

**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**

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**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 Personal Medicine Program of Brigham and Women's Hospital, Harvard Medical School  
 11/13-present      Instructor, Department of Neurology, Harvard Medical School  
 09/13-11/16      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  
 2013 - present      Bioinformatics team lead in Neurogenomics Laboratory, Harvard Medical School

**Professional Societies**

2016 - present      American Academy of Neurology (AAN), Member  
 2006 - present      International Society for Computational Biology (ISCB), Member  
 2013 - present      American Society for Human Genetics (ASHG), Member  
 2015                  The 10<sup>th</sup> Annual DNA Day Essay Contest, Judge

**Honors and Prizes**

2000                  2<sup>nd</sup> prize of the National Undergraduate Mathematical Contest in Modeling  
 2000                  *Liu Yonglin* Fellowship Award, Southeast University, China  
 2000                  Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China  
 2001                  1<sup>st</sup> prize of 2001 "Sony Cup" National Undergraduate Electronic Design Contest, China (winning by designing a robot-controlled electronic car)  
 2001                  **Meritorious** winner (top 10%) in the international Mathematical Contest in Modeling (MCM) (winning by modeling the growth control of zebra mussels in the Great Lakes)  
 2001                  Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China  
 2002                  Distinguished Graduate Student Award, Southeast University, China  
 2009                  Full Scholarship, "Chromatin Domains and Insulators" Workshop, Spain  
 2009                  Travel Fellowship, MCB Research School, University of Bergen, Norway  
 2010                  Chinese Government Award for Outstanding Self-financed Students Abroad, Ministry of Education, China (1 of 500 annual awardees in the world wide)  
 2015                  Reviewers' Choice – top 10% best posters in the American Society of Human Genetics (ASHG) meeting, US

**Service to Professional Publications****- Ad hoc reviewer -** (Total: **26** times for **15** journals)

2011 - present	<i>PLoS Computational Biology</i> (1 paper)
2011 - present	<i>Genome Research</i> (1 paper)
2012 - present	<i>Nature Biotechnology</i> (1 paper)
2013 - present	<i>PLoS ONE</i> (2 paper)
2013 - present	<i>Genome Biology</i> (2 paper)
2014 - present	<i>Bioinformatics</i> (5 paper)
2014 - present	<i>PLoS Genetics</i> (1 paper)
2014 - present	<i>Evolutionary Bioinformatics</i> (2 paper)
2014 - present	<i>International Journal of Biological Sciences</i> (3 paper)
2014 - present	<i>Journal of Biomedical Informatics</i> (2 paper)
2014 - present	<i>Movement Disorders</i> (1 paper)
2014 - present	<i>The Pharmacogenomics Journal</i> (1 paper)
2015 - present	<i>Current Bioinformatics</i> (2 paper)
2015 - present	<i>Neurogenetics</i> (1 paper)
2015 - present	<i>Journal of Bioinformatics and Computational Biologys</i> (1 paper)

**Funding Information****- Past -**

2008 - 2012	<u>Title:</u> EDAC: ENCODE Data Analysis Center <u>Grant number:</u> U01 HG004695-04 <u>Goal:</u> The goal of this project is to perform integrative analysis on CHIP-Seq, FAIRE-Seq and RNA-Seq data as a part of the ENCODE data analysis center. <u>Role:</u> Bioinformatics engineer
2011 - 2016	<u>Title:</u> Epigenetic Markers in Huntington's Disease Brain <u>Grant number:</u> R01 NS073947 <u>Goal:</u> The goal of this project is to map, genome-wide HD disease-related changes in histone methylation markings in prefrontal neurons. <u>Role:</u> Bioinformatics analyst
2013 - 2016	<u>Title:</u> A Next Generation of Biomarkers for Incipient Huntington's Disease <u>Grant number:</u> U01 NS082080 <u>Goal:</u> The goal of this project is to establish a national RNA biobank resource and develop digital biofluid markers useful for tracking disease progression. <u>Role:</u> Co-investigator

**- Current -**

2016 – 2019	<u>Title:</u> Parkinson Disease: Predicting the Future <u>Grant number:</u> U01 NS095736-01A1 <u>Goal:</u> 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. <u>Role:</u> Co-investigator
2016 – 2021	<u>Title:</u> GBA pathway markers for Lewy body dementias <u>Grant number:</u> U01 NS100603-01 <u>Role:</u> Bioinformatics engineer

**- Pending -**

2017-2018	<u>Title:</u> Cracking the Code of Chromosome 17q21 for Parkinson: From GWAS to Novel Drug Targets <u>Grant:</u> American Parkinson Disease Association (APDA) Research Grant
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**Goal:** The goal of this project is to discover the causal variants in chr17q21 locus and validate them in iPSC-derived neurons.

**Role:** PI

## **PART II: REPORT OF TEACHING, TRAINING, AND PRESENTATIONS**

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

2007                    EnsEMBL in a Nutshell, Bergen Center of Computational Science, University of Bergen, Norway  
 Role: Lecturer  
 National-wide bioinformatics students / researchers, 8-hr sessions per day for 5 days

### **Laboratory and Other Research Supervisory and Training Responsibilities**

2013 - present        Bioinformatics training and supervision of the bioinformatics staff, students, engineers  
 Daily mentorship for 3 years

### **Formally Supervised Trainees / Students**

2009 - 2012        Yogita Sharma (graduate student in University of Bergen, Norway)  
 Mentor, co-supervisor for her research project & thesis, and co-author of one 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        Alyssa Ehrlich (medical student in Harvard Medical School)  
 Supervisor, research advisor for her proposal and her internship in the laboratory

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 - 2016        Dr. Yunfei Bai (visiting scholar from Southeast University, China)  
 Co-supervisor, Bioinformatics trainer

2015 - 2017        Tao Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)  
 Supervisor, research advisor for his two-year bioinformatics training in Harvard

2016 -2016        Ellen DeGennaro (graduate student in Harvard-MIT HST PhD program)  
 Supervisor, research advisor for her proposal and her internship in the laboratory

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

### **Invited Presentations**

#### **- Local -**

2011                    Correlate histone modifications and gene expression / BIB seminar (UMass Medical School)

2012                    Redefining the piRNA-producing loci of the mouse testis as genes / Invited Bioinformatics talk (UMass Medical School)

2014                    From ENCODE to PD Brain Map: Bioinformatics in Big Data Research / The Center for Neurologic Diseases' ADPD seminar series (Harvard Institute of Medicine, BWH)

2015                    The BRAINCODE consortium: Decoding neuronal genome function in human brain / The Center for Neurologic Diseases' ADPD seminar series (Harvard Institute of Medicine, BWH)

#### **- Regional -**

2007                    Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks (BREW 2007, Norway)

2012                    Modeling gene expression with chromatin features (ENCODE conference, MIT)

2013 Studying gene regulation using comparative genomics and epigenomics (DFCI / HMS)  
 2013 Studying gene regulation using comparative genomics and epigenomics (BWH / HMS)

#### - National -

2011 Modeling gene expression with chromatin features / Invited talk (ENCODE conference, Stanford University)  
 2013 Long-range gene regulation in vertebrates genome (Berkeley Lawrence Laboratory)

#### - International -

2010 Translog, a web browser for studying the expression divergence of homologous genes (The 8<sup>th</sup> Asia Pacific Bioinformatics Conference, India)  
 2010 Web resources to study the expression divergence of homologous genes (Huazhong Agricultural University, China)  
 2010 Evolutionary mechanisms of developmental long-range gene regulation in vertebrate genomes (GIS, Singapore)  
 2013 Studying gene regulation using comparative genomics and epigenomics (Southeast University / Huazhong Agricultural University / Tongji University, China)  
 2015 NGS and its application in translational medicine (Tongji Hospital, China)

### **PART III: REPORT OF ACTIVITIES AND INNOVATIONS**

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#### **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 the ENCODE consortium  
 URL: <http://factorbook.org>  
 Published as co-author on *Nucleic Acid Research* (Impact factor: 8.28), 4 citations

#### **Educational Activities to the Community**

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>

2008 – present Founder of bioinformatics blog, “One Tip Per Day” (<http://onetipperday.blogspot.com/>), which has 200 visit per day on average and more than 520,000 visits in total

#### **Media Coverage**

ENCODE consortium, Dong 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](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>  
 Washington Post: [http://www.washingtonpost.com/national/health-science/junk-dna-concept-debunked-by-new-analysis-of-human-genome/2012/09/05/cf296720-f772-11e1-8398-0327ab83ab91\\_story.html](http://www.washingtonpost.com/national/health-science/junk-dna-concept-debunked-by-new-analysis-of-human-genome/2012/09/05/cf296720-f772-11e1-8398-0327ab83ab91_story.html)

Dong et al. *Genome* Genomeweb: <http://www.genomeweb.com/blog/week-genome-biology-59>

## PART IV: PUBLICATIONS

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### Original Articles:

1. Mungpakdee S, Seo HC, Angotzi AR, **Dong X**, Akalin A, et al. Differential evolution of the 13 Atlantic salmon Hox clusters. *Molecular biology and evolution*. 2008; 25(7):1333-43. PMID: 18424774
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, PMCID: PMC2745767
3. Akalin A, Fredman D, Arner E, **Dong X**, Bryne JC, et al. Transcriptional features of genomic regulatory blocks. *Genome biology*. 2009; 10(4):R38. PMID: 19374772, PMCID: PMC2688929
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, PMCID: PMC3009532
5. **Dong X**, Navratilova P, Fredman D, Drivenes Ø, Becker TS, et al. Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. *Nucleic acids research*. 2010; 38(4):1071-85. PMID: 19969543, PMCID: PMC2831330
6. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS biology*. 2011; 9(4):e1001046. PMID: 21526222, PMCID: PMC3079585
7. Yildirim O, Li R, Hung JH, Chen PB, **Dong X**, et al. Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells. *Cell*. 2011; 147(7):1498-510. NIHMSID: NIHMS343144 PMID: 22196727, PMCID: PMC3252821
8. **Dong X**, Greven MC, Kundaje A, Djebali S, Brown JB, et al. Modeling gene expression using chromatin features in various cellular contexts. *Genome biology*. 2012; 13(9):R53. PMID: 22950368, PMCID: PMC3491397
9. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, et al. Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome research*. 2012; 22(9):1798-812. PMID: 22955990, PMCID: PMC3431495
10. Cheng C, Alexander R, Min R, Leng J, Yip KY, et al. Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome research*. 2012; 22(9):1658-67. PMID: 22955978, PMCID: PMC3431483
11. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012; 489(7414):57-74. NIHMSID: NIHMS381381, PMID: 22955616, PMCID: PMC3439153
12. Wang J, Zhuang J, Iyer S, Lin XY, Greven MC, et al. 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, PMCID: PMC3531197
13. Li XZ, Roy CK, **Dong X**, Bolcun-Filas E, Wang J, et al. An ancient transcription factor initiates the burst of piRNA production during early meiosis in mouse testes. *Molecular cell*. 2013; 50(1):67-81. NIHMSID: HHMIMS469552 PMID: 23523368, PMCID: PMC3671569
14. Hoss AG, Kartha VK, **Dong X**, Latourelle JC, Dumitriu A, et al. MicroRNAs located in the Hox gene clusters are implicated in huntington's disease pathogenesis. *PLoS genetics*. 2014; 10(2):e1004188. PMID: 24586208, PMCID: PMC3937267
15. Haberle V, Li N, Hadzhiev Y, Plessy C, Previti C, et al. Two independent transcription initiation codes overlap on vertebrate core promoters. *Nature*. 2014; 507(7492):381-5. PMID: 24531765
16. **Dong X**, Tsuji J, Labadorf A, Roussos P, Chen JF, et al. The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. *PloS one*. 2015; 10(12):e0144398. PMID: 26636336, PMCID: PMC4670094

17. Bai G, Cheung I, Shulha HP, Coelho JE, Li P, et al. 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, PMCID: PMC4321450
18. Locascio JJ, Eberly S, Liao Z, Liu G, Hoising AN, et al. Association between  $\alpha$ -synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. *Brain*. 2015; 138(Pt 9):2659-71. PMID: 26220939, PMCID: PMC4643625
19. Liu G, Boot B, Locascio JJ, Jansen IE, Winder-Rhodes S, et al. Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. *Ann Neurol*. 2016 Nov;80(5):674-685. PMID: 27717005; PMCID: PMC5244667.

#### Reviews:

1. Fredman D, **Dong X**, Lenhard B. Making enhancers from spare parts of the genome. *Genome biology*. 2011; 12(12):138. PMID: 22206586, PMCID: PMC3334608
2. **Dong X**, Weng Z. The correlation between histone modifications and gene expression. *Epigenomics*. 2013; 5(2):113-6. NIHMSID: NIHMS598474, PMID: 23566087, PMCID: PMC4230708

#### Public Science:

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

#### 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**, 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. **Dong X**. Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks. *Bioinformatics Research and Education Workshops (BREW)*, Bergen, Norway, 2007. **(Oral)**
5. **Dong X**, Fredman D, Engström P, Lenhard B. Reconstructing the Evolutionary History of Genomic Regulatory Blocks in Vertebrates. *The 15<sup>th</sup> Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Austria, 2007.
6. **Dong X**, Akalin A, Fredman D, Lenhard B. Distribution of highly conserved non-coding elements in *Danio rerio*. *The 5<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Hong Kong, 2007.
7. **Dong X**, Sheng Y, Gupta P, Lenhard B. Computational prediction of ncRNAs as target genes in genomic regulatory blocks. *The 6<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Japan, 2008.
8. **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.
9. **Dong X**, Akalin A, Fredman D, Lenhard B. Evolutionary dynamics of genomic regulatory blocks: HCNEs and HARs, the content and the boundaries. *The 7<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, China, 2009.
10. **Dong X**. Translog, a web browser for studying the expression divergence of homologous genes. *The 8<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Bangalore, India, 2010. **(Oral)**
11. **Dong X**. Predicting gene expression using histone modifications. ENCODE Conference, Stanford, 2011.
12. **Dong X**. Correlating histone modifications and gene expression. *Systems Biology: Global Regulation of Gene Expression*, CSHL, 2012.
13. **Dong X**. Modeling gene expression with chromatin features. ENCODE Conference, MIT, 2012. **(Oral)**

14. 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.
15. **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.