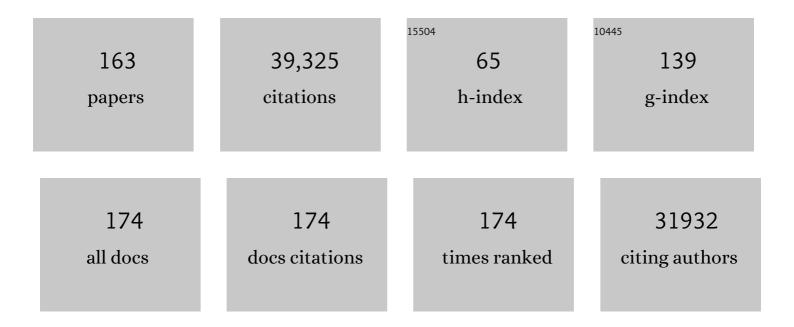
## Andrew Z Fire

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Potent and specific genetic interference by double-stranded RNA in Caenorhabditis elegans. Nature, 1998, 391, 806-811.	27.8	13,137
2	Genes and Mechanisms Related to RNA Interference Regulate Expression of the Small Temporal RNAs that Control C. elegans Developmental Timing. Cell, 2001, 106, 23-34.	28.9	1,731
3	Specific interference by ingested dsRNA. Nature, 1998, 395, 854-854.	27.8	1,655
4	Ingestion of bacterially expressed dsRNAs can produce specific and potent genetic interference in Caenorhabditis elegans. Gene, 2001, 263, 103-112.	2.2	1,605
5	The rde-1 Gene, RNA Interference, and Transposon Silencing in C. elegans. Cell, 1999, 99, 123-132.	28.9	1,180
6	On the Role of RNA Amplification in dsRNA-Triggered Gene Silencing. Cell, 2001, 107, 465-476.	28.9	1,172
7	Chapter 19 DNA Transformation. Methods in Cell Biology, 1995, , 451-482.	1.1	1,063
8	Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. Nature, 2013, 496, 469-476.	27.8	961
9	Efficient Marker-Free Recovery of Custom Genetic Modifications with CRISPR/Cas9 in <i>Caenorhabditis elegans</i> . Genetics, 2014, 198, 837-846.	2.9	738
10	A modular set of lacZ fusion vectors for studying gene expression in Caenorhabditis elegans. Gene, 1990, 93, 189-198.	2.2	620
11	Human tRNA-derived small RNAs in the global regulation of RNA silencing. Rna, 2010, 16, 673-695.	3.5	583
12	Determinants of nucleosome organization in primary human cells. Nature, 2011, 474, 516-520.	27.8	567
13	RNA-triggered gene silencing. Trends in Genetics, 1999, 15, 358-363.	6.7	565
14	Distinct Populations of Primary and Secondary Effectors During RNAi in C. elegans. Science, 2007, 315, 241-244.	12.6	530
15	Loss of the Putative RNA-Directed RNA Polymerase RRF-3 Makes C. elegans Hypersensitive to RNAi. Current Biology, 2002, 12, 1317-1319.	3.9	529
16	A high-resolution, nucleosome position map of <i>C. elegans</i> reveals a lack of universal sequence-dictated positioning. Genome Research, 2008, 18, 1051-1063.	5.5	503
17	A nuclear Argonaute promotes multigenerational epigenetic inheritance and germline immortality. Nature, 2012, 489, 447-451.	27.8	450
18	Distinct Requirements for Somatic and Germline Expression of a Generally Expressed <i>Caernorhabditis elegans</i> Gene. Genetics, 1997, 146, 227-238.	2.9	444

#	Article	IF	CITATIONS
19	Patterns of Known and Novel Small RNAs in Human Cervical Cancer. Cancer Research, 2007, 67, 6031-6043.	0.9	416
20	Functional Anatomy of a dsRNA Trigger. Molecular Cell, 2000, 6, 1077-1087.	9.7	391
21	Integrative transformation of <i>Caenorhabditis elegans</i> . EMBO Journal, 1986, 5, 2673-2680.	7.8	383
22	Essential Roles for <i>Caenorhabditis elegans</i> Lamin Gene in Nuclear Organization, Cell Cycle Progression, and Spatial Organization of Nuclear Pore Complexes. Molecular Biology of the Cell, 2000, 11, 3937-3947.	2.1	378
23	Measurement and Clinical Monitoring of Human Lymphocyte Clonality by Massively Parallel V-D-J Pyrosequencing. Science Translational Medicine, 2009, 1, 12ra23.	12.4	372
24	[35] In Vitro transcription: Whole-cell extract. Methods in Enzymology, 1983, 101, 568-582.	1.0	309
25	A pyrosequencing-tailored nucleotide barcode design unveils opportunities for large-scale sample multiplexing. Nucleic Acids Research, 2007, 35, e130.	14.5	306
26	Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody. Cell, 2016, 165, 449-463.	28.9	305
27	<i>Caenorhabditis elegans</i> Levamisole Resistance Genes <i>lev-1</i> , <i>unc-29</i> , and <i>unc-38</i> Encode Functional Nicotinic Acetylcholine Receptor Subunits. Journal of Neuroscience, 1997, 17, 5843-5857.	3.6	301
28	Repression of gene expression in the embryonic germ lineage of C. elegans. Nature, 1996, 382, 713-716.	27.8	299
29	Convergent Antibody Signatures in Human Dengue. Cell Host and Microbe, 2013, 13, 691-700.	11.0	271
30	Individual Variation in the Germline Ig Gene Repertoire Inferred from Variable Region Gene Rearrangements. Journal of Immunology, 2010, 184, 6986-6992.	0.8	261
31	Human Responses to Influenza Vaccination Show Seroconversion Signatures and Convergent Antibody Rearrangements. Cell Host and Microbe, 2014, 16, 105-114.	11.0	246
32	Amplification of siRNA in Caenorhabditis elegans generates a transgenerational sequence-targeted histone H3 lysine 9 methylation footprint. Nature Genetics, 2012, 44, 157-164.	21.4	239
33	Six RNA Viruses and Forty-One Hosts: Viral Small RNAs and Modulation of Small RNA Repertoires in Vertebrate and Invertebrate Systems. PLoS Pathogens, 2010, 6, e1000764.	4.7	234
34	dsRNA-mediated gene silencing in cultured Drosophila cells: a tissue culture model for the analysis of RNA interference. Gene, 2000, 252, 95-105.	2.2	229
35	Double-stranded RNA as a mediator in sequence-specific genetic silencing and co-suppression. Trends in Genetics, 1998, 14, 255-258.	6.7	222
36	CeMyoD accumulation defines the body wall muscle cell fate during C. elegans embryogenesis. Cell, 1990, 63, 907-919.	28.9	211

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37	Initial antibodies binding to HIV-1 gp41 in acutely infected subjects are polyreactive and highly mutated. Journal of Experimental Medicine, 2011, 208, 2237-2249.	8.5	198
38	Distinct Phases of siRNA Synthesis in an Endogenous RNAi Pathway in C. elegans Soma. Molecular Cell, 2010, 37, 679-689.	9.7	177
39	Transmission Dynamics of Heritable Silencing Induced by Double-Stranded RNA in <i>Caenorhabditis elegans</i> . Genetics, 2008, 180, 1275-1288.	2.9	174
40	Direct CRISPR spacer acquisition from RNA by a natural reverse transcriptase–Cas1 fusion protein. Science, 2016, 351, aad4234.	12.6	170
41	Flexibility and constraint in the nucleosome core landscape of Caenorhabditis elegans chromatin. Genome Research, 2006, 16, 1505-1516.	5.5	169
42	Effects of Aging, Cytomegalovirus Infection, and EBV Infection on Human B Cell Repertoires. Journal of Immunology, 2014, 192, 603-611.	0.8	166
43	High-throughput VDJ sequencing for quantification of minimal residual disease in chronic lymphocytic leukemia and immune reconstitution assessment. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21194-21199.	7.1	160
44	Wobble base-pairing slows in vivo translation elongation in metazoans. Rna, 2011, 17, 2063-2073.	3.5	159
45	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270.	13.3	156
46	Ultra-high throughput sequencing-based small RNA discovery and discrete statistical biomarker analysis in a collection of cervical tumours and matched controls. BMC Biology, 2010, 8, 58.	3.8	148
47	Immunoglobulin Gene Insertions and Deletions in the Affinity Maturation of HIV-1 Broadly Reactive Neutralizing Antibodies. Cell Host and Microbe, 2014, 16, 304-313.	11.0	137
48	Inducible Systemic RNA Silencing in Caenorhabditis elegans. Molecular Biology of the Cell, 2003, 14, 2972-2983.	2.1	135
49	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. Science, 2009, 323, 401-404.	12.6	122
50	Gene Silencing by Doubleâ€ <del>S</del> tranded RNA (Nobel Lecture). Angewandte Chemie - International Edition, 2007, 46, 6966-6984.	13.8	112
51	Recompleting the <i>Caenorhabditis elegans</i> genome. Genome Research, 2019, 29, 1009-1022.	5.5	108
52	Minicircle DNA Vectors Achieve Sustained Expression Reflected by Active Chromatin and Transcriptional Level. Molecular Therapy, 2013, 21, 131-138.	8.2	103
53	The Inference of Phased Haplotypes for the Immunoglobulin H Chain V Region Gene Loci by Analysis of VDJ Gene Rearrangements. Journal of Immunology, 2012, 188, 1333-1340.	0.8	102
54	Rescue of polyglutamine-mediated cytotoxicity by double-stranded RNA-mediated RNA interference. Human Molecular Genetics, 2002, 11, 175-184.	2.9	100

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55	Elements Regulating Cell- and Stage-Specific Expression of the C. elegans MyoD Family Homolog hlh-1. Developmental Biology, 1994, 166, 133-148.	2.0	99
56	Recognition and Silencing of Repeated DNA. Annual Review of Genetics, 2000, 34, 187-204.	7.6	99
57	An Abundant Class of Non-coding DNA Can Prevent Stochastic Gene Silencing in the C.Âelegans Germline. Cell, 2016, 166, 343-357.	28.9	92
58	Translation readthrough mitigation. Nature, 2016, 534, 719-723.	27.8	90
59	Inhibition of transcription factor activity by poliovirus. Cell, 1981, 27, 555-561.	28.9	87
60	Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in <i>Caenorhabditis elegans</i> and <i>Homo sapiens</i> . G3: Genes, Genomes, Genetics, 2017, 7, 3295-3303.	1.8	87
61	Histochemical techniques for locating Escherichia coli β-galactosidase activity in transgenic organisms. Genetic Analysis, Techniques and Applications, 1992, 9, 151-158.	1.5	84
62	Type III CRISPR-Cas systems can provide redundancy to counteract viral escape from type I systems. ELife, 2017, 6, .	6.0	81
63	A <i>Caenorhabditis elegans</i> RNA-Directed RNA Polymerase in Sperm Development and Endogenous RNA Interference. Genetics, 2009, 183, 1297-1314.	2.9	80
64	EGO-1, a C.Âelegans RdRP, Modulates Gene Expression via Production of mRNA-Templated Short Antisense RNAs. Current Biology, 2011, 21, 449-459.	3.9	75
65	Competition between ADAR and RNAi pathways for an extensive class of RNA targets. Nature Structural and Molecular Biology, 2011, 18, 1094-1101.	8.2	73
66	Capped small RNAs and MOV10 in human hepatitis delta virus replication. Nature Structural and Molecular Biology, 2008, 15, 714-721.	8.2	72
67	Protection from Feed-Forward Amplification in an Amplified RNAi Mechanism. Cell, 2012, 151, 885-899.	28.9	70
68	Aberrant B cell repertoire selection associated with HIV neutralizing antibody breadth. Nature Immunology, 2020, 21, 199-209.	14.5	68
69	Chapter 14 Whole-Mount in Situ Hybridization for the Detection of RNA in Caenorhabditis elegans Embryos. Methods in Cell Biology, 1995, 48, 323-337.	1.1	65
70	Landscape of target:guide homology effects on Cas9-mediated cleavage. Nucleic Acids Research, 2014, 42, 13778-13787.	14.5	65
71	A Requirement for ERK-Dependent Dicer Phosphorylation in Coordinating Oocyte-to-Embryo Transition in C.Âelegans. Developmental Cell, 2014, 31, 614-628.	7.0	63
72	Distinct patterns of Cas9 mismatch tolerance <i>in vitro</i> and <i>in vivo</i> . Nucleic Acids Research, 2016, 44, 5365-5377.	14.5	62

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73	Unusual DNA Structures Associated With Germline Genetic Activity in Caenorhabditis elegans. Genetics, 2006, 173, 1259-1273.	2.9	61
74	The transcription start site landscape of <i>C. elegans</i> . Genome Research, 2013, 23, 1348-1361.	5.5	58
75	An antagonistic role for the C. elegans Schnurri homolog SMA-9 in modulating TGFÎ <sup>2</sup> signaling during mesodermal patterning. Development (Cambridge), 2006, 133, 2887-2896.	2.5	57
76	Contributions of mRNA abundance, ribosome loading, and post- or peri-translational effects to temporal repression of <i>C. elegans</i> heterochronic miRNA targets. Genome Research, 2012, 22, 2418-2426.	5.5	56
77	Up-Regulated Dicer Expression in Patients with Cutaneous Melanoma. PLoS ONE, 2011, 6, e20494.	2.5	56
78	Partitioning the C. elegans genome by nucleosome modification, occupancy, and positioning. Chromosoma, 2010, 119, 73-87.	2.2	55
79	The Extragenic Spacer Length Between the 5′ and 3′ Ends of the Transgene Expression Cassette Affects Transgene Silencing From Plasmid-based Vectors. Molecular Therapy, 2012, 20, 2111-2119.	8.2	55
80	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. MBio, 2017, 8, .	4.1	52
81	The T-box factor MLS-1 acts as a molecular switch during specification of nonstriated muscle in C. elegans. Genes and Development, 2002, 16, 257-269.	5.9	50
82	Target-dependent nickase activities of the CRISPR–Cas nucleases Cpf1 and Cas9. Nature Microbiology, 2019, 4, 888-897.	13.3	49
83	Vectors for low copy transformation of C. elegans. Nucleic Acids Research, 1990, 18, 4269-4269.	14.5	47
84	Nonsense mRNA suppression via nonstop decay. ELife, 2018, 7, .	6.0	46
85	An Extensive Meta-Metagenomic Search Identifies SARS-CoV-2-Homologous Sequences in Pangolin Lung Viromes. MSphere, 2020, 5, .	2.9	46
86	Evolutionary Conservation of MyoD Function and Differential Utilization of E Proteins. Developmental Biology, 1999, 208, 465-472.	2.0	42
87	Conserved Translatome Remodeling in Nematode Species Executing a Shared Developmental Transition. PLoS Genetics, 2013, 9, e1003739.	3.5	42
88	Persistence and evolution of allergen-specific IgE repertoires during subcutaneous specific immunotherapy. Journal of Allergy and Clinical Immunology, 2016, 137, 1535-1544.	2.9	41
89	CED-9 and mitochondrial homeostasis in <i>C. elegans</i> muscle. Journal of Cell Science, 2008, 121, 3373-3382.	2.0	40
90	Profiling and Discovery of Novel miRNAs from Formalin-Fixed, Paraffin-Embedded Melanoma and Nodal Specimens. Journal of Molecular Diagnostics, 2009, 11, 420-429.	2.8	40

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91	Caudal-like PAL-1 directly activates the bodywall muscle module regulator <i>hlh-1</i> in <i>C. elegans</i> to initiate the embryonic muscle gene regulatory network. Development (Cambridge), 2009, 136, 1241-1249.	2.5	38
92	Multimodal RNA-seq using single-strand, double-strand, and CircLigase-based capture yields a refined and extended description of the <i>C. elegans</i> transcriptome. Genome Research, 2011, 21, 265-275.	5.5	38
93	Intron and gene size expansion during nervous system evolution. BMC Genomics, 2020, 21, 360.	2.8	38
94	Connector Inversion Probe Technology: A Powerful One-Primer Multiplex DNA Amplification System for Numerous Scientific Applications. PLoS ONE, 2007, 2, e915.	2.5	38
95	Structural analysis of hyperperiodic DNA from Caenorhabditis elegans. Nucleic Acids Research, 2006, 34, 3057-3066.	14.5	37
96	Immunobiology of naÃ <sup>-</sup> ve and genetically modified HLA-class-I-knockdown human embryonic stem cells. Journal of Cell Science, 2011, 124, 3029-3037.	2.0	36
97	The MADS-Box Factor CeMEF2 Is Not Essential for Caenorhabditis elegans Myogenesis and Development. Developmental Biology, 2000, 223, 431-440.	2.0	34
98	Maternal Ribosomes Are Sufficient for Tissue Diversification during Embryonic Development in C.Âelegans. Developmental Cell, 2019, 48, 811-826.e6.	7.0	32
99	An essential role for the piRNA pathway in regulating the ribosomal RNA pool in C.Âelegans. Developmental Cell, 2021, 56, 2295-2312.e6.	7.0	31
100	Imprinting Capacity of Gamete Lineages in Caenorhabditis elegans. Genetics, 2005, 170, 1633-1652.	2.9	29
101	Human Leukocyte Antigen I Knockdown Human Embryonic Stem Cells Induce Host Ignorance and Achieve Prolonged Xenogeneic Survival. Circulation, 2011, 124, S3-9.	1.6	28
102	Prospective Biopsy-Based Study of CKD of Unknown Etiology in Sri Lanka. Clinical Journal of the American Society of Nephrology: CJASN, 2019, 14, 224-232.	4.5	27
103	Cell autonomous specification of temporal identity by Caenorhabditis elegans microRNA lin-4. Developmental Biology, 2010, 344, 603-610.	2.0	26
104	UNC-39, the C. elegans homolog of the human myotonic dystrophy-associated homeodomain protein Six5, regulates cell motility and differentiation. Developmental Biology, 2004, 272, 389-402.	2.0	25
105	Functional relevance of "seed―and "non-seed―sequences in microRNA-mediated promotion of <i>C. elegans</i> developmental progression. Rna, 2015, 21, 1980-1992.	3.5	25
106	A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition. Molecular Cell, 2018, 72, 700-714.e8.	9.7	25
107	High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences. Genetics, 2017, 206, 1727-1738.	2.9	23
108	Cas9 Variants Expand the Target Repertoire in <i>Caenorhabditis elegans</i> . Genetics, 2016, 202, 381-388.	2.9	22

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109	Distributed probing of chromatin structure in vivo reveals pervasive chromatin accessibility for expressed and non-expressed genes during tissue differentiation in C. elegans. BMC Genomics, 2010, 11, 465.	2.8	21
110	Assessment and Maintenance of Unigametic Germline Inheritance for C.Âelegans. Developmental Cell, 2019, 48, 827-839.e9.	7.0	21
111	A Differential Cytolocalization Assay for Analysis of Macromolecular Assemblies in the Eukaryotic Cytoplasm. Molecular and Cellular Proteomics, 2006, 5, 2175-2184.	3.8	20
112	An in vitro-identified high-affinity nucleosome-positioning signal is capable of transiently positioning a nucleosome in vivo. Epigenetics and Chromatin, 2010, 3, 13.	3.9	20
113	On the nature of in vivo requirements forrde-4in RNAi and developmental pathways inC. elegans. RNA Biology, 2011, 8, 458-467.	3.1	20
114	Transcription polymerase–catalyzed emergence of novel RNA replicons. Science, 2020, 368, .	12.6	19
115	Nucleic acid structure and intracellular immunity: some recent ideas from the world of RNAi. Quarterly Reviews of Biophysics, 2005, 38, 303-309.	5.7	18
116	Distinct ribonucleoprotein reservoirs for microRNA and siRNA populations in <i>C. elegans</i> . Rna, 2007, 13, 1492-1504.	3.5	18
117	Functional conservation of nematode and vertebrate myogenic regulatory factors. Journal of Cell Science, 1992, 1992, 111-115.	2.0	17
118	Cyclin D involvement demarcates a late transition in C. elegans embryogenesis. Developmental Biology, 2005, 279, 244-251.	2.0	17
119	A streamlined tethered chromosome conformation capture protocol. BMC Genomics, 2016, 17, 274.	2.8	17
120	Chikungunya Virus Sequences Across the First Epidemic in Nicaragua, 2014–2015. American Journal of Tropical Medicine and Hygiene, 2016, 94, 400-403.	1.4	17
121	A novel TRIP11-FLT3 fusion in a patient with a myeloid/lymphoid neoplasm with eosinophilia. Cancer Genetics, 2017, 216-217, 10-15.	0.4	17
122	Epidemiology, molecular, and genetic methodologies to evaluate causes ofÂCKDuÂaroundÂthe world: report of the Working GroupÂfrom the ISN InternationalÂConsortium ofÂCollaborators onÂCKDu. Kidney International, 2019, 96, 1254-1260.	5.2	16
123	Lymphoid blast transformation in an MPN with <i>BCR-JAK2</i> treated with ruxolitinib: putative mechanisms of resistance. Blood Advances, 2021, 5, 3492-3496.	5.2	14
124	A four-dimensional digital image archiving system for cell lineage tracing and retrospective embryology. Bioinformatics, 1994, 10, 443-447.	4.1	12
125	Ribosome clearance during RNA interference. Rna, 2019, 25, 963-974.	3.5	11
126	Comprehensive whole-genome sequencing of an early-stage primary myelofibrosis patient defines low mutational burden and non-recurrent candidate genes. Haematologica, 2013, 98, 1689-1696.	3.5	10

Andrew Z Fire

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127	Gamete-Type Dependent Crossover Interference Levels in a Defined Region of <i>Caenorhabditis elegans</i> Chromosome V. G3: Genes, Genomes, Genetics, 2014, 4, 117-120.	1.8	10
128	Sequence-Modified Antibiotic Resistance Genes Provide Sustained Plasmid-Mediated Transgene Expression in Mammals. Molecular Therapy, 2017, 25, 1187-1198.	8.2	10
129	Deconvolution of nucleic-acid length distributions: a gel electrophoresis analysis tool and applications. Nucleic Acids Research, 2019, 47, e92-e92.	14.5	10
130	â€~Inc-miRs': functional intron-interrupted miRNA genes. Genes and Development, 2011, 25, 1589-1594.	5.9	8
131	Unusual DNA packaging characteristics in endoreduplicated Caenorhabditis elegans oocytes defined by in vivo accessibility to an endogenous nuclease activity. Epigenetics and Chromatin, 2013, 6, 37.	3.9	5
132	A Small RNA Isolation and Sequencing Protocol and Its Application to Assay CRISPR RNA Biogenesis in Bacteria. Bio-protocol, 2018, 8, .	0.4	5
133	In ovoRNAi opens new possibilities for functional genomics in vertebrates. , 2005, , 220-232.		3
134	Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species. BMC Genomics, 2015, 16, 978.	2.8	3
135	PLP-1 is essential for germ cell development and germline gene silencing in <i>C. elegans</i> . Development (Cambridge), 2020, 147, .	2.5	3
136	Context-dependent DNA polymerization effects can masquerade as DNA modification signals. BMC Genomics, 2022, 23, 249.	2.8	2
137	Sexist ads. Nature, 1986, 321, 106-106.	27.8	1
138	Dicer in RNAi: Its roles in vivo and utility in vitro. , 2005, , 29-54.		1
139	Viral delivery of shRNA. , 2005, , 161-173.		1
140	Genes required for RNA interference. , 2005, , 55-68.		1
141	RNAi and gene silencing phenomena mediated by viral suppressors in plants. , 2005, , 280-300.		1
142	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47.		1
143	RNAi, genome ultrastructure, and other unexpected tales from the analysis of genetic silencing. , 2004, , .		0
144	Design and synthesis of small interfering RNA (siRNA). , 2005, , 103-117.		0

#	Article	IF	CITATIONS
145	<i>Foreword by</i> Andrew Fire. , 2005, , xi-xii.		Ο
146	RNAi beginnings, Overview of the pathway in C. elegans. , 2005, , 17-28.		0
147	MicroRNAs: A small contribution from worms. , 2005, , 69-83.		0
148	miRNAs in the brain and the application of RNAi to neurons. , 2005, , 84-100.		0
149	Liposomal delivery of siRNAs in mice. , 2005, , 186-193.		Ο
150	Chemical modifications to achieve increased stability and sensitive detection of siRNA. , 2005, , 194-206.		0
151	Practical applications of RNAi in C. elegans. , 2005, , 235-246.		0
152	Inducible RNAi as a forward genetic tool in Trypanosoma brucei. , 2005, , 247-256.		0
153	RNA-mediated gene silencing in fission yeast. , 2005, , 257-269.		0
154	RNA interference technology in the discovery and validation of druggable targets. , 2005, , 347-360.		0
155	RNAi-mediated silencing of viral gene expression and replication. , 2005, , 363-383.		Ο
156	Tools for integrative genomics: Genome-wide RNAi and expression profiling in Drosophila. , 2005, , 433-446.		0
157	Microarray analysis and RNA silencing to determine genes functionally important in mesothelioma. , 2005, , 447-469.		Ο
158	High-throughput RNA interference. , 2005, , 470-479.		0
159	Clonality: Point estimation. Annals of Applied Statistics, 2019, 13, .	1.1	0
160	Cellular responses to genetic change. FASEB Journal, 2008, 22, 397.2.	0.5	0
161	High-Throughput Sequencing for Diagnosis, Prognosis and Monitoring of Lymphoid Malignancies. Blood, 2008, 112, 3779-3779.	1.4	0
162	High-Throughput VDJ Sequencing Is Superior to Quantitative PCR and Flow Cytometry for the Quantification of Minimal Residual Disease In Chronic Lymphocytic Leukemia After Hematopoietic Cell Transplantation Blood, 2010, 116, 1290-1290.	1.4	0

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163	Whole Genome Sequence Analysis of Primary Myelofibrosis Blood, 2012, 120, 2863-2863.	1.4	Ο