

**Xianjun Dong, PhD****Address:** 60 Fenwood Road, 9002M, Boston, MA 02115, USA**Phone:** +1 857-307-5423**Email:** [xdong@rics.bwh.harvard.edu](mailto:xdong@rics.bwh.harvard.edu)**Web:** <http://www.sterding.com>**Education**

2002	B.Sc.	Biomedical Engineering	Southeast University, China
2005	M.Sc.	Biomedical Engineering	Southeast University, China
2010	Ph.D.	Bioinformatics & Genomics (Advisor: Dr. Boris Lenhard)	University of Bergen, Norway

**Postdoctoral Training**

09/10 - 09/13	Postdoc Fellow	Program of Bioinformatics and Integrative Biology	University of Massachusetts Medical School
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**Faculty Academic Appointments**

11/13 – 03/20	Instructor	Neurology	Harvard Medical School
04/20 - present	Assistant Professor	Neurology	Harvard Medical School
07/20 - present	Faculty member	HMS Initiative for RNA Medicine	Harvard Medical School
08/20 - present	Associate member	Broad Institute	Harvard and MIT

**Appointments at Hospitals/Affiliated Institutions**

09/13 - present	Assistant Scientist	Ann Romney Center for Neurologic Diseases	Brigham and Women's Hospital
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**Major Administrative Leadership Positions**

2016 – present	Director of Computational Neuroscience	Center for Advanced Parkinson Research	Brigham & Women's Hospital
2020 – present	Director	Genomics and Bioinformatics Hub	Brigham and Women's Hospital

**Professional Societies**

2006 – present	International Society for Computational Biology (ISCB), Member
2013 – present	American Society for Human Genetics (ASHG), Member
2015	The 10 <sup>th</sup> Annual DNA Day Essay Contest, Judge
2016 – present	American Academy of Neurology (AAN), Member
2021	MJFF/ASAP Data Repository Working Group, Chair

**Grant Review Activities**

2021	NIH NINDS Special Emphasis Panel study section
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**Editorial Activities****- Ad-hoc Reviewer –****General:** *Nature Biotechnology, Nature Communication, Genome Research, Genome Biology, PloS Genetics, International Journal of Biological Sciences, The Pharmacogenomics Journal, Nucleic Acids Research***Bioinformatics:** *Bioinformatics, PloS Computational Biology, Evolutionary Bioinformatics, Journal of Biomedical Informatics, Current Bioinformatics, Journal of Bioinformatics and Computational Biology***Neurology:** *Movement Disorders, Neurogenetics*

**- Editorial Roles -**

2017 – present *Personalized Medicine* (Editorial Board)  
 2017 – present *PeerJ* (Academic Editor)  
 2018 – present *Frontiers in Neuroscience, Frontiers in Genetics* (Academic Editor)  
 2019 – present *iScience* (Editorial Board)

**Honors and Prizes**

2000 Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China  
 2000 2<sup>nd</sup> prize of the National Undergraduate Mathematical Contest in Modeling  
 2000 *Liu Yonglin* Fellowship Award, Southeast University, China  
 2001 1<sup>st</sup> prize of 2001 “Sony Cup” National Undergraduate Electronic Design Contest, China  
 (winning by designing a self-driving electronic toy car)  
 2001 Meritorious winner (top 10%) in the International Mathematical Contest in Modeling  
 (MCM) (winning by modeling the growth control of zebra mussels in the Great Lakes)  
 2001 Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China  
 2002 Distinguished Graduate Student Award, Southeast University, China  
 2009 Full Scholarship, “Chromatin Domains and Insulators” Workshop, Spain  
 2009 Travel Fellowship, MCB Research School, University of Bergen, Norway  
 2010 Chinese Government Award for Outstanding Self-financed Students Abroad, Ministry of  
 Education, China (1 of 500 annual awardees worldwide)  
 2015 Reviewers’ Choice – top 10% best posters in the American Society of Human Genetics  
 (ASHG) meeting, US  
 2018 Finalist of the PacBio Structural Variant SMRT Grant program  
 2018 Research Excellence Award, Brigham and Women’s Hospital  
 2019 Advanced Center for Parkinson’s Disease Research (ACEPD) Seed Award

**Report of Funded and Unfunded Projects****Funding Information****Past Grants:**

2011 – 2016 *Epigenetic Markers in Huntington’s Disease Brain*  
 NIH R01 NS073947  
 Role: Co-Investigator (PI: Richard H. Myers)  
 The goal of this project is to map genome-wide HD disease-related changes in histone  
 methylation markings in prefrontal neurons.

2012 – 2016 *EDAC: ENCODE Data Analysis Center*  
 NIH U41 HG007000  
 Role: Co-Investigator (PI: Zhiping Weng)  
 The goal of this project is to perform integrative analysis on ChIP-Seq, CAGE, and RNA-  
 Seq data as a part of the ENCODE data analysis center.

2012 – 2018 *Biomarkers for Early Intervention in Parkinson Disease*  
 U01 NS082157  
 Role: Director, Computational Neuroscience Core (PI: Clemens Scherzer)

The goal of this project is to discover, confirm, and translate viable non-coding RNA biomarkers useful for the early detection of high-risk individuals.

- 2015 – 2017 *The PD Brain Map: From Genome to Function*  
Department of Defense USAMRMC W81XWH-15-1-0007  
Role: Director, Bioinformatics Core  
The specific aims of this project are: Aim 1, we will characterize the landscape of bidirectionally transcribed enhancer RNAs in laser-captured nigral dopamine neurons. In Aim 2, we will clarify the genetic control of non-coding transcription in nigral dopamine neurons. In Aim 3, we will translate expression traits into potential precision markers.
- 2018 – 2018 *Identification of Gene Modifiers of Disease Penetrance and Age at Onset (Planning Grant)*  
Michael J. Fox Foundation  
Role: Co-Investigator (PI: Clemens Scherzer)  
The goal of this project is to develop a project plan for the identification of gene modifiers of disease penetrance and age at onset.
- 2017 – 2019 *Cracking the Code of chr17q21 for Parkinson: From GWAS to Novel Drug Targets*  
American Parkinson Disease Association (APDA) Research Grant - \$50,000  
Role: **Principal Investigator**  
The goal of this project is to discover the causal variants in the chr17q21 locus and validate them in iPSC-derived neurons.
- 2016 – 2019 *Parkinson Disease: Predicting the Future*  
NIH U01 NS095736  
Role: Co-investigator (PI: Clemens Scherzer)  
The goal of this project is to identify genetic variants in susceptibility loci and familial genes that predict cognitive or motor progression and to replicate and verify forwarded genetic variants in independent populations.
- 2018 – 2019 (NCE 2020) *Bioinformatics Club: A Weekly Meetup to Learn and Share Bioinformatics at BWH Brigham Research Institute (BRI) NextGen Awards - \$5,000*  
Role: *Principal Investigator*  
*This award is for my leadership in the Bioinformatics Club to further improve the bioinformatics education environment in Brigham and Women's Hospital.*
- 2019 – 2020 (NCE 2021) *Circular RNAs: A novel link between genetic susceptibility and Parkinson's disease?*  
American Parkinson Disease Association (APDA) Research Grant - \$75,000  
Role: **Principal Investigator**  
The goal of this project is to identify the role of the novel class of circular RNAs (circRNAs) in the early development of Parkinson's disease and their linkage to the susceptibility of PD.

**Active grants (9 in total):**

- 2018 – 2023 *Translating GWAS peaks into novel drug targets*  
APDA Advanced Center for Parkinson's Disease Research (ACEPD) Seed Award

Role: **Co-Principal Investigator (\$10,000)**

The ACEPD Seed Award is “for young rising stars in Parkinson’s research to study precision neurology of Parkinson from basic neuroscience to clinical.” Working together with a yeast genetic scientist, I will integrate the powers of human genomics, transcriptomics, and epigenomics data to identify novel, potentially druggable mechanisms for PD.

2017 – 2022

*Integrative Multi-omic Discovery of Proximal Mechanisms Driving Age-Dependent Neurodegeneration*

NIA RF1AG057331

Role: **Bioinformatics Director** (PIs: Mel Feany, Ernest Fraenkel, Clemens Scherzer)

I will lead the analysis of computational transcriptomics in this multi-institutional grant and test my hypothesis that Alzheimer’s disease risk loci specifically in human pyramidal neurons drive age-dependent neurodegeneration through dysregulation of variant-associated genes and networks in AD.

2019 – 2021

*400 Virtual Clinical Trials for Parkinson’s Disease.*

The Michael J. Fox Foundation for Parkinson’s Disease

Role: **Lead Bioinformatics Investigator** (PIs: Clemens Scherzer, Trond Riise)

The goal is to discover and confirm candidate drugs with a known safety profile that can be repurposed and developed for patients with PD. I will lead the bioinformatics analysis done at Harvard site in this dual-institute grant.

2020 – 2021

*AI2AMP-PD: Accelerating Parkinson’s Diagnosis Using Multi-Omics and Artificial Intelligence*

NIH 1U01NS120637-01

Role: **Principal Investigator** (PIs: Dong, Scherzer) **\$300,000**

The goal is to leverage the harmonized, large-scale dataset in the AMP PD consortium to build a multi-omics classifier for Parkinson’s diagnosis using advanced machine learning data analytic methods.

2020 – 2023

*Parkinson5D: Deconstructing Proximal Disease Mechanisms across Cells, Space and Progression*

The Michael J. Fox Foundation for Parkinson’s Disease

Role: **Principal Investigator** (PIs: Scherzer, Dong, Feany, Levin, Zhang) **\$9,000,000**

The goal is to reveal the complex human genetics of Parkinson’s disease through a dynamic, five-dimensional view of proximal cellular mechanisms across brain cells (1D), brain space (3D), and disease stage (1D).

2022 – 2023

*An inverse translational research project for identifying new treatments for Parkinson’s disease: The Epi-screening project*

The Research Council of Norway

Role: **Subcontract Instructor** (Subcontract PI: Clemens Scherzer)

The goal of this study is to evaluate whether existing drugs (molecules) can be repurposed as an effective treatment of PD. I will lead the analysis of computational pharmacome analysis based on Harvard Biomarkers Study longitudinal data.

- 2021 – 2022 *Developing RNA biomarkers of early PD pathology from brain organoids and extracellular vesicles*  
American Parkinson Disease Association (APDA) Research Grant - **\$75,000**  
Role: **Principal Investigator**  
The goal of the study is to develop RNA biomarkers of early PD pathology from brain 3D organoids and extracellular vesicles (EV).
- 2021 - 2022 *EXODUS-enabled High-throughput Multi-omics Profiling of Extracellular Vesicles for Diagnosis of Preclinical Alzheimer's Disease*  
NIH R41 AG076098-01  
Role: **Principal Investigator** (PIs: Chen, Dong) - **\$250,000**  
The goal of this STTR is to develop a platform and workflow for biomarker discovery and diagnosis of preclinical Alzheimer's disease (AD) based on multi-omics profiling of circulating extracellular vesicles.
- 2021 – 2026 *Systematic study of extracellular vesicles and their integrative analysis with Parkinson's organoids MAP*  
NIH R01 NS124916-01  
Role: **Principal Investigator** (PIs: Dong, Lee) - **\$2,500,000**  
The goal of this study is to develop a new 3D mini-brain microphysiological analysis platform (MAP) to recapitulate the dopamine neurons' interconnectivity and study molecular neurodegeneration systematically.

### **Projects Submitted for Funding**

- 2022 - 2027 *MIA: Multi-omics Interface for Alzheimer's disease related dementias*  
NIH R01 - **\$2,500,000**  
Role: **Principal Investigator**  
The goal of this study is to harmonize the existing brain multi-omics datasets relevant to Alzheimer's disease related dementias (ADRD) to identify ADRD-associated RNAs, their regulatory networks, and genetic association in expression, splicing, and chromatin accessibility, and from there to develop a comprehensive, cloud-based, interactive web portal -- Multi-omics Interface for ADRD (MIA).
- 2022 - 2027 *Regulation mechanism and functional genomics of LINE1 RNA in TDP-43 linked neurodegeneration*  
NIH R01 - **\$2,500,000**  
Role: **Principal Investigator** (PIs: Sun, Dong)  
The goal of this project is to study the regulation mechanism and functional genomics of LINE1 RNA in TDP-43 linked neurodegeneration.

### **Report of Local Teaching and Training**

#### **Teaching of Students in Courses**

- 2007 "Ensembl in a Nutshell" bioinformatics workshop, University of Bergen, Norway  
Bioinformatics students and researchers, 1-hr sessions per day for five days

- 2017 – present Lecture in the Bioinformatics Club, Brigham and Women’s Hospital  
Bioinformatics students and researchers, 1 hour per lecture for six lectures
- 2021 Single-cell RNA-seq analysis, Brigham and Women’s Hospital  
40 students and researchers, a 2-day in-person course

### Laboratory and Other Research Supervisory and Training Responsibilities

- 2013 – present Supervision of Harvard learners (incl. HMS graduate students and postdoctoral fellows with a formal appointment at BWH) for bioinformatics in the Lab of Neurogenomics, Brigham and Women’s Hospital (average of 2 students per year)  
1:1 supervision one hour per week per student
- 2013 – present Informal mentorship and consultancy to non-Harvard visiting scholars and summer interns in the Lab of Neurogenomics, Brigham and Women’s Hospital (average of 3 students per year)  
1 hour per week per student

### Formally Mentored Harvard Medical and Graduate Students

- 2014 – 2016 Alyssa Ehrlich (Medical student in Harvard Medical School)  
Conducted her rotation in the bioinformatics team. Presented a poster titled “Discovering Circular RNAs in Dopamine Neurons of Human Brain: Implications for Parkinson’s Disease” at the 2016 Soma Weiss Student Research Day in Harvard Medical School. She got all “Excellent” assessments for her PiM funding proposal.
- 2015 -2016 Ellen DeGennaro (PhD student in Harvard-MIT HST PhD program)  
Conducted her internship in the laboratory and worked on a Huntington’s disease project. Co-authored a manuscript.
- 2016 – 2016 Rebeca Borges Monroy (PhD student in the BIG program at Harvard University)  
Conducted her PhD rotation in the laboratory and worked together on a circRNA project. Drafting a co-authored manuscript.
- 2020 – 2020 Varshini Odayar (Freshman at Harvard College)  
She chose us from the HUROS Fair as her first laboratory for research and participated in a top-secret project in the lab.

### Other Mentored Trainees and Faculty

- 2009 – 2012 Yogita Sharma (Graduate student at University of Bergen, Norway)  
Mentor, co-supervisor for her research project & thesis, and co-author of an article in *BMC Bioinformatics*
- 2013 – 2014 Carmen Portenkirchner (Medical student in Paracelsus Medical University, Austria)  
Thesis co-advisor, research advisor
- 2013 – 2014 Dr. Shuilin Jin (Visiting research scholar from Harbin Institute of Technology, China)  
Co-supervisor, Bioinformatics trainer
- 2014 – 2015 Ruoting Wang (Undergraduate in University of Massachusetts)  
Supervisor, research advisor for his summer internship in the Neurogenomics Laboratory
- 2014 – 2016 Dr. David Gritsch (Postdoc in BWH Neurogenomics laboratory)  
Research advisor for his research in the laboratory, and co-authored an article published in *Nature Neuroscience* and a manuscript
- 2015 – 2015 Will Nemirovsky (Junior high school student in Buckingham Browne & Nichols School)  
Supervisor, research advisor for his summer bioinformatics training at Harvard
- 2015 – 2017 Kristy Abo (Medical student in School of Medicine, Boston University)  
Supervisor and project manager for her summer bioinformatics training at Harvard
- 2015 – 2018 Tao Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)

- Supervisor, research advisor for his three-year bioinformatics training in Harvard, and co-authored an article published in *Nature Neuroscience* and a manuscript
- 2016 – 2018 **Zhuo Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)**  
Supervisor, research advisor for her two-year bioinformatics training in Harvard, and co-authored a manuscript
- 2016 – 2018 **Dr. Miguel E. Renteria (Postdoc in QIMR Berghofer Medicine Research Institute, Australia)**  
Supervisor, research advisor for his two-year bioinformatics training in the lab, and drafting a co-authored manuscript
- 2018 – 2019 **Yaiza Van Waes Rubio (M.S. student in Universidad Complutense of Madrid, Spain)**  
Supervisor, research advisor for her five-month research traineeship in Bioinformatics, and co-authored a manuscript.
- 2018 – 2020 **Dr. Jiajie Peng (Associate Professor in Northwest Polytechnical University, China)**  
Co-supervisor, research advisor for his two-year visiting scholarship in Brigham
- 2018 – 2020 **Dr. Young Eun Huh (Assistant Professor of Neurology at CHA University School of Medicine, South Korea)**  
Supervisor, research advisor for her two-year bioinformatics training at Harvard
- 2018 – 2019 **Haotian Liao (Graduate student in West China Medical School, Sichuan University, China)**  
Supervisor, research advisor for his two-year bioinformatics training at Brigham
- 2019 – 2019 **Carmen Domínguez (Undergraduate student from National Autonomous University of Mexico, Mexico)**  
Career stage: postgraduate 5-month internship.  
Mentoring role: research advisor and mentor.  
Accomplishments: awarded a Summer Student Fellowship from the Parkinson's Foundation; invited to give an oral presentation on the "Genomics of Brain Disorders 2020" conference (Wellcome Genome Campus, Cambridge, UK); published a first-author paper in *Scientific Reports*.
- 2020 - 2021 **Xiaoqi Li (Undergraduate student from University of Wisconsin–Madison)**  
Career stage: postgraduate 11-month internship.  
Mentoring role: research advisor and mentor.  
Accomplishments: implemented an R shiny application in 1 month; led two innovative projects (PD imaging genetics based on UK Biobank data; SARS-Cov-2 circRNAs); three poster presentations in local and national scientific conferences; published one co-first author paper in the journal of *Bioinformatics*; received Data Science Internship Program award (\$20,800) by Massachusetts Life Sciences Center; three manuscripts in preparation
- 2021 - 2021 **Ariela Buxbaum Grice (Undergraduate student from Connecticut College)**  
Career stage: postgraduate 8-month internship.  
Mentoring role: research advisor and mentor.  
Accomplishments: Led an exploratory project (pathogen detection in AD brain); prepared a first-author manuscript.
- 2021 - 2021 **Mrinal Subash (Master student in Northeastern University)**  
Research advisor and mentor for his 5-months co-op internship in bioinformatics.
- 2021 - **Dr. Tingting Zhao (Full-time research scientist in the Bioinformatics Hub)**  
Career stage: transition from molecular biologist to bioinformatics specialist.  
Mentoring role: supervisor  
Accomplishments: leading the bioinformatics analysis for three collaborative projects; two poster presentations in the local conference; TA in the Single-cell RNA-seq course

- 2021 - Dr. Ruifeng Hu (Postdoctoral Research Fellow)  
Mentoring role: supervisor  
Accomplishments: leading an NIH-sponsored research project (AMP PD); one poster presentation at the local conference; preparing a first-author manuscript
- 2021 - Dr. Jie Yuan (Postdoctoral Research Fellow)  
Mentoring role: supervisor  
Accomplishments: leading an ASAP-sponsored research project (Parkinson5D); two poster presentations in the local and international conference; preparing a first-author manuscript

### Formal Teaching of Peers (e.g., CME and other continuing education courses)

No presentations below were sponsored by outside entities

2017	Make Interactive Web Applications Using Shiny Bioinformatics Club, Brigham and Women's Hospital	Single presentation Boston
2017	Introducing the UCSC Genome Browser Bioinformatics Club, Brigham and Women's Hospital	Single presentation Boston
2018	Using <i>reshape2</i> and <i>tidyr</i> for Data Transformation The "Mini R Camp" talk series, Brigham and Women's Hospital	Single presentation Boston
2019	Introducing Artificial Intelligence (AI) and the AI Camp The "2019 AI Camp" talk series, Brigham and Women's Hospital	Single presentation Boston
2019	Making Your First AI Program Using CoLab and TensorFlow The "2019 AI Camp" talk series, Brigham and Women's Hospital	Teaching assistant Boston
2019	Unsolved Problems and Future Challenges of Using AI in Medicine The "2019 AI Camp" talk series, Brigham and Women's Hospital	Single presentation Boston

### Local Invited Presentations

No presentations below were sponsored by outside entities

2011	Correlate histone modifications and gene expression / BIB seminar Program of Bioinformatics and Integrative Biology, UMass Medical School
2012	Redefining the piRNA-producing loci of the mouse testis as genes / Bioinformatics Seminar Program of Bioinformatics and Integrative Biology, UMass Medical School
2014	From ENCODE to PD Brain Map: Bioinformatics in Big Data Research / ADPD seminar Center of Neurologic Diseases, Brigham and Women's Hospital
2015	BRAINCODE: Decoding neuronal genome function in human brain / ADPD seminar Center for Neurologic Diseases, Brigham and Women's Hospital
2016	Barcodes of neuronal genome function in human brain / ADPD seminar Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital
2017	An encyclopedia of transcribed elements in human brain dopamine neurons / ADPD seminar Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital
2018	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease / ADPD seminar Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital



- 2018 BRAINcode: An encyclopedia of human neuron transcriptomes in health and disease  
**Award Speaker** of Discover Brigham Day  
Brigham and Women's Hospital
- 2018 Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease  
**Featured Speaker**  
2018 HMS Epigenetics Symposium  
Department of Genetics, Harvard Medical School
- 2019 Circular or not: Cell specificity of circRNAs in human brain neurons / ADPD seminar  
Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital
- 2020 Exploring the dark matter in the human brain neurons  
**Invited Speaker**  
Harvard Initiative of RNA Medicine seminar  
Beth Israel Deaconess Medical Center (BIDMC)
- 2020 Circular RNAs: Challenging linear thinking of neurodegenerative diseases / ADPD seminar  
Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital
- 2021 Making Every Bit Count in Your RNA Sequencing Data / ADPD seminar  
Ann Romney Center for Neurologic Diseases, Brigham and Women's Hospital

**Report of Regional, National, and International Invited Teaching and Presentations**

No presentations below were sponsored by outside entities

**Regional**

- 2013 Studying gene regulation using comparative genomics and epigenomics  
Dana-Farber Cancer Institute, Boston, MA
- 2017 7<sup>th</sup> Bioinformatics Strategy Meeting USA (East Coast)  
The Westin Boston Waterfront, Boston, MA

**National**

- 2007 Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks  
Bioinformatics Research and Education Workshop (BREW) 2007, Norway
- 2011 Modeling gene expression with chromatin features  
ENCODE conference, Stanford University
- 2012 Modeling gene expression using chromatin features in various cellular contexts  
ENCODE conference, MIT
- 2013 Long-range gene regulation in the vertebrate genome  
Berkeley Lawrence Laboratory, CA
- 2017 From the known world to an expanding universe of genomic dark matter  
**Invited Speaker**  
NIH Huntington's Disease Biomarkers Workshop

National Institute of Health, Bethesda, MD

2018 Update on current PD brain transcriptomics analysis  
**Invited Speaker**  
NIH Accelerating Medicine Partnership (AMP) – Parkinson’s Disease Conference  
National Institute of Health, Bethesda, MD

2019 Bioinformatics Strategy Meeting USA East Coast 2019  
**Invited Panelist**  
The Le Meridien Cambridge, Boston, MA

2021 Online sandboxes and tools for open science: AMP-PD, BRAINcode, power-eQTL  
ASAP Collaborative Research Network (CRN) Tech 1 meeting  
Aligning Science Across Parkinson’s (ASAP) foundation

### **International**

2010 Translog, a web browser for studying the expression divergence of homologous genes  
The 8<sup>th</sup> Asia Pacific Bioinformatics Conference  
Bangalore, India

2010 Web resources to study the long-range gene regulation  
Huazhong Agricultural University, Wuhan, China

2010 Evolutionary mechanisms of developmental long-range gene regulation in vertebrate genomes  
Genome Institute of Singapore, Singapore

2013 Studying gene regulation using comparative genomics and epigenomics  
Tongji University, Shanghai, China

2015 NGS and its application in translational medicine  
Huazhong University of Science and Technology, Tongji Hospital, Wuhan, China

2019 Dark matter in the human genome and its regulation in complex diseases  
**Invited Speaker**  
The 2<sup>nd</sup> Academic Symposium of Rare Disease  
Sichuan Medical Association, Chengdu, China

2020 Exploring the Dark Matters in the Human Brain Neurons  
**Invited Speaker and Panelist**  
NextGen Omics Series – the 6<sup>th</sup> Single Cell Analysis Congress  
Boston, USA

2021 Decoding the dark matters in the human genome  
**Invited Speaker**  
The 11<sup>th</sup> International Forum on Post-Genome Technologies (11’IFPT) -- virtual  
Nanjing, China

### **Report of Activities and Innovations**

#### **Technological and Other Scientific Innovations**

Synorth A website designed for genome research, allowing to explore the evolution of synteny and long-range regulatory interactions between vertebrate genomes

Translog	<p>URL: <a href="http://synorth.genereg.net">http://synorth.genereg.net</a>          Published as first author on <i>Genome Biology</i> (Impact factor: 11.91), 25 citations          A website designed to study the expression divergence of homologous genes          URL: <a href="http://translog.genereg.net">http://translog.genereg.net</a></p>
Factorbook	<p>Published as the first author on <i>BMC Bioinformatics</i> (Impact factor: 2.21)          A Wiki-based database for transcription factor-binding data generated by ENCODE          URL: <a href="http://factorbook.org">http://factorbook.org</a></p>
BRAINcode	<p>Published as co-author on <i>Nucleic Acid Research</i> (Impact factor: 10.16), 158 citations          A web resource allowing users to query the gene expression profile and eQTL result in human brain neurons.          URL: <a href="http://humanbraincode.org">http://humanbraincode.org</a></p>
powerEQTl	<p>An R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis          URL: <a href="https://bwhbioinfo.shinyapps.io/powerEQTl">https://bwhbioinfo.shinyapps.io/powerEQTl</a>          Published as the first author on <i>Bioinformatics</i> (Impact factor: 6.94)</p>

### Educational Activities to the Community

2008 – present	Owner of the bioinformatics blog, “ <i>One Tip Per Day</i> ” ( <a href="http://onetipperday.sterding.com">http://onetipperday.sterding.com</a> ), which has 200 visits per day on average and more than 1,000,000 visits in total
2012	Innovation Month in the Worcester Public Schools: How to extract DNA from an onion Claremont Academy, Worcester <a href="http://www.umassmed.edu/news/2012/education/gsbs-students-take-science-on-road.aspx">http://www.umassmed.edu/news/2012/education/gsbs-students-take-science-on-road.aspx</a>
2017 – present	Founder and Director of the <i>Bioinformatics Club</i> ( <a href="http://bioinformatics.bwh.harvard.edu/training">http://bioinformatics.bwh.harvard.edu/training</a> ), which is a weekly forum for learning and sharing bioinformatics at the whole hospital level. To date, we have already scheduled over 70 talks, serving more than 1000 persons.
2021	Lecture in the course of “Single-cell RNA-seq Analysis” ( <a href="https://singlecellcourse.org">https://singlecellcourse.org</a> ) at Brigham and Women’s Hospital, with 40 participants

### Media Coverage

<u>ENCODE consortium et al. <i>Nature</i>, 2012</u>	<p>CNN: <a href="http://www.cnn.com/2012/09/05/health/encode-human-genome/">http://www.cnn.com/2012/09/05/health/encode-human-genome/</a>          BBC: <a href="http://www.bbc.com/news/health-19202141">http://www.bbc.com/news/health-19202141</a>          Scientific American: <a href="http://www.scientificamerican.com/article/junk-dna-encode/">http://www.scientificamerican.com/article/junk-dna-encode/</a>          Evolution News:  <a href="http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html">http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html</a>          New York Times: <a href="http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html">http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html</a>          LA Times: <a href="http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906">http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906</a>          The Guardian: <a href="http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode">http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode</a></p>
<u>Dong et al. <i>Genome Biology</i>, 2012</u>	<p>GenomeWeb: <a href="http://www.genomeweb.com/blog/week-genome-biology-59">http://www.genomeweb.com/blog/week-genome-biology-59</a>          Biomed Central: <a href="http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/">http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/</a>          UmassMed News: <a href="http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/">http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/</a></p>
<u>Dong et al. <i>Nature Neuroscience</i>, 2018</u>	<p>EurekaAlert!: <a href="https://www.eurekaalert.org/pub_releases/2018-09/bawh-gdm092018.php">https://www.eurekaalert.org/pub_releases/2018-09/bawh-gdm092018.php</a>          Alzforum: <a href="https://www.alzforum.org/news/research-news/noncoding-rnas-evince-world-">https://www.alzforum.org/news/research-news/noncoding-rnas-evince-world-</a></p>

gene-regulation-dopaminergic-neurons

Neurology Today:

[https://journals.lww.com/neurotodayonline/Fulltext/2018/11010/Disease\\_Mechanisms\\_Parkinson\\_s\\_Disease\\_Activity.2.aspx](https://journals.lww.com/neurotodayonline/Fulltext/2018/11010/Disease_Mechanisms_Parkinson_s_Disease_Activity.2.aspx)

R&D: <https://www.rdmag.com/news/2018/09/laser-capture-method-investigates-parkinsons-and-psychiatric-diseases>

**Report of Scholarship****Peer-Reviewed Scholarship in print or other media:**

**In total, 34 publications, over 17,000 citations, H-index = 21, 60% articles with Impact Factor > 10**

- **Research Investigation** (including 9 first-author publications\* and 3 corresponding-author publications<sup>†</sup>)
1. Mungpakdee S, Seo HC, Angotzi AR, **Dong X**, Akalin A, Chourrout D. Differential evolution of the 13 Atlantic salmon Hox clusters. *Molecular Biology and Evolution*. 2008; 25(7):1333-43. PMID: 18424774 (**IF = 14.8**)
  - \*2. \***Dong X**, Fredman D, Lenhard B. Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. *Genome Biology*. 2009; 10(8):R86. PMID: 19698106 (**IF = 14.0**)
  3. Akalin A, Fredman D, Arner E, **Dong X**, Bryne JC, Suzuki H, Daub CO, Hayashizaki Y, Lenhard B. Transcriptional features of genomic regulatory blocks. *Genome Biology*. 2009; 10(4):R38. PMID: 19374772 (**IF = 14.0**)
  - \*4. \***Dong X**, Akalin A, Sharma Y, Lenhard B. Translog, a web browser for studying the expression divergence of homologous genes. *BMC Bioinformatics*. 2010; 11 Suppl 1:S59. PMID: 20122234 (IF = 2.5)
  - \*5. \***Dong X**, Navratilova P, Fredman D, Drivenes Ø, Becker TS, Lenhard B. Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. *Nucleic Acids Research*. 2010; 38(4):1071-85. PMID: 19969543 (**IF = 11.2**)
  6. Yildirim O, Li R, Hung JH, Chen PB, **Dong X**, Ee LS, Weng Z, Rando OJ, Fazzio TG. Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells. *Cell*. 2011; 147(7):1498-510. PMID: 22196727 (**IF = 36.2**)
  7. Fredman D, **Dong X**, Lenhard B. Making enhancers from spare parts of the genome. *Genome Biology*. 2011; 12(12):138. PMID: 22206586 (**IF = 14.0**)
  - \*8. \***Dong X**, Greven MC, Kundaje A, Djebali S, Brown JB, Cheng C, Gingeras TR, Gerstein M, Guigó R, Birney E, Weng Z. Modeling gene expression using chromatin features in various cellular contexts. *Genome Biology*. 2012; 13(9):R53. PMID: 22950368 (**IF = 14.0**)
    - \*\* Cited 203 times so far
    - \*\* In the top 5% of all research outputs scored by Altmetric
    - \*\* High Attention Score (95th percentile) compared to outputs of the same age tracked by Altmetric
  9. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, Greven MC, Pierce BG, **Dong X**, Kundaje A, Cheng Y, Rando OJ, Birney E, Myers RM, Noble WS, Snyder M, Weng Z. Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome Research*. 2012; 22(9):1798-812. PMID: 22955990 (**IF = 10.1**)
  10. Cheng C, Alexander R, Min R, Leng J, Yip KY, Rozowsky J, Yan KK, **Dong X**, Djebali S, Ruan Y, Davis CA, Carninci P, Lassman T, Gingeras TR, Guigó R, Birney E, Weng Z, Snyder M, Gerstein M. Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Research*. 2012; 22(9):1658-67. PMID: 22955978 (**IF = 10.1**)
  11. ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012; 489(7414):57-74. PMID: 22955616 (**IF = 43.1**)
    - \*\* **Dong X** is listed as “Lead Analyst” among the authorship
    - \*\* Cited more than 800 times in the first year of publication
    - \*\* Featured as “Top 10 Breakthroughs of the Year 2012”
  12. Wang J, Zhuang J, Iyer S, Lin XY, Greven MC, Kim BH, Moore J, Pierce BG, **Dong X**, Virgil D, Birney E, Hung JH, Weng Z. Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. *Nucleic Acids Research*. 2013; 41(Database issue):D171-6. PMID: 23203885 (**IF = 11.2**)

13. Li XZ, Roy CK, **Dong X**, Bolcun-Filas E, Wang J, Han BW, Xu J, Moore MJ, Schimenti JC, Weng Z, Zamore PD. An ancient transcription factor initiates the burst of piRNA production during early meiosis in mouse testes. *Molecular Cell*. 2013; 50(1):67-81. PMID: 23523368 (IF = 14.6)  
 \*\* Dong X is the lead bioinformatics analyst  
 \*\* Recommended by the *Faculty of 1000*
14. Hoss AG, Kartha VK, **Dong X**, Latourelle JC, Dumitriu A, Hadzi TC, Macdonald ME, Gusella JF, Akbarian S, Chen JF, Weng Z, Myers RH. MicroRNAs located in the Hox gene clusters are implicated in huntington's disease pathogenesis. *PLoS Genetics*. 2014; 10(2):e1004188. PMID: 24586208 (IF = 5.2)
15. Haberle V, Li N, Hadzhiev Y, Plessy C, Previti C, Nepal C, Gehrig J, **Dong X**, Akalin A, Suzuki AM, van IJcken WFJ, Armant O, Ferg M, Strähle U, Carninci P, Müller F, Lenhard B. Two independent transcription initiation codes overlap on vertebrate core promoters. *Nature*. 2014; 507(7492):381-5. PMID: 24531765 (IF = 43.1)
- \*16. \***Dong X**, \*Tsuji J, Labadorf A, Roussos P, Chen JF, Myers RH, Akbarian S, Weng Z. The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. *PLoS ONE*. 2015; 10(12):e0144398. PMID: 26636336 (IF = 2.8)  
 \*\* Cited 27 times by top journals including *Nature Neuroscience*, *Molecular Psychiatry*, *Trends in Neuroscience*
17. Bai G, Cheung I, Shulha HP, Coelho JE, Li P, **Dong X**, Jakovcevski M, Wang Y, Grigorenko A, Jiang Y, Hoss A, Patel K, Zheng M, Rogaev E, Myers RH, Weng Z, Akbarian S, Chen JF. Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. *Human Molecular Genetics*. 2015; 24(5):1441-56. PMID: 25480889 (IF = 4.5)
18. Locascio JJ, Eberly S, Liao Z, Liu G, Hoising AN, Duong K, Trisini-Lipsanopoulos A, Dhima K, Hung AY, Flaherty AW, Schwarzschild MA, Hayes MT, Wills AM, Shivraj Sohur U, Mejia NI, Selkoe DJ, Oakes D, Shoulson I, **Dong X**, Marek K, Zheng B, Iverson A, Hyman BT, Growdon JH, Sudarsky LR, Schlossmacher MG, Ravina B, Scherzer CR. Association between  $\alpha$ -synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. *Brain*. 2015; 138(Pt 9):2659-71. PMID: 26220939 (IF = 11.8)
19. Mittal S, Bjornevik K, Im DS, Flierl A, **Dong X**, Abo KM, Long E, Jin M, Xu B, Xiang YK, Rochet JC, Engeland A, Rizzu P, Heutink P, Bartels T, Selkoe DJ, Caldarone BJ, Glicksman MA, Khurana V, Schüle B, Park DS, Riise T, and Scherzer CR.  $\beta$ 2-adrenoreceptor is a regulator of the  $\alpha$ -synuclein gene driving risk of Parkinson's disease. *Science*. 2017; 357 (6354), 891-898. PMID: 28860381 (IF = 41.0)  
 \*\* Dong X is the lead bioinformatics analyst  
 \*\* Featured on NIH Director Francis Collins's blog  
 \*\* Recommended by the *Faculty of 1000*  
 \*\* In the 99<sup>th</sup> percentile (top 5%) of all research outputs ever tracked by Altmetric
- \*20. \***Dong X**, Liao Z, Gritsch D, Hadzhiev Y, Bai Y, Locascio J, Guennewig B, Liu G, Blauwendraat C, Wang T, Adler CH, Frosch MP, Nelson PT, Rizzu P, Cooper AA, Heutink P, Beach TG, Mattick JS, Mueller F, Scherzer CR. Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. *Nature Neuroscience*. 2018; 21(10):1482-1492. PMID: 30224808 (IF = 21.1)  
 \*\* Featured in NIH Press Release, Alzforum, Neurology Today, Michael J Fox Foundation News.  
 \*\* Featured in 10 news outlets including EurekAlert!, R&D, BWH Bulletin, Science Daily, MedicalXpress, GEN, Drug Discovery and Development, The Medical News  
 \*\* Recommended by the *Faculty of 1000*  
 \*\* In the 98<sup>th</sup> percentile (top 1.5%) of all articles of a similar age in all journals tracked by Altmetric
- +21. Bao Z, Zhu Y, Ge Q, Gu W, **Dong X**<sup>+</sup>, Bai Y<sup>+</sup>. gwSPIA: Improved signaling pathway impact analysis with gene weights. *IEEE Access*. 2019; 7:69172-69183. (IF = 4.1)
22. Tsuji J, Thomson T, Chan E, Brown CK, Oppenheimer J, Bigelow C, **Dong X**, Theurkauf WE, Weng Z, Schwartz LM. High-resolution analysis of differential gene expression during skeletal muscle atrophy and programmed cell death. *Physiology Genomics*. 2020 Oct 1;52(10):492-511. PMID: 32926651. (IF = 2.7)

23. Tokarew JM, El-Kodsi DN, Lengacher NA, Fehr TK, Nguyen AP, Shutinoski B, O'Nuallain B, Jin M, Khan JM, Ng ACH, Li J, Jiang Q, Zhang M, Wang L, Sengupta R, Barber KR, Tran A, Im DS, Callaghan S, Park DS, Zandee S, **Dong X**, Scherzer CR, Prat A, Tsai EC, Takanashi M, Hattori N, Chan JA, Zecca L, West AB, Holmgren A, Puente L, Shaw GS, Toth G, Woulfe JM, Taylor P, Tomlinson JJ, Schlossmacher MG. Age-associated insolubility of parkin in human midbrain is linked to redox balance and sequestration of reactive dopamine metabolites. *Acta Neuropathology*. 2021 Mar 10. PMID: 33694021. (IF = 18.2)
24. Chen Y, Zhu Q, Cheng L, Wang Y, Li M, Yang Q, Hu L, Lou D, Li J, **Dong X**, Lee LP, Liu F. Exosome detection via the ultrafast-isolation system: EXODUS. *Nature Methods*. 2021 Feb;18(2):212-218. PMID: 33432243. (IF = 30.8)
25. Zhu Q, Cheng L, Deng C, Huang L, Li J, Wang Y, Li M, Yang Q, **Dong X**, Su J, Lee LP, Liu F. The genetic source tracking of human urinary exosomes. *PNAS*. 2021 Oct 26;118(43):e2108876118. doi:10.1073/pnas.2108876118. PMID: 34663731. (IF = 11.2)
26. Wang T, Liu Y, Ruan J, **Dong X**, Wang Y, Peng J. A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. *BMC Bioinformatics*. 2021 Aug 25;22(Suppl 9):403. doi: 10.1186/s12859-021-04307-0. PMID: 34433407; PMCID: PMC8386049. (IF = 3.24)
- <sup>+</sup>27. Domínguez-Baleón C, Ong JS, Scherzer CR, Rentería ME, **Dong X**. Understanding the effect of smoking and drinking behavior on Parkinson's disease risk: a Mendelian randomization study. *Sci Rep*. 2021 Jul 7;11(1):13980. doi:10.1038/s41598-021-93105-y. PMID: 34234189; PMCID: PMC8263722. (IF = 5.13)
- <sup>++</sup>28. **Dong X**, Li X, Chang TW, Scherzer CR, Weiss ST, Qiu W. powerEQTL: An R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis. *Bioinformatics*. 2021 May 19;btab385. doi:10.1093/bioinformatics/btab385. PMID: 34009297. (IF = 6.94)
- <sup>++</sup>29. **Dong X**, Liu C, Dozmorov M. Review of multi-omics data resources and integrative analysis for human brain disorders. *Brief Funct Genomics*. 2021 Jul 17;20(4):223-234. doi: 10.1093/bfpg/elab024. PMID: 33969380; PMCID: PMC8287916. (IF = 4.23)
30. Iwaki H, Leonard HL, Makarios MB, Bookman M, Landin B, Vismer D, Casey B, Gibbs JR, Hernandez DG, Blauwendraat C, Vitale D, Song Y, Kumar D, Dalgard CL, Sadeghi M, **Dong X**, Misquitta L, Scholz SW, Scherzer CR, Nalls MA, Biswas S, Singleton AB; Uniformed Services University of the Health Sciences Associates; AMP PD Whole Genome Sequencing Working Group; AMP PD consortium. Accelerating Medicines Partnership: Parkinson's Disease. Genetic Resource. *Mov Disord*. 2021 Aug;36(8):1795-1804. doi: 10.1002/mds.28549. Epub 2021 May 7. PMID: 33960523; PMCID: PMC8453903. (IF = 8.32)
31. Liu G, Peng J, Liao Z, Locascio JJ, Corvol JC, Zhu F, **Dong X**, Maple-Grødem J, Campbell MC, Elbaz A, Lesage S, Brice A, Mangone G, Growdon JH, Hung AY, Schwarzschild MA, Hayes MT, Wills AM, Herrington TM, Ravina B, Shoulson I, Taba P, Kóks S, Beach TG, Cormier-Dequaire F, Alves G, Tysnes OB, Perlmutter JS, Heutink P, Amr SS, van Hilten JJ, Kasten M, Mollenhauer B, Trenkwalder C, Klein C, Barker RA, Williams-Gray CH, Marinus J; International Genetics of Parkinson Disease Progression (IGPP) Consortium, Scherzer CR. Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinson's disease. *Nat Genet*. 2021 Jun;53(6):787-793. PMID: 33958783; PMCID: PMC8459648. (IF = 38.33)
32. Li C, Ou R, Chen Y, Gu X, Wei Q, Cao B, Zhang L, Hou Y, Liu K, Chen X, Song W, Zhao B, Wu Y, Li T, **Dong X**, Shang H. Genetic Modifiers of Age at Onset for Parkinson's Disease in Asians: A Genome-Wide Association Study. *Mov Disord*. 2021 Sep;36(9):2077-2084. PMID: 33884653. (IF = 8.32)
- **Scholarship listed as a collaborator in PUBMED**
33. ENCODE Project Consortium\*. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*. 2011; 9(4):e1001046. PMID: 21526222. (IF = 8.4)  
(\* member of the data analysis group cited in the appendix of the manuscript)
34. Liu G, Boot B, Locascio JJ, Jansen IE, Winder-Rhodes S, Eberly S, Elbaz A, Brice A, Ravina B, van Hilten JJ, Cormier-Dequaire F, Corvol JC, Barker RA, Heutink P, Marinus J, Williams-Gray CH, Scherzer CR;

International Genetics of Parkinson Disease Progression (IGPP) Consortium\*. Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. *Annals of Neurology*. 2016 Nov;80(5):674-685. PMID: 27717005. (IF = 10.2)

(\* member of the IGPP group cited in the appendix of the manuscript)

### **Non-peer reviewed Scholarship in print or other media:**

#### **Science-fiction essay**

1. \*Dong X. The brainstorm. *IEEE Potential*. 2009 Vol. 28, No.1.

#### **Editorial and review**

2. \*Dong X, Weng Z. The correlation between histone modifications and gene expression. *Epigenomics*. 2013; 5(2):113-6. PMID: 23566087 (IF = 4.4)

#### **Proceedings of meetings and other non-peer reviewed scholarship:**

3. Dong X, Xie J, Lu Z. PatternExplorer2.0: a tool to explore related genes with random pattern sequence in genome. *The International Forum on Biochip Technologies (IFBT2004)*, Beijing, China, 2004.
4. Dong X, Zhang L, Lu Z. Why SARS virus only infects the lung of human? A model to analyze the association of virus attachment proteins and cell receptors. *The 2nd International Forum on Post-Genome Technologies (2'IFPT)*, Nanjing, 2004.
5. Xie J, Sun X, Lu Z, Xue W, Dong X, Lu Z. gWord: A Tool for Genome-Wide Word Search and Count. *Proceeding of Bioinformatics and Biomedical Engineering*, 2007. ICBBE 2007.
6. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, Greven MC, Pierce BG, Dong X, Kundaje A, Cheng Y, Rando OJ, Birney E, Myers RM, Noble WS, Snyder M, Weng Z. Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Journal of Biomolecular Structure and Dynamics*. 2013; 31:sup1, 49-50

#### **Thesis:**

1. Dong X. Evolutionary mechanisms of developmental long-range gene regulation in vertebrate genomes. 2010.

#### **Abstracts, Poster Presentations Presented at Professional Meetings:**

1. Dong X, Fredman D, Engström P, Lenhard B. Reconstructing the Evolutionary History of Genomic Regulatory Blocks in Vertebrates. *The 15<sup>th</sup> Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Austria, 2007.
2. Dong X, Akalin A, Fredman D, Lenhard B. Distribution of highly conserved non-coding elements in *Danio rerio*. *The 5<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Hong Kong, 2007.
3. Dong X, Sheng Y, Gupta P, Lenhard B. Computational prediction of ncRNAs as target genes in genomic regulatory blocks. *The 6<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Japan, 2008.
4. Dong X, Fredman D, Lenhard B. GRB Evolution Browser: a web resource for exploring evolutionary behaviours of vertebrate genomic regulatory blocks. *The 4th EMBO Conference: From Functional Genomics to Systems Biology*, Germany, 2008.
5. Dong X, Akalin A, Fredman D, Lenhard B. Evolutionary dynamics of genomic regulatory blocks: HCNEs and HARs, the content and the boundaries. *The 7<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, China, 2009.
6. Dong X. Predicting gene expression using histone modifications. ENCODE Conference, Stanford, 2011.
7. Dong X. Correlating histone modifications and gene expression. *Systems Biology: Global Regulation of Gene Expression*, CSHL, 2012.
8. Liao Z, Zheng B, Dong X, Vanderburg CR, Locascio JJ, Pochet N, Regev A, Portenkirchner C, Altmann P, Jin S, Beach TG, Adler CH and Scherzer CR. The PD Brain Map: Mapping the Transcriptional Architecture of Dopamine Neurons in Human Brain. *The American Society of Human Genetics (ASHG)*, Boston, 2013.
9. Dong X, Liao Z, Gritsch D, Guennewig B, Hadzhiev Y, Bai Y, Liu G, Zheng B, Blauwendraat C, Hu Q, Adler CH, Hedreen JC, Frosch MP, Faull R, Nelson PT, Locascio J, Vanderburg C, Rizzu P, Cooper AA, Heutink P, Beach TG, Mueller F, Mattick JS, Scherzer CR. BRAINCODE: How does the Human Genome Function in Specific Brain Neurons? *The American Society of Human Genetics (ASHG)*, Baltimore, 2015.



10. Liu G, Boot B, Locascio JJ, Liao Z, Franco D, Duong K, Page K, Jansen I, Yi T, Trisini-Lipsanopoulos A, **Dong X**, Hutten SJ, Winder-Rhodes S, Amr S, Tanner C, Lang A, Nalls M, Eberly S, CamPaIGN HBS, PROPARK PICNICS, DIGPD PSG, Sudarsky L, Elbaz A, Brice A, Ravina B, Shoulson I, van Hilten J, Cormier-Dequaire F, Corvol JC, Barker R, Heutink P, Marinus J, Williams-Gray C, Scherzer CR, International Genetics of Parkinson Disease Progression (IGPP) Consortium. Neuropathic Gaucher's Mutations: Shifting Parkinson's Into High Gear. *Neurology*. 2017; 88 (16 Supplement) S1.002.
11. **Dong X**. BRAINcode: an encyclopedia of human dopamine neurons in health and disease. *The NINDS Parkinson's Disease Biomarkers Program (PDBP) Annual Meeting*, Bethesda, MD, 2018.
12. **Dong X**, Liao Z, Bai Y, Monroy RB, Wang T, Ehrlich A, Scherzer CR. Circular RNAs: A novel link between genetic susceptibility and Parkinson's disease? *The 84th Cold Spring Harbor Laboratory Symposium on Quantitative Biology: RNA Control & Regulation*, CSHL, NY, 2019.
13. Li X, Mariani M, Bustos S, Frieze S, Cohrs R, **Dong X**. Circular RNAs detected in Varicella-Zoster Virus (VZV): a possible association to latency. *Colorado Alpha herpesvirus Latency Symposium 2021*. - Poster oral presentation
14. Li X and **Dong X**. Circular RNAs detected in SARS-Cov-2: A potential robust biomarker for COVID19. *Discover Brigham 2020*. - Poster oral presentation
15. Li X, Renteria M, and **Dong X**. Polygenic Risk Assessment: Genetics Supported Imaging Diagnosis for Parkinson's Disease. *2020 PQG Conference*. - Poster oral presentation
16. Yuan J#, Haywood N#, Liao Z, Tuncali I, Adiconis X, Simmons S, Kuras Y, Lin Z, Parker J, Zhang SC, Feany MB, Scherzer CR, Levin JZ\*, **Dong X\***. Integrating spatial transcriptomics and known regulatory elements to elucidate mechanisms of Parkinson's disease. *ASAP Celebration of Scientific Achievement*, 2021.
17. Hu R, Yuan J, Scherzer CR\*, **Dong X\***. Accelerating Parkinson's Diagnosis using Multi-omics and Artificial Intelligence. *Discover Brigham 2021*. Boston, MA, 2021.