

Xianjun Dong, PhD**Address:** 60 Fenwood Road, 9002U, Boston, MA 02115 USA**Phone:** +1 857-307-5423**Email:** 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 (Advisor: 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 (Mentor: Dr. Clemens Scherzer)	Brigham and Women's Hospital
02/20 - present	Director	Genomics and Bioinformatics Hub	Brigham and Women's Hospital

Major Administrative Leadership Positions

2016 - present	Director of Computational Neuroscience, Neurogenomics Lab and Precision Neurology Program, Brigham & Women's Hospital
2017 - present	Founder and Organizer, the Bioinformatics Club, 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

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 1st grade Scholarship, Southeast University, China
 2000 2nd prize of the National Undergraduate Mathematical Contest in Modeling
 2000 *Liu Yonglin* Fellowship Award, Southeast University, China
 2001 1st 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 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 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 identification of gene modifiers of disease penetrance and age at onset.

Active grants (seven in total):

- 2019 – 2020 *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.
- 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 chr17q21 locus and validate them in iPSC-derived neurons.
- 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.
- 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.
- 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.
- 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 in Harvard site in this dual-institute grant.

Projects Submitted for Funding

- 2019 - 2020 *Developing circular RNA biomarkers in cerebrospinal fluid for Parkinson's disease*
The Michael J. Fox Foundation for Parkinson's Disease - \$300,000 for two years
Role: **Principal Investigator**
In this proposal, we aim to investigate the expression profiles of circular RNA (circRNA) in CSF from patients with Parkinson's disease to identify suitable biomarkers for the early diagnosis of Parkinson's disease.
- 2020 - 2023 *Genetics to Therapeutic Targets: Single-Cell Transcriptomics of Non-motor Parkinson's Disease*
US Department of Defense (DoD) - CDMRP
Role: Co-Investigator and Director, Bioinformatics Core with 45% effort (PI: Clemens Scherzer)
I lead the Bioinformatics Core for this project, performing single-cell RNAseq analysis to profile the transcriptome of hundreds of thousands of human neurons and glia cells during cognitive disease progression in Parkinson's disease, and eQTL analysis to systematically decode the function of Parkinson's disease-linked genetic variants in single cortical neurons and glia cells.

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 5 days
- 2017 – present Lecture in the Bioinformatics Club, Brigham and Women’s Hospital
Bioinformatics students and researchers, 1 hour per lecture for 6 lectures

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 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.
- 2020 – 2020 Varshini Odayar (Freshman at Harvard College)
She chose us from the HUROS Fair as her first laboratory for research and participated a top-secret project in the lab.

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 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 in Harvard
- 2015 – 2017 Kristy Abo (Medical student in School of Medicine, Boston University)

2015 – 2018	Supervisor and project manager, for her summer bioinformatics training in Harvard 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 <i>Nature Neuroscience</i> 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. Jijie 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 in Harvard
2018 – 2020	Haotian Liao (Graduate student in West China Medical School, Sichuan University, China) Supervisor, research advisor for his two-year bioinformatics training in 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); submitting a manuscript together.

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

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

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 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

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
- 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

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 the first author on <i>Genome Biology</i> (Impact factor: 11.91), 25 citations
Translog	A website designed to study the expression divergence of homologous genes URL: http://translog.genereg.net Published as first author on <i>BMC Bioinformatics</i> (Impact factor: 2.21)
Factorbook	A Wiki-based database for transcription factor-binding data generated by ENCODE URL: http://factorbook.org Published as co-author on <i>Nucleic Acid Research</i> (Impact factor: 10.16), 158 citations
BRAINcode	A web resource allowing users to query the gene expression profile and eQTL result in human brain neurons. URL: http://humanbraincode.org

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 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/gpbs-students-take-science-on-road.aspx
2017 – present	Founder and Director of the <i>Bioinformatics Club</i> (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

<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>	EurekaAlert!: https://www.eurekaalert.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**In total, 25 publications, over 12,000 citations, H-index = 21, 70% articles with IF > 10****Peer-Reviewed Scholarship in print or other media:**

- **Research Investigation** (including seven first-author publications* and one corresponding-author publication[†])
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, Fazio 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, 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 = 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. 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 = 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 99th 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 98th percentile (top 1.5%) of all articles of a similar age in all journals tracked by Altmetric
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