# Andrew Z Fire

List of Publications by Year
in descending order



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|---|---|---|---|
| 163 papers | 39,325 citations | 15504 65 h-index | 10445 139 g-index |
| 174 all docs | 174 docs citations | 174 times ranked | 31932 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Context-dependent DNA polymerization effects can masquerade as DNA modification signals. BMC Genomics, 2022, 23, 249. | 2.8 | 2 |
| 2 | 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 |
| 3 | Lymphoid blast transformation in an MPN with BCR-JAK2 treated with ruxolitinib: putative mechanisms of resistance. Blood Advances, 2021, 5, 3492-3496. | 5.2 | 14 |
| 4 | PLP-1 is essential for germ cell development and germline gene silencing inC. elegans. Development (Cambridge), 2020, 147, . | 2.5 | 3 |
| 5 | Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270. | 13.3 | 156 |
| 6 | An Extensive Meta-Metagenomic Search Identifies SARS-CoV-2-Homologous Sequences in Pangolin Lung Viromes. MSphere, 2020, 5, . | 2.9 | 46 |
| 7 | Intron and gene size expansion during nervous system evolution. BMC Genomics, 2020, 21, 360. | 2.8 | 38 |
| 8 | Transcription polymeraseâ€“catalyzed emergence of novel RNA replicons. Science, 2020, 368, . | 12.6 | 19 |
| 9 | Aberrant B cell repertoire selection associated with HIV neutralizing antibody breadth. Nature Immunology, 2020, 21, 199-209. | 14.5 | 68 |
| 10 | Clonality: Point estimation. Annals of Applied Statistics, 2019, 13, . | 1.1 | 0 |
| 11 | 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 |
| 12 | Recompleting the Caenorhabditis elegans genome. Genome Research, 2019, 29, 1009-1022. | 5.5 | 108 |
| 13 | Deconvolution of nucleic-acid length distributions: a gel electrophoresis analysis tool and applications. Nucleic Acids Research, 2019, 47, e92-e92. | 14.5 | 10 |
| 14 | Ribosome clearance during RNA interference. Rna, 2019, 25, 963-974. | 3.5 | 11 |
| 15 | Target-dependent nickase activities of the CRISPRâ€“Cas nucleases Cpf1 and Cas9. Nature Microbiology, 2019, 4, 888-897. | 13.3 | 49 |
| 16 | Maternal Ribosomes Are Sufficient for Tissue Diversification during Embryonic Development in C.Âelegans. Developmental Cell, 2019, 48, 811-826.e6. | 7.0 | 32 |
| 17 | Assessment and Maintenance of Unigametic Germline Inheritance for C.Âelegans. Developmental Cell, 2019, 48, 827-839.e9. | 7.0 | 21 |
| 18 | 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 |

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|---|---|---|---|
| 19 | A Small RNA Isolation and Sequencing Protocol and Its Application to Assay CRISPR RNA Biogenesis in Bacteria. Bio-protocol, 2018, 8, . | 0.4 | 5 |
| 20 | 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 |
| 21 | Nonsense mRNA suppression via nonstop decay. ELife, 2018, 7, . | 6.0 | 46 |
| 22 | 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 |
| 23 | Sequence-Modified Antibiotic Resistance Genes Provide Sustained Plasmid-Mediated Transgene Expression in Mammals. Molecular Therapy, 2017, 25, 1187-1198. | 8.2 | 10 |
| 24 | 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 |
| 25 | Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in Caenorhabditis elegans and Homo sapiens. G3: Genes, Genomes, Genetics, 2017, 7, 3295-3303. | 1.8 | 87 |
| 26 | On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. MBio, 2017, 8, . | 4.1 | 52 |
| 27 | Type III CRISPR-Cas systems can provide redundancy to counteract viral escape from type I systems. ELife, 2017, 6, . | 6.0 | 81 |
| 28 | 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 |
| 29 | Distinct patterns of Cas9 mismatch tolerancein vitroandin vivo. Nucleic Acids Research, 2016, 44, 5365-5377. | 14.5 | 62 |
| 30 | 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 |
| 31 | Translation readthrough mitigation. Nature, 2016, 534, 719-723. | 27.8 | 90 |
| 32 | A streamlined tethered chromosome conformation capture protocol. BMC Genomics, 2016, 17, 274. | 2.8 | 17 |
| 33 | Cas9 Variants Expand the Target Repertoire in Caenorhabditis elegans. Genetics, 2016, 202, 381-388. | 2.9 | 22 |
| 34 | Direct CRISPR spacer acquisition from RNA by a natural reverse transcriptaseâ€“Cas1 fusion protein. Science, 2016, 351, aad4234. | 12.6 | 170 |
| 35 | Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody. Cell, 2016, 165, 449-463. | 28.9 | 305 |
| 36 | Chikungunya Virus Sequences Across the First Epidemic in Nicaragua, 2014â€“2015. American Journal of Tropical Medicine and Hygiene, 2016, 94, 400-403. | 1.4 | 17 |

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| 37 | 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 |
| 38 | Functional relevance of â€œseedâ€•and â€œnon-seedâ€•sequences in microRNA-mediated promotion of C. elegans developmental progression. Rna, 2015, 21, 1980-1992. | 3.5 | 25 |
| 39 | Landscape of target:guide homology effects on Cas9-mediated cleavage. Nucleic Acids Research, 2014, 42, 13778-13787. | 14.5 | 65 |
| 40 | Gamete-Type Dependent Crossover Interference Levels in a Defined Region ofCaenorhabditis elegansChromosome V. G3: Genes, Genomes, Genetics, 2014, 4, 117-120. | 1.8 | 10 |
| 41 | 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 |
| 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 | Efficient Marker-Free Recovery of Custom Genetic Modifications with CRISPR/Cas9 in Caenorhabditis elegans. Genetics, 2014, 198, 837-846. | 2.9 | 738 |
| 44 | 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 |
| 45 | Human Responses to Influenza Vaccination Show Seroconversion Signatures and Convergent Antibody Rearrangements. Cell Host and Microbe, 2014, 16, 105-114. | 11.0 | 246 |
| 46 | 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 |
| 47 | Minicircle DNA Vectors Achieve Sustained Expression Reflected by Active Chromatin and Transcriptional Level. Molecular Therapy, 2013, 21, 131-138. | 8.2 | 103 |
| 48 | Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. Nature, 2013, 496, 469-476. | 27.8 | 961 |
| 49 | Convergent Antibody Signatures in Human Dengue. Cell Host and Microbe, 2013, 13, 691-700. | 11.0 | 271 |
| 50 | The transcription start site landscape of C. elegans. Genome Research, 2013, 23, 1348-1361. | 5.5 | 58 |
| 51 | Conserved Translatome Remodeling in Nematode Species Executing a Shared Developmental Transition. PLoS Genetics, 2013, 9, e1003739. | 3.5 | 42 |
| 52 | 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 |
| 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 | Contributions of mRNA abundance, ribosome loading, and post- or peri-translational effects to temporal repression of C. elegans heterochronic miRNA targets. Genome Research, 2012, 22, 2418-2426. | 5.5 | 56 |

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| 55 | Protection from Feed-Forward Amplification in an Amplified RNAi Mechanism. Cell, 2012, 151, 885-899. | 28.9 | 70 |
| 56 | The Extragenic Spacer Length Between the 5â€² and 3â€² Ends of the Transgene Expression Cassette Affects Transgene Silencing From Plasmid-based Vectors. Molecular Therapy, 2012, 20, 2111-2119. | 8.2 | 55 |
| 57 | 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 |
| 58 | A nuclear Argonaute promotes multigenerational epigenetic inheritance and germline immortality. Nature, 2012, 489, 447-451. | 27.8 | 450 |
| 59 | Whole Genome Sequence Analysis of Primary Myelofibrosis.. Blood, 2012, 120, 2863-2863. | 1.4 | 0 |
| 60 | 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 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | Determinants of nucleosome organization in primary human cells. Nature, 2011, 474, 516-520. | 27.8 | 567 |
| 65 | Multimodal RNA-seq using single-strand, double-strand, and CircLigase-based capture yields a refined and extended description of the C. elegans transcriptome. Genome Research, 2011, 21, 265-275. | 5.5 | 38 |
| 66 | Immunobiology of naÃ¯ve and genetically modified HLA-class-I-knockdown human embryonic stem cells. Journal of Cell Science, 2011, 124, 3029-3037. | 2.0 | 36 |
| 67 | Wobble base-pairing slows in vivo translation elongation in metazoans. Rna, 2011, 17, 2063-2073. | 3.5 | 159 |
| 68 | â€¯Inc-miRsâ€™: functional intron-interrupted miRNA genes. Genes and Development, 2011, 25, 1589-1594. | 5.9 | 8 |
| 69 | On the nature of in vivo requirements forrde-4in RNAi and developmental pathways inC. elegans. RNA Biology, 2011, 8, 458-467. | 3.1 | 20 |
| 70 | 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 |
| 71 | Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47. | | 1 |
| 72 | Up-Regulated Dicer Expression in Patients with Cutaneous Melanoma. PLoS ONE, 2011, 6, e20494. | 2.5 | 56 |

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| 73 | Partitioning the C. elegans genome by nucleosome modification, occupancy, and positioning. Chromosoma, 2010, 119, 73-87. | 2.2 | 55 |
| 74 | 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 |
| 75 | 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 |
| 76 | 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 |
| 77 | Human tRNA-derived small RNAs in the global regulation of RNA silencing. Rna, 2010, 16, 673-695. | 3.5 | 583 |
| 78 | Individual Variation in the Germline Ig Gene Repertoire Inferred from Variable Region Gene Rearrangements. Journal of Immunology, 2010, 184, 6986-6992. | 0.8 | 261 |
| 79 | 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 |
| 80 | Distinct Phases of siRNA Synthesis in an Endogenous RNAi Pathway in C. elegans Soma. Molecular Cell, 2010, 37, 679-689. | 9.7 | 177 |
| 81 | Cell autonomous specification of temporal identity by Caenorhabditis elegans microRNA lin-4. Developmental Biology, 2010, 344, 603-610. | 2.0 | 26 |
| 82 | 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 |
| 83 | Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. Science, 2009, 323, 401-404. | 12.6 | 122 |
| 84 | ACaenorhabditis elegansRNA-Directed RNA Polymerase in Sperm Development and Endogenous RNA Interference. Genetics, 2009, 183, 1297-1314. | 2.9 | 80 |
| 85 | Caudal-like PAL-1 directly activates the bodywall muscle module regulator hlh-1 in C. elegans to initiate the embryonic muscle gene regulatory network. Development (Cambridge), 2009, 136, 1241-1249. | 2.5 | 38 |
| 86 | 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 |
| 87 | Measurement and Clinical Monitoring of Human Lymphocyte Clonality by Massively Parallel V-D-J Pyrosequencing. Science Translational Medicine, 2009, 1, 12ra23. | 12.4 | 372 |
| 88 | Capped small RNAs and MOV10 in human hepatitis delta virus replication. Nature Structural and Molecular Biology, 2008, 15, 714-721. | 8.2 | 72 |
| 89 | A high-resolution, nucleosome position map of C. elegans reveals a lack of universal sequence-dictated positioning. Genome Research, 2008, 18, 1051-1063. | 5.5 | 503 |
| 90 | CED-9 and mitochondrial homeostasis inC. elegansmuscle. Journal of Cell Science, 2008, 121, 3373-3382. | 2.0 | 40 |

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| 91 | Transmission Dynamics of Heritable Silencing Induced by Double-Stranded RNA inCaenorhabditis elegans. Genetics, 2008, 180, 1275-1288. | 2.9 | 174 |
| 92 | Cellular responses to genetic change. FASEB Journal, 2008, 22, 397.2. | 0.5 | 0 |
| 93 | High-Throughput Sequencing for Diagnosis, Prognosis and Monitoring of Lymphoid Malignancies. Blood, 2008, 112, 3779-3779. | 1.4 | 0 |
| 94 | Distinct ribonucleoprotein reservoirs for microRNA and siRNA populations in C. elegans. Rna, 2007, 13, 1492-1504. | 3.5 | 18 |
| 95 | Distinct Populations of Primary and Secondary Effectors During RNAi in C. elegans. Science, 2007, 315, 241-244. | 12.6 | 530 |
| 96 | Patterns of Known and Novel Small RNAs in Human Cervical Cancer. Cancer Research, 2007, 67, 6031-6043. | 0.9 | 416 |
| 97 | A pyrosequencing-tailored nucleotide barcode design unveils opportunities for large-scale sample multiplexing. Nucleic Acids Research, 2007, 35, e130. | 14.5 | 306 |
| 98 | Gene Silencing by Doubleâ€Stranded RNA (Nobel Lecture). Angewandte Chemie - International Edition, 2007, 46, 6966-6984. | 13.8 | 112 |
| 99 | Connector Inversion Probe Technology: A Powerful One-Primer Multiplex DNA Amplification System for Numerous Scientific Applications. PLoS ONE, 2007, 2, e915. | 2.5 | 38 |
| 100 | Structural analysis of hyperperiodic DNA from Caenorhabditis elegans. Nucleic Acids Research, 2006, 34, 3057-3066. | 14.5 | 37 |
| 101 | A Differential Cytolocalization Assay for Analysis of Macromolecular Assemblies in the Eukaryotic Cytoplasm. Molecular and Cellular Proteomics, 2006, 5, 2175-2184. | 3.8 | 20 |
| 102 | Unusual DNA Structures Associated With Germline Genetic Activity in Caenorhabditis elegans. Genetics, 2006, 173, 1259-1273. | 2.9 | 61 |
| 103 | Flexibility and constraint in the nucleosome core landscape of Caenorhabditis elegans chromatin. Genome Research, 2006, 16, 1505-1516. | 5.5 | 169 |
| 104 | An antagonistic role for the C. elegans Schnurri homolog SMA-9 in modulating TGFÎ²2 signaling during mesodermal patterning. Development (Cambridge), 2006, 133, 2887-2896. | 2.5 | 57 |
| 105 | Design and synthesis of small interfering RNA (siRNA). , 2005, , 103-117. | | 0 |
| 106 | Dicer in RNAi: Its roles in vivo and utility in vitro. , 2005, , 29-54. | | 1 |
| 107 | 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 |
| 108 | Viral delivery of shRNA. , 2005, , 161-173. | | 1 |

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| 109 | Foreword by Andrew Fire. , 2005, , xi-xii. | | 0 |
| 110 | RNAi beginnings, Overview of the pathway in C. elegans. , 2005, , 17-28. | | 0 |
| 111 | Genes required for RNA interference. , 2005, , 55-68. | | 1 |
| 112 | MicroRNAs: A small contribution from worms. , 2005, , 69-83. | | 0 |
| 113 | miRNAs in the brain and the application of RNAi to neurons. , 2005, , 84-100. | | 0 |
| 114 | Liposomal delivery of siRNAs in mice. , 2005, , 186-193. | | 0 |
| 115 | Chemical modifications to achieve increased stability and sensitive detection of siRNA. , 2005, , 194-206. | | 0 |
| 116 | In ovoRNAi opens new possibilities for functional genomics in vertebrates. , 2005, , 220-232. | | 3 |
| 117 | Practical applications of RNAi in C. elegans. , 2005, , 235-246. | | 0 |
| 118 | Inducible RNAi as a forward genetic tool in Trypanosoma brucei. , 2005, , 247-256. | | 0 |
| 119 | RNA-mediated gene silencing in fission yeast. , 2005, , 257-269. | | 0 |
| 120 | RNAi and gene silencing phenomena mediated by viral suppressors in plants. , 2005, , 280-300. | | 1 |
| 121 | RNA interference technology in the discovery and validation of druggable targets. , 2005, , 347-360. | | 0 |
| 122 | RNAi-mediated silencing of viral gene expression and replication. , 2005, , 363-383. | | 0 |
| 123 | Tools for integrative genomics: Genome-wide RNAi and expression profiling in Drosophila. , 2005, , 433-446. | | 0 |
| 124 | Microarray analysis and RNA silencing to determine genes functionally important in mesothelioma. , 2005, , 447-469. | | 0 |
| 125 | High-throughput RNA interference. , 2005, , 470-479. | | 0 |
| 126 | Imprinting Capacity of Gamete Lineages in Caenorhabditis elegans. Genetics, 2005, 170, 1633-1652. | 2.9 | 29 |

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| 127 | Cyclin D involvement demarcates a late transition in C. elegans embryogenesis. Developmental Biology, 2005, 279, 244-251. | 2.0 | 17 |
| 128 | RNAi, genome ultrastructure, and other unexpected tales from the analysis of genetic silencing. , 2004, , . | | 0 |
| 129 | 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 |
| 130 | Inducible Systemic RNA Silencing in Caenorhabditis elegans. Molecular Biology of the Cell, 2003, 14, 2972-2983. | 2.1 | 135 |
| 131 | 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 |
| 132 | Rescue of polyglutamine-mediated cytotoxicity by double-stranded RNA-mediated RNA interference. Human Molecular Genetics, 2002, 11, 175-184. | 2.9 | 100 |
| 133 | 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 |
| 134 | Ingestion of bacterially expressed dsRNAs can produce specific and potent genetic interference in Caenorhabditis elegans. Gene, 2001, 263, 103-112. | 2.2 | 1,605 |
| 135 | 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 |
| 136 | On the Role of RNA Amplification in dsRNA-Triggered Gene Silencing. Cell, 2001, 107, 465-476. | 28.9 | 1,172 |
| 137 | Recognition and Silencing of Repeated DNA. Annual Review of Genetics, 2000, 34, 187-204. | 7.6 | 99 |
| 138 | Essential Roles forCaenorhabditis elegansLamin 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 |
| 139 | The MADS-Box Factor CeMEF2 Is Not Essential for Caenorhabditis elegans Myogenesis and Development. Developmental Biology, 2000, 223, 431-440. | 2.0 | 34 |
| 140 | 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 |
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| 142 | RNA-triggered gene silencing. Trends in Genetics, 1999, 15, 358-363. | 6.7 | 565 |
| 143 | The rde-1 Gene, RNA Interference, and Transposon Silencing in C. elegans. Cell, 1999, 99, 123-132. | 28.9 | 1,180 |
| 144 | Evolutionary Conservation of MyoD Function and Differential Utilization of E Proteins. Developmental Biology, 1999, 208, 465-472. | 2.0 | 42 |

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| 146 | Specific interference by ingested dsRNA. Nature, 1998, 395, 854-854. | 27.8 | 1,655 |
| 147 | Double-stranded RNA as a mediator in sequence-specific genetic silencing and co-suppression. Trends in Genetics, 1998, 14, 255-258. | 6.7 | 222 |
| 148 | Caenorhabditis elegansLevamisole Resistance Geneslev-1,unc-29, andunc-38Encode Functional Nicotinic Acetylcholine Receptor Subunits. Journal of Neuroscience, 1997, 17, 5843-5857. | 3.6 | 301 |
| 149 | Distinct Requirements for Somatic and Germline Expression of a Generally Expressed Caernorhabditis elegans Gene. Genetics, 1997, 146, 227-238. | 2.9 | 444 |
| 150 | Repression of gene expression in the embryonic germ lineage of C. elegans. Nature, 1996, 382, 713-716. | 27.8 | 299 |
| 151 | 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 |
| 152 | Chapter 19 DNA Transformation. Methods in Cell Biology, 1995, , 451-482. | 1.1 | 1,063 |
| 153 | A four-dimensional digital image archiving system for cell lineage tracing and retrospective embryology. Bioinformatics, 1994, 10, 443-447. | 4.1 | 12 |
| 154 | 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 |
| 155 | Functional conservation of nematode and vertebrate myogenic regulatory factors. Journal of Cell Science, 1992, 1992, 111-115. | 2.0 | 17 |
| 156 | Histochemical techniques for locating Escherichia coli Î²-galactosidase activity in transgenic organisms. Genetic Analysis, Techniques and Applications, 1992, 9, 151-158. | 1.5 | 84 |
| 157 | Vectors for low copy transformation ofC. elegans. Nucleic Acids Research, 1990, 18, 4269-4269. | 14.5 | 47 |
| 158 | A modular set of lacZ fusion vectors for studying gene expression in Caenorhabditis elegans. Gene, 1990, 93, 189-198. | 2.2 | 620 |
| 159 | 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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| 161 | Sexist ads. Nature, 1986, 321, 106-106. | 27.8 | 1 |
| 162 | [35] In Vitro transcription: Whole-cell extract. Methods in Enzymology, 1983, 101, 568-582. | 1.0 | 309 |

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| 163 | Inhibition of transcription factor activity by poliovirus. Cell, 1981, 27, 555-561. | 28.9 | 87 |