Xianjun Dong, Ph.D.

Address: 60 Fenwood Road, 9th Floor, BTM 09002EE**,** Boston, MA 02115 USA
Phone: +1 857-307-5423
Fax: +1 857-307-5476
Email: xdong@rics.bwh.harvard.edu
Website: http://www.sterding.com

PART I: GENERAL INFORMATION

Education

1998 - 2002	B.Sc., Biomedical Engineering, Southeast University, China
2002 - 2005	M.Sc., Biomedical Engineering, Southeast University, China
2005 - 2010	Ph.D., Bioinformatics, University of Bergen, Norway (Advisor: Dr. Boris Lenhard)

Postdoctoral Training

09/10 - 09/13	Postdoctoral Associate, Program of Bioinformatics and Integrative Biology, University of Massachusetts Medical School (Supervisor: Dr. Zhiping Weng)

Appointments at Hospitals/Affiliated Institutions

12/16 - present	Director of Computational Neuroscience, Neurogenomics Lab and Parkinson Personalized Medicine (PPM), Harvard Medical School and Brigham & Women's Hospital
11/13 - present	Instructor, Department of Neurology, Harvard Medical School
09/13 - present	Faculty in Neurology, Brigham and Women's Hospital (Mentor: Dr. Clemens Scherzer)

Other Professional Positions

2005 - 2005	Manager Trainee / Process Engineer, P&G

Major Administrative Leadership Positions

2005 - 2007	President, Chinese Students and Scholars Association (CSSA) of Bergen, Norway
2007 - 2007	Organizer of the "EnsEMBL in a Nutshell" Bioinformatics Workshop, University of Bergen
2017 - present	Founder of the Bioinformatics Club in 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 10th Annual DNA Day Essay Contest, Judge
2016 - present	American Academy of Neurology (AAN), Member

Honors and Prizes

2000	*Liu Yonglin* Fellowship Award, Southeast University, China
2000	Distinguished Student with 1st grade Scholarship, Southeast University, China
2000	2nd prize of the National Undergraduate Mathematical Contest in Modeling
2001	1st prize of 2001 "Sony Cup" National Undergraduate Electronic Design Contest, China
2001	Meritorious winner (top 10%) in the International Mathematical Contest in Modeling (MCM)
2001	Distinguished Student with 1st 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 in the world wide)
2015	Reviewers' Choice – best abstract in the American Society of Human Genetics meeting, US
2018	Finalist of the PacBio Structural Variant SMRT Grant program
2018	Research Excellence Award, Brigham and Women's Hospital
2019	Center for Advanced Parkinson's Research (CAPR) Seed Award

Service to Professional Publications

- 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*

- Other editorial Roles -

2017 - present	*Personalized Medicine* (Editorial Board)
2017 - present	*PeerJ* (Academic Editor)
2018 - present	*Frontiers in Neuroscience - Neurogenomics* (Editorial Board)
2018 – present	*PLoS ONE* (Editorial Board)

Funding Information

- Past -

2011 - 2016
Epigenetic Markers in Huntington's Disease Brain
NIH R01 NS073947
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
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
Co-investigator (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.

- Current -

2016 – 2019
Parkinson Disease: Predicting the Future
NIH U01 NS095736
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 replicate and verify forwarded genetic variants in independent populations.

2017 – 2018
(NEC 2019)
Cracking the code of chr17q21 for Parkinson: From GWAS to novel drug targets
American Parkinson Disease Association (APDA) Research Grant
Principal Investigator **($50,000)**
The goal of this project is to discover the causal variants in chr17q21 locus and validate them in iPSC-derived neurons.

2017 - 2022
Integrative Multi-Omic Discovery of Proximal Mechanisms Driving Age-Dependent Neurodegeneration
NIA RF1AG057331
Bioinformatics Director (PI: 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.

2018 – 2023 *Translating GWAS peaks into novel drug targets*
American Parkinson Disease Association (APDA) Center for Advanced Parkinson's Research (CAPR) Seed Award
Co-Principal Investigator ($10,000)
The CAPR 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 integrates the powers of human genomics, transcriptomics, and epigenomics data to identify novel, potentially druggable mechanisms for PD.

2018 – 2019 *Bioinformatics Club: A Weekly Meetup to Learn and Share Bioinformatics at BWH*
Brigham Research Institute (BRI) NextGen Awards
Principal Investigator ($5,000)
This award is for my leadership in the Bioinformatics Club to further improve the bioinformatics education environment in Brigham and Women's Hospital.

PART II: REPORT OF TEACHING, TRAINING, AND PRESENTATIONS

Teaching of Students in Courses

2007 "EnsEMBL in a Nutshell" workshop, University of Bergen, Norway
Bioinformatics students / researchers, 8-hr sessions per day for 5 days

2017 - present Lecture in the Bioinformatics Club, Brigham and Women's Hospital
Bioinformatics students and researchers, 1 hour per lecture for 3 lectures

Laboratory and Other Research Supervisory and Training Responsibilities

2013 – present Supervision of graduate students and visiting scholars in Bioinformatics, Lab of Neurogenomics, Brigham and Women's Hospital
1:1 supervision one hour per week per student (avg. 2-3 students)

2013 – present Informal mentorship and consultancy to researchers in the Lab of Neurogenomics, Brigham and Women's Hospital
1 hour per week

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 title "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. Got all "Excellent" assessment 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 BIG program at Harvard University)
Conducted her PhD rotation in the laboratory and worked together on circRNA project. Drafting a co-authored manuscript.

Other Mentored Trainees and Faculty

2009 – 2012 Yogita Sharma (graduate student in 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	David Gritsch (postdoc in BWH Neurogenomics laboratory) Research advisor for his research in the laboratory
2015 – 2015	Will Nemirovsky (junior high school student in BB&N) Supervisor, research advisor for his summer bioinformatics training in Harvard
2015 – 2017	Kristy Abo (medical student in School of Medicine, Boston University) Supervisor and project manager, for her summer bioinformatics training in 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 Neuroscience, Universidad Complutense of Madrid, Spain) Supervisor, research advisor for her five-month research traineeship in Bioinformatics.
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 in Harvard

Local Invited Presentations

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 Center for Neurologic Diseases, Brigham and Women's Hospital
2017	An encyclopedia of transcribed elements in human brain dopamine neurons / ADPD seminar 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 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

Report of Regional, National and International Invited Teaching and Presentations

Regional

2013 Studying gene regulation using comparative genomics and epigenomics
Dana-Farber Cancer Institute, Boston, MA

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

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 vertebrates 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 – Parkinson's Disease Conference
National Institute of Health, Bethesda, MD

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

PART III: 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
URL: http://synorth.genereg.net
Published as first author on *Genome Biology* (Impact factor: 10.30), 13 citations

Translog — A website designed to study the expression divergence of homologous genes
URL: http://translog.genereg.net
Published as first author on *BMC Bioinformatics* (Impact factor: 3.02)

Factorbook	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: 8.28), 4 citations
BRAINcode	A web resource allowing users to query the gene expression profile and eQTL result in human dopamine neurons. URL: http://humanbraincode.org

Educational Activities to the Community

2008 – present	Owner of the bioinformatics blog, "*One Tip Per Day*" (http://onetipperday.sterding.com), which has 200 visit 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 *Bioinformatics Club* (http://bioinformatics.bwh.harvard.edu), which is a weekly forum for learning and sharing bioinformatics in the whole hospital level. To date, we have already scheduled over 30 talks, serving more than 500 persons.

Media Coverage

ENCODE consortium et al. *Nature*, 2012	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
Dong et al. *Genome Biology*, 2012	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/
Dong et al. *Nature Neuroscience*, 2018	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

PART IV: PUBLICATIONS

Peer-Reviewed Scholarship in print or other media:

In total, 25 publications, over 11,000 citations, H-index = 20, 70% articles with IF > 10

- **Research Investigation** (incl. seven first-author articles marked with *, and one corresponding-author article)

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 = 10.2)**

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 = 13.2)**

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 = 13.2)**

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 = 2.2)

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 = 11.6)**

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 = 31.4)**

7. Fredman D, **Dong X**, Lenhard B. Making enhancers from spare parts of the genome. ***Genome Biology***. 2011; 12(12):138. PMID: 22206586 **(IF = 13.2)**

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 = 13.2)**
**** Cited 187 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 = 41.6)**
**** 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**. ***Dong X**, Weng Z. The correlation between histone modifications and gene expression. ***Epigenomics. 2013; 5(2):113-6. PMID: 23566087 (IF = 5.0)
**** Invited review**

13. 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 = 11.6)**

14. 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 = 14.2)**

15. 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 = 5.5)

16. 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 = 41.6)**

17**. ***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 26 times by top journals including *Nature Neuroscience, Molecular Psychiatry, Trends in Neuroscience*

18. 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 = 6.0)

19. Locascio JJ, Eberly S, Liao Z, Liu G, Hoesing 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, Ivinson 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 = 10.8)**

20. 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. β2-adrenoreceptor is a regulator of the α-synuclein gene driving risk of Parkinson's disease. ***Science***. 2017; 357 (6354), 891-898. PMID: 28860381 **(IF = 37.2)**
** Dong X is the lead bioinformatics analyst
** Featured on NIH Director Francis Collins's blog
** Recommended by the ***Faculty of 1000***
** In the 99th percentile (top 5%) of all research outputs ever tracked by Altmetric

21. 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. (IF = 8.1)

22.** ***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 = 19.9)**
**** 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 98th percentile (top 1.5%) of all articles of a similar age in all journals tracked by Altmetric**

[+]**23**. Bao Z, Zhu Y, Ge Q, Gu W, **Dong X**[+], Bai Y[+]. gwSPIA: Improved signaling pathway impact analysis with gene weights. ***IEEE Access*** (In press)

- **Scholarship without named authorship**

24. ENCODE Project Consortium*. A user's guide to the encyclopedia of DNA elements (ENCODE). ***PLoS Biology***. 2011; 9(4):e1001046. PMID: 21526222 (IF = 9.2)
(* member of the data analysis group cited in the appendix of the manuscript)

25. 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. ***Ann Neurol***. 2016 Nov;80(5):674-685. PMID: 27717005 **(IF = 10.2)**
(* member of the IGPP group cited in the appendix of the manuscript)

- **Scholarship in submission**

26. **Dong X***, Wang Z*, Liao Z, Liu X, Long J, Paulsen JS, Bockholt HJ, Jin S[+], Scherzer CR[+]. MicroRNAs differentially expressed in blood of huntingtin gene-positive cases. ***JAMA Neurology*** (submitted)

27. **Dong X***, Rubio VWY, Locascio JJ, Scherzer CR. Long introns of synapse genes drive the evolution of human. (In preparation)

28. **Dong X***, Bai Y, Liao Z, Ehrlich A, Monroy RB, Guennewig B, Cooper AA, Scherzer CR. Circular RNAs in human brain neurons link genetic susceptibility and synaptopathy. (In preparation)

29. **Dong X***, Wang T, Xue H, Peng J, Scherzer CR. BRAINcode: A web resource for human brain transcriptome and eQTL study. (In preparation)

Non-peer reviewed Scholarship in print or other media:

Science-fiction assay

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

Proceedings of meetings and other non-peer reviewed scholarship:

1. **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.
2. **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.
3. 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.
4. 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 15th 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 5th 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 6th 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 7th 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. **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.
11. **Dong X,** Bai Y, Liao Z, Borges-Monroy R, Wang T, Ehrlich A, Locascio JJ, Adler CH, Hedreen JC, Frosch MP, Faull RLM, Nelson PT, Beach TG, Scherzer CR. Circular RNAs in human brain neurons and their linkage to neuropsychiatric diseases. *The 84th Cold Spring Harbor Laboratory Symposium on Quantitative Biology: RNA Control & Regulation*, Cold Spring Harbor, NY, 2019.