

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://sites.stanford.edu/firelab/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

->What We Do:

Our lab studies the mechanisms by which cells and organisms respond to genetic change.

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 natural mechanisms that are utilized by cells adapting to genetic change. These include mechanisms activated during normal development and systems for detecting and responding to foreign or unwanted genetic activity. At the root of these studies are questions of how a cell can distinguish "self" versus "nonself" and "wanted" versus "unwanted" gene expression.

We primarily make use of the nematode *C. elegans* 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. Much of the current effort in the lab is directed toward a molecular understanding of the RNAi machinery and its roles in the cell. 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.

->Who we are:

PI: Andrew Fire, Professor of Pathology and Genetics, Stanford University School of Medicine

Postdoctoral Fellows:

Dae-Eun Jeong (Ph.D. Pohang University of Science and Technology, Life Sciences, 2017)

Maya Kasowski (M.D./Ph.D. Yale University School of Medicine, 2016)

Matthew McCoy (Ph.D. Washington University, Molecular Genetics and Genomics 2018)

Massa Shoura (Ph.D. Univ. Texas at Dallas, Molecular-Cellular Biology 2013, Bioengineering 2014)

Lamia Wahba (Ph.D. Johns Hopkins University, Biology, 2013)

Graduate Students:

Nelson Hall (Stanford Bioengineering Ph.D. Program; B.S. MIT, 2016)

Nimit Jain (Stanford Bioengineering Ph.D. Program; B.S. Yale, 2011)

Undergraduate Students:

Alizeh Ahmad (Stanford Human Biology, 2019)

Visiting Scientist (Stanford Thinking-Matters Fellows Program):

Saumya Sankaran (Ph.D. Stanford, Biology, 2016)

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 positions for undergraduate researchers in the lab (especially summers, and particularly straightforward for current or incoming Stanford students). Email the PI at the above address.

Teaching

COURSES

2023-24

- Advanced Genetics: GENE 205 (Win)
- Computational Analysis of Biological Information: Introduction to Python for Biologists: 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)

2021-22

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

2020-21

- Advanced Genetics: GENE 205 (Win)
- C. Elegans Genetics: GENE 235 (Spr)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Alex Adams, Sierra Bowden, Ching Pin Cheng, Kelsey Fryer, Yannick Lee-Yow, Rahul Nagvekar, Lucero Rogel, Jack Shanahan, Liesl Strand, Gabriel Tauber, Tee Udomlumleart, Alyssa Yoxsimer

Postdoctoral Faculty Sponsor

Orkan Ilbay, Dae-Eun Jeong, Matthew McCoy

Doctoral Dissertation Advisor (AC)

Colette Benko, Usman Enam, Drew Galls, Janie Kim, Ivan Zheludev

Doctoral Dissertation Co-Advisor (AC)

Emily Greenwald

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Parallel gene size and isoform expansion of ancient neuronal genes.** *Current biology : CB*
McCoy, M. J., Fire, A. Z.
2024
- **Viroid-like colonists of human microbiomes.** *bioRxiv : the preprint server for biology*
Zheludev, I. N., Edgar, R. C., Lopez-Galiano, M. J., de la Pena, M., Babaian, A., Bhatt, A. S., 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
- **Ancient origins of complex neuronal genes.** *bioRxiv : the preprint server for biology*
McCoy, M. J., 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
 - **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., Cururu, 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 CKD of Unknown Etiology in Sri Lanka** *CLINICAL JOURNAL OF THE AMERICAN SOCIETY OF NEPHROLOGY*
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; 14 (2): 224–32

- **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
- **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
- **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
- **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 nuclelease 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.
2013; 23 (8): 1348-1361
- **Convergent antibody signatures in human dengue.** *Cell host & microbe*
Parameswaran, P., Liu, Y., Roskin, K. M., Jackson, K. K., Dixit, V. P., Lee, J., Artiles, K. L., Zompi, S., Vargas, M. J., Simen, B. B., Hanczaruk, B., McGowan, K. R., Tariq, et al
2013; 13 (6): 691-700
- **Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus.** *Nature*
Liao, H., Lynch, R., Zhou, T., Gao, F., Alam, S. M., Boyd, S. D., Fire, A. Z., Roskin, K. M., Schramm, C. A., Zhang, Z., Zhu, J., Shapiro, L., Mullikin, et al
2013; 496 (7446): 469-476
- **Minicircle DNA vectors achieve sustained expression reflected by active chromatin and transcriptional level.** *Molecular therapy : the journal of the American Society of Gene Therapy*
Gracey Maniar, L. E., Maniar, J. M., Chen, Z., Lu, J., Fire, A. Z., Kay, M. A.
2013; 21 (1): 131-138
- **Contributions of mRNA abundance, ribosome loading, and post- or peri-translational effects to temporal repression of *C-elegans* heterochronic miRNA targets** *GENOME RESEARCH*
Stadler, M., Artiles, K., Pak, J., Fire, A.
2012; 22 (12): 2418-2426
- **Whole Genome Sequence Analysis of Primary Myelofibrosis.** *54th Annual Meeting and Exposition of the American-Society-of-Hematology (ASH)*
Merker, J. D., Roskin, K., Ng, D., Pan, C., Fisk, D. G., Jones, C. D., Gojenola, L., Clark, M. J., Zhang, B., Cherry, M., Snyder, M., Boyd, S. D., Zehnder, et al

AMER SOC HEMATOLOGY.2012

● **Protection from Feed-Forward Amplification in an Amplified RNAi Mechanism** *CELL*

Pak, J., Maniar, J. M., Mello, C. C., Fire, A.
2012; 151 (4): 885-899

● **The Exogenous Spacer Length Between the 5' and 3' Ends of the Transgene Expression Cassette Affects Transgene Silencing From Plasmid-based Vectors** *MOLECULAR THERAPY*

Lu, J., Zhang, F., Xu, S., Fire, A. Z., Kay, M. A.
2012; 20 (11): 2111-2119

● **A nuclear Argonaute promotes multigenerational epigenetic inheritance and germline immortality** *NATURE*

Buckley, B. A., Burkhart, K. B., Gu, S. G., Spracklin, G., Kershner, A., Fritz, H., Kimble, J., Fire, A., Kennedy, S.
2012; 489 (7416): 447-451

● **Amplification of siRNA in Caenorhabditis elegans generates a transgenerational sequence-targeted histone H3 lysine 9 methylation footprint** *NATURE GENETICS*

Gu, S. G., Pak, J., Guang, S., Maniar, J. M., Kennedy, S., Fire, A.
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