CURRICULUM VITAE

Xiuxia Du, Ph.D.

Professor
Department of Bioinformatics and Genomics
College of Computing and Informatics
University of North Carolina at Charlotte
Charlotte, NC 28223

500 Laureate Way
North Carolina Research Campus
Kannapolis, NC 28081
Phone: 704-687-7307
Email: xiuxia.du@uncc.edu

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1. Education

1999 – 2005	D.Sc.	Systems Science and Mathematics Washington University in St. Louis
1991 – 1994	M.S.	Electrical Engineering Hefei University of Technology, China
1987 – 1991	B.S.	Electrical Engineering Hefei University of Technology, China

2. Professional Experience

2019 – present	Professor Department of Bioinformatics & Genomics College of Computing and Informatics University of North Carolina at Charlotte
2014 – 2019	Associate Professor with tenure Department of Bioinformatics & Genomics College of Computing and Informatics University of North Carolina at Charlotte
2008 – 2014	Assistant Professor College of Computing and Informatics Department of Bioinformatics & Genomics University of North Carolina at Charlotte
2005 – 2008	Postdoctoral Fellow Computational Proteomics Laboratory of Dr. Richard Smith Pacific Northwest National Laboratory
1994 – 1999	Assistant Investigator Institute of Electrical Engineering Chinese Academy of Sciences, Beijing, China
1999 – 1999	Production Engineer China Test & Measurement Operation Hewlett-Packard Company, Beijing, China

3. Funding

3.1 Active Grants

- NIH/NCI U01CA235507-01 Xiuxia Du, PI

Cross-platform and graphical software tool for adaptive LC/MS and GC/MS metabolomics data preprocessing
09/19/18 – 08/31/22 $1,128,717 (direct cost) 2.0 summer months
Role: PI
Dr. Du manages the entire project and designs the computational workflow proposed in the project.

- NIH/NHLBI 1R01 HL143885-01A1
  Christy Avery, Penny Gordon-Larson, Kari North, Susan Sumner, MPI
  Leveraging multi-omics approaches to examine metabolic challenges of obesity in relation to cardiovascular diseases
  04/01/19 – 03/31/23
  Dr. Du will lead the preprocessing of raw untargeted mass spectrometry-based metabolomics data.

  Subaward to University of North Carolina at Charlotte:
  Role: MPI
  04/01/20 – 03/31/24 $833,557 (total cost)

- NIH/NIEHS 1U2CES030857-01 Timmothy Fennell, Susan Sumner, Xiuxia Du, MPIs
  Human Health Exposure Analysis Resource Core (HHEAR): Untargeted Analysis
  08/01/19 – 07/31/24 $12,787,872.00 (total cost)
  Dr. Du will lead the Big Data Analytics for Computational Exposome.

  Subaward to University of North Carolina at Charlotte:
  Role: PI
  08/01/19 – 07/31/24 $2,265,000 (total cost)

3.3 Completed Grants

- NSF 1262416 Xiuxia Du, PI
  ABI Innovation: A systematic computational approach to creating libraries of high-quality mass spectra for unidentified metabolites
  9/1/2013 – 8/31/2018 $580,611 (total cost) 2.0 summer months
  Role: PI
  Dr. Du manages the entire project and designs the computational workflow proposed in the project.

- NIH/NCI 1R03CA222450-01 Xiuxia Du, PI
  Parameter-free peak detection algorithm for reducing false positive/negative compound identification from raw mass spectrometry metabolomics data
  09/19/17 – 08/31/19 $108,956 (direct cost) 1.28 summer months
  Role: PI
  Dr. Du manages the project and designs the computational workflow proposed in the project.

- NIH/NIDDK 5P30 DK 056350-13 Steven Zeisel, PI
  UNC Nutrition Obesity Research Center (NORC)
  9/30/1999 – 3/31/2016
  Dr. Du worked on projects in the Bioinformatics Core.

  Subaward to University of North Carolina at Charlotte:
  Role: PI
  4/5/11 – 3/31/14 $68,255 (total cost)

- NIH/NIGMS 1R25GM103802 Martin Kohlmeier, PI
  Online learning platform: Introducing clinicians and researchers to metabolomics
  09/01/12 – 08/31/17

Subaward to University of North Carolina at Charlotte:
Role: PI
09/01/12 – 08/31/17 $41,928 (total cost)

- NIH/NEI 3R01EY012224-10S1 Ellen Weiss, PI
  Desensitization of cone visual signaling pathways
  4/01/2012 – 3/31/2013

  Subaward to University of North Carolina at Charlotte:
  Role: PI
  4/01/2012 – 3/31/2013 $16,308 (total cost)

- **Protein data management system**
  Funded by: Carolinas Medical Center
  Role: PI
  10/1/08 – 9/31/09 $5,000 (direct cost)

4. Awards

- 2018 **Outstanding Faculty Research Award**
  College of Computing and Informatics
  University of North Carolina at Charlotte

5. Teaching

5.1 Graduate Courses

- **ITCS 6156: Machine Learning** (computer science)
  2017 Fall (cross listed with BINF 6210/8210: Machine Learning for Bioinformatics)

- **BINF 6210/8210: Machine Learning for Bioinformatics**
  2010 Fall, 2012 Spring, 2014 Fall, 2015 Fall, 2016 Fall, 2017 Fall, 2018 Fall

- **BINF 6200/8200: Statistics for Bioinformatics**
  2009 Fall, 2011 Fall

- **BINF 6010/8010: Computational Proteomics and Metabolomics**
  2011 Spring, 2013 Fall

- **BINF 6210/8210: Numerical Methods**
  2009 Spring

5.2 Undergraduate Courses

- **BINF 4211: Applied Data Mining for Bioinformatics**
  2018 Spring, 2019 Spring

- **BINF 3121: Statistics for Bioinformatics**
  2015 Spring, 2016 Spring

6. Postdoctoral Fellow and Student Supervision

6.1 Postdoctoral Fellows Supervised

- Aleksandr Smirnov, Ph.D. 06/2016 – present
  Development of ADAP-GC and ADAP demonstration spectral library for unknown compounds

Number of journal publications: 2

- Owen Myers, Ph.D. 01/2016 – 06/2017
  Comparative evaluation of XCMS and MZmine 2 and development of ADAP peak picking
  Number of journal publications: 2
  Job placement: Data Engineer at Sharp Action

- Wenchao Zhang, Ph.D. 06/2010 – 06/2012
  Development of computational algorithms for preprocessing LC-MS metabolomics data and continued development of Xlink-Identifier
  Number of journal publications: 1
  Job placement: Computational biologist at the Noble Research Institute

- Wenxin Jiang, Ph.D. 05/2009 – 11/2010
  Development of computational algorithms for preprocessing GC-MS metabolomics data
  Number of journal publications: 2
  Job placement: Software Engineer at Fred Hutchinson Cancer Research Center

6.2 Doctoral Students Supervised

- Md Sajjad Hossain 2019 Spring – present
  Department of Physics and Optical Science
  Dissertation: **Adaptive peak picking and alignment for preprocessing untargeted LC-MS and GC-MS metabolomics data**

- Yan Ni 09/2009 – 05/2014
  Department of Bioinformatics and Genomics
  Dissertation: **Data analysis workflow for GC-MS metabolomics studies**
  Job placement: Assistant Professor/Specialist at the University of Hawaii Cancer Center

6.3 Master's Students Supervised

- Prashant Madaan 11/2018 – present
  Coding mummichog (a software tool for metabolic pathway analysis) from Python to Java

- Anup Bharade 10/2018 – present
  Comparison of alignment algorithms for metabolomics data preprocessing

- Nilanjan Mhatre 7/2018 – present
  Development of ADAP demonstration spectral library for unknown compounds

- Matthew Kovacs 2018 Summer
  Prediction of compound sub-structures
  Job placement: Data Scientist at TIAA-CREF

- Dharak Shah 2017 Google Summer of Code (GSoC) student
  Implementation of ADAP-3D in Java
  Job placement: Software Engineer at TriNet

- Matthew Deitz 06/2015 – 12/2015

Big Data Metabolomics: parsing data files from PubChem, HMDB, and KEGG with information on close to 100 million compounds
Job placement: Bioinformatics Specialist at Santa Cruz Biotechnology

- Peter Pham — 01/2011 – 07/2012
  Development of ADAP-GC software graphical user interface in Java
  Job placement: Bioinformatician at Walter Reed Army Institute of Research

- Adam Baxter — 01/2012 – 08/2012
  Continued development of Xlink-Identifier
  Job placement: Senior middleware consultant at Red Hat

- Kyle Suttlemyre — 06/2009 – 08/2012
  Development of web-based visualization of analysis results from Xlink-Identifier
  Job placement: Bioinformatics staff scientist at David H. Murdock Research Institute

6.4 Bachelor's Students Supervised

- Xiao Song — 2009 Summer
  Parsing large protein fasta files using MATLAB

6.5 Non-Degree Students Supervised

- Jason Zhou — 2016 and 2017 Summer as a high school student from North Carolina
  Feature extraction from mass spectrometry-based metabolomics data
  Currently: Undergraduate student at Georgia Tech

- Zhuqiu Chen — December 2016 as a visiting undergraduate student from China
  Feature extraction from mass spectrometry-based metabolomics data
  Currently: Graduate student at University of Melbourne, Australia

7. Service and Outreach

7.1 External Services

7.1.1 Invited talks to train researchers to use metabolomics

Similar topics underwent significant updates each year.

- Annual UAB Metabolomics Workshop, jointly sponsored by NIH/NIGMS as part of the NIH Common Fund Metabolomics Initiative and the University of Alabama at Birmingham.
  https://www.uab.edu/proteomics/metabolomics/workshop.php

  - 6th Workshop, July 22 – 27, 2018.

    Metabolite Databases
    Hands-on Analysis with MZmine 2
    Introduction to XCMS in R
    Introduction to Preprocessing of Untargeted Metabolomics Data

  - 5th Workshop, July 16 – 21, 2017.

    Metabolite Databases
    Hands-on Analysis with MZmine 2
    Introduction to XCMS in R

Introduction to Preprocessing of Untargeted Metabolomics Data

- 4th Workshop, July 17 – 21, 2016.

  Data Analysis with R (XCMS)
  Metabolite Databases
  Data Analysis with MZmine 2
  LC-MS Data Preprocessing

- 3rd Workshop, June 14 – 18, 2015.

  Principles of Pre-processing LC-MS-Based Untargeted Metabolomics Data
  Software Tools in Metabolomics
  Construct Consensus Mass Spectra for Unknown Metabolites

- 2nd Workshop, June 2 – 5, 2014.

  XCMS Command Line Introduction
  Running XCMS Data Analysis on Your Computer
  Principles of Pre-processing LC-MS-Based Untargeted Metabolomics Data

- 1st Workshop, July 22-25, 2013.

  Pre-processing of LC-MS Metabolomics Data
  Statistical Analysis of GC-MS and LC-MS Metabolomics Data

- NIH-sponsored program to train bioinformatics students in Mali, Africa about metabolomics data analysis, April 7, 2016.

  LC-MS Data Processing and Use of XCMS

- Workshop on the Analysis of Metabolomics Data, University of Alabama at Birmingham, December 17, 2013.

  Principles of Pre-processing LC-MS-Based Untargeted Metabolomics Data
  Basic use of XCMS - local
  Statistical Analysis of Metabolomics Data

7.1.2 Journal/Conference Reviewer

Journals

- Analyst
- Journal of Proteome Research
- Oxford Bioinformatics
- Analytical Methods
- Proteomics
- Journal of Proteomics
- Journal of American Society for Mass Spectrometry
- Analytical Chemistry
- Journal of Chromatography
- Toxicology Mechanisms and Methods
- Analytical and Bioanalytical Chemistry
- Journal of Mass Spectrometry
- Journal of Chromatography A

Conferences

- American Society for Mass Spectrometry Conference on Mass Spectrometry and Allied Topics

7.1.3 Program Committees

- Chair, "**Metabolomics Informatics**", American Society of Mass Spectrometry Conference on Mass Spectrometry and Allied Topics, Indianapolis, Indiana, June 4-8, 2017.

- Chair, "**Informatics Tools for Pharmaceutical Applications of Mass Spectrometry**", American Society of Mass Spectrometry Conference on Mass Spectrometry and Allied Topics, June 5-9, 2011, Denver, CO.

7.1.4 Editorial Boards/Panels

- Frontiers in Nutrigenomics, since January 2018.
- Frontiers in Bioinformatics and Computational Biology, since April 2011

7.1.5 Professional Affiliations/Memberships

- Metabolomics Society.
- The American Society for Mass Spectrometry, 2005 - present.
- American Association for the Advancement of Science, 2005 - 2006.

7.1.6 Dissertation/Thesis committees

- Hameed Khan — Ph.D. dissertation committee, Department of Chemistry, George Mason University — 2018 – present

- Grey Madison — M.S. thesis committee, Department of Chemistry, George Mason University — 2018 – present
  Serum metabolomics: characterization of total pancreatectomy and islet autotransplantation patients

7.1.7 Community Service

- Presented a lecture to the local Kannapolis community about computational proteomics and metabolomics and applications of mass spectrometry to life science research. 2011 Summer.

7.2 Internal Services

7.2.1 Department Committees

- Ph.D. Admission Committee: 2008 - 2016
  Reviewing applications, discussions, interviewing (phone and onsite) candidates, and making recommendations
- Graduate Curriculum Committee: 2008 – 2016, 2018 - 2019
- Bioinformatics Faculty Search Committee for a research assistant professor: 2011
  Reviewing applications, discussions, interviewing (phone and onsite) candidates, and making recommendations.
- Department Review Committee: 2014 - 2017
- Chair, Department Review Committee: 2017 – 2018
- Department Infrastructure Committee: 2016 – 2017
- Awards and Fellowship Committee: 2018 – 2019

7.2.2 College Committees

- College Diversity committee: 2009 - 2010
- College Graduate Curriculum Committee: 2011 - 2013
- College Faculty Advisory Library Committee: 2012 - 2013
- College Graduate Education Committee: 2016 – 2019

7.2.3 Ph.D. Dissertation Committees

- Robert W. Reid (Advisor: Dr. Anthony Fodor), 2009 – 2010
- Christopher Overall (Advisor: Dr. Jennifer Weller), 2012
- Ivetth Corona (Advisor: Dr. Jun-tao Guo), 2012 – present
- Balasubramanian Karthik Kumar (Advisor: Dr. Robin Coger), Graduate Faculty Representative, Department of Mechanical Engineering, UNC Charlotte, 2010 – 2012
- Erik Broemsen, Graduate Faculty Representative
  Department of Biology, UNC Charlotte, 2017 – present

7.2.4 Other Departmental Services

- While my department does not have a standing committee for Ph.D. qualifying exams in the past, I have been involved in the *statistics* section of the qualifying exams in 2010, 2011, and 2012. Services include advising students, preparing written questions, grading the exams, and participating in students' oral exams.
- My department revised the format of qualifying exams in 2018. Since then, I have been on the qualifying committee of four Ph.D. candidates and responsible for designing qualifying questions for the section on computational methods, grading their written answers, and assess their computational and data analysis skills via face-to-face meetings.
- Outreach talks for introducing bioinformatics to potential graduate students in universities and colleges in North Carolina.
  Catawba College, 2013
  Wingate University, 2017
  Belmont Abbey College, 2018

8. Publications

8.1 Journal Publications (underlined - Du-Lab members; * - corresponding author)

- Smirnov A, Jia W, Walker DI, Jones DP, **Du X***: ADAP-GC 3.2: Graphical Software Tool for Efficient Spectral Deconvolution of Gas Chromatography-High-Resolution Mass Spectrometry Metabolomics Data. Journal of proteome research 2018, 17(1):470-478.
  [https://pubs.acs.org/doi/10.1021/acs.jproteome.7b00633]
- **Du X***, Smirnov A, Jia W: A preparatory study of how to construct consensus mass spectra of recurrent unknown metabolites from untargeted GC-MS metabolomics data. International Journal of Mass Spectrometry 2017, 427, 73-78.
  [https://www.sciencedirect.com/science/article/pii/S1387380617302269?via%3Dihub]
- Myers OD, Sumner SJ, Li S, Barnes S, **Du X***: One Step Forward for Reducing False Positive and False Negative Compound Identifications from Mass Spectrometry Metabolomics Data: New Algorithms for Constructing Extracted Ion Chromatograms and Detecting Chromatographic Peaks. Analytical chemistry 2017, 89(17):8696-8703.
  [https://pubs.acs.org/doi/10.1021/acs.analchem.7b00947]
- Myers OD, Sumner SJ, Li S, Barnes S, **Du X***: Detailed Investigation and Comparison of the XCMS and MZmine 2 Chromatogram Construction and Chromatographic Peak Detection Methods for Preprocessing Mass Spectrometry Metabolomics Data. Analytical chemistry 2017, 89(17):8689-8695.
  [https://pubs.acs.org/doi/10.1021/acs.analchem.7b01069]
- Ashkavand Z, O'Flanagan C, Hennig M, **Du X**, Hursting SD, Krupenko SA: Metabolic Reprogramming by Folate Restriction Leads to a Less Aggressive Cancer Phenotype. Mol Cancer Res 2017, 15(2):189-200.

[http://mcr.aacrjournals.org/content/15/2/189.long]

- Ni Y, Su M, Qiu Y, Jia W, **Du X***: ADAP-GC 3.0: Improved Peak Detection and Deconvolution of Co-eluting Metabolites from GC/TOF-MS Data for Metabolomics Studies. Analytical chemistry 2016, 88(17):8802-8811.
  [https://pubs.acs.org/doi/abs/10.1021/acs.analchem.6b02222]
- Barnes S, Benton HP, Casazza K, Cooper SJ, Cui X, **Du X**, Engler J, Kabarowski JH, Li S, Pathmasiri W et al: Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. J Mass Spectrom 2016, 51(8):ii-iii.
  [http://onlinelibrary.wiley.com/doi/10.1002/jms.3780/abstract]
- Barnes S, Benton HP, Casazza K, Cooper SJ, Cui X, **Du X**, Engler J, Kabarowski JH, Li S, Pathmasiri W et al: Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. J Mass Spectrom 2016, 51(7):461-475.
  [http://onlinelibrary.wiley.com/doi/10.1002/jms.3782/abstract]
- Clavier, S.; **Du, X.**; Sagan, S.; Bolbach, G.; Sachon, E.: An integrated cross-linking-MS approach to investigate cell penetrating peptides interacting partners. EuPA OPEN PROTEOMICS 2014, 3:229-238.
  [http://www.sciencedirect.com/science/article/pii/S2212968514000233]
- **Du, X.***, Zeisel, S., Spectral deconvolution for gas chromatography-based metabolomics: current status and future perspectives. Computational and structural biotechnology journal 2013, 4 (5).
  [https://www.sciencedirect.com/science/article/pii/S2001037014600568]
- Ni, Y.; Qiu, Y.; Jiang, W.; Suttlemyre, K.; Su, M.; Zhang, W.; Jia, W.; **Du, X.***, ADAP-GC 2.0: deconvolution of coeluting metabolites from GC/TOF-MS data for metabolomics studies. Analytical chemistry 2012, 84 (15), 6619-29.
  [http://pubs.acs.org/doi/pdf/10.1021/ac300898h]
- Watson, A. A.; Mahajan, P.; Mertens, H. D.; Deery, M. J.; Zhang, W.; Pham, P.; **Du, X.**; Bartke, T.; Zhang, W.; Edlich, C.; Berridge, G.; Chen, Y.; Burgess-Brown, N. A.; Kouzarides, T.; Wiechens, N.; Owen-Hughes, T.; Svergun, D. I.; Gileadi, O.; Laue, E. D., The PHD and chromo domains regulate the ATPase activity of the human chromatin remodeler CHD4. Journal of molecular biology 2012, 422 (1), 3-17.
  [http://www.sciencedirect.com/science/article/pii/S0022283612003737]
- **Du, X.***; Chowdhury, S. M.; Manes, N. P.; Wu, S.; Mayer, M. U.; Adkins, J. N.; Anderson, G. A.; Smith, R. D., Xlink-identifier: an automated data analysis platform for confident identifications of chemically cross-linked peptides using tandem mass spectrometry. J Proteome Res 2011, 10 (3), 923-31.
  [http://pubs.acs.org/doi/pdf/10.1021/pr100848a]
- Manes, N. P.; Dong, L.; Zhou, W.; **Du, X.**; Reghu, N.; Kool, A. C.; Choi, D.; Bailey, C. L.; Petricoin, E. F., 3rd; Liotta, L. A.; Popov, S. G., Discovery of Mouse Spleen Signaling Responses to Anthrax using Label-Free Quantitative Phosphoproteomics via Mass Spectrometry. Mol Cell Proteomics 2011, 10 (3), M110 000927.
  [http://www.mcponline.org/content/10/3/M110.000927.long]
- Yang, F.; Waters, K. M.; Miller, J. H.; Gritsenko, M. A.; Zhao, R.; **Du, X.**; Livesay, E. A.; Purvine, S. O.; Monroe, M. E.; Wang, Y.; Camp, D. G., 2nd; Smith, R. D.; Stenoien, D. L., Phosphoproteomics profiling of human skin fibroblast cells reveals pathways and proteins affected by low doses of ionizing radiation. PLoS One 2010, 5 (11), e14152.
  [http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0014152]
- Jiang, W.; Qiu, Y.; Ni, Y.; Su, M.; Jia, W.; **Du, X.***, An automated data analysis pipeline for GC-TOF-MS metabonomics studies. J Proteome Res 2010, 9 (11), 5974-81.
  [http://pubs.acs.org/doi/pdf/10.1021/pr1007703]
- Chowdhury, S. M.; **Du, X.**; Tolic, N.; Wu, S.; Moore, R. J.; Mayer, M. U.; Smith, R. D.; Adkins, J. N., Identification of cross-linked peptides after click-based enrichment using sequential collision-induced dissociation and electron transfer dissociation tandem mass spectrometry. Analytical chemistry 2009, 81 (13), 5524-32.
  [http://pubs.acs.org/doi/pdf/10.1021/ac900853k]

- Ding, S. J.; Wang, Y.; Jacobs, J. M.; Qian, W. J.; Yang, F.; Tolmachev, A. V.; **Du, X.**; Wang, W.; Moore, R. J.; Monroe, M. E.; Purvine, S. O.; Waters, K.; Heibeck, T. H.; Adkins, J. N.; Camp, D. G., 2nd; Klemke, R. L.; Smith, R. D., Quantitative phosphoproteome analysis of lysophosphatidic acid induced chemotaxis applying dual-step (18)O labeling coupled with immobilized metal-ion affinity chromatography. Journal of proteome research 2008, 7 (10), 4215-24. [http://pubs.acs.org/doi/pdf/10.1021/pr7007785]
- **Du, X.**; Callister, S. J.; Manes, N. P.; Adkins, J. N.; Alexandridis, R. A.; Zeng, X.; Roh, J. H.; Smith, W. E.; Donohue, T. J.; Kaplan, S.; Smith, R. D.; Lipton, M. S., A computational strategy to analyze label-free temporal bottom-up proteomics data. Journal of proteome research 2008, 7 (7), 2595-604. [http://pubs.acs.org/doi/pdf/10.1021/pr0704837]
- **Du, X.**; Yang, F.; Manes, N. P.; Stenoien, D. L.; Monroe, M. E.; Adkins, J. N.; States, D. J.; Purvine, S. O.; Camp, D. G., 2nd; Smith, R. D., Linear discriminant analysis-based estimation of the false discovery rate for phosphopeptide identifications. Journal of proteome research 2008, 7 (6), 2195-203. [http://pubs.acs.org/doi/pdf/10.1021/pr070510t]
- Manes, N. P.; Estep, R. D.; Mottaz, H. M.; Moore, R. J.; Clauss, T. R.; Monroe, M. E.; **Du, X.**; Adkins, J. N.; Wong, S. W.; Smith, R. D., Comparative proteomics of human monkeypox and vaccinia intracellular mature and extracellular enveloped virions. Journal of proteome research 2008, 7 (3), 960-8. [http://pubs.acs.org/doi/pdf/10.1021/pr070432%2B]
- Yang, F.; Jaitly, N.; Jayachandran, H.; Luo, Q.; Monroe, M. E.; **Du, X.**; Gritsenko, M. A.; Zhang, R.; Anderson, D. J.; Purvine, S. O.; Adkins, J. N.; Moore, R. J.; Mottaz, H. M.; Ding, S. J.; Lipton, M. S.; Camp, D. G., 2nd; Udseth, H. R.; Smith, R. D.; Rossie, S., Applying a targeted label-free approach using LC-MS AMT tags to evaluate changes in protein phosphorylation following phosphatase inhibition. Journal of proteome research 2007, 6 (11), 4489-97. [http://pubs.acs.org/doi/pdf/10.1021/pr070068e]
- **Du, X.**; Ghosh, B. K.; Ulinski, P., Encoding of motion targets by waves in turtle visual cortex. IEEE transactions on biomedical engineering 2006, 53 (8), 1688-95. [http://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=1658164]
- **Du, X.**; Ghosh, B. K.; Ulinski, P., Encoding and decoding target locations with waves in the turtle visual cortex. IEEE transactions on biomedical engineering 2005, 52 (4), 566-77. [http://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=1408113]
- **Du, X.**; Ni, S., Analysis and design of variable speed constant frequency (VSCF) pump storage system. Advanced technology of electrical engineering and energy 1999, ISSN 1003-3076, Issue 3, pp. 13-7. [http://en.cnki.com.cn/Article_en/CJFDTotal-DGDN903.003.htm]
- Ding, Y.; **Du, X.**, Design of the triggering circuit for the inverter in a VSCF wave power station. Power electronics 1998, ISSN 1000-100x, No. 2, pp. 76-8.
- **Du, X.**; Li, K; Ni, S., Research on the control and protection system for the VSCF wave power station. Advanced technology of electrical engineering and energy 1997, ISSN 1003-3076, Issue 2, pp. 56-9. [http://en.cnki.com.cn/Article_en/CJFDTOTAL-DGDN702.012.htm]
- Li, K.; **Du, X.**, R&D of the controller for a VSCF wave power station based on the 89c51 microprocessor. Power electronics 1997, ISSN 1000-100x, No.3, pp. 55-7.

8.2 Conference Publications

- **Du, X.**; Ghosh, B.K., Information-Theoretic Analysis of Turtle Cortical Waves, *Proceedings of the 42nd IEEE Conference on Decision and Control* **200***3*, pp. 6423--28. [https://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=1272355]
- **Du, X.,** Ghosh, B., Ulinski, P., Decoding the position of a visual stimulus from the cortical waves of turtles, *Proceedings of the American Control Conference* **2003**, 477-82. [http://ieeexplore.ieee.org/xpls/abs_all.jsp?arnumber=1239055]

8.3 Book Chapters

- Artigues A, Nadeau OW, Rimmer MA, Villar MT, **Du X,** Fenton AW, Carlson GM: Protein Structural Analysis via Mass Spectrometry-Based Proteomics. *Adv Exp Med Biol* 2016, **919**:397-431. [https://link.springer.com/chapter/10.1007%2F978-3-319-41448-5_19]