global analyses of the effect of different cellular contexts on microRNA targeting. *Molecular Cell*, **2014**, 53, 1031-1043	17.6	205

112	Assessing the ceRNA hypothesis with quantitative measurements of miRNA and target abundance. *Molecular Cell*, **2014**, 54, 766-76	17.6	451
111	Poly(A)-tail profiling reveals an embryonic switch in translational control. *Nature*, **2014**, 508, 66-71	50.4	397
110	Expanded identification and characterization of mammalian circular RNAs. *Genome Biology*, **2014**, 15, 409	18.3	1039
109	mRNA destabilization is the dominant effect of mammalian microRNAs by the time substantial repression ensues. *Molecular Cell*, **2014**, 56, 104-15	17.6	317
108	Widespread changes in the posttranscriptional landscape at the Drosophila oocyte-to-embryo transition. *Cell Reports*, **2014**, 7, 1495-1508	10.6	81
107	Beyond secondary structure: primary-sequence determinants license pri-miRNA hairpins for processing. *Cell*, **2013**, 152, 844-58	56.2	281
106	Stalled spliceosomes are a signal for RNAi-mediated genome defense. *Cell*, **2013**, 152, 957-68	56.2	124
105	lincRNAs: genomics, evolution, and mechanisms. *Cell*, **2013**, 154, 26-46	56.2	1841
104	3UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. *Genome Research*, **2013**, 23, 2078-90	9.7	123
103	Structure of yeast Argonaute with guide RNA. *Nature*, **2012**, 486, 368-74	50.4	226
102	Extensive alternative polyadenylation during zebrafish development. *Genome Research*, **2012**, 22, 2054-66	9.7	220
101	Candida albicans 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, 523-8	11.5	43
100	The structural basis of RNA-catalyzed RNA polymerization. *Nature Structural and Molecular Biology*, **2011**, 18, 1036-42	17.6	32
99	The inside-out mechanism of Dicers from budding yeasts. *Cell*, **2011**, 146, 262-76	56.2	57
98	Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. *Cell*, **2011**, 147, 1537-50	56.2	882
97	Compatibility with killer explains the rise of RNAi-deficient fungi. *Science*, **2011**, 333, 1592	33.3	164
96	MicroRNA destabilization enables dynamic regulation of the miR-16 family in response to cell-cycle changes. *Molecular Cell*, **2011**, 43, 993-1004	17.6	141
95	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, 1139-46	17.6	701

94	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. *Nature Structural and Molecular Biology*, **2011**, 18, 100-6	17.6	56
93	Formation, regulation and evolution of Caenorhabditis elegans 3ΨTRs. *Nature*, **2011**, 469, 97-101	50.4	353
92	Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. *Genome Research*, **2011**, 21, 1395-403	9.7	102
91	Mammalian microRNAs predominantly act to decrease target mRNA levels. *Nature*, **2010**, 466, 835-40	50.4	3074
90	MicroRNAs prevent precocious gene expression and enable pattern formation during plant embryogenesis. *Genes and Development*, **2010**, 24, 2678-92	12.6	266
89	Mammalian microRNAs: experimental evaluation of novel and previously annotated genes. *Genes and Development*, **2010**, 24, 992-1009	12.6	610
88	Expanding the microRNA targeting code: functional sites with centered pairing. *Molecular Cell*, **2010**, 38, 789-802	17.6	466
87	A class I ligase ribozyme with reduced Mg2+ dependence: Selection, sequence analysis, and identification of functional tertiary interactions. *Rna*, **2009**, 15, 2129-46	5.8	17
86	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, 18610-5	11.5	74
85	Coherent but overlapping expression of microRNAs and their targets during vertebrate development. *Genes and Development*, **2009**, 23, 466-81	12.6	89
84	MicroRNAs: target recognition and regulatory functions. *Cell*, **2009**, 136, 215-33	56.2	15104
83	Widespread shortening of 3ΨTRs by alternative cleavage and polyadenylation activates oncogenes in cancer cells. *Cell*, **2009**, 138, 673-84	56.2	1129
82	Crystal structure of the catalytic core of an RNA-polymerase ribozyme. *Science*, **2009**, 326, 1271-5	33.3	95
81	Allelic imbalance sequencing reveals that single-nucleotide polymorphisms frequently alter microRNA-directed repression. *Nature Biotechnology*, **2009**, 27, 472-7	44.5	57
80	RNAi in budding yeast. *Science*, **2009**, 326, 544-550	33.3	398
79	Most mammalian mRNAs are conserved targets of microRNAs. *Genome Research*, **2009**, 19, 92-105	9.7	5919
78	The impact of microRNAs on protein output. *Nature*, **2008**, 455, 64-71	50.4	2911
77	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. *Nature*, **2008**, 455, 1193-7	50.4	522

76	TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the Schizosaccharomyces pombe siRNA pathway. *Nature Structural and Molecular Biology*, **2008**, 15, 1015-23	17.6	151
75	Endogenous siRNA and miRNA targets identified by sequencing of the Arabidopsis degradome. *Current Biology*, **2008**, 18, 758-762	6.3	597
74	Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. *Cell*, **2008**, 134, 521-33	56.2	1228
73	MicroRNAs in the Hox network: an apparent link to posterior prevalence. *Nature Reviews Genetics*, **2008**, 9, 789-96	30.1	151
72	A single Hox locus in Drosophila produces functional microRNAs from opposite DNA strands. *Genes and Development*, **2008**, 22, 8-13	12.6	188
71	Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. *Genes and Development*, **2008**, 22, 2773-85	12.6	606
70	Intronic microRNA precursors that bypass Drosha processing. *Nature*, **2007**, 448, 83-6	50.4	1138
69	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. *Nature*, **2007**, 450, 219-32	50.4	506
68	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, 7080-5	11.5	505
67	Common functions for diverse small RNAs of land plants. *Plant Cell*, **2007**, 19, 1750-69	11.6	340
66	Most Caenorhabditis elegans microRNAs are individually not essential for development or viability. *PLoS Genetics*, **2007**, 3, e215	6	368
65	MicroRNA targeting specificity in mammals: determinants beyond seed pairing. *Molecular Cell*, **2007**, 27, 91-105	17.6	2989
64	Disrupting the pairing between let-7 and Hmga2 enhances oncogenic transformation. *Science*, **2007** , 315, 1576-9	33.3	960
63	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of Drosophila microRNAs. *Genome Research*, **2007**, 17, 1850-64	9.7	462
62	A diverse and evolutionarily fluid set of microRNAs in Arabidopsis thaliana. *Genes and Development*, **2006**, 20, 3407-25	12.6	1058
61	A two-hit trigger for siRNA biogenesis in plants. *Cell*, **2006**, 127, 565-77	56.2	517
60	Large-scale sequencing reveals 21U-RNAs and additional microRNAs and endogenous siRNAs in C. elegans. *Cell*, **2006**, 127, 1193-207	56.2	774
59	AGO1 homeostasis entails coexpression of MIR168 and AGO1 and preferential stabilization of miR168 by AGO1. *Molecular Cell*, **2006**, 22, 129-36	17.6	272

58	MicroRNAS and their regulatory roles in plants. *Annual Review of Plant Biology*, **2006**, 57, 19-53	30.7	2102
57	MicroRNAs regulate brain morphogenesis in zebrafish. *Science*, **2005**, 308, 833-8	33.3	1080
56	Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell*, **2005**, 120, 15-20	56.2	9564
55	Passenger-strand cleavage facilitates assembly of siRNA into Ago2-containing RNAi enzyme complexes. *Cell*, **2005**, 123, 607-20	56.2	880
54	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, 403-14	10.2	379
53	Regulatory mutations of mir-48, a C. elegans let-7 family MicroRNA, cause developmental timing defects. *Developmental Cell*, **2005**, 9, 415-22	10.2	84
52	Antiquity of microRNAs and their targets in land plants. *Plant Cell*, **2005**, 17, 1658-73	11.6	461
51	The widespread impact of mammalian MicroRNAs on mRNA repression and evolution. *Science*, **2005**, 310, 1817-21	33.3	1249
50	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. *Nature*, **2005**, 433, 769-73	50.4	3967
49	The microRNA miR-196 acts upstream of Hoxb8 and Shh in limb development. *Nature*, **2005**, 438, 671-4	50.4	343
48	Partially redundant functions of Arabidopsis DICER-like enzymes and a role for DCL4 in producing trans-acting siRNAs. *Current Biology*, **2005**, 15, 1494-500	6.3	480
47	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, 1360-75	11.6	682
46	New ligase-derived RNA polymerase ribozymes. *Rna*, **2005**, 11, 1173-80	5.8	43
45	Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes. *Rna*, **2005**, 11, 241-7	5.8	1109
44	Most Caenorhabditis elegans microRNAs are individually not essential for development or viability. *PLoS Genetics*, **2005**, preprint, e215	6	
43	Patterns of flanking sequence conservation and a characteristic upstream motif for microRNA gene identification. *Rna*, **2004**, 10, 1309-22	5.8	138
42	The three-dimensional architecture of the class I ligase ribozyme. *Rna*, **2004**, 10, 176-84	5.8	36
41	Micromanagers of gene expression: the potentially widespread influence of metazoan microRNAs. *Nature Reviews Genetics*, **2004**, 5, 396-400	30.1	1141

40	MicroRNA control of PHABULOSA in leaf development: importance of pairing to the microRNA 5U region. *EMBO Journal*, **2004**, 23, 3356-64	13	538
39	MicroRNA regulation of NAC-domain targets is required for proper formation and separation of adjacent embryonic, vegetative, and floral organs. *Current Biology*, **2004**, 14, 1035-46	6.3	540
38	MicroRNAs modulate hematopoietic lineage differentiation. *Science*, **2004**, 303, 83-6	33.3	2736
37	MicroRNA-directed cleavage of HOXB8 mRNA. *Science*, **2004**, 304, 594-6	33.3	1428
36	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, 1187-97	12.6	719
35	Computational identification of plant microRNAs and their targets, including a stress-induced miRNA. *Molecular Cell*, **2004**, 14, 787-99	17.6	1839
34	Endogenous trans-acting siRNAs regulate the accumulation of Arabidopsis mRNAs. *Molecular Cell*, **2004**, 16, 69-79	17.6	671
33	MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell*, **2004**, 116, 281-97	56.2	28094
32	The microRNAs of Caenorhabditis elegans. *Genes and Development*, **2003**, 17, 991-1008	12.6	926
31	Substrate 2Uhydroxyl groups required for ribozyme-catalyzed polymerization. *Chemistry and Biology*, **2003**, 10, 799-806		22
30	Vertebrate microRNA genes. *Science*, **2003**, 299, 1540	33.3	899
29	A biochemical framework for RNA silencing in plants. *Genes and Development*, **2003**, 17, 49-63	12.6	738
28	Processivity of ribozyme-catalyzed RNA polymerization. *Biochemistry*, **2003**, 42, 8748-55	3.2	49
27	A uniform system for microRNA annotation. *Rna*, **2003**, 9, 277-9	5.8	1332
26	Prediction of mammalian microRNA targets. *Cell*, **2003**, 115, 787-98	56.2	4144
25	MicroRNAs: at the root of plant development?. *Plant Physiology*, **2003**, 132, 709-17	6.6	354
24	MicroRNAs in plants. *Genes and Development*, **2002**, 16, 1616-26	12.6	1607
23	Metal ion requirements for structure and catalysis of an RNA ligase ribozyme. *Biochemistry*, **2002**, 41, 8103-12	3.2	34

22	Prediction of plant microRNA targets. *Cell*, **2002**, 110, 513-20	56.2	1809
21	Small RNAs correspond to centromere heterochromatic repeats. *Science*, **2002**, 297, 1831	33.3	368
20	An abundant class of tiny RNAs with probable regulatory roles in Caenorhabditis elegans. *Science*, **2001**, 294, 858-62	33.3	2719
19	RNA-catalyzed RNA polymerization: accurate and general RNA-templated primer extension. *Science* , **2001**, 292, 1319-25	33.3	523
18	A ribozyme selected from variants of U6 snRNA promotes 2′,5′-branch formation. *Rna*, **2001**, 7, 29-43	5.8	16
17	The hammerhead cleavage reaction in monovalent cations. *Rna*, **2001**, 7, 546-52	5.8	118
16	RNAi: double-stranded RNA directs the ATP-dependent cleavage of mRNA at 21 to 23 nucleotide intervals. *Cell*, **2000**, 101, 25-33	56.2	2137
15	One sequence, two ribozymes: implications for the emergence of new ribozyme folds. *Science*, **2000**, 289, 448-52	33.3	296
14	Kinetic framework for ligation by an efficient RNA ligase ribozyme. *Biochemistry*, **2000**, 39, 3115-23	3.2	51
13	Recognition of nucleoside triphosphates during RNA-catalyzed primer extension. *Biochemistry*, **2000**, 39, 15556-62	3.2	16
12	The PUMILIO-RNA interaction: a single RNA-binding domain monomer recognizes a bipartite target sequence. *Biochemistry*, **1999**, 38, 596-604	3.2	78
11	RNA-catalysed nucleotide synthesis. *Nature*, **1998**, 395, 260-3	50.4	237
10	RNA-catalysed RNA polymerization using nucleoside triphosphates. *Nature*, **1996**, 382, 373-6	50.4	197
9	The secondary structure and sequence optimization of an RNA ligase ribozyme. *Nucleic Acids Research*, **1995**, 23, 3231-8	20.1	111
8	Reverse transcriptase reads through a 2′-5′ linkage and a 2′-thiophosphate in a template. *Nucleic Acids Research*, **1995**, 23, 2811-4	20.1	65
7	Xrn1p Acts at Multiple Steps in the Budding-Yeast RNAi Pathway to Enhance the Efficiency of Silencing		1
6	A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain		1
5	The biochemical basis of microRNA targeting efficacy		3

4	MicroRNAs Cause Accelerated Decay of Short-Tailed Target mRNAs	2
3	The Dynamics of Cytoplasmic mRNA Metabolism	3
2	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences	1
1	Pairing to the microRNA 3? region occurs through two alternative binding modes, with affinity shaped by nucleotide identity as well as pairing position	1