**Xianjun Dong, PhD**

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**Web**: http://www.sterding.com

Education

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

Postdoctoral Training

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| 09/10 – 09/13 | Postdoc Fellow | Program of Bioinformatics and Integrative Biology  (Supervisor: Dr. Zhiping Weng) | University of Massachusetts Medical School |

Faculty Academic Appointments

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| 11/13 – present | Instructor | Neurology | Harvard Medical School |

Appointments at Hospitals/Affiliated Institutions

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| 09/13 – present | Assistant Scientist | Neurology (Ann Romney Center for Neurologic Diseases) | Brigham and Women’s Hospital |

Major Administrative Leadership Positions

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| 2007 – 2007 | Course director of the “Ensembl in a Nutshell” Workshop, University of Bergen |
| 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

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| 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 |

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 –

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

Honors and Prizes

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| 2000 | 2nd prize of the National Undergraduate Mathematical Contest in Modeling |
| 2000 | *Liu Yonglin* Fellowship Award, Southeast University, China |
| 2000 | Distinguished Student with 1st grade Scholarship, 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 world wide) |
| 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 | Brigham Research Institute (BRI) NextGen Award |
| 2019 | Advanced Center for Parkinson’s Disease Research (ACEPD) Seed Award |

Report of Funded and Unfunded Projects

Funding Information

- Past –

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| 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 –

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| 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  (NCE 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** (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. |
| 2018 – 2023 | *Translating GWAS peaks into novel drug targets*  APDA Advanced Center for Parkinson’s Disease Research (ACEPD) Seed Award  **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. |
| 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. |
| 2019 – 2022 | *Study in Norwegian Population to Identify Therapies with Repurposing Potential for Parkinson’s Disease.*  The Michael J. Fox Foundation for Parkinson’s Disease  **Lead Bioinformatics Investigator** (PIs: Clemens Scherzer, Trond Riise)  The goal of the study is to identify existing drugs that could be tested for impact on Parkinson’s disease through virtual drug screening in a database from the Norwegian population. I will lead the bioinformatics analysis done in Harvard site in this dual-institute grant. |
| 2019 – 2020 | *Circular RNAs: A novel link between genetic susceptibility and Parkinson’s disease?*  American Parkinson Disease Association (APDA) Research Grant  **Principal Investigator ($75,000)**  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. |

Projects Submitted for Funding

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| 2018 – 2020 | *Identifying Modifiers of GBA Penetrance and Age-at-onset*  Michael J. Fox Foundation  Co-investigator (PI: Clemens Scherzer, Tatiana Foroud)  The aim of the project is to identify modifiers of GBA penetrance and age-at-onset. |
| 2019 - 2021 | *Circular RNAs: A novel link between genetic susceptibility and Alzheimer’s disease?*  NIH R21  **Principal Investigator** ($275,000)  The aim of the project is to identify novel circular RNAs in the Alzheimer’s disease-associated pyramidal neurons, its role in early development of AD, and their associated genetic risk variants. |

Report of Local Teaching and Training

Teaching of Students in Courses

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| 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 3 lectures |

Laboratory and Other Research Supervisory and Training Responsibilities

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| 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

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| 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

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| 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 |
| 2019 -- 2019 | Carmen Domínguez (Undergraduate student from National Autonomous University of Mexico, Mexico)  Supervisor for her 5-month summer intern in Harvard Medical School; Mentor for her American Parkinson Disease Association (APDA) Summer Student Fellowships |

Local Invited Presentations

No presentations below were sponsored by outside entities

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| 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** ofDiscover Brigham Day Brigham and Women’s Hospital |

Report of Regional, National and International Invited Teaching and Presentations

No presentations below were sponsored by outside entities

Regional

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| 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

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| 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 – Parkinson’s Disease Conference  National Institute of Health, Bethesda, MD |

International

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| 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 |

**Report of Activities and Innovations**

Technological and Other Scientific Innovations

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| 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](http://synorth.genereg.net/)  Published as first author on *Genome Biology* (Impact factor: 11.91), 25 citations |
| Translog | A website designed to study the expression divergence of homologous genes  URL: [http://translog.genereg.net](http://translog.genereg.net/)  Published as first author on *BMC Bioinformatics* (Impact factor: 2.21) |
| Factorbook | A Wiki-based database for transcription factor-binding data generated by ENCODE  URL: [http://factorbook.org](http://factorbook.org/)  Published as co-author on *Nucleic Acid Research* (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](http://humanbraincode.org/) |

Educational Activities to the Community

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| 2008 – present | Owner of the bioinformatics blog, “*One Tip Per Day*” ([http://onetipperday.sterding.com](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](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

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| --- | --- |
| 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> |

**Report of Scholarship**

Peer-Reviewed Scholarship in print or other media:

In total, 24 publications, over 11,000 citations, H-index = 20, 70% articles with IF > 10

* **Research Investigation** (including **seven** first-author publications, marked with \*)

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)**  
\*\* Dong X is the lead bioinformatics analyst

\*\* Recommended by the ***Faculty of 1000***

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.* 2019; 7:69172-69183.

* **Scholarship without named authorship**

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