Stanford

Andrew Fire

George D. Smith Professor of Molecular and Genetic Medicine and Professor of Pathology and of Genetics

Bio

ACADEMIC APPOINTMENTS

- Professor, Pathology
- Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Professor of Pathology and Genetics, Stanford University School of Medicine, (2003- present)
- Assistant Professor -> Professor of Biology (Adjunct), Johns Hopkins University, (1989-2009)
- Scientific Staff, Carnegie Institution of Washington, (1989-2003)
- Staff Associate, Carnegie Institution of Washington, (1986-1989)

LINKS

- Fire Lab: https://firelab.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

->What We Do:

Our lab studies novel (non-chromosomal) agents of genetic constancy and change and the mechanisms by which organisms and cells respond to such agents.

The genetic landscape faced by a living cell is constantly changing. Developmental transitions, environmental shifts, and pathogenic invasions lend a dynamic character to both the genome and its activity pattern. We study a variety of genetic change agents, as well as the natural mechanisms that are utilized by cells adapting to such agents. The change agents include a panoply of previously (and often still) uncharacterized DNA and RNA elements that straddle boundaries between genome, virome, and mobilome. The corresponding propagation and control mechanisms likewise span a spectrum between systems activated during normal development and systems for detecting and responding to foreign or unwanted genetic activity. At the root of

these studies are searches for unexpected genetic and genomic entities and questions of how a cell can distinguish "self" versus "nonself" and "wanted" versus "unwanted" gene activity.

We make use of both model and non-model organisms in our work. The "simple" nematode C. elegans in a recurring tool in our experimental studies. C. elegans is small, easily cultured, and can readily be made to accept foreign DNA or RNA. The results of such experiments have outlined a number of concerted responses that recognize (and in most cases work to silence) the foreign nucleic acid. One such mechanism ("RNAi") responds to double stranded character in RNA: either as introduced experimentally into the organism or as produced from foreign DNA that has not undergone selection to avoid a dsRNA response. RNAi is not the only cellular defense against unwanted nucleic acid, and substantial current effort in the lab is also directed at identification of other triggers and mechanisms used in recognition and response to foreign information. Beyond C. elegans, we seek novel processes driving genetic constancy and change the lie outside of standard chromosomal inheritance. The latter studies have taken us to a number of studies with non-model organisms and toward a view that biology is best expanded by combining model organism approaches with a wide net for novel phenomena that includes examining wide diversity of non-model organisms.

------>Who we are:
PI: Andrew Fire, Professor of Pathology and Genetics

Postdoctoral Fellows:
Dr. Dae-Eun Jeong (Ph.D. Pohang University of Science and Technology, 2017)
Dr. Orkan Ilbay (Ph.D. University of Massachusetts, 2019)

Graduate Students:
Usman Enam [Stanford Genetics Ph.D. Program] (B.S. Johns Hopkins, 2020)
Drew Galls [Stanford Genetics Ph.D. Program] (B.S. Yale, 2021)
Janie Kim [Stanford Biology Ph.D. Program; Joint with Nicole Martinez Lab] (A.B. Princeton 2021)
Colette Benko [Stanford Developmental Biology, Ph.D. Program] (BMSc Biochemistry, WesternU 2022)
Haim Krupkin [Stanford Genetics Ph.D Program; Joint with Stephen Montgomery Lab] (B.Sc., M.Sc. Bar Ilan University 2021, 2024)

Undergraduate Students:
Talha Rao [Stanford '2026]

Visiting Scientist:
David Lipman (FDA CFSAN)

Laboratory Manager:
Karen Artiles (Ph.D. UC Santa Cruz, 2008)

Laboratory Specialist:
Krisztina Perez

-> Joining The Fire Lab

We welcome new applicants to the lab.

Prospective postdoctoral applicants should send a resume and summary of research to Dr. Fire (afire <at> stanford <dot> edu), and arrange to have 3-4 letters of reference likewise sent to this address.

Prospective graduate students are encouraged to apply to the Stanford Genetics Ph.D. program (or to any of the biosciences Ph.D. programs): http://biosciences.stanford.edu/prospective/

Rotation Students: We welcome rotation students from any program at Stanford, with Spring being the preferred quarter. Email the PI.

We occasionally have undergraduate research opportunities. Email the PI at the above address.

Teaching

COURSES

2025-26

- Advanced Genetics: GENE 205 (Win)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Genetics of Viral Emergence and Emerging Viruses: GENE 242 (Win)

2024-25

- Advanced Genetics: GENE 205 (Win)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Genetics of Viral Emergence and Emerging Viruses: GENE 242 (Win)

2023-24

- Advanced Genetics: GENE 205 (Win)
- Computational Analysis of Biological Information: Introduction to Python for Biologists: GENE 218, MI 218, PATH 218 (Sum)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Genetics of Viral Emergence and Emerging Viruses: GENE 242 (Win)

2022-23

- Advanced Genetics: GENE 205 (Win)
- Computational Analysis of Biological Information: Introduction to Python for Biologists: GENE 218, MI 218, PATH 218 (Sum)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Genetics of Viral Emergence and Emerging Viruses: GENE 242 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Simone Evans, Matthew Gill, Gokul Kannan, Yannick Lee-Yow, Gabriel Tauber, Tee Udomlumleart, Sidney Vermeulen

Doctoral Dissertation Advisor (AC)

Colette Benko, Usman Enam, Drew Galls, Haim Krupkin

Doctoral Dissertation Co-Advisor (AC)

Janie Kim

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Cancer Biology (Phd Program)
- Genetics (Phd Program)
- Immunology (Phd Program)

Publications

PUBLICATIONS

- **Case-control study of water and agricultural exposures among women in CKDu-endemic Sri Lanka.** *Journal of water and health*
  Contreras Nieves, M., Hewapathiranage, S., Zabel, F. Q., Mahalekam, D., Yu, X., Weerakoon, C., Bandara, M., Bandara, I., Maduwantha, I., Hearth, D., Athauda, I., Rathnayake, B., Erandika, et al
  2026; 24 (2): 160-175
- **Case-control study of water and agricultural exposures among women in CKDu-endemic Sri Lanka** *JOURNAL OF WATER AND HEALTH*
  Contreras Nieves, M., Hewapathiranage, S., Zabel, F., Mahalekam, D., Yu, X., Weerakoon, C., Bandara, M., Bandara, I., Maduwantha, I., Hearth, D., Athauda, I., Rathnayake, B., Erandika, et al
  2026
- **A default silencing mechanism restrains stress-induced genes in C. elegans.** *bioRxiv : the preprint server for biology*
  Ilbay, O., Gama, A. R., Jarosz, D. F., Morimoto, R. I., Fire, A.
  2025
- **CGC1, a new reference genome for Caenorhabditis elegans.** *Genome research*
  Ichikawa, K., Shoura, M. J., Artiles, K. L., Jeong, D. E., Owa, C., Kobayashi, H., Suzuki, Y., Kanamori, M., Toyoshima, Y., Iino, Y., Rougvie, A. E., Wahba, L., Fire, et al
  2025
- **DragonRNA: Generality of DNA-primed RNA-extension activities by DNA-directed RNA polymerases.** *Nucleic acids research*
  Greenwald, E., Galls, D., Park, J., Jain, N., Montgomery, S. B., Roy, B., Yin, Y. W., Fire, A. Z.
  2025; 53 (6)
- **A general RNA-templated RNA extension activity of E. coli RNA polymerase.** *RNA (New York, N.Y.)*
  Galls, D., Mueller, A. U., Greenwald, E., Fire, A.
  2025
- **Viroid-like colonists of human microbiomes.** *Cell*
  Zheludev, I. N., Edgar, R. C., Lopez-Galiano, M. J., de la Peña, M., Babaian, A., Bhatt, A. S., Fire, A. Z.
  2024
- **A genetic and microscopy toolkit for manipulating and monitoring regeneration in Macrostomum lignano.** *Cell reports*
  Hall, R. N., Li, H., Chai, C., Vermeulen, S., Bigasin, R. R., Song, E. S., Sarkar, S. R., Gibson, J., Prakash, M., Fire, A. Z., Wang, B.
  2024; 43 (11): 114892
- **Pachytene piRNAs control discrete meiotic events during spermatogenesis and restrict gene expression in space and time.** *Science advances*
  Ortega, J., Wahba, L., Seemann, J., Chen, S., Fire, A. Z., Arur, S.
  2024; 10 (40): eadp0466
- **Parallel gene size and isoform expansion of ancient neuronal genes.** *Current biology : CB*
  McCoy, M. J., Fire, A. Z.
  2024
- **Kidney biopsies among persons living in hotspots of CKDu: A position statement from the International Society of Nephrology's Consortium of Collaborators on CKDu.** *Kidney international*

Wijewickrama, E., Behera, S., Garcia, P., Avila-Casado, C., Caplin, B., Paolo, V. S., Courville, K., Friedman, D., Madero, M., Jha, V., Kambham, N., Levin, A., Anand, et al
2023

- **DNA polymerase diversity reveals multiple incursions of Polintons during nematode evolution.** *Molecular biology and evolution*
  Jeong, D. E., Sundrani, S., Hall, R. N., Krupovic, M., Koonin, E. V., Fire, A. Z.
  2023

- **Describing Natural History and Exploring Risk Factors for Kidney Function Decline in Persons With CKD of Uncertain Etiology in Sri Lanka.** *Kidney international reports*
  Hewavitharana, P., Schensul, S., Lee, E., Montez-Rath, M., Senarathne, S., Liu, S., Harold, K., Hewapathiranage, S., Erandika, N., Abeysundara, H. T., Yu, X., Bhalla, V., Fire, et al
  2023; 8 (7): 1430-1438

- **Challenges and opportunities in interventions for chronic kidney disease of unknown origin (CKDu): report from the International Society of Nephrology Consortium of Collaborators on CKDu.** *Kidney international*
  Smyth, B., Glaser, J., Butler-Dawson, J., Nanayakkara, N., Wegman, D. H., Anand, S., Levin, A., International Society of Nephrologys International Consortium of Collaborators on Chronic Kidney Disease of Unknown Etiology (i3C), Caplin, B., Correa Rotter, R., Eckardt, K., Fire, A., Friedman, D., et al
  2023; 103 (1): 6-12

- **Restriction Endonuclease-Based Modification-Dependent Enrichment (REMoDE) of DNA for Metagenomic Sequencing.** *Applied and environmental microbiology*
  Enam, S. U., Cherry, J. L., Leonard, S. R., Zheludev, I. N., Lipman, D. J., Fire, A. Z.
  2022: e0167022

- **Heterologous reporter expression in the planarian Schmidtea mediterranea through somatic mRNA transfection.** *Cell reports methods*
  Hall, R. N., Weill, U., Drees, L., Leal-Ortiz, S., Li, H., Khariton, M., Chai, C., Xue, Y., Rosental, B., Quake, S. R., Sanchez Alvarado, A., Melosh, N. A., Fire, et al
  2022; 2 (10): 100298

- **Context-dependent DNA polymerization effects can masquerade as DNA modification signals.** *BMC genomics*
  Takahashi, Y., Shoura, M., Fire, A., Morishita, S.
  2022; 23 (1): 249

- **Lymphoid blast transformation in an MPN with BCR-JAK2 treated with ruxolitinib: putative mechanisms of resistance.** *Blood advances*
  Chen, J. A., Hou, Y., Roskin, K. M., Arber, D. A., Bangs, C. D., Baughn, L. B., Cherry, A. M., Ewalt, M. D., Fire, A. Z., Fresard, L., Kearney, H. M., Montgomery, S. B., Ohgami, et al
  2021; 5 (17): 3492-3496

- **An essential role for the piRNA pathway in regulating the ribosomal RNA pool in C.elegans.** *Developmental cell*
  Wahba, L., Hansen, L., Fire, A. Z.
  2021

- **PLP-1 is essential for germ cell development and germline gene silencing in C. elegans.** *Development (Cambridge, England)*
  Vishnupriya, R., Thomas, L., Wahba, L., Fire, A., Subramaniam, K.
  2020

- **Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome.** *Nature microbiology*
  Wolf, Y. I., Silas, S., Wang, Y., Wu, S., Bocek, M., Kazlauskas, D., Krupovic, M., Fire, A., Dolja, V. V., Koonin, E. V.
  2020

- **An Extensive Meta-Metagenomic Search Identifies SARS-CoV-2-Homologous Sequences in Pangolin Lung Viromes.** *mSphere*
  Wahba, L., Jain, N., Fire, A. Z., Shoura, M. J., Artiles, K. L., McCoy, M. J., Jeong, D.
  2020; 5 (3)

- **Aberrant B cell repertoire selection associated with HIV neutralizing antibody breadth.** *Nature immunology*
  Roskin, K. M., Jackson, K. J., Lee, J., Hoh, R. A., Joshi, S. A., Hwang, K., Bonsignori, M., Pedroza-Pacheco, I., Liao, H., Moody, M. A., Fire, A. Z., Borrow, P., Haynes, et al
  2020

- **Transcription polymerase-catalyzed emergence of novel RNA replicons.** *Science (New York, N.Y.)*
  Jain, N. n., Blauch, L. R., Szymanski, M. R., Das, R. n., Tang, S. K., Yin, Y. W., Fire, A. Z.
  2020
- **Intron and gene size expansion during nervous system evolution.** *BMC genomics*
  McCoy, M. J., Fire, A. Z.
  2020; 21 (1): 360
- **Deconvolution of nucleic-acid length distributions: a gel electrophoresis analysis tool and applications.** *Nucleic acids research*
  Ziraldo, R., Shoura, M. J., Fire, A. Z., Levene, S. D.
  2019
- **Ribosome clearance during RNA interference.** *RNA (New York, N.Y.)*
  Pule, M. N., Glover, M. L., Fire, A. Z., Arribere, J. A.
  2019
- **Maternal Ribosomes Are Sufficient for Tissue Diversification during Embryonic Development in C-elegans** *DEVELOPMENTAL CELL*
  Cenik, E., Meng, X., Tang, N., Hall, R., Arribere, J. A., Cenik, C., Jin, Y., Fire, A.
  2019; 48 (6): 811-+
- **Assessment and Maintenance of Unigametic Germline Inheritance for C. elegans** *DEVELOPMENTAL CELL*
  Artiles, K. L., Fire, A. Z., Frokjaer-Jensen, C.
  2019; 48 (6): 827-+
- **Target-dependent nickase activities of the CRISPR-Cas nucleases Cpf1 and Cas9.** *Nature microbiology*
  Fu, B. X., Smith, J. D., Fuchs, R. T., Mabuchi, M., Curcuru, J., Robb, G. B., Fire, A. Z.
  2019
- **CLONALITY: POINT ESTIMATION** *ANNALS OF APPLIED STATISTICS*
  Tian, L., Liu, Y., Fire, A. Z., Boyd, S. D., Olshen, R. A.
  2019; 13 (1): 113–31
- **Assessment and Maintenance of Unigametic Germline Inheritance for C.elegans.** *Developmental cell*
  Artiles, K. L., Fire, A. Z., Frokjar-Jensen, C.
  2019
- **Maternal Ribosomes Are Sufficient for Tissue Diversification during Embryonic Development in C.elegans.** *Developmental cell*
  Cenik, E. S., Meng, X., Tang, N. H., Hall, R. N., Arribere, J. A., Cenik, C., Jin, Y., Fire, A.
  2019
- **Prospective Biopsy-Based Study of Chronic Kidney Disease of Unknown Etiology in Sri Lanka.** *Clinical journal of the American Society of Nephrology : CJASN*
  Anand, S., Montez-Rath, M. E., Adasooriya, D., Ratnatunga, N., Kambham, N., Wazil, A., Wijetunge, S., Badurdeen, Z., Ratnayake, C., Karunasena, N., Schensul, S. L., Valhos, P., Haider, et al
  2019
- **Recompleting the Caenorhabditis elegans genome.** *Genome research*
  Yoshimura, J. n., Ichikawa, K. n., Shoura, M. J., Artiles, K. L., Gabdank, I. n., Wahba, L. n., Smith, C. L., Edgley, M. L., Rougvie, A. E., Fire, A. Z., Morishita, S. n., Schwarz, E. M.
  2019
- **Epidemiology, molecular, and genetic methodologies to evaluate causes of CKDu around the world: report of the Working Group from the ISN International Consortium of Collaborators on CKDu.** *Kidney international*
  Anand, S. n., Caplin, B. n., Gonzalez-Quiroz, M. n., Schensul, S. L., Bhalla, V. n., Parada, X. n., Nanayakkara, N. n., Fire, A. n., Levin, A. n., Friedman, D. J.
  2019; 96 (6): 1254–60
- **A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition** *MOLECULAR CELL*
  Mohr, G., Silas, S., Stamos, J. L., Makarova, K. S., Markham, L. M., Yao, J., Lucas-Elio, P., Sanchez-Amat, A., Fire, A. Z., Koonin, E., Lambowitz, A. M.

2018; 72 (4): 700-+

- **A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition.** *Molecular cell*
  Mohr, G., Silas, S., Stamos, J. L., Makarova, K. S., Markham, L. M., Yao, J., Lucas-Elio, P., Sanchez-Amat, A., Fire, A. Z., Koonin, E. V., Lambowitz, A. M.
  2018
- **A Small RNA Isolation and Sequencing Protocol and Its Application to Assay CRISPR RNA Biogenesis in Bacteria** *BIO-PROTOCOL*
  Silas, S., Jain, N., Stadler, M., Fu, B., Sanchez-Amat, A., Fire, A. Z., Arribere, J.
  2018; 8 (4)
- **Nonsense mRNA suppression via nonstop decay** *ELIFE*
  Arribere, J. A., Fire, A. Z.
  2018; 7
- **Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in Caenorhabditis elegans and Homo sapiens.** *G3 (Bethesda, Md.)*
  Shoura, M. J., Gabdank, I., Hansen, L., Merker, J., Gotlib, J., Levene, S. D., Fire, A. Z.
  2017; 7 (10): 3295-3303
- **A novel TRIP11-FLT3 fusion in a patient with a myeloid/lymphoid neoplasm with eosinophilia** *CANCER GENETICS*
  Chung, A., Hou, Y., Ohgami, R. S., Von Gehr, A., Fisk, D. G., Roskin, K. M., Li, X., Gojenola, L., Bangs, C. D., Arber, D. A., Fire, A. Z., Cherry, A. M., Zehnder, et al
  2017; 216: 10–15
- **Type III CRISPR-Cas systems can provide redundancy to counteract viral escape from type I systems** *ELIFE*
  Silas, S., Lucas-Elio, P., Jackson, S. A., Aroca-Crevillen, A., Hansen, L. L., Fineran, P. C., Fire, A. Z., Sanchez-Amat, A.
  2017; 6
- **Sequence-Modified Antibiotic Resistance Genes Provide Sustained Plasmid-Mediated Transgene Expression in Mammals** *MOLECULAR THERAPY*
  Lu, J., Zhang, F., Fire, A. Z., Kay, M. A.
  2017; 25 (5): 1187-1198
- **High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences.** *Genetics*
  Fu, B. X., Wainberg, M. n., Kundaje, A. n., Fire, A. Z.
  2017; 206 (4): 1727–38
- **Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in Caenorhabditis elegans and Homo sapiens** *G3: GENES, GENOMES, GENETICS*
  Shoura, M., Gabdank, I., Merker, J., Gotlib, J., Levene, S., Fire, A.
  2017; 7: 3295-3303
- **On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires.** *mBio*
  Silas, S. n., Makarova, K. S., Shmakov, S. n., Páez-Espino, D. n., Mohr, G. n., Liu, Y. n., Davison, M. n., Roux, S. n., Krishnamurthy, S. R., Fu, B. X., Hansen, L. L., Wang, D. n., Sullivan, et al
  2017; 8 (4)
- **An Abundant Class of Non-coding DNA Can Prevent Stochastic Gene Silencing in the C. elegans Germline** *CELL*
  Frokjaer-Jensen, C., Jain, N., Hansen, L., Davis, M. W., Li, Y., Zhao, D., Rebora, K., Millet, J. R., Liu, X., Kim, S. K., Dupuy, D., Jorgensen, E. M., Fire, et al
  2016; 166 (2): 343-357
- **Translation readthrough mitigation** *NATURE*
  Arribere, J. A., Cenik, E. S., Jain, N., Hess, G. T., Lee, C. H., Bassik, M. C., Fire, A. Z.
  2016; 534 (7609): 719-?
- **Distinct patterns of Cas9 mismatch tolerance in vitro and in vivo** *NUCLEIC ACIDS RESEARCH*
  Fu, B. X., Onge, R. P., Fire, A. Z., Smith, J. D.

2016; 44 (11): 5365-5377

- **Persistence and evolution of allergen-specific IgE repertoires during subcutaneous specific immunotherapy** *JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY*
  Levin, M., King, J. J., Glanville, J., Jackson, K. J., Looney, T. J., Hoh, R. A., Mari, A., Andersson, M., Greiff, L., Fire, A. Z., Boyd, S. D., Ohlin, M.
  2016; 137 (5): 1535-1544
- **Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody.** *Cell*
  Bonsignori, M., Zhou, T., Sheng, Z., Chen, L., Gao, F., Joyce, M. G., Ozorowski, G., Chuang, G., Schramm, C. A., Wiehe, K., Alam, S. M., Bradley, T., Gladden, et al
  2016; 165 (2): 449-463
- **A streamlined tethered chromosome conformation capture protocol** *BMC GENOMICS*
  Gabdank, I., Ramakrishnan, S., Villeneuve, A. M., Fire, A. Z.
  2016; 17
- **Direct CRISPR spacer acquisition from RNA by a natural reverse transcriptase-Cas1 fusion protein** *SCIENCE*
  Silas, S., Mohr, G., Sidote, D. J., Markham, L. M., Sanchez-Amat, A., Bhaya, D., Lambowitz, A. M., Fire, A. Z.
  2016; 351 (6276): 932-?
- **Chikungunya Virus Sequences Across the First Epidemic in Nicaragua, 2014-2015.** *American journal of tropical medicine and hygiene*
  Wang, C., Saborio, S., Gresh, L., Eswarappa, M., Wu, D., Fire, A., Parameswaran, P., Balmaseda, A., Harris, E.
  2016; 94 (2): 400-403
- **Cas9 Variants Expand the Target Repertoire in Caenorhabditis elegans.** *Genetics*
  Bell, R. T., Fu, B. X., Fire, A. Z.
  2016; 202 (2): 381-388
- **Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species** *BMC GENOMICS*
  Nakatani, Y., Mello, C. C., Hashimoto, S., Shimada, A., Nakamura, R., Tsukahara, T., Qu, W., Yoshimura, J., Suzuki, Y., Sugano, S., Takeda, H., Fire, A., Morishita, et al
  2015; 16
- **Functional relevance of "seed" and "non-seed" sequences in microRNA-mediated promotion of C. elegans developmental progression** *RNA*
  Zhang, H., Artiles, K. L., Fire, A. Z.
  2015; 21 (11): 1980-1992
- **Landscape of target:guide homology effects on Cas9-mediated cleavage.** *Nucleic acids research*
  Fu, B. X., Hansen, L. L., Artiles, K. L., Nonet, M. L., Fire, A. Z.
  2014; 42 (22): 13778-13787
- **Efficient Marker-Free Recovery of Custom Genetic Modifications with CRISPR/Cas9 in Caenorhabditis elegans** *GENETICS*
  Arribere, J. A., Bell, R. T., Fu, B. X., Artiles, K. L., Hartman, P. S., Fire, A. Z.
  2014; 198 (3): 837-U842
- **Immunoglobulin Gene Insertions and Deletions in the Affinity Maturation of HIV-1 Broadly Reactive Neutralizing Antibodies** *CELL HOST & MICROBE*
  Kepler, T. B., Liao, H., Alam, S. M., Bhaskarabhatla, R., Zhang, R., Yandava, C., Stewart, S., Anasti, K., Kelsoe, G., Parks, R., Lloyd, K. E., Stolarchuk, C., Pritchett, et al
  2014; 16 (3): 304-313
- **Human responses to influenza vaccination show seroconversion signatures and convergent antibody rearrangements.** *Cell host & microbe*
  Jackson, K. J., Liu, Y., Roskin, K. M., Glanville, J., Hoh, R. A., Seo, K., Marshall, E. L., Gurley, T. C., Moody, M. A., Haynes, B. F., Walter, E. B., Liao, H., Albrecht, et al
  2014; 16 (1): 105-114
- **Effects of Aging, Cytomegalovirus Infection, and EBV Infection on Human B Cell Repertoires** *JOURNAL OF IMMUNOLOGY*
  Wang, C., Liu, Y., Xu, L. T., Jackson, K. J., Roskin, K. M., Pham, T. D., Laserson, J., Marshall, E. L., Seo, K., Lee, J., Furman, D., Koller, D., Dekker, et al

2014; 192 (2): 603-611

- **Gamete-Type Dependent Crossover Interference Levels in a Defined Region of Caenorhabditis elegans Chromosome V.** *G3 (Bethesda, Md.)*
  Gabdank, I., Fire, A. Z.
  2014; 4 (1): 117-120
- **A requirement for ERK-dependent Dicer phosphorylation in coordinating oocyte-to-embryo transition in C. elegans.** *Developmental cell*
  Drake, M. n., Furuta, T. n., Suen, K. M., Gonzalez, G. n., Liu, B. n., Kalia, A. n., Ladbury, J. E., Fire, A. Z., Skeath, J. B., Arur, S. n.
  2014; 31 (5): 614–28
- **Comprehensive whole-genome sequencing of an early-stage primary myelofibrosis patient defines low mutational burden and non-recurrent candidate genes.** *Haematologica*
  Merker, J. D., Roskin, K. M., Ng, D., Pan, C., Fisk, D. G., King, J. J., Hoh, R., Stadler, M., Okumoto, L. M., Abidi, P., Hewitt, R., Jones, C. D., Gojenola, et al
  2013; 98 (11): 1689-1696
- **Unusual DNA packaging characteristics in endoreduplicated Caenorhabditis elegans oocytes defined by in vivo accessibility to an endogenous nuclease activity** *EPIGENETICS & CHROMATIN*
  Gu, S. G., Goszczynski, B., McGhee, J. D., Fire, A. Z.
  2013; 6
- **Conserved translatome remodeling in nematode species executing a shared developmental transition.** *PLoS genetics*
  Stadler, M., Fire, A.
  2013; 9 (10)
- **The transcription start site landscape of C. elegans** *GENOME RESEARCH*
  Saito, T. L., Hashimoto, S., Gu, S. G., Morton, J. J., Stadler, M., Blumenthal, T., Fire, A., Morishita, S.
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