

Xianjun Dong, PhD**Office Address:** 60 Fenwood Road, 9002R, Boston, MA 02115, USA**Phone:** +1 857-307-5423**Email:** xdong@rics.bwh.harvard.edu**Web:** <https://bioinformatics.bwh.harvard.edu>**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 (Supervisor: Dr. Zhiping Weng)	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

Appointments at Hospitals/Affiliated Institutions

09/13 - present	Assistant Scientist	Ann Romney Center for Neurologic Diseases	Brigham and Women's Hospital
07/20 - present	Full member	HMS Initiative for RNA Medicine	BIDMC Cancer Center / Harvard Medical School
08/20 - present	Associate member	Broad Institute	Harvard and MIT

Major Administrative Leadership Positions

2016 – present	Director of Computational Neuroscience	Center for Advanced Parkinson Research (Director: Dr. Clemens Scherzer)	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 th Annual DNA Day Essay Contest, Judge		
2016 – present	American Academy of Neurology (AAN), Member		
2021 – present	MJFF/ASAP Data Repository Alignment Working Group, Chair		
2022 – present	MJFF/ASAP Spatial Transcriptomics Working Group, Co-chair		
2022 - 2023	MJFF/ASAP 2023 Meetings Advisory Committee		
2023 – present	NIH PRECISION Human Pain Data Subcommittee, chair		

Grant Review Activities

2021	NIH NINDS Special Emphasis Panel study section Ad hoc Reviewer
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2022	European Science Foundation – CORE program Ad hoc Reviewer
2022	European Science Foundation – FWO Strategic Basic Research Program Ad hoc Reviewer

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, npj Parkinson's Disease*

- Editorial Roles –

2017 – present	<i>Personalized Medicine</i> (Editorial Board)
2017 – 2023	<i>PeerJ</i> (Academic Editor)
2018 – present	<i>Frontiers in Neuroscience, Frontiers in Genetics</i> (Academic Editor)
2019 – present	<i>iScience</i> (Editorial Board)

Honors and Prizes

2000	Distinguished Student with 1 st grade Scholarship, Southeast University, China
2000	2 nd prize in the National Undergraduate Mathematical Contest in Modeling
2000	<i>Liu Yonglin</i> Fellowship Award, Southeast University, China
2001	1 st 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 st 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	<i>Epigenetic Markers in Huntington’s Disease Brain</i> NIH R01 NS073947 Role: Co-Investigator (PI: Richard H. Myers)
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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's 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 at 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.
- 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 the Harvard site in this dual-institute grant.
- 2020 – 2021
(NCE 2022) *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.
- 2018 – 2018 *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.

Active grants (9 in total):

- 2020 – 2023 *Genomics and Bioinformatics Hub*
Fidelity Foundation
Role: **Principal Investigator -- \$436,800**
The goal is to develop a collaborative hub providing a genomics and bioinformatics service hub to the Neurology research community at Brigham and Women's Hospital.

- 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 (\$560,000 total cost to Dong)**
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).
- 2021 – 2022
(NCE 2023) *Developing RNA biomarkers of early PD pathology from brain organoids and extracellular vesicles*
American Parkinson Disease Association (APDA) Research Grant
Role: **Principal Investigator -- \$75,000**
The goal of the study is to develop RNA biomarkers of early PD pathology from brain 3D organoids and extracellular vesicles (EV).
- 2021 – 2022
(NCE 2023) *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) -- **\$251,359 (\$109,906 total cost to Dong)**
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) -- **\$3,691,875 (\$1,671,386 total to Dong)**
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.
- 2022 – 2027 *Regulation mechanism and functional genomics of LINE1 RNA in TDP-43 linked neurodegeneration*
NIH R01 AG078948-01
Role: **Principal Investigator** (Pis: Sun, Dong) -- **\$4,255,070 (\$1,566,250 total cost to Dong)**
The goal of this project is to study the regulation mechanism and functional genomics of LINE1 RNA in TDP-43 linked neurodegeneration.
- 2022 – 2027 *Human PRECISION Human Pain Center – Data Core*
NIH U19 1U19NS130617
Role: **Data Core lead -- \$13,015,149 (\$1,790,000 total cost to Dong)**
The goal of this core is to act as a data center for large-scale multi-omics datasets generated by the U19 Center by building infrastructure and providing data management, coordination, analysis, and sharing.

2023 – 2024 *A Large-scale Extracellular Vesicle RNA-seq Resource for Parkinson's Disease*
NIH R24 1R24NS132738-01
Role: **Principal Investigator** (PI: Dong, Jensen, Eitan) – \$2,250,000 (**\$520,935 total cost to Dong**)
The goal of this project is to develop a comprehensive, plasma-based, extracellular RNA (exRNA) resource that can easily be accessed and utilized by the PD research community.

2023 -2024 *Data Science Internship Program*
Massachusetts Life Sciences Center
Role: **Principal Investigator -- \$67,600**
The aim of this program is to support three prospective interns to advance their data analytics and data science applications to the life sciences.

Projects Submitted for Funding

2023 – 2028 *Parkinson's Disease Analysis via Sensitive and Systematic Integrated multi-Omics Networks: PASSION*
NIH RM1
Role: **Principal Investigator** (PI: Dong, Lee, Scherzer, Guo) – **\$11,643,556**
This multi-disciplinary project is poised to establish a versatile and scalable human on-chip platform with an unprecedented single-cell and spatial resolution, real-time detection of metabolites, dopamine release, secreted proteins, and electrophysiological brainwaves.

2023 – 2024 *Building subcellular spatial maps of non-coding regulatory RNAs in PD brain organoids with Xenium in situ*
American Parkinson Disease Association (APDA) Research Grant
Role: **Principal Investigator -- \$75,000**
The goal of the study is to build high-resolution subcellular spatial maps of non-coding regulatory RNAs in PD brain organoids.

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 at 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 at Harvard Medical School. She got all “Excellent” assessments for her PiM funding proposal.

2015 -2016 Ellen DeGennaro (PhD student in the 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 (Undergraduate student 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.

2022 - 2024 Xiaohe Lucy Tian (Master student in the Computational Biology and Quantitative Genetics program at Harvard T.H. Chan Public Health)
Conducted her master's thesis in the Dong Lab where Dr. Dong is her thesis mentor.
Received the Data Science Internship Program award (\$20,800) from Massachusetts Life Sciences Center

Other Mentored Trainees and Faculty

2009 – 2012 Yogita Sharma (Graduate student at the 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 at 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 at the University of Massachusetts)
Supervisor, and 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 at Buckingham Browne & Nichols School)
Supervisor, and research advisor for his summer bioinformatics training at Harvard

2015 – 2017 Kristy Abo (Medical student at the 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 at Harbin Institute of Technology, China)
Supervisor, and research advisor for his three-year bioinformatics training at Harvard, and co-authored an article published in *Nature Neuroscience* and a manuscript

2016 – 2018 Zhuo Wang (PhD Joint Training Program student at Harbin Institute of Technology, China)

	Supervisor, and research advisor for her two-year bioinformatics training at Harvard, and co-authored a manuscript
2016 – 2018	Dr. Miguel E. Renteria (Postdoc in QIMR Berghofer Medicine Research Institute, Australia) Supervisor, and 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 at Universidad Complutense of Madrid, Spain) Supervisor, and research advisor for her five-month research traineeship in Bioinformatics, and co-authored a manuscript.
2018 – 2020	Dr. Jiajie Peng (Associate Professor at Northwest Polytechnical University, China) Co-supervisor, and research advisor for his two-year visiting scholarship at Brigham
2018 – 2020	Dr. Young Eun Huh (Assistant Professor of Neurology at CHA University School of Medicine, South Korea) Supervisor, and research advisor for her two-year bioinformatics training at Harvard
2018 – 2019	Haotian Liao (Graduate student at West China Medical School, Sichuan University, China) Supervisor, and research advisor for his two-year bioinformatics training at Brigham
2019 – 2019	Carmen Domínguez (Undergraduate from the National Autonomous University of 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 at the "Genomics of Brain Disorders 2020" conference (Wellcome Genome Campus, Cambridge, UK); published a first-author paper in <i>Scientific Reports</i> .
2020 - 2021	Xiaoqi Li (Undergraduate from the University of Wisconsin–Madison) <u>Career stage</u> : postgraduate 11-month internship. <u>Mentoring role</u> : research advisor and mentor. <u>Accomplishments</u> : 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 <i>Bioinformatics</i> ; received Data Science Internship Program award (\$20,800) by Massachusetts Life Sciences Center; three manuscripts in preparation
2021 - 2021	Ariela Buxbaum Grice (Undergraduate from Connecticut College) <u>Career stage</u> : postgraduate 8-month internship. <u>Mentoring role</u> : research advisor and mentor. <u>Accomplishments</u> : Led an exploratory project (pathogen detection in AD brain); prepared a first-author manuscript.
2021 - 2021	Mrinal Subash (Master's student at Northeastern University) Research advisor and mentor for his 5-month co-op internship in bioinformatics.
2021 – 2022	Dr. Tingting Zhao (Full-time research scientist in the Bioinformatics Hub) <u>Career stage</u> : transition from molecular biologist to bioinformatics specialist. <u>Mentoring role</u> : supervisor <u>Accomplishments</u> : Led the bioinformatics analysis for three collaborative projects; two poster presentations at the local conference; TA in the Single-cell RNA-seq course
2021 -	Dr. Ruifeng Hu (Postdoctoral Research Fellow) <u>Mentoring role</u> : supervisor <u>Accomplishments</u> : Led an NIH-sponsored research project (AMP PD); one poster presentation at the local conference; prepared a first-author manuscript

- 2021 - Dr. Jie Yuan (Postdoctoral Research Fellow)
Mentoring role: supervisor
Accomplishments: Led an ASAP-sponsored research project (Parkinson5D); two poster presentations at local and international conferences; prepared a first-author manuscript
- 2022 - Ziqin Wang (Master student at UC Davis)
Career stage: transition from biostatistics to bioinformatics/genomics.
Mentoring role: supervisor
Accomplishments: Led a project of modeling the evolutionary change of intron size expansion; funded by the Data Science Internship Program (\$20,800) of Massachusetts Life Sciences Center
- 2022 - Rosan Ruoxuan Wang (Undergraduate student at Northeastern University)
Career stage: one-year co-op internship in genomics and bioinformatics.
Mentoring role: Research advisor and mentor
Accomplishments: identifying PD-associated enhancer RNAs (eRNAs) in the AMP-PD cohort; funded by the Data Science Internship Program (\$20,800) of Massachusetts Life Sciences Center; preparing a review and a manuscript.
- 2022 - 2022 Qinyun Lin (Master student of Computer Science at Northeastern University)
Career stage: an internship in genomics and bioinformatics.
Mentoring role: Research advisor and mentor
Accomplishments: implemented Nextflow pipelines on AWS cloud for RNA-seq and circRNAs analysis.
- 2022 - 2022 Daianna González (Undergraduate student at the National Autonomous University of Mexico)
 Research advisor and mentor for her summer internship in the lab
- 2022 - Miles Waits (Undergraduate from Yale University)
 Research supervisor and trainer for his one-year remote internship in the lab
- 2022 - Dr. Ewa Grassin (Postdoctoral Research Fellow)
Mentoring role: co-supervisor (together with Dr. Luke Lee at BWH)
Accomplishments: Led an NIH-sponsored R01 project (PD-MAP) to study PD brain organogenesis using iPSC-derived midbrain organoids in dish as a platform; preparing a review and a manuscript; Awardee of Swiss National Science Foundation Early Postdoc Mobility Fellowship;
- 2023 - Anthony Cicalo (Full-time bioinformatician in the Bioinformatics Hub)
Mentoring role: supervisor
Accomplishments: Led the single-cell RNAseq analysis for five collaborative projects;
- 2023 - Dr. Maoxuan Lin (Postdoctoral Research Fellow)
Mentoring role: Supervisor
Accomplishments: Led an NIH-sponsored U19 project to study human pain mechanisms using single-cell multi-omics integrative analysis.

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

No presentations below were sponsored by outside entities

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|------|---|---------------------|
| 2017 | Make Interactive Web Applications Using Shiny | Single presentation |
| | Bioinformatics Club, Brigham and Women's Hospital | Boston |
| 2017 | Introducing the UCSC Genome Browser | Single presentation |

	Bioinformatics Club, Brigham and Women's Hospital	Boston
2018	Using <i>reshape2</i> and <i>tidyr</i> for Data Transformation	Single presentation
	The "Mini R Camp" talk series, Brigham and Women's Hospital	Boston
2019	Introducing Artificial Intelligence (AI) and the AI Camp	Single presentation
	The "2019 AI Camp" talk series, Brigham and Women's Hospital	Boston
2019	Making Your First AI Program Using CoLab and TensorFlow	Teaching Assistant
	The "2019 AI Camp" talk series, Brigham and Women's Hospital	Boston
2019	Unsolved Problems and Future Challenges of Using AI in Medicine	Single presentation
	The "2019 AI Camp" talk series, Brigham and Women's Hospital	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 <u>Award Speaker</u> 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 <u>Featured Speaker</u> 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 <u>Invited Speaker</u> 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
- 2023 Decoding the Dark Matter in the Human Brain Genome
Neurology Grand Rounds, Yale University

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 7th Bioinformatics Strategy Meeting USA (East Coast)
The Westin Boston Waterfront, Boston, MA
- 2021 Circular RNAs Detected in SARS-Cov-2: A Potential Robust Biomarker for COVID-19
MGBCCI Horizon Technologies Forum, Boston, MA
- 2023 Integrative Multi-Omics Analysis to Study Brain Disorders
Invited Speaker
Longwood Bioinformatics Exchange, Boston, MA
April 21, 2023

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
- 2020 Exploring the Dark Matters in the Human Brain Neurons
Invited Speaker and Panelist
NextGen Omics Series – the 6th Single Cell Analysis Congress
Boston, USA
- 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
- 2022 Towards a spatial atlas of Parkinson's brain: Single-cell and spatial transcriptomics
integrative analysis of 200 human brains
Invited Speaker
Oxford Global Spatial Biology Conference (US)
Boston, USA
- 2022 Integrative Multi-Omics Analysis to Study Brain Disorders
Invited Speaker
Tri-Omics Summit
Boston, MA
- 2022 Parkinson Brain Atlas: Single-cell and spatial transcriptomics integrative analysis of 200
human brains
ASAP Collaborative Research Network (CRN) Tech 1 Sequencing/Omics Meeting
Aligning Science Across Parkinson's (ASAP) Foundation
- 2022 Circular RNAs and Exosome: A Promising Candidate for Earlier Diagnosis and Therapy
Invited Speaker and Panelist
APDA Connecticut Annual Parkinson's Symposium
Hartford, CT
- 2022 Exploring PD-associated enhancer RNAs in the AMP-PD RNA sequencing data
Invited Speaker
NIH AMP-PD Steering Committee Meeting
Dec 5th, 2022. Zoom

International

- 2010 Translog, a web browser for studying the expression divergence of homologous genes
The 8th 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 2nd Academic Symposium of Rare Disease
Sichuan Medical Association, Chengdu, China
- 2021 Decoding the dark matters in the human genome
Invited Speaker
The 11th International Conference on Post-Genome Technologies (11'IFPT) – virtual
Nanjing, China
- 2021 Mathematics challenges in high-dimensional multi-omics biomedical data analysis
Invited Speaker
Soochow University, China
- 2021 Exploring the dark matters in the human genome and their relationship with complex diseases
Institute of Basic Medicine and Cancer (IBMC), Chinese Academy of Sciences
Hangzhou, China
- 2022 Seeing the unseen dark matter in the human brain genome
Workshop organizer and Speaker
ASAP Annual Conference – Non-coding Workshop
Nassau, Bahamas

Report of Activities and Innovations

Technological and Other Scientific Innovations

- Synorth
(2009) A website designed for genome research, allowing to explore the evolution of synteny and long-range regulatory interactions between vertebrate genomes
URL: <http://synorth.genereg.net>
Published as the first author on *Genome Biology* (Impact factor: 11.91), 25 citations
- Translog
(2010) A website designed to study the expression divergence of homologous genes
URL: <http://translog.genereg.net>
Published as the first author on *BMC Bioinformatics* (Impact factor: 2.21)
- Factorbook
(2012) A Wiki-based database for transcription factor-binding data generated by ENCODE
URL: <http://factorbook.org>
Published as co-author on *Nucleic Acid Research* (Impact factor: 10.16), 158 citations
- BRAINcode
(2018) A web resource allowing users to query the gene expression profile and eQTL result in human brain neurons.
URL: <http://humanbraincode.org>
- powerEQTL
(2021) An R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis
URL: <https://bwhbioinfo.shinyapps.io/powerEQTL>
Published as the first author on *Bioinformatics* (Impact factor: 6.94)

Educational Activities to the Community

2008 – present	Owner of the bioinformatics blog, “ <i>One Tip Per Day</i> ” (http://onetipperday.sterding.com), 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 http://www.umassmed.edu/news/2012/education/gsbs-students-take-science-on-road.aspx
2017 – present	Founder and Director of the <i>Bioinformatics Club</i> (http://bioinformatics.bwh.harvard.edu/training), 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 “Single-cell RNA-seq Analysis” (https://singlecellcourse.org) at Brigham and Women’s Hospital, with 40 participants

Media Coverage

<u>ENCODE consortium et al. <i>Nature</i>, 2012</u>	CNN: http://www.cnn.com/2012/09/05/health/encode-human-genome/ BBC: http://www.bbc.com/news/health-19202141 Scientific American: http://www.scientificamerican.com/article/junk-dna-encode/ Evolution News: http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html New York Times: http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html LA Times: http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906 The Guardian: http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode
<u>Dong et al. <i>Genome Biology</i>, 2012</u>	GenomeWeb: http://www.genomeweb.com/blog/week-genome-biology-59 Biomed Central: http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/ UmassMed News: http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/
<u>Dong et al. <i>Nature Neuroscience</i>, 2018</u>	EurekAlert!: https://www.eurekalert.org/pub_releases/2018-09/bawh-gdm092018.php Alzforum: https://www.alzforum.org/news/research-news/noncoding-rnas-evince-world-gene-regulation-dopaminergic-neurons Neurology Today: 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, 41 publications, over 21,000 citations, H-index = 27, over 65% articles with Impact Factor > 10

- **Research Investigation** (including 9 first-author publications* and 4 corresponding-author publications⁺)
- 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 = 17.9**)
- 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 = 17.9**)
- *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 = 19.16**)
- 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 = 66.86**)
- 7. Fredman D, **Dong X**, Lenhard B. Making enhancers from spare parts of the genome. *Genome Biology*. 2011; 12(12):138. PMID: 22206586 (**IF = 17.9**)
- *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 = 17.9**)
 - ** 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 = 19.16**)

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 = 19.33**)
 ** 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 = 6.02)
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 = 69.5**)
- *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 = 3.75)
 ** 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 = 6.15)
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 α -synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. *Brain*. 2015; 138(Pt 9):2659-71. PMID: 26220939 (**IF = 15.26**)
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. β 2-adrenoreceptor is a regulator of the α -synuclein gene driving risk of Parkinson's disease. *Science*. 2017; 357 (6354), 891-898. PMID: 28860381 (**IF = 63.71**)
 ** Dong X is the lead bioinformatics analyst
 ** Featured on NIH Director Francis Collins's blog
 ** Recommended by the *Faculty of 1000*
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- *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 = 24.88**)
 ** **Featured in NIH Press Release, Alzforum, Neurology Today, Michael J Fox Foundation News.**
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- +21. Bao Z, Zhu Y, Ge Q, Gu W, **Dong X**⁺, Bai Y⁺. 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 = 4.29)

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 = 17.09)
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 = 47.99)
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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 = 4.34)
- ⁺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 = 5.00)
- ⁺⁺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)
- ⁺⁺29. **Dong X**, Liu C, Dozmorov M. Review of multi-omics data resources and integrative analysis for human brain disorders. *Briefings in Functional Genomics*. 2021 Jul 17;20(4):223-234. doi: 10.1093/bfpg/elab024. PMID: 33969380; PMCID: PMC8287916. (IF = 4.84)
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. *Movement Disorders*. 2021 Aug;36(8):1795-1804. doi: 10.1002/mds.28549. Epub 2021 May 7. PMID: 33960523; PMCID: PMC8453903. (IF = 9.69)
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, Köks 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. *Nature Genetics*. 2021 Jun;53(6):787-793. PMID: 33958783; PMCID: PMC8459648. (IF = 41.38)
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. *Movement Disorders*. 2021 Sep;36(9):2077-2084. PMID: 33884653. (IF = 9.69)
33. Mitchell BL, Saklatvala JR, Dand N, Hagenbeek FA, Li X, Min JL, Thomas L, Bartels M, Jan Hottenga J, Lupton MK, Boomsma DI, **Dong X**, Hveem K, Løset M, Martin NG, Barker JN, Han J, Smith CH, Rentería ME, Simpson MA. Genome-wide association meta-analysis identifies 29 new acne susceptibility loci. *Nature Communications*. 2022 Feb 7;13(1):702. doi: 10.1038/s41467-022-28252-5. PMID: 35132056; PMCID: PMC8821634. (IF = 17.69)

34. Dai Y, Hu R, Liu A, Cho KS, Manuel AM, Li X, **Dong X**, Jia P, Zhao Z. WebCSEA: web-based cell-type-specific enrichment analysis of genes. *Nucleic Acids Research*. 2022 May 24;gkac392. doi: 10.1093/nar/gkac392. Epub ahead of print. PMID: 35610053. (IF = 19.16)
35. Hallacli E, Kayatekin C, Nazeen S, Wang XH, Sheinkopf Z, Sathyakumar S, Sarkar S, Jiang X, **Dong X**, Di Maio R, Wang W, Keeney MT, Felsky D, Sandoe J, Vahdatshoar A, Udeshi ND, Mani DR, Carr SA, Lindquist S, De Jager PL, Bartel DP, Myers CL, Greenamyre JT, Feany MB, Sunyaev SR, Chung CY, Khurana V. The Parkinson's disease protein alpha-synuclein is a modulator of processing bodies and mRNA stability. *Cell*. 2022 Jun 9;185(12):2035-2056.e33. doi: 10.1016/j.cell.2022.05.008. PMID: 35688132; PMCID: PMC9394447. (IF = 66.85)
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- *37. ***Dong X**, Bai Y, Liao Z, Gritsch D, Liu X, Wang T, Borges-Monroy R, Ehrlich A, Serano GE, Feany MB, Beach TG, Scherzer CR. Circular RNAs in the human brain are tailored to neuron identity and neuropsychiatric disease. *Nature Communications*. in press. (IF = 17.69)
38. Han X, Gharahkhani P, Hamel AR, Ong JS, Rentería ME, Mehta P, **Dong X**, Pasutto F, Hammond C, Young TL, Hysi P, Lotery AJ, Jorgenson E, Choquet H, Hauser M, Cooke Bailey JN, Nakazawa T, Akiyama M, Shiga Y, Fuller ZL, Wang X, Hewitt AW, Craig JE, Pasquale LR, Mackey DA, Wiggs JL, Khawaja AP, Segrè AV, 23andMe Research Team, International Glaucoma Genetics Consortium, MacGregor S. Large-scale multi-trait genome-wide association analyses identify hundreds of glaucoma risk loci. *Nature Genetics*. in press. (IF = 41.38)

• **Scholarship listed as a collaborator in PUBMED**

39. ENCODE Project Consortium*. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*. 2011; 9(4):e1001046. PMID: 21526222. (IF = 9.59)
(* member of the data analysis group cited in the appendix of the manuscript)
40. 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 = 11.27)
(* member of the IGPP group cited in the appendix of the manuscript)
41. Liu G, Ni C, Zhan J, Li W, Luo J, Liao Z, Locascio JJ, Xian W, Chen L, Pei Z, Corvol JC, Maple-Grødem J, Campbell MC, Elbaz A, Lesage S, Brice A, Hung AY, Schwarzschild MA, Hayes MT, Wills AM, Ravina B, Shoulson I, Taba P, Köks S, Beach TG, Cormier-Dequaire F, Alves G, Tysnes OB, Perlmutter JS, Heutink P, van Hilten JJ, Barker RA, Williams-Gray CH, Scherzer CR; International Genetics of Parkinson Disease Progression (IGPP) Consortium*. Mitochondrial haplogroups and cognitive progression in Parkinson's disease. *Brain*. 2023 Jan 5;146(1):42-49. PMID: 36343661. (IF = 15.26)
(* member of the IGPP group)

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.
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Thesis:

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

Abstracts, Poster Presentations Presented at Professional Meetings (since 2020):

1. Li X, Mariani M, Bustos S, Fietze 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
2. Li X and **Dong X**. Circular RNAs detected in SARS-Cov-2: A potential robust biomarker for COVID19. *Discover Brigham 2020*. - Poster oral presentation
3. Li X, Renteria M, and **Dong X**. Polygenic Risk Assessment: Genetics Supported Imaging Diagnosis for Parkinson's Disease. *2020 PQG Conference*. - Poster oral presentation
4. 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.
5. Hu R, Yuan J, Scherzer CR*, **Dong X***. Accelerating Parkinson's Diagnosis using Multi-omics and Artificial Intelligence. *Discover Brigham 2021*. Boston, MA, 2021.
6. Yuan J#, Haywood N#, Liao Z, Tuncali I, Adiconis X, Simmons S, Kuras Y, Lin Z, Parker J, Zhang SZ, Feany MB, Scherzer C*, Levin J*, and **Dong X*** for the PD5D Consortium. Parkinson Brain Atlas: A multi-facet view of Parkinson's brain by integrating single-cell and spatial data for 100 human brains. *ASAP Celebration of Scientific Achievement (COSA)*, 2022.