

**CURRICULUM VITAE**

**Name:** Antonio J. Giraldez, Ph.D.  
Fergus Wallace Professor, Department of Genetics

**School:** Yale University School of Medicine and the Graduate School

**Education:** B.S. Chemistry. University Autonoma of Madrid (Spain) 1998  
Ph.D. Developmental Biology, European Molecular Biology Laboratory,  
(Germany) 2002

**CAREER/ACADEMIC APPOINTMENTS**

1998-2002 Ph.D with Dr. Stephen M. Cohen. Developmental Genetics. European Molecular Biology Laboratory. Heidelberg. Germany.

2003-2005 Postdoctoral Research, with Dr. Alexander F. Schier. Skirball Institute. New York University School of Medicine. NY.

2006 Postdoctoral Research, with Dr. Alexander F. Schier. Harvard University. Cambridge. MA.

2006-2011 Assistant Professor. Yale University School of Medicine. New Haven, Connecticut. USA

2011-2012 Associate Professor. Yale University School of Medicine. New Haven, Connecticut. USA

2013-2015 Associate Professor with Tenure. Yale University School of Medicine. New Haven, CT.

2012-2016 Director of Graduate Studies in Genetics. Yale University School of Medicine. New Haven, CT.

2015-Present Professor with Tenure. Yale University School of Medicine. New Haven, CT.

2016-2017 Interim Chair of the Department of Genetics Yale University School of Medicine. New Haven, CT.

2017-2023 Chair of the Department of Genetics Yale University School of Medicine. New Haven, CT.

**Administrative positions**

- 2012-2016 Director of Graduate Studies Genetics Department. Yale University School of Medicine. New Haven, Connecticut. USA
- 2016-2017 Interim Chair of the Department of Genetics Yale University School of Medicine. New Haven, CT.
- 2017-2023 Chair of the Department of Genetics Yale University School of Medicine. New Haven, CT.

**PROFESSIONAL HONORS & RECOGNITION****International/National/Regional**

- 2021 Member of the Connecticut Academy of Science and Engineering
- 2017 Blavatnik National Award for Young Scientists (Finalist)
- 2016 Whitman Center Research Fellow MBL (2016, 2017)
- 2016-2021 HHMI Faculty Scholar
- 2016 Blavatnik National Award for Young Scientists (Finalist)
- 2016 Whitman Center Research Fellow MBL
- 2015 Damon Runyon Fellowship Award Committee
- 2014 Vilcek Prize for Creative Promise in Biomedical Sciences
- 2008-2012 Pew Scholar
- 2007 John Kendrew Young investigator Award EMBL, Heidelberg
- 2007 NYAS Blavatnik Young Investigator Award (Finalist)
- 2004-2006 HFSP Postdoctoral Fellowship
- 2003-2004 EMBO Postdoctoral Fellowship
- 2001-2002 EMBL Postdoctoral bridging fellowship.
- 1998-2001 EMBL PhD fellowship
- 1998 3rd National Prize in Chemistry Degree. Ministry of Science. Spain
- 1997-1998 Undergraduate Research Fellowship. CBMSO. UAM.

**University**

- 2007-2010 Lois E. and Franklin H. Top, Jr., Yale Scholar Award
- 2016-present Wallace Professor of Genetics

**PERSONAL STATEMENT**

My laboratory combines Genomics, Imaging, Biochemical, Developmental and Computational approaches to investigate the molecular mechanisms of gene regulation and how they shape

embryonic development after fertilization. My contribution to science has resulted in paradigm shifts within several areas: i) the identification of a novel miRNA family (miR-430) that regulates the maternal to zygotic transition, later shown to provide a conserved regulatory mechanism in drosophila (miR-309) and xenopus (miR-430/427), ii) the identification of deadenylation as one of the molecular mechanisms that mediate miRNA-mediated repression, iii) the discovery of alternative processing pathways for microRNAs independent of Dicer and required for blood development; iv) the translation of micropeptides encoded in genes thought to be non-coding RNAs; v) the identification of a global gene regulatory layer in vertebrates by translated uORFs (~50%) of genes; vi) Identification of a new layer in the genetic code in animals (identified also by the Collier lab in Yeast), where translation of specific triplet codons, mediate mRNA deadenylation, decay and translation efficiency to shape gene expression across animals; vii) Identification of a novel function of nanog, oct4, and sox1 as key transcription factors to mediate activation of the zygotic genome after fertilization. Our interdisciplinary approach has begun to uncover the regulatory codes that shape embryogenesis from new coding regions in the genome to new transcriptional codes that regulate genome activation and cell fate identity, and we have developed innovative imaging approaches to gene regulation and chromatin architecture. We have also developed experimental approaches to define the targeting rules of Cas9, developing CRISPCan to identify the most active sgRNAs across species, which is now broadly used in the community (CRISPRscan.org). Finally, we are currently applying the genomic approaches developed over the last 18 years in my laboratory to develop novel therapeutic mRNAs with tissue specificity and using this technology I have founded an RNA therapeutics company called RESA therapeutics inc.

My broader contributions to science beyond scientific discoveries include a demonstrated commitment to mentoring, diversity and service to the community and can be divided in four areas:

**a)** In my laboratory, my trainees receive a multidisciplinary training in a multicultural environment with 11 nationalities currently represented in my 15-member laboratory. Trainees have now taken faculty positions in leading universities (D. Cifuentes, **Boston University**; M. Lee, **University of Pittsburg**; A Bazzini, **Stowers Institute**; Y Mishima, **Kyoto University**; JD Beudoin, **UCONN**; C Takacs, **Quinnipiac University**, E. Hoffman, **Yale University**; V. Tornini, **UCLA**, L. Miao **Florida State University**) and students have also taken positions within and outside academia (Pownall M, Faculty Fellow **UCSF**, Stahlhut C Postdoc, **CSHL**; Staton AA, Scientific writer **Infusion Communications**; Johnstone T, **Juno pharmaceuticals** Data scientist; Yartseva V Scientist at **Genentech**; Bonneau A, Postdoc at **MIT**; Musaef D , Science Advisor at **Goodwin and Procter**). Witnessing this thriving group of outstanding scientists, scholars, mentors, and colleagues is certainly one of the highlights of my career.

**b)** I served for 5 years at Yale University, as **Director of Graduate Studies** in the Department of Genetics where I shaped the curriculum to encourage students to focus on their scientific projects early on, reducing the time to graduation to 4.8 years from (6 years before I was DGS). ii) mentor and encourage students to get exposure to a wide range of different professional careers (within and outside academia) serving as advisor to the Biomedical Careers Science Committee and the annual career symposium, and more recently Chair of the Genetics Department and co-founder of the center for genomic health.

**c)** I served as **Chair of the Department of Genetics** at Yale for seven years, during which I shaped the department's direction through the recruitment of 16 faculty members, including ten tenure-track basic science faculty, five clinical faculty, and one clinical educator. I also led the establishment of the Yale Center for Genomic Health, culminating in the recruitment of its director, Dr. Ira Hall, and the re-invigoration of the clinical genetics program with the recruitment of the Clinical Chief of Genetics, Dr. Yong-Hui Jiang. Among the junior faculty recruited, five

were awarded the NIH Director's New Innovator Award (this represents 30% of all the Innovator Awards at Yale University), and one received the prestigious HHMI Freeman Hrabowski Scholarship. Additionally, I established the Office for Strategic Research Development, beginning with the recruitment of a Scientific Director, Dr. Caroline Hendry, and comprising four outstanding scientists, including three former journal editors from top journals (*Development*, *Nature Genetics*, and *Nature Cell Biology*). This initiative fostered a supportive environment for scientific management, mentoring, and grant applications, resulting in a significant increase in overall departmental funding (~126% over seven 7 years) and clinical revenue, with the NIH funding Blue Ridge Rank rising from 17 in 2017 (\$12,443,151) to 8 in 2023 (\$28,143,168). Funding is only a means to an end, and the junior faculty recruited during this time have made landmark discoveries, publishing eight articles in *Nature*, *Science*, and *Cell* as last authors over the past five years, with a median of nine papers per newly recruited faculty during this period. Contributing to building a thriving and diverse department at Yale has been one of the highlights of my career as a scientist and a member of the Yale community.

d) Within the broader scientific community, I participate in multiple **scientific review boards** for young investigators and fellowships (Pew, Damon Runyon, Smith Science fellows). Most significantly, I spearheaded, in collaboration with several postdocs and the Yale Office of Diversity, a major initiative to showcase the research of and mentor a diverse group of postdocs entering the job market. Inspired by the **Leading Edge Symposium**, this effort resulted in the creation of the Intersection Science Fellows Symposium. I leveraged my scientific network to engage 25 institutions across the USA, and together with the team we were able to attract 400 applicants, select 51 fellows and finalists, with over 1,500 participants in total. This initiative has become one of the prime recruitment opportunities across institutions in the USA, and this diverse cohort of outstanding fellows are now faculty across many of the top leading universities. I continued to serve as a senior advisor to this initiative for 2 years and later leadership in this project moved to the DEI office at Yale. More information can be found at: <https://www.intersectionssciencefellows.com/>

## SCIENTIFIC CONTRIBUTIONS

### 1. Identification of key factors that activate the vertebrate genome after fertilization:

A central question in biology is how embryonic development is initiated in the fertilized egg. Upon fertilization the zygotic genome is silent, and the first steps of development are instructed by maternal mRNAs and proteins deposited in the egg. However, the factors that initiate gene expression in the silent vertebrate embryo to trigger embryonic development were unknown. We have identified the Nanog, Oct4 and SoxB1 as long sought-after transcription factors key to activating the genome, and provide an entry point to understand how the embryo activates transcription. Nanog, Oct4 and SoxB1 maintain stem cell identity and function during reprogramming in vitro, while in vivo they initiate the zygotic program of development by reprogramming terminally differentiated cells, sperm and oocyte, to transient totipotency. These link stem cell biology, cellular reprogramming and early embryonic development. We have also undertaken follow up molecular mechanisms to understand the machinery required to activate the genome and how these factors remodel the chromatin, showing they are required to open the chromatin and mediate histone acetylation at promoters and enhancers. Finally we have developed ChromExM to visualize this machinery with single molecule resolution and proposed a model of genome activation called Kiss-and-Kick, where promoter enhancer contacts are set apart by activation of RNA-Pol II. I was senior author in these studies.

- a. Lee MT, Bonneau AR, Takacs CM, Bazzini AA, DiVito KR, Fleming ES & **Giraldez AJ**<sup>‡</sup>. Nanog, SoxB1 and Pou5f1/Oct4 regulate widespread zygotic gene activation during the maternal-to-zygotic transition. **Nature**, 2013 Nov 21;503(7476):360-4.
- b. Miao L, Tang Y, Bonneau AR, Chan SH, Kojima ML, Pownall ME, Vejnar CE, Giraldez AJ Synergistic activity of Nanog, Pou5f3, and Sox19b establishes chromatin accessibility and developmental competence in a context-dependent manner. **Molecular Cell** 2022
- c. Chan SH, Tang Y, Miao L, Darwich-Codore H, Vejnar CE, JBeaudoin JD, Musaev D, Fernandez JP, Benitez MDJ, Moreno-Mateos MA<sup>‡</sup>, **Giraldez AJ**<sup>‡</sup> Brd4 and p300 confer transcriptional competency during zygotic genome activation. **Developmental Cell**. 2019. Jun 17;49(6):867-881.e8. doi: 10.1016/j.devcel.2019.05.037.
- d. Pownall ME, Miao L, Vejnar CE, M'Saad O, Sherrard A, Frederick MA, Benitez MDJ, Boswell CW, Zaret KS, Bewersdorf J, **Giraldez AJ**<sup>‡</sup>. Chromatin expansion microscopy reveals nanoscale organization of transcription and chromatin. **Science** July 5, 2023. doi: 10.1126/science.ade5308.

## 2. Regulation of the maternal program, and how the cells clear the past during cellular transitions:

All animals inherit maternal information in the oocyte in the form of mRNAs and proteins needed to undergo the first developmental processes after fertilization. A large fraction of this information is degraded upon activation of the zygotic genome. This represents one of the most profound remodeling of gene expression in biology, but the effectors and the molecular mechanisms underlying this global regulation remained poorly understood. Our contribution is meaningful in two ways: First, we have uncovered a novel function for microRNAs (miR-430) in the clearance of a large fraction (~20-30%) of the maternal mRNAs during the maternal to zygotic transition in zebrafish. Indeed, this uncovered a conserved mechanism across several species through the same (Xenopus) or different (Drosophila) microRNAs. Second, we have identified that translation of specific codons induces mRNA stabilization or decay, and that this mechanism regulates differential mRNA decay during the maternal to zygotic transition across species (zebrafish, mouse, xenopus and drosophila). Finally, we identified a pathway called ORF mediated decay (OMD), whereby the NMD machinery UPF1 recognizes long and lowly translated coding sequences without premature stop codons to provide a major mechanism controlling global mRNA stability. Together this provides novel paradigms of how embryos regulate the previous developmental program (microRNAs and coding sequence), with implications reaching from cellular transitions, to mRNA homeostasis and fertility. I was leading or corresponding author in these studies.

- a. **Giraldez AJ**<sup>‡</sup>, Mishima Y, Rihel J, Grocock R, Dongen S, Inoue, K, Enright A, and Schier AF<sup>‡</sup>. Zebrafish miR-430 promotes deadenylation and clearance of maternal mRNAs. **Science**. 2006.Apr 7;312(5770):75-9. Epub 2006 Feb 16. <sup>‡</sup>Corresponding author.
- b. **Giraldez AJ**<sup>‡</sup>, Cinalli RM, Glasner ME, Enright A, Thomson JM, Baskerville S, Hammond SM, Bartel D, and Schier AF<sup>‡</sup>. MicroRNAs regulate brain morphogenesis in zebrafish. **Science**. 2005 May 6;308(5723):833-8.
- c. Bazzini A<sup>‡</sup>, del Viso F, Moreno-Mateos MA, Johnstone TG, Vejnar CE, Qin Y, Yao J, Khokha MK, and **Giraldez AJ**<sup>‡</sup>. Codon identity regulates mRNA stability and translation efficiency during the maternal-to-zygotic transition. **EMBOJ**. 2016 Jul 19. pii: e201694699.
- d. Kontur C<sup>‡</sup>, Jeong M, Cifuentes D, **Giraldez AJ**<sup>‡</sup>. Ythdf m6A Readers Function Redundantly during Zebrafish Development. **Cell Rep**. 2020 Dec 29;33(13):108598. doi: 10.1016/j.celrep.2020.108598. PMID: 33378672
- e. Musaev D, Abdelmessih M, Vejnar CE, Yartseva V, Weiss LA, Strayer EC, Takacs CM, **Giraldez AJ**<sup>‡</sup>. UPF1 regulates mRNA stability by sensing poorly translated coding sequences. **Cell Reports**. 2024 Apr 23;43(4):114074. doi: 10.1016/j.celrep.2024.114074.

Epub 2024 Apr 15. PMID: 38625794

### 3. Uncovered novel mechanisms of microRNA processing and function:

The discoveries of microRNAs lead to the identification of a new layer gene regulation, with far reaching implications in all aspects of biology, however the mechanism remained poorly understood. At a time when the field was solely focussed on the regulation of translation, our contribution resulted in a paradigm shift with the discovery that microRNAs cause mRNA decay through deadenylation of their endogenous targets. The dynamic analysis of miRNA function in vivo combined with ribosome footprinting lead to the discovery that translation is repressed by reducing the initiation rate, before triggering deadenylation of the message. These findings have provided some of the basis to understand the molecular mechanisms of miRNA function.

- a. Bazzini AA, Lee MT, **Giraldez AJ<sup>‡</sup>**. Ribosome Profiling Shows That miR-430 Reduces Translation Before Causing mRNA Decay in Zebrafish. **Science** 13 April 2012: 233-237.
- b. Takacs C<sup>‡</sup> and **Giraldez. AJ<sup>‡</sup>**. miR-430 regulates oriented cell division during neural tube development in zebrafish. **Developmental Biology**, 2015 Nov 30.

Over the last decade, Dicer was thought to be strictly required for the biogenesis of all miRNAs and siRNAs. Combining high-throughput sequencing of small RNAs in mutants of the miRNA-processing pathway, we identified a novel miRNA processing pathway independent of Dicer, but dependent on the catalytic activity of Argonaute2 (Ago2). We showed that this pathway is required for the processing of miR-451, a miRNA conserved in all vertebrates, expressed in the blood. This revealed important roles for this pathway in erythrocyte maturation across species. Furthermore, in a follow-up study, we uncovered PolyA ribonuclease (Yoda et al., Cell Reports 2013) as the enzyme that acts downstream of Ago2 in the processing of miRNAs. This enzyme provides an entry point to study small RNA turnover, as it is likely involved in the trimming of other small regulatory RNAs. This work helped to pave the way for new avenues of research in the study of miRNAs, by challenging a dogma, and defining a novel cellular pathway to produce small RNAs.

- c. Cifuentes D, Xue H, Taylor DW, Patnode H, Mishima Y, Cheloufi S, Ma E, Mane S, Hannon GJ, Lawson N, Wolfe S, **Giraldez AJ<sup>‡</sup>**. A novel miRNA processing pathway independent of Dicer requires Argonaute2. **Science**. 2010, Jun 25;328(5986):1694-8. Epub 2010 May 6
- d. Yoda M, Cifuentes D, Izumi N, Sakaguchi Y, Suzuki T, **Giraldez AJ<sup>‡</sup>** and Tomari Y<sup>‡</sup>. PARN mediates 3'-end trimming of Argonaute2-cleaved precursor microRNAs. **Cell Reports**, 2013, 5, 1–12, Nov. 14.

### 4. Characterization of the coding potential of the vertebrate genome:

Analysis of the eukaryotic genome has identified a large class of transcripts known as long-noncoding RNAs that lack classical hallmarks of protein-coding genes. However, many of these transcripts harbor short open reading frames, but their coding potential has not been experimentally addressed. Conversely, short peptides have emerged as important regulators of development and physiology, but their identification has been limited by their size. We have pioneered the combination of high resolution ribosome footprinting, with mass spectrometry, conservation analysis and a novel computational method (ORFscore) to define the actively translated open reading frame in individual transcripts. This approach enabled us to identify several hundred novel micropeptide-encoding genes (20-100 amino acids) in zebrafish and humans, within genes thought to lack coding potential. This study provides a conceptual shift in the study of predicted non-coding RNAs, uncovering previously unidentified small peptide-encoding genes with potential regulatory potential in vivo. This opens new areas of inquiry in genomics, cell biology and developmental biology for understanding the function of these

micropeptide-encoding genes in the context of a whole organism.

a. Bazzini AA<sup>#</sup>, Johnstone TG<sup>#</sup>, Christiano R, Mackowiak SD, Obermayer B, Fleming ES, Vejnar CE, Lee MT, Rajewsky N<sup>‡</sup>, Walther TC and **Giraldez AJ<sup>‡</sup>**. Identification of smallORFs in animals using ribosome footprinting and evolutionary conservation. **EMBO J**. 2014, May 2;33(9):981-93.

b. Johnstone TG, Bazzini AB and **Giraldez AJ<sup>‡</sup>**. Upstream ORFs act as prevalent translational repressors in vertebrates. **EMBO J**, 2016, Apr 1;35(7):706-23.

#### 5. Identification of the features governing CRISPR/Cas9 mediated targeting:

CRISPR-Cas9 technology provides a powerful system for genome engineering. However, variable activity across different single guide RNAs (sgRNAs) remains a significant limitation. In this study, we have analyzed the molecular features that influence sgRNA stability, activity and loading into Cas9 in vivo. On the basis of these results, we created a predictive sgRNA-scoring algorithm, CRISPRscan.org, that effectively captures the sequence features affecting the activity of CRISPR-Cas9 in vivo. These results identify determinants that influence Cas9 activity and provide a framework for the design of highly efficient sgRNAs for genome targeting in vivo across different species.

a. Moreno-Mateos MA, Vejnar CE, Beaudoin JD, Fernandez JP, Mis EK, Khokha MK, **Giraldez AJ**. CRISPRscan: designing highly efficient sgRNAs for CRISPR-Cas9 targeting in vivo. **Nature Methods**. 2015 Oct;12(10):982-8. doi: 10.1038/nmeth.3543. Epub 2015 Aug 31.

b. Moreno-Mateos MA, Fernandez JP, Rouet R, Vejnar CE, Lane MA, Mis E, Khokha MK, Doudna JA, **Giraldez AJ**. CRISPR-Cpf1 mediates efficient homology-directed repair and temperature-controlled genome editing. **Nature Communications**. 2017 Dec 8;8(1):2024. doi: 10.1038/s41467-017-01836-2.

#### 6. Scientific collaborations:

As part of our scientific collaborations and **team science**, our genomic contributions have allowed us to identify novel pathways regulating gene expression through genetic compensation, identify the gene mutated in long sought mutants for blood development, develop resources for the scientific community (crisprscan.org, LabxDB, GEARs) and undertake molecular biology experiments aboard the international space station among others.

a. El-Brolosy MA, Kontarakis Z, Rossi A, Kuenne C, Günther S, Fukuda N, Kikhi K, Boezio GLM, Takacs CM, Lai SL, Fukuda R, Gerri C, **Giraldez AJ**, Stainier DYR. Genetic compensation triggered by mutant mRNA degradation. **Nature**. 2019 Apr;568(7751):193-197. doi: 10.1038/s41586-019-1064-z. Epub 2019 Apr 3.

b. Reischauer S, Stone OA, Villasenor A, Chi N, Jin SW, Martin M, Lee MT, Fukuda N, Marass M, Witty A, Fiddes I, Kuo T, Chung WS, Salek S, Lerrigo R, Alsö J, Luo S, Tworus D, Augustine SM, Mucenieks S, Nystedt B, **Giraldez AJ**, Schroth GP, Andersson O, Stainier DY<sup>‡</sup>. Cloche is a bHLH-PAS transcription factor that drives haemato-vascular specification. **Nature**. 2016 Jul 13;535(7611):294-8. doi: 10.1038/nature18614.

c. Moreno-Mateos MA, Fernandez JP, Rouet R, Vejnar CE, Lane MA, Mis E, Khokha MK, Doudna JA, **Giraldez AJ<sup>‡</sup>**. CRISPR-Cpf1 mediates efficient homology-directed repair and temperature-controlled genome editing. **Nature Communications**. 2017 Dec 8;8(1):2024. doi: 10.1038/s41467-017-01836-2.

- d. Vicencio J, Sánchez-Bolaños C, Moreno-Sánchez I, Brena D, Vejnar CE, Kukhtar D, Ruiz-López M, Cots-Ponjoan M, Rubio A, Melero NR, Crespo-Cuadrado J, Carolis C, Pérez-Pulido AJ, **Giraldez AJ**, Kleinstiver BP, Cerón J, Moreno-Mateos MA. Genome editing in animals with minimal PAM CRISPR-Cas9 enzymes. **Nat Commun.** 2022 May 12;13(1):2601. doi: 10.1038/s41467-022-30228-4.
- e. Kasper DM, Moro A, Ristori E, Narayanan A, Hill-Teran G, Fleming E, Moreno-Mateos M, Vejnar CE, Zhang J, Lee D, Gu M, Gerstein M, **Giraldez A**, Nicoli S. MicroRNAs Establish Uniform Traits during the Architecture of Vertebrate Embryos. **Developmental Cell.** 2017 Mar 27;40(6):552-565.e5. doi: 10.1016/j.devcel.2017.02.021
- f. Boswell CW, Hoppe C, Sherrard A, Miao L, Kojima ML, Krishna S, Musaev D, Zhao N, Stasevich TJ, **Giraldez AJ**. Genetically encoded affinity reagents (GEARs): A toolkit for visualizing and manipulating endogenous protein function in vivo. **bioRxiv** 2024. doi: 10.1101/2023.11.15.567075.
- g. Boguraev AS, Christensen HC, Bonneau AR, Pezza JA, Nichols NM, **Giraldez AJ**, Gray MM, Wagner BM, Aken JT, Foley KD, Copeland DS, Kraves S, Alvarez Saavedra E. Successful amplification of DNA aboard the International Space Station. **NPJ Microgravity.** 2017 Nov 16;3:26

Complete List of Published Work in MyBibliography:

<https://pubmed.ncbi.nlm.nih.gov/?term=giraldez+aj&sort=date&size=100>

## GRANT HISTORY

[https://reporter.nih.gov/search/EY02Hlo7rkyKL8Uix5\\_3Sw/projects](https://reporter.nih.gov/search/EY02Hlo7rkyKL8Uix5_3Sw/projects)

## OTHER SUPPORT

### Active

**R01MH118554** (Giraldez, PI) 03/15/19-01/31/24 1.56 cal mos

NIH/NIMHS \$2,955,469  
Functional analysis of autism risk genes during neural development using single cell seq

We combine single cell sequencing, with genetic, genomic and computational approaches in zebrafish and embryoid bodies to i) characterize the role of ASD-risk genes in healthy neural gene regulatory networks.

**R01HD100035** (Giraldez, PI) 05/07/20-02/28/25 1.8 cal mos

NIH/NCHD \$2,848,442

Deciphering the regulatory code that specifies different cell fates in development using single cell

This proposal aims to understand how different cell types in the developing embryo are generated, the transcription factors involved and the sequences in the genome activated in different cells

**R35GM122580-06** (Giraldez, PI) 05/01/22-04/30/27 6.12 cal mos

NIH/ NIGMS \$5,778,750

Molecular mechanisms of the maternal to zygotic transition

The goal of understanding basic conserved principles of how genes are regulated that can be applied to other systems, including reprogramming of the cellular fates and cancer.

**1R01HG012969-01A1** (Giraldez PI, Bewersdorf Co-PI, Wang Co-PI) 03/01/2024 - 02/29/2028

NIH/NHGRI

Multimodal Analysis of the Genome Architecture Using Expansion Microscopy

Major Goals: This proposal aims to develop a novel method of expansion microscopy to visualize the structure of the chromatin with sequence and nucleosomal resolution while allowing multimodal labeling to other chromatin proteins.

### Past Grants

Agency: **Simons Foundation**  
 I.D.# 504633  
 Title: "Effect of Autism risk genes in neural cell identity using single cell seq"  
 P.I.: Antonio Giraldez  
 Percent effort: 5%  
 Direct costs per year: \$229,397  
 Project period: 09/01/17-08/31/20

Agency: **HHMI**  
 I.D.# 55108524  
 Title: "Molecular analysis of the maternal to zygotic transition"  
 P.I.: Antonio Giraldez  
 Percent effort: 5%  
 Direct costs per year: \$125,000  
 Project period: 11/01/16-10/30/22

Agency: **NIH**  
 I.D.# **R01GM103789 (NCE)**  
 Title: "Analysis of the gene networks regulating the maternal to zygotic transition"  
 P.I.: Antonio Giraldez  
 Percent effort: 19%  
 Direct costs per year: \$255,726

Total costs for project period: \$1,748,355  
 Project period: 09/01/2012-08/31/2016

Agency: NIH  
 I.D.# **R01HD074078 (NCE)**  
 Title: "Functional analysis of the zebrafish genome through RNA-seq and ribosome profile"  
 P.I.: Antonio Giraldez  
 Percent effort: 10%  
 Direct costs per year: \$305,617  
 Total costs for project period: \$2,377,640  
 Project period: 08/15/2012-04/30/2017 (Pre award 7/1/12)

Agency: NIH  
 I.D.# **R01 GM101108-03**  
 Title: "Molecular Characterization of the microRNA Processing Pathways"  
 P.I.: Antonio Giraldez  
 Percent effort: 20%  
 Direct costs per year: \$ 300,696  
 Total costs for project period: \$1,982,821  
 Project period 5/1/2012-2/29/2016 (Pre-award 2/1/12)

Agency: NIH  
 I.D.# **R01GM102251-01**  
 Title: "Molecular mechanisms of miRNA mediated regulation"  
 P.I.: Antonio Giraldez  
 Percent effort: 19%  
 Direct costs per year: \$183,350  
 Total costs for project period: \$1,253,302  
 Project period: 08/10/2012-05/31/2016

Agency: NIH  
 I.D.# **R21HD073768-01**  
 Title: "Development of RNA interference in zebrafish"  
 P.I.: Antonio Giraldez  
 Percent effort: 5 %  
 Direct costs per year: \$ 142,350  
 Total costs for project period: \$ 444,513  
 Project period: 7/1/2012-6/31/2014

Agency: MOD  
 I.D.# **MARCH OF DIMES #1-FY12-230**  
 Title: "The role of microRNAs during vertebrate development "  
 P.I.: Antonio Giraldez  
 Percent effort: 2%  
 Direct costs per year: \$100,186  
 Total costs for project period: \$ 334,312

Project period: 6/1/2012-5/31/2015

Agency: NIH  
 I.D.# **RC2 MH089956-01**  
 Title: " Genomic profiling and Functional Mutation Analysis in Autism Spectrum Disorders "  
 P.I.: Mathew State (Giraldez Co-Pi)  
 Percent effort: 20%  
 Direct costs per year: \$220,000  
 Total costs for project period: \$2,245,836  
 Project period: 09/30/2009-08/31/2012 (no cost ext)

Agency: Pew Charitable Trusts  
 I.D.# **Pew Scholars in the Biomedical Sciences**  
 Title: "The role of microRNAs in vertebrate development "  
 P.I.: Antonio Giraldez  
 Percent effort: 1%  
 Direct costs per year: \$ 23,076  
 Total costs for project period: \$ 240,000  
 Project period: 07/01/2008-6/30/2013 (no cost ext)

Agency: Yale Center for Genomics and Proteomics  
 I.D.# **Yale Genomics Grant**  
 Title: "Identification of the microRNA regulatory networks in vertebrates"  
 P.I.: Antonio Giraldez  
 Percent effort: 0%  
 Direct costs per year: \$25,000  
 Total costs for project period: \$25,000  
 Project period: 04/01/2008-03/31/2009

Agency: NIH  
 I.D.# **R01 GM081602-01**  
 Title: "The Role of microRNAs in Vertebrate Development"  
 P.I.: Antonio Giraldez  
 Percent effort: 75%  
 Direct costs per year: \$ 188,000  
 Total costs for project period: \$ 1,545,536  
 Project period: 08/01/2007-05/31/2012

Agency: MDA  
 I.D.# **115608**  
 Title: "The role of microRNAs in muscle development and muscular dystrophy "  
 P.I.: Antonio Giraldez  
 Percent effort: 15.25 %  
 Direct costs per year: \$113,913  
 Total costs for project period: \$385,180  
 Project period: 01/01/2009-12/31/2011

Agency: NIH

I.D.# **GM081602 ARRA Supplement**  
 Title: "The role of microRNAs in vertebrate development "  
 P.I.: Antonio Giraldez  
 Percent effort: 0%  
 Direct costs per year: \$63,819  
 Total costs for project period: \$105,620  
 Project period: 02/12/2010-12/31/2010

## **INVITED SPEAKING ENGAGEMENTS, PRESENTATIONS, SYMPOSIA & WORKSHOPS**

### **International/National**

- 2025 Invited Speaker EMBO | EMBL symposium "Cell biology of the nucleus".
- 2025 Invited speaker Mount Sinai Medical Center, New York, USA
- 2025 Invited speaker Tsinghua University, Beijing, China
- 2025 Invited Speaker Institute for Biochemistry and Cell biology, Shanghai.
- 2025 Invited speaker Gene Regulation Workshop, Lausanne, Switzerland.
- 2025 Invited speaker Telluride RNA conference, USA
- 2025 Invited speaker Expansion Microscopy Forum, Goettingen, Germany
- 2025 Selected talk, International Stem Cell Society meeting, Hong Kong,.
- 2025 Invited speaker Center for Developmental Biology, Seville, Spain
- 2025 Invited speaker Institute for Biomedical Research, Barcelona, Spain
  
- 2024 Invited speaker Italian Zebrafish meeting
- 2024 Invited speaker Center for Genomic Regulation Barcelona
- 2024 Invited speaker Universidad Autonoma of Madrid
- 2023 Invited speaker UCONN
- 2023 Invited speaker Hubrecht institute
- 2023 Invited speaker UT Southwestern
- 2023 Invited speaker Stanford university Frontiers in Biology
- 2023 Invited speaker Caltech
  
- 2022 Invited speaker NYU
- 2022 Invited speaker UMASS med School
- 2022 Invited speaker MBL zebrafish course
- 2022 Invited speaker MBL embryology course
- 2022 NCI seminar Series. Genome integrity
- 2022 EMBO workshop on Awakening the Genome, Vienna

- 2022 Invited Speaker, Vienna Biocenter, IMP, Vienna
- 2022 Invited Speaker Developmental Biology, UPenn.
  
- 2021 Invited Speaker Cancer Research Center of Salamanca (CIC) of Salamanca
- 2021 GRC Fertilization and Activation of Development
- 2021 IMB seminar series. University of Oregon
  
- 2020 Invited Speaker Department of Cell and Developmental Biology. Mount Sinai
- 2020 Invited Speaker Department of Cell Biology. Duke University
- 2020 Albert Einstein Stem Cell institute
- 2019 International Symposium on Early Embryonic Development in Beijing
- 2019 Invited Speaker, International Zebrafish Conference, Suzhou, China
- 2019 Invited Speaker, Gene regulation in development. Atacama, Chile
  
- 2018 Seminar Speaker Hubrecht University. The Netherlands
- 2018 International meeting in RNA biology Seoul, Korea
- 2018 Keynote Speaker CSHL meeting in translational control
- 2018 Society of Developmental Biology international meeting. Portland Oregon.
- 2018 Seminar Speaker Brandeis University
- 2018 Keystone Symposia Noncoding RNAs
- 2018 Seminar Speaker MIT Whitehead,
  
- 2017 Biochemistry & Biophysics Seminar series at UCSF
- 2017 HHMI Conference, Washington DC
- 2017 Congress in Molecular Biology and Biochemistry, Gijon Asturias Spain
- 2017 University of Minnesota Symposium.
- 2017 Annual meeting and Workshop NIH. Washington
- 2017 EMBO Symposium, Awakening the genome. Germany, Dresden
- 2017 University of Utah, Department of Human Genetics
- 2017 Center for genomic Regulation. Spain Barcelona
- 2017 Institute for Research in Biomedicine. IRB. Spain, Barcelona
- 2017 Gene regulatory systems in Development. Spain, Carmona
- 2017 Brown University. Department of Biology
- 2017 Upenn. Developmental Biology Seminar Series
- 2017 Zebrafish Strategic Conference. Asilomar

- 2016 Columbia University
- 2016 Keystone Symposia Stem Cells and Regeneration- Silverthorne, CO
- 2016 3rd Developmental Biology Workshop NIH
- 2016 MARC NU-STAR Seminar at Northeastern Illinois University
- 2016 EMBL epitranscriptome. EMBL Heidelberg.
- 2016 Vienna microsposium IMBA-IMP
- 2016 Computational biology conference Florida
- 2016 Blavatnik Science Symposium NYC
- 2016 Complex life of RNA
- 2016 IMB conference
- 2016 Heidelberg Steve Cohen symposium
- 2016 The Hospital for Sick Children Seminar Series
- 2016 Frontiers of Biology Stanford University, Developmental Biology Department
  
- 2015 6th Strategic Conference of Zebrafish Investigators, Pacific Grove, CA
- 2015 Seminar NYU Department of Biology
- 2015 University of Wisconsin School of Medicine and Public Health, Seminar
- 2015 Annual Meeting of Korean Society for Biochemistry and Molecular Biology (KSBMB)
- 2015 9th European Zebrafish Meeting Oslo Norway
- 2015 Gordon Conference, Fertilization and Activation of Development, NH
  
- 2014 13th Annual McGill Workshop on Bioinformatics in Barbados
- 2014 Keystone Symposium RNA Silencing Sheraton Seattle Hotel in Seattle, Washington
- 2014 UCB CDB Seminar
- 2014 EMBO/EMBL SYMPOSIA
- 2014 Northwestern University
- 2014 Santa Cruz Developmental Meeting
- 2014 RNA meeting in Quebec Ribo Club
- 2014 Ohio State University
- 2014 Towards an encyclopedia of DNA elements in zebrafish London, UK
- 2014 Santa Cruz Developmental Biology Meeting.
- 2014 Non-coding RNA - From Basic Mechanisms to Cancer, DKFZ, Germany
- 2014 Biochemistry Department, Northwestern University, Chicago, USA
- 2014 Department of Biochemistry, University of Washington, Seattle, USA
- 2014 University of California Berkeley, Division of Cell & Developmental Biology, USA
- 2014 MicroRNA workshop. McGill University's Bellairs Research Station, Barbados

- 2014 Keystone Symposium RNA silencing, Seattle, Washington. USA
- 2013 RNA Program in Academia Sinica (RPAS), Taipei, Taiwan
- 2013 Molecular Biology Society of Japan, Kobe, Japan
- 2013 RNA Symposium: Nobel Forum Karolinska Institute, Stockholm, Sweden
- 2013 EMBO|EMBL Symposium: Non-Coding Genome, Heidelberg, Germany
- 2013 EMBO, Protein Synthesis and Translational Control, Heidelberg, Germany
- 2013 Gordon Conference in Developmental Biology, Il Ciocco, Italy
- 2013 Cellular aspects of mRNA fate, Université Pierre et Marie Curie, Paris, France
- 2013 Micro Symposium, IMP, Vienna.
- 2013 National Institute of Child Health and Human Development, NIH, Bethesda, ME
- 2013 Keystone Meeting, Noncoding RNAs in Development and Cancer, Vancouver, CA
- 2012 Cincinnati Children's Hospital Medical Center, Cincinnati, OH.
- 2012 Annual Developmental Biology symposium, McGill University, Montreal, CA.
- 2012 CRG, Centre de Regulacio Genomica, Barcelona, Spain.
- 2012 FMI, Friedrich Miescher Institute for Biomedical Research , Basel, Switzerland.
- 2012 RIKEN, Center for Developmental Biology, Kobe, Japan.
- 2012 Max Plank Institute for Biochemistry, Munich, Germany.
- 2012 Institute of Molecular Biology, Mainz, Germany.
- 2012 EMBL, Developmental Biology Department, Heidelberg, Germany
- 2012 Keystone Meeting, RNA Silencing, Vancouver, CA
- 2012 Department of Developmental and Molecular Biology, Albert Einstein, NY.
- 2011 Microsymposium on small RNAs. IMP. Vienna. Austria.
- 2011 Non-coding RNAs and Cancer Symposium. UCL Cancer Institute. London, England.
- 2011 Department of Medicine. New York University School of Medicine. New York.
- 2011 Keystone Symposium on Mechanism and Biology of Silencing, Monterey, California.
- 2010 Genetics department. Skirball Institute. NYU. New York.
- 2010 EMBO/EMBL Non Coding Genome Symposium. Heidelberg. Germany
- 2010 Regulatory roles of small RNAs. Weizmann Institute of Science. Rehovot, Israel.
- 2010 Santa Cruz Developmental Biology Meeting. Santa Cruz. California.
- 2009 4th Barossa Meeting. Cell signaling in Cancer and Development. Adelaide, Australia.
- 2009 Twenty-first Annual Kavli Frontiers of Science symposium. Irvine California.
- 2009 International PhD program, Gulbenkian Institute, Oeiras. Portugal
- 2009 Institute of Molecular Medicine, Lisbon, Portugal
- 2009 European Zebrafish meeting. Rome. Italy

- 2009 The Biology of RNA silencing. Keystone meeting. Victoria, British Columbia. Canada.
- 2009 Pew Meeting on Biomedical Sciences. Puerto Rico.
- 2009 Center for Research on Reproduction. University of Pennsylvania. Philadelphia.
- 2009 Strategic Conference of Zebrafish Investigators. Asilomar, CA. USA.
- 2008 48th Annual Meeting of the American Society for Cell Biology. San Francisco, CA.
- 2008 University of Connecticut Health Center. Farmington, CT. USA.
- 2008 European Molecular Biology Laboratory. Heidelberg. Germany
- 2008 MicroRNA Symposium. Vienna, Austria.
- 2008 Regulatory RNA Symposium. Symposium. Toronto, Canada.
- 2008 National Center for Biological Sciences. Bangalore, India.
- 2008 Temasek Life Science Laboratory, Singapore.
- 2008 Institute of Molecular and Cell Biology. Singapore.
- 2008 Vanderbilt University, Nashville, Tennessee, USA
- 2007 Keystone Symposia. MicroRNAs and cancer. Keystone, Colorado. USA
- 2007 Molecular Biology Society of Japan Spring Symposium, Awajishima Island, Japan.
- 2007 New York Academy of Sciences. RNAi discussion group. New York. USA
- 2007 Keystone Symposia 'miRNAs and siRNAs' at Keystone, Colorado. USA
- 2007 Strategic Conference of Zebrafish Investigators. Asilomar, CA. USA.
- 2006 Keystone Symposia. RNAi and Related Pathways. Vancouver, BC, Canada.
- 2006 Department of Physiology. Columbia University. New York
- 2006 Cold Spring Harbor Laboratory. Cold Spring Harbor. New York.
- 2006 Genetics Department. Yale University School of Medicine. New Haven Connecticut.
- 2006 Department of Biology. New York University. New York.
- 2006 Department of Gene expression. UMASS Medical School. Worcester, Massachusetts
- 2006 Center for RNA. Case Western Reserve University. Cincinnati, Ohio.
- 2006 Department of Biochemistry. UMASS Medical School. Worcester, Massachusetts.
- 2005 CSHL RNAi meeting. Cold Spring Harbor Laboratory, New York.
- 2005 New York Academy of Sciences. RNAi discussion group. New York.
- 2005 Keystone Symposia Meeting. Beaver Run Resort Breckenridge, Colorado. USA
- 2002 ELSO 2002. Nice, France.

## **PROFESSIONAL SERVICE**

### **Peer Review Groups/Grant Study Sections**

- 2017-2021 NIH Dev1 study section permanent member.
- 2016-2019 Pew Scholars Alumni Review Board

2016-2019	Damon Runyon Cancer Research Foundation Fellowship Award Committee
2016	NIH/NIAMS ad hoc reviewer Board of Scientific Counselors
2015	NIH Dev1 study section ad hoc reviewer
2014	NIH/SREA reviewer for a CSR study section, ad hoc reviewer
2008	NIH reviewer for a Molecular Neurogenetics study section, ad hoc reviewer

### **Journal Service**

#### Reviewer

2007-present Reviewer for Cell, Nature, Nature Genetics, Science, Current Biology, Cell Metabolism, Developmental Cell, EMBO Journal, Genome Biology, Nature Molecular Structural Biology, PLoS ONE, Proceedings of the National Academy of Sciences, BMC Genomics, RNA,

### **Professional Organizations**

2004-present New York Academy of Science

### **Meeting Planning**

2007-2011	Co-Organizer, Genetics Department Retreat
2019	Faculty Founder Inaugural Intersection Science Fellows Symposium
2021	Faculty Advisor Intersection Science Fellows Symposium

### **Yale University Service**

2012-2016	Director of Graduate Studies, Genetics.
2016-2023	Chair of the Department of Genetics

### **University Committees**

2012-2016	Member, executive committee of the Developmental Biology Training Grant
2012-2016	Member, executive committee for the Human Genetics Training Grant
2012-2016	Member, executive committee MCGD
2011-2016	Member, advisory committee for the Genetics Training Grant
2009-2011	Vertebrate Developmental Biology/Pediatrics Faculty Search Committee
2014-2016	Member of the Tenure and Promotion University Committee

**Departmental Committees**

- 2010-2016 Co-Organizer Genetics Seminar Series
- 2009-2010 Co-Organizer of the Interdepartmental Junior Faculty Meetings
- 2014 Member of the systems biology Search committee (Faculty recruited: Sidi Chen)
- 2015 Member of the Genetics Department Search Committee (Faculty recruited Smita Krishnaswami)
- 2016-2017 Chair of the Genetics Department search committee (Recruited Bluma Lesch, Monkol Lek and Steven Wang)
- 2017 Chair of the Personalized medicine search committee (Recruited Dr. Michael Murray)
- 2018 Chair of the Genetics Department Clinical search committee (Recruited Rama Kastury)
- 2018 Chair of the Clinical Chief Search committee (Recruited Dr. Yong Hui Jiang)
- 2018-2019 Chair of the Genetics Department search committee (Recruited Kaelyn Sumigray)
- 2019-2020 Member of the Stem cell center Search committee (Faculty Recruited Zach Smith)
- 2019-2020 Chair of the Genetics Department search committee (Recruited Berna Sozen)
- 2018-2019 Chair of the Genetics Department YCGH search committee (Recruited Ira Hall and Sabrina Nuñez)
- 2020-2021 Chair of the Genetics Department search committee (Recruited Steven Reilly)
- 2021 Member of the Genetics Clinical search committee (Recruited Theo Gerves, Nada Derar)
- 2021-2022 Chair of the Genetics Search committee (Recruited Trevor Sorrels and Diyendo Massilani)
- 2022 Member of the Search committee for the Chair of Dermatology (Chair appointed Keith Choate)

**Faculty mentoring**

Participant in the 1st Junior faculty retreat as a faculty in the discussion panel

Co-organizer of the junior faculty meeting in group/organizational psychology (David Berg)

## BIBLIOGRAPHY

### Peer-Reviewed Original Research

<https://www.ncbi.nlm.nih.gov/pubmed?term=giraldez+AJ&cmd=DetailsSearch>

1. Youtten SE, Miao L, Hoppe C, Boswell CW, Musaev D, Abdelmessih M, Krishnaswamy S, **Giraldez AJ†**, Tornini VA†. Novel cell states arise in embryonic cells devoid of key reprogramming factors. *bioRxiv* [Preprint]. Accepted **Cell Rep.** 2025 15:2024.05.13.593729. doi: 10.1101/2024.05.13.593729. PMID: 38798464.
2. Kojima ML, Hoppe C, **Giraldez AJ†**. The maternal-to-zygotic transition: reprogramming of the cytoplasm and nucleus. *Nat Rev Genet.* 2025 Apr;26(4):245–267. doi: 10.1038/s41576-024-00792-0. Epub 2024 Nov 25. PMID: 39587307.
3. Vock IW, Tang D, **Giraldez AJ**, Simon MD. RNA DecayCafe, a uniformly processed atlas of RNA half-life estimates across multiple human cell lines. *bioRxiv* [Preprint]. 2025 Aug 21:2025.08.19.671151. doi: 10.1101/2025.08.19.671151. PMID: 40894569.
4. Young LN, Sherrard A, Zhou H, Shaikh F, Hutchings J, Riggi M, Rosen MK, **Giraldez AJ†**, Villa E†. ExoSloNano: Multi-Modal Nanogold Tags for identification of Macromolecules in Live Cells & Cryo-Electron Tomograms. *bioRxiv* 2024 Oct 13:2024.10.12.617288. doi: 10.1101/2024.10.12.617288. Accepted **Nature Methods**
5. Boswell CW, Hoppe C, Sherrard A, Miao L, Kojima ML, Martino P, Zhao N, Stasevich TJ, S Nicoli, **Giraldez AJ†**. Genetically encoded affinity reagents (GEARs): A toolkit for visualizing and manipulating endogenous protein function in vivo. *bioRxiv* 2024. doi: 10.1101/2023.11.15.567075. **Nature Commun.** 2025 Jul 1;16(1):5503. doi: 10.1038/s41467-025-61003-w.
6. Boraas LC, Hu M, Martino P, Thornton L, Vejnar CE, Zhen G, Zeng L, Parker DM, Cox AL, **Giraldez AJ**, Su X, Mayr C, Wang S, Nicoli S. G3BP1 ribonucleoprotein complexes regulate focal adhesion protein mobility and cell migration. **Cell Rep.** 2025 Feb 25;44(2):115237. doi: 10.1016/j.celrep.2025.115237. Epub 2025 Feb 1. PMID: 39883578.
7. Strayer EC, Krishna S, Lee H, Vejnar C, Beaudoin JD\*, **Giraldez AJ†**. NaP-TRAP, a novel massively parallel reporter assay to quantify translation control. *bioRxiv*. doi: 10.1101/2023.11.09.566434. **Nature communications.** 2024 Dec 30;15(1):10898. doi: 10.1038/s41467-024-55274-y. PMID: 39738051
8. Fuentes R, Marlow FL, Abrams EW, Zhang H, Kobayashi M, Gupta T, Kapp LD, DiNardo Z, Heller R, Cisternas R, García-Castro P, Segovia-Miranda F, Montecinos-Franjola F, Vought W, Vejnar CE, **Giraldez AJ**, Mullins MC. Maternal regulation of the vertebrate oocyte-to-embryo transition. **PLoS Genetics.** 2024 Jul 25; 20(7): e1011343. doi: 10.1371/journal.pgen.1011343. eCollection 2024 Jul. PMID: 39052672.

9. Musaev D, Abdelmessih M, Vejnar CE, Yartseva V, Weiss LA, Strayer EC, Takacs CM, **Giraldez AJ†**. UPF1 regulates mRNA stability by sensing poorly translated coding sequences. **Cell Reports**. 2024 Apr 23;43(4):114074. doi: 10.1016/j.celrep.2024.114074. Epub 2024 Apr 15. PMID: 38625794.
10. Hendry C‡, **Giraldez AJ†**. The scientific director: A complimentary model for academic leadership. **Cell**. 2023 Jul 6;186(14):2951-2955. doi: 10.1016/j.cell.2023.05.036. PMID: 37419083.
11. Pownall ME, Miao L, Vejnar CE, M'Saad O, Sherrard A, Frederick MA, Benitez MDJ, Boswell CW, Zaret KS, Bewersdorf J, Giraldez AJ†. Chromatin expansion microscopy reveals nanoscale organization of transcription and chromatin. **Science**. 2023 Jul 7;381(6653):92-100. doi: 10.1126/science.ade5308. Epub 2023 Jul 6. PMID: 37410825.
12. Tornini VA, Miao L, Lee HJ, Gerson T, Dube SE, Schmidt V, Kroll F, Tang Y, Du K, Kuchroo M, Vejnar CE, Bazzini AA, Krishnaswamy S, Rihel J, **Giraldez AJ†**. linc-mipep and linc-wrb encode micropeptides that regulate chromatin accessibility in vertebrate-specific neural cells. **Elife**. 2023 May 16;12. doi: 10.7554/eLife.82249. PMID: 37191016.
13. Begik O, Diensthuber G, Liu H, Delgado-Tejedor A, Kontur C, Niazi AM, Valen E, **Giraldez AJ**, Beaudoin JD, Mattick JS, Novoa EM. Nano3P-seq: transcriptome-wide analysis of gene expression and tail dynamics using end-capture nanopore cDNA sequencing. **Nat Methods**. 2023 Jan;20(1):75-85. doi: 10.1038/s41592-022-01714-w. Epub 2022 Dec 19. PMID: 36536091
14. Bogoch Y, Jamieson-Lucy A, Vejnar CE, Levy K, **Giraldez AJ**, Mullins MC, Elkouby YM. Stage Specific Transcriptomic Analysis and Database for Zebrafish Oogenesis. **Front Cell Dev Biol**. 2022 Jun 6;10:826892. doi: 10.3389/fcell.2022.826892. eCollection 2022. PMID: 35733854 Free PMC article.
15. Greco V\*, Politi K\*, Eisenbarth S\*, Colón-Ramos D\*, **Giraldez AJ\***, Bewersdorf J\*, Berg DN\*. A group approach to growing as a principal investigator. **Curr Biol**. 2022 Jun 6;32(11):R498-R504. doi: 10.1016/j.cub.2022.04.082. PMID: 35671717
16. Vicencio J, Sánchez-Bolaños C, Moreno-Sánchez I, Brena D, Vejnar CE, Kukhtar D, Ruiz-López M, Cots-Ponjoan M, Rubio A, Melero NR, Crespo-Cuadrado J, Carolis C, Pérez-Pulido AJ, **Giraldez AJ**, Kleinstiver BP, Cerón J, Moreno-Mateos MA. Genome editing in animals with minimal PAM CRISPR-Cas9 enzymes. **Nat Commun**. 2022 May 12;13(1):2601. doi: 10.1038/s41467-022-30228-4.
17. Miao L†\*, Tang Y\*, Bonneau AR, Chan SH, Kojima ML, Pownall ME, Vejnar CE, Gao F, Krishnaswamy S, Hendry CE, **Giraldez AJ†** The landscape of pioneer factor activity reveals the mechanisms of chromatin reprogramming and genome activation. **Molecular Cell**. 2022 Mar 3;82(5):986-1002.e9. doi: 10.1016/j.molcel.2022.01.024. Epub 2022 Feb 18.
18. Burkhardt DB, Stanley JS 3rd, Tong A, Perdigoto AL, Gigante SA, Herold KC, Wolf G, **Giraldez AJ**, van Dijk D, Krishnaswamy S. Quantifying the effect of experimental perturbations at single-cell resolution. **Nat Biotechnol**. 2021 May;39(5):619-629. doi: 10.1038/s41587-020-00803-5. Epub 2021 Feb 8. PMID: 33558698 Free PMC article.

19. Pradhan SJ, Reddy PC, Smutny M, Sharma A, Sako K, Oak MS, Shah R, Pal M, Deshpande O, Dsilva G, Tang Y, Mishra R, Deshpande G, **Giraldez AJ**, Sonawane M, Heisenberg CP, Galande S. Satb2 acts as a gatekeeper for major developmental transitions during early vertebrate embryogenesis. **Nat Commun.** 2021 Oct 19;12(1):6094. doi: 10.1038/s41467-021-26234-7.
20. Kontur C, Jeong M, Cifuentes D, **Giraldez AJ†**. Ythdf m6A Readers Function Redundantly during Zebrafish Development. **Cell Rep.** 2020 Dec 29;33(13):108598. doi: 10.1016/j.celrep.2020.108598. PMID: 33378672 Free article.
21. Liu X, Beaudoin JD, Davison CA, Kosmaczewski SG, Meyer BI, **Giraldez AJ†**, Hammarlund M. A Functional Non-coding RNA Is Produced from xbp-1 mRNA. **Neuron.** 2020 Sep 9;107(5):854-863.e6. doi: 10.1016/j.neuron.2020.06.015. Epub 2020 Jul 7. PMID: 32640191 Free PMC article.
22. Vejnar CE, **Giraldez AJ†**. LabxDB: versatile databases for genomic sequencing and lab management. **Bioinformatics.** 2020 Aug 15;36(16):4530-4531. doi: 10.1093/bioinformatics/btaa557. PMID: 32502232 Free PMC article.
23. El-Brolosy MA, Kontarakis Z, Rossi A, Kuenne C, Günther S, Fukuda N, Kikhi K, Boezio GLM, Takacs CM, Lai SL, Fukuda R, Gerri C, **Giraldez AJ**, Stainier DYR. Genetic compensation triggered by mutant mRNA degradation. **Nature.** 2019 Apr;568(7751):193-197. doi: 10.1038/s41586-019-1064-z. Epub 2019 Apr 3.
24. Vejnar CE\*, Messih MA\*, Takacs CM\*, Yartseva V\*, Oikonomou P \*, Christiano R , Stoeckius M, Lau S, Lee MT, Beaudoin JD, Musaev D, Darwich-Codore H, Walther TC, Tavazoie S, Cifuentes D†, **Giraldez AJ†** Genome wide analysis of 3'-UTR sequence elements and proteins regulating mRNA stability during maternal-to-zygotic transition in zebrafish.. **Genome Research.** 2019. Jul;29(7):1100-1114. doi: 10.1101/gr.245159.118.
25. Chan SH, Tang Y, Miao L, Darwich-Codore H, Vejnar CE, JBeaudoin JD, Musaev D, Fernandez JP, Benitez MDJ, Moreno-Mateos MA†, **Giraldez AJ†** Brd4 and p300 confer transcriptional competency during zygotic genome activation. **Developmental Cell.** 2019. Jun 17;49(6):867-881.e8. doi: 10.1016/j.devcel.2019.05.037.
26. Beaudoin JD\*†, Novoa EM\*, Vejnar CE, Yartseva V, Takacs CM, Kellis M, **Giraldez AJ†**. Analyses of mRNA structure dynamics identify embryonic gene regulatory programs. **Nature Struct Mol Biol.** 2018 Aug;25(8):677-686. doi: 10.1038/s41594-018-0091-z. Epub 2018 Jul 30.
27. Fernandez JP, Moreno-Mateos MA, Gohr A, Miao L, Chan SH, Irimia M, **Giraldez AJ†**. RES complex is associated with intron definition and required for zebrafish early embryogenesis. **PLoS Genet.** 2018 Jul 3;14(7):e1007473. doi: 10.1371/journal.pgen.1007473. eCollection 2018 Jul.
28. Fernandez JP, Vejnar CE, **Giraldez AJ**, Rouet R, Moreno-Mateos MA. Optimized CRISPR-Cpf1 system for genome editing in zebrafish. **Methods.** 2018 Jun 28. pii: S1046-2023(18)30021-5. doi: 10.1016/j.ymeth.2018.06.014.
29. Moreno-Mateos MA, Fernandez JP, Rouet R, Vejnar CE, Lane MA, Mis E, Khokha MK, Doudna JA, **Giraldez AJ†**. CRISPR-Cpf1 mediates efficient homology-directed repair and temperature-controlled genome editing. **Nature Communications.** 2017 Dec 8;8(1):2024. doi: 10.1038/s41467-017-01836-2.
30. Boguraev AS, Christensen HC, Bonneau AR, Pezza JA, Nichols NM, **Giraldez AJ**, Gray MM, Wagner BM, Aken JT, Foley KD, Copeland DS, Kraves S, Alvarez Saavedra E.

- Successful amplification of DNA aboard the International Space Station. **NPJ Microgravity**. 2017 Nov 16;3:26
31. Kasper DM, Moro A, Ristori E, Narayanan A, Hill-Teran G, Fleming E, Moreno-Mateos M, Vejnar CE, Zhang J, Lee D, Gu M, Gerstein M, **Giraldez A**, Nicoli S. MicroRNAs Establish Uniform Traits during the Architecture of Vertebrate Embryos. **Developmental Cell**. 2017 Mar 27;40(6):552-565.e5. doi: 10.1016/j.devcel.2017.02.021.
  32. Kontur C, **Giraldez AJ**. RNA Methylation Clears the Way. **Developmental Cell**. 2017 Mar 13;40(5):427-428. doi: 10.1016/j.devcel.2017.02.024.
  33. Yartseva V, Takacs CM, Vejnar CE, Lee MT<sup>‡</sup>, **Giraldez AJ**<sup>‡</sup>. RESA identifies mRNA regulatory sequences with high resolution. **Nature Methods**. 2017 Feb;14(2):201-207. doi: 10.1038/nmeth.4121. Epub 2016 Dec 26.
  34. Bazzini AA<sup>‡</sup>, Del Viso F, Moreno-Mateos MA, Johnstone TG, Vejnar CE, Qin Y, Yao J, Khokha MK, **Giraldez AJ**<sup>‡</sup>. Codon identity regulates mRNA stability and translation efficiency during the maternal-to-zygotic transition. **EMBO J**. 2016 Oct 4;35(19):2087-2103.
  35. Reischauer S, Stone OA, Villasenor A, Chi N, Jin SW, Martin M, Lee MT, Fukuda N, Marass M, Witty A, Fiddes I, Kuo T, Chung WS, Salek S, Lerrigo R, Alsiö J, Luo S, Tworus D, Augustine SM, Mucenieks S, Nystedt B, **Giraldez AJ**, Schroth GP, Andersson O, Stainier DY<sup>‡</sup>. Cloche is a bHLH-PAS transcription factor that drives haemato-vascular specification. **Nature**. 2016 Jul 13;535(7611):294-8. doi: 10.1038/nature18614.
  36. Johnstone TG, Bazzini AA, **Giraldez AJ**<sup>‡</sup>. Upstream ORFs are prevalent translational repressors in vertebrates. **EMBO J**. 2016 Apr 1;35(7):706-23. doi: 10.15252/embj.201592759.
  37. Hoffman EJ, Turner KJ, Fernandez JM, Cifuentes D, Ghosh M, Ijaz S, Jain RA, Kubo F, Bill BR, Baier H, Granato M, Barresi MJ, Wilson SW, Rihel J<sup>‡</sup>, State MW<sup>‡</sup>, **Giraldez AJ**<sup>‡</sup>. Estrogens Suppress a Behavioral Phenotype in Zebrafish Mutants of the Autism Risk Gene, CNTNAP2. **Neuron**. 2016 Feb 17;89(4):725-33. doi: 10.1016/j.neuron.2015.12.039.
  38. Moreno-Mateos MA, Vejnar CE, Beaudoin JD, Fernandez JP, Mis EK, Khokha MK and **Giraldez AJ**<sup>‡</sup>. CRISPRscan: designing highly efficient sgRNAs for CRISPR/Cas9 targeting in vivo. **Nature Methods**. 2015. Oct;12(10):982-8.
  39. Bazzini AA<sup>#</sup>, Johnstone TG<sup>#</sup>, Christiano R, Mackowiak SD, Obermayer B, Fleming ES, Vejnar CE, Lee MT, Rajewsky N<sup>‡</sup>, Walther TC and **Giraldez AJ**<sup>‡</sup>. Identification of small ORFs in animals using ribosome footprinting and evolutionary conservation. **EMBO J**. 2014 Apr 4.
  40. Lee MT<sup>#</sup>, Bonneau AR<sup>#</sup>, Takacs CM, Bazzini AA, DiVito KR, Fleming ES, **Giraldez AJ**<sup>‡</sup>. Nanog, SoxB1 and Pou5f1/Oct4 regulate widespread zygotic gene activation during the maternal-to-zygotic transition. **Nature**, 2013 Sep 22. doi: 10.1038/nature12632.
  41. Yoda M<sup>#</sup>, Cifuentes D<sup>#</sup>, Izumi N, Sakaguchi Y, Suzuki T, **Giraldez AJ**<sup>‡</sup> and Tomari Y<sup>‡</sup>. PARN mediates 3'-end trimming of Argonaute2-cleaved precursor microRNAs. **Cell Reports**, 2013, 5, 1–12, November 14,

42. Lewellis SW, Nagelberg D, Subedi A, Staton A, LeBlanc M, **Giraldez A**, and Knaut H. Precise SDF1-mediated cell guidance is achieved through ligand clearance and microRNA-mediated decay. **J Cell Biol.** 2013 Feb 4;200(3):337-55.
43. Stahlhut C, Suarez Y, Lu J, Mishima Y‡, and **Giraldez AJ‡**. miR-1/206 regulate angiogenesis by modulating Vegf-A expression. **Development**, 2012.
44. Bazzini AA, Lee MT, **Giraldez AJ‡**. Ribosome Profiling Shows That miR-430 Reduces Translation Before Causing mRNA Decay in Zebrafish. **Science** 13 April 2012: 233-23
45. Staton AA, **Giraldez AJ‡**. Use of target protector morpholinos to analyze the physiological roles of specific miRNA-mRNA pairs in vivo. **Nature Protocols.** 2011 Dec 1;6(12):2035-49. doi: 10.1038/nprot.2011.423.
46. Zhu C, Smith T, McNulty J, Rayla AL, Lakshmanan A, Siekmann AF, Buffardi M, Meng X, Shin J, Padmanabhan A, Cifuentes D, **Giraldez AJ**, Look AT, Epstein JA, Lawson ND, Wolfe SA. Evaluation and application of modularly assembled zinc-finger nucleases in zebrafish. **Development.** 2011 Oct;138(20):4555-64.
47. Staton AA, Knaut H and **Giraldez AJ‡**. miRNA regulation of SDF1 chemokine signaling provides genetic robustness to germ cell migration. **Nature Genetics.** Mar;43(3):204-11. Epub 2011 Jan 23
48. Zhu C, Smith T, McNulty J, Rayla AL, Lakshmanan A, Siekmann AF, Buffardi M, Meng X, Shin J, Padmanabhan A, Cifuentes D, **Giraldez AJ**, Look AT, Epstein JA, Lawson ND, Wolfe SA. Evaluation and application of modularly assembled zinc-finger nucleases in zebrafish. **Development.** 2011 Oct;138(20):4555-64.
49. Sander JD, Dahlborg EJ, Goodwin MJ, Cade L, Zhang F, Cifuentes D, Curtin SJ, Blackburn JS, Thibodeau-Beganny S, Qi Y, Pierick CJ, Hoffman E, Maeder ML, Khayter C, Reyon D, Dobbs D, Langenau DM, Stupar RM, **Giraldez AJ**, Voytas DF, Peterson RT, Yeh JR, Joung JK. Selection-free zinc-finger-nuclease engineering by context-dependent assembly (CoDA). **Nature Methods.** 2011 Jan;8(1):67-9. Epub 2010 Dec 12.
50. Cifuentes D, Xue H, Taylor DW, Patnode H, Mishima Y, Cheloufi S, Ma E, Mane S, Hannon GJ, Lawson N, Wolfe S, **Giraldez AJ‡**. A novel miRNA processing pathway independent of Dicer requires Argonaute2. **Science.** 2010, Jun 25;328(5986):1694-8. Epub 2010 May 6
51. Mishima Y, Abreu-Goodger C, Staton AA, Stahlhut C, Shou C, Cheng C, Gerstein M, Enright AJ and **Giraldez AJ‡**. Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. **Genes & Development.** 2009 Mar 1;23(5):619-32. Epub 2009 Feb 24. PMID: 19240126
52. Choi PS, Zakhary L, Choi WY, Caron S, Alvarez-Saavedra E, Miska EA, McManus M, Harfe B, **Giraldez AJ**, Horvitz RH, Schier AF, and Dulac C. Members of the miRNA-200 Family Regulate Olfactory Neurogenesis. **Neuron.** 2008. Jan 10, 57, 1–15.
53. Choi WY, **Giraldez AJ‡**, Schier AF‡. Target Protectors Reveal Dampening and Balancing of Nodal Agonist and Antagonist by miR-430. **Science.** 2007. Oct 12;318(5848):271-4. ‡Corresponding authors.
54. Mishima Y<sup>#</sup>, **Giraldez AJ<sup>#</sup>**, Takeda Y, Fujiwara T, Sakamoto H, Schier AF and Inoue K. Differential regulation of germline mRNAs in soma and germ cells by zebrafish miR-430. **Current Biology,** 2006. Nov 7;16(21):2135-42.

55. **Giraldez AJ‡**, Mishima Y, Rihel J, Grocock R, van Dongen S, Inoue, K, Enright A, and Schier AF‡. Zebrafish miR-430 promotes deadenylation and clearance of maternal mRNAs. **Science**. 2006 Apr 7;312(5770):75-9.
56. **Giraldez AJ‡**, Cinalli RM, Glasner ME, Enright A, Thomson JM, Baskerville S, Hammond SM, Bartel D, and Schier AF‡. MicroRNAs regulate brain morphogenesis in zebrafish. **Science**. 2005 May 6;308(5723):833-8.
57. Le Good JA, Joubin K#, **Giraldez AJ#**, Ben-Haim N#, Beck S, Chen Y, Schier AF and Constam DB. Nodal stability determines signaling range. **Current Biology**. 2005 Jan 11;15(1):31-6.
58. Kreuger J, Perez L, **Giraldez AJ**, Cohen SM. Opposing activities of Dally-like glypican at high and low levels of Wingless morphogen activity. **Developmental Cell**. 2004 Oct;7(4):503-12.
59. **Giraldez AJ**, Cohen SM. Wingless and Notch signaling provide cell survival cues and control cell proliferation during wing development. **Development**. 2003 Dec;130(26):6533-43.
60. **Giraldez AJ**, Perez L, Cohen SM. A naturally occurring alternative product of the mastermind locus that represses notch signaling. **Mechanisms of Development**. 2002 Jul;115(1-2):101-5.
61. **Giraldez AJ**, Copley RR, Cohen SM. HSPG modification by the secreted enzyme Notum shapes the Wingless morphogen gradient. **Developmental Cell**. 2002 May; 2(5):667-76.

‡ Corresponding authors.

# Equal contribution

### Reviews, Chapters, Books

1. Kojima M, Hoppe C, Giraldez AJ‡ The maternal-to-zygotic transition: reprogramming of the cytoplasm and nucleus. **Nature Reviews in Genetics**. Accepted
2. Strayer EC, Tornini VA, **Giraldez AJ‡**. Giving translation a hand. **Dev Cell**. 2021 Nov 8;56(21):2921-2923. doi: 10.1016/j.devcel.2021.10.016. PMID: 34752744
3. Kontur C, Giraldez A. RNA Methylation Clears the Way. **Dev Cell**. 2017 Mar 13;40(5):427-428. doi: 10.1016/j.devcel.2017.02.024. PMID: 28292421 Free article.
4. Yartseva V‡, **Giraldez AJ‡**. The Maternal-to-Zygotic Transition During Vertebrate Development: A Model for Reprogramming. **Curr Top Dev Biol**. 2015;113:191-232. doi: 10.1016/bs.ctdb.2015.07.020. Epub 2015 Aug 13.
5. Lee MT‡#, Bonneau AR#, **Giraldez AJ‡**. Activation of the zygotic genome during the maternal to zygotic transition in animals. **Annu Rev Cell Dev Biol**. 2014;30:581-613. Review.
6. Bazzini AA, **Giraldez AJ‡**. MicroRNAs sculpt gene expression in embryonic development new insights from plants. **Dev Cell**. 2011 Jan 18;20(1):3-4.
7. **Giraldez AJ‡**. microRNAs, the cell's Nepenthe: clearing the past during the maternal-to-zygotic transition and cellular reprogramming. **Curr Opin Genet Dev**. 2010. Volume 20, Issue 4, August 2010, Pages 369-375 (Review)

8. Takacs CM, **Giraldez AJ†**. MicroRNAs as genetic sculptors: Fishing for clues. **Semin Cell Dev Biol.** 2010 Epub 2010 Feb 10. (Review)
9. Staton, A.A. and **Giraldez AJ†**. MicroRNAs in development and disease. **Encyclopedia of Life Sciences.** 2008. pp. 1–10. (Review)
10. Mishima Y, Stahlhut C, **Giraldez AJ†**. miR-1-2 gets to the heart of the matter. **Cell.** 2007 Apr 20;129(2):247-9. (Review).
11. Schier AF, **Giraldez AJ**. MicroRNA function and mechanism: insights from zebra fish. **Cold Spring Harb Symp Quant Biol.** 2006. 71:195-203. (Review).

#### **SELECTED PATENTS**

1. **Giraldez AJ**, Copley RR, Cohen SM. TORERO Protein. 2003 WO 03062410 A3
2. Choi WY, **Giraldez AJ**, Schier AF. Methods of increasing gene expression through rna protection. 2008. WO2009032083A1
3. Moreno-Mateos MA, **Giraldez AJ**. Tailed gRNAs used in single cell sequence to identify the loss of function genes caused in individual cells. Provisional patent. 2016. OCR 7071