

CURRICULUM VITAE



Xusheng Wang, Ph.D.

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Department of Biology
University of North Dakota

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EMPLOYMENT

Assistant Professor	Department of Biology, University of North Dakota	2019--
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ACADEMIC DEGREES

Ph.D.	Zhejiang University (China)/University of California, Davis (USA)	2006
M.S.	Zhejiang University (China)/International Rice Research Institute (Philippines)	2003
B.S.	Zhejiang University (China)	2000

PROFESSIONAL EXPERIENCES

Bioinformatics Group Lead	Center for Proteomics and Metabolomics; Department of Structural Biology, St. Jude Children's Research Hospital	2015—2019
Sr. Bioinformatics Research Scientist	Department of Structural Biology, St. Jude Children's Research Hospital	2014—2015
Bioinformatics Research Scientist	Department of Structural Biology, St. Jude Children's Research Hospital	2012—2014
Bioinformatics Research Associate	Proteomics Facility and Department of Structural Biology, St. Jude Children's Research Hospital	2011—2012
Director of Bioinformatics	Center for Integrative and Translational Genomics, University of Tennessee Health Science Center, USA	2010—2011
Research Associate	Department of Anatomy and Neurobiology, University of Tennessee Health Science Center, USA	2008—2011
Post-doctoral Fellow	Department of Anatomy and Neurobiology, University of Tennessee Health Science Center, USA	2007—2008
Assistant Professor Junior Scientist	Zhejiang University, China	2006—2007
	Education Aboard Program of University of California, Davis in China (Peking University)	2006—2007

Junior Specialist
Visiting Scholar

University of California, Davis, USA
International Rice Research Institute, Philippine

2005—2006
2002—2003

RESEARCH DIRECTIONS

- Computational proteomics and metabolomics
- Bioinformatics and computational biology
- Systems biology, integrative biology
- Quantitative genetics and Statistical Genomics
- Genetics of complex diseases

PROFESSIONAL SOCIETIES

- American Society for Mass Spectrometry
- International Complex Trait Consortium
- International Behavioral and Neural Genetics Society
- International Mouse Genome
- International Human Genetics Society

JOURNAL EDITOR AND REVIEWER

Editor

Frontiers in Genetics (In genetic disorders)
PLoS One
Metabolites

Associate Editor

Frontiers in Evolutionary and Population Genetics

Reviewer

Nature Communications, Cell Systems, Journal of Proteome Research, Proteomics, Bioinformatics, Nature Communication Biology, Molecular Metabolism, Metabolite, Acta Pharmaceutica Sinica B

TEACHING EXPERIENCES

Biostatistics	Zhejiang University	Spring 2007
Bioinformatics	China Jiliang University (Invited)	Spring 2007
Bioinformatics	Zhejiang Forest College (Invited)	Spring 2007
Bioinformatics	University of Tennessee, Health Science Center (Invited)	Spring 2010
Bioinformatics	University of Tennessee, Health Science Center (Invited)	Spring 2012
Bioinformatics	University of Tennessee, Health Science Center (Invited)	Spring 2014
Genetics	University of North Dakota	Fall 2019, 2021
Genomics	University of North Dakota	Spring 2020, 2021

ACTIVITIES & SERVICES

Internal advisor board	NSF stem; UND	2021-2024
External advisor board	NIH R24; University of Arkansas for Medical Sciences	2021-2026
Faculty search committee	Department of Chemistry, UND	2021
President	College Graduate Student Union, Zhejiang University	2001—2002
President	College Student Union, Zhejiang University	1999—2000

INVITED TALKS IN CONFERENCES

High-throughput sequencing of the DBA/2J mouse genome. UT-ORNL-KBRIN Bioinformatics Summit 2010. March 19-21, 2010. Lake Barkley State Resort Park Cadiz, KY.

Whole-genome sequence of DBA/2J and its use for reverse complex trait analysis. The 9th annual meeting of the Complex Trait Community. Chicago, IL, USA. May 2010.

Reverse genetics. The 5th symposium of animal and plant quantitative genetics and breeding. Chengdu, Sichuan, China. Sept 2011.

JUMP: A tag-based database search program for peptide identification by mass spectrometry. 5th International Conference on Proteomics and Bioinformatics. Aug 2014. (http://omicsonline.org/speaker/Xusheng_Wang_Research_Scientist_At_St_Jude_Childrens_Research_HospitalUSA_Proteomics2014/)

JUMPM: A Pipeline for Mass Spectrometry-based Identification of Small Molecules. UND, Department of Chemistry. Feb 20, 2021.

Protein Expression and its Regulation in Mouse Brain. UND Epigenetics group. April 27, 2021.

Genetic Architecture of Protein Expression in Rat Brain. NIDA Genetics and Epigenetics Consortium Meeting. March 8-10, 2021.

PUBLICATIONS

1. Ling Li, Mingming Niu, Alyssa Erickson, Jie Luo, He Huang, Yuxin Li, Yi Jiang, Chunyu Liu, Junmin Peng, **Xusheng Wang (corresponding author)**. SMAP: A pipeline for sample matching in proteogenomics. 2021. Submitted to *Nature Communications*. 2022. 13:744.
2. Erickson, Alyssa, Suiping Zhou, Jie Luo, Ling Li, He Huang, Hai-Ming Xu, Junmin Peng, Lu Lu, **Xusheng Wang (corresponding author)**. Genetic Architecture of Protein Expression and its Regulation in the Mouse Brain. 2021. Submitted to *BMC Genomics*. 2021. 22:875.
3. Hazal Haytural, Rui Benfeitas, Sophia Schedin-Weiss, Erika Bereczki, Melinda Rezeli, Richard D Unwin, **Xusheng Wang**, Eric B Dammer, Erik CB Johnson, Nicholas T Seyfried, Bengt Winblad, Betty M Tijms, Pieter Jelle Visser, Susanne Frykman, Lars O Tjernberg. Insights into the changes in the proteome of Alzheimer's disease elucidated by a meta-analysis. *Scientific Data*. 2021. 8:312.
4. Bai, Bing, David Vanderwall, Yuxin Li, **Xusheng Wang**, Suresh Poudel, Hong Wang, Kaushik Kumar Dey, Ping-Chung Chen, Ka Yang, and Junmin Peng. Proteomic landscape of Alzheimer's Disease: novel insights into pathogenesis and biomarker discovery. *Molecular Neurodegeneration*. 2021. 16:1-16.

5. Maria Marti-Solano, Stephanie E Crilly, Duccio Malinverni, Christian Munk, Matthew Harris, Abigail Pearce, Tezz Quon, Amanda E Mackenzie, **Xusheng Wang**, Junmin Peng, Andrew B Tobin, Graham Ladds, Graeme Milligan, David E Gloriam, Manojkumar A Puthenveedu, M Madan Babu. Combinatorial expression of GPCR isoforms affects signalling and drug responses. *Nature*. 2020. 587:650-6.
6. Hong Wang, Kaushik Kumar Dey, Ping-Chung Chen, Yuxin Li, Mingming Niu, Ji-Hoon Cho, **Xusheng Wang**, Bing Bai, Yun Jiao, Surendhar Reddy Chepyala, Vahram Haroutunian, Bin Zhang, Thomas G Beach, Junmin Peng. Integrated analysis of ultra-deep proteomes in cortex, cerebrospinal fluid and serum reveals a mitochondrial signature in Alzheimer's disease. *Molecular neurodegeneration*. 2020. 15(1):1-20.
7. **Xusheng Wang (co-corresponding author)**, Ji-Hoon Cho, Suresh Poudel, Yuxin Li, Drew R Jones, Timothy I Shaw, Haiyan Tan, Boer Xie, Junmin Peng. JUMPm: A Tool for Large-Scale Identification of Metabolites in Untargeted Metabolomics. *Metabolites*. 2020. 10(5):190.
8. Pingping Liu, Jie Luo, Qingxia Zheng, Qiansi Chen, Niu Zhai, Shengchun Xu, Yalong Xu, Lifeng Jin, Guoyun Xu, Xin Lu, Guowang Xu, Gangjun Wang, Jianfeng Shao, Hai - Ming Xu, Peijian Cao, Huina Zhou, **Xusheng Wang (corresponding author)**. Integrating transcriptome and metabolome reveals molecular networks involved in genetic and environmental variation in tobacco. *DNA Research*. 2020. 27(2):dsaa006.
9. Bing Bai, **Xusheng Wang (co-first and co-corresponding author)**, Yuxin Li, Ping-Chung Chen, Kaiwen Yu, Kaushik Kumar Dey, Jay M Yarbrow, Xian Han, Brianna M Lutz, Shuquan Rao, Yun Jiao, Jeffrey M Sifford, Jonghee Han, Minghui Wang, Haiyan Tan, Timothy I Shaw, Ji-Hoon Cho, Suiping Zhou, Hong Wang, Mingming Niu, Ariana Mancieri, Kaitlynn A Messler, Xiaojun Sun, Zhiping Wu, Vishwajeeth Pagala, Anthony A High, Wenjian Bi, Hui Zhang, Hongbo Chi, Vahram Haroutunian, Bin Zhang, Thomas G Beach, Gang Yu, Junmin Peng. Deep multilayer brain proteomics identifies molecular networks in Alzheimer's disease progression. *Neuron*. 2020. 105(6):975-91.
10. Kaushik Kumar Dey, Hong Wang, Mingming Niu, Bing Bai, **Xusheng Wang**, Yuxin Li, Ji-Hoon Cho, Haiyan Tan, Ashutosh Mishra, Anthony A. High, Ping-Chung Chen, Zhiping Wu, Thomas G. Beach, Junmin Peng. Deep undepleted human serum proteome profiling toward biomarker discovery for Alzheimer's disease. *Clinical proteomics*. 2019. (1):1-2.
11. Hong Wang, Alexander K. Diaz, Timothy I. Shaw, Yuxin Li, Mingming Niu, Ji-Hoon Cho, Barbara S. Paugh, Yang Zhang, Jeffrey Sifford, Bing Bai, Zhiping Wu, Haiyan Tan, Suiping Zhou, Laura D. Hover, Heather S. Tillman, Abbas Shirinifard, Suresh Thiagarajan, Andras Sablauer, Vishwajeeth Pagala, Anthony A. High, **Xusheng Wang**, Chunliang Li, Suzanne J. Baker, Junmin Peng. Deep multiple-omics profiling of brain tumors measures oncogenic potency of cancer driver genes. *Nature Communications*. 2019. 10: 3718.
12. Dey, Kaushik Kumar, Hong Wang, Mingming Niu, Bing Bai, **Xusheng Wang**, Yuxin Li, Ji-Hoon Cho, Haiyan Tan, Ashutosh Mishra, Anthony A. High, Ping-Chung Chen, Zhiping Wu, Thomas G. Beach, Junmin Peng. Deep undepleted human serum proteome profiling toward biomarker discovery for Alzheimer's disease. *Clinical proteomics*. 2019. 16:1.
13. Mulligan, Megan K., Timothy Abreo, Sarah M. Neuner, Cory Parks, Christine E. Watkins, M. Trevor Houseal, Thomas M. Shapaker, Mike Hook, Haiyan Tan, **Xusheng Wang**, Jesse Ingels, Junmin Peng, Lu Lu, Catherine C. Kaczorowski, Camron D. Bryant, Gregg E. Homanics, Robert W. Williams. Identification of a functional non-coding variant in the GABAA receptor $\alpha 2$ subunit of the C57BL/6J mouse reference genome: Major implications for neuroscience research. 2019; DOI: 10.3389/fgene.2019.00188/*Frontier in Genetics*.

14. Jianqiao Shen, Vishwajeeth Reddy Pagala, Junmin Peng, Bin Ma, **Xusheng Wang (corresponding author)**. Spectral library search improves assignment of TMT labeled MS/MS spectra. *Journal of Proteome Research*. 2018; 17(9):3325–3331.
15. Wang, Daifeng, Shuang Liu, Jonathan Warrell, Hyejung Won, Xu Shi, Fabio CP Navarro, Declan Clarke, ... PsychENCODE Consortium [...**Xusheng Wang** ...].... Comprehensive functional genomic resource and integrative model for the human brain. *Science*, 2018; 362(6420). DOI: 10.1126/science.aat8464.
16. Ying Cheng, Zhao-Qian Teng, Weiqi Tan, Bing Bai, Yujing Li, Hai-Liang Yan, Zhi-Meng Wang, Hong Wang, Yunhee Kang, Xiaona Wang, Li Lin, Zhenping Chen, Nina Xie, **Xusheng Wang**, Junmin Peng, Dahua Chen & Peng Jin. Neuropsychiatric risk gene MIR137 modulates neurodevelopment and behavior. *Nature Neuroscience*. 2018; 5:1. DOI: 10.1038/s41593-018-0261-7.
17. Elizabeth Stewart, Justina McEvoy, Hong Wang, Xiang Chen, Yanlin Yang, Yuxin Li, Timothy I. Shaw, Ji-Hoon Cho, **Xusheng Wang**, Lyra Griffiths, Jongrye Jeon, Burgess Freeman, Michael R. Clay, Alberto Pappo, John Easton, Sheila Shurtleff, Anang Shelat, Xin Zhou, Kristy Boggs, Heather Mulder, Donald Yergeau, Armita Bahrami, Elaine R. Mardis, Richard K. Wilson, Jinghui Zhang, Junmin Peng, James R. Downing, and Michael A. Dyer. Identification of therapeutic targets in rhabdomyosarcoma through integrated genomic, epigenomic, and proteomic analyses. *Cancer Cell*. 2018; 34(3):411–426.e19.
18. Boer Xie, Yuanyuan Wang, Drew R Jones, Kaushik Kumar Dey, **Xusheng Wang**, Yuxin Li, Ji-Hoon Cho, Timothy I Shaw, Haiyan Tan, Junmin Peng. Isotope labeling-assisted evaluation of hydrophilic and hydrophobic liquid chromatograph–mass spectrometry for metabolomics profiling. *Analytical Chemistry*, 2018; 90(14), 8538-8545.
19. Jie Luo, Pei Xu, Hongjian Wan, Xiaonan Lv, Melloni N. Cook, Byron C. Jones, Lu Lu, **Xusheng Wang (corresponding author)**. Integrating genetic and gene co-expression analysis identifies gene networks involved in alcohol and stress responses. *Frontiers in Molecular Neuroscience*, 2018; 11:102.
20. **Xusheng Wang (corresponding author)**, Drew Jones, Timothy Shaw, Ji-Hoon Cho, Yuanyuan Wang, Haiyan Tan, Boer Xie, Suiping Zhou, Yuxin Li, Junmin Peng. Target-decoy–based false discovery rate estimation for large-scale metabolite identification. *Journal of Proteome Research*. 2018; 17(7):2328–2334.
21. Daniel C. Scott, Jared T. Hammill, Jaeki Min, David Y. Rhee, Michele Connelly, Vladislav O. Sviderskiy, Deepak Bhasin, Yizhe Chen, Su-Sien Ong, Sergio C. Chai, Asli N. Goktug, Guochang Huang, Julie K. Monda, Jonathan Low, Ho Shin Kim, Joao A. Paulo, Joe R. Cannon, Anang Shelat, Taosheng Chen, Ian R. Kelsall, Arno F. Alpi, Vishwajeeth Pagala, **Xusheng Wang**, Junmin Peng, Bhuvanesh Singh, J. Wade Harper, Brenda A. Schulman, R. Kip Guy. Blocking an N-terminal acetylation-dependent protein interaction inhibits an E3 ligase. *Nature Chemical Biology*. 2017; 13:850–857.
22. Anthony A. High, Haiyan Tan, Vishwajeeth R. Pagala, Mingming Niu, Ji-Hoon Cho, **Xusheng Wang**, Bing Bai, Junmin Peng. Deep proteome profiling by isobaric labeling, extensive liquid chromatography, mass spectrometry, and software-assisted quantification. *J. Vis. Exp.* 2017; 129, e56474, doi:10.3791/56474.
23. Haiyan Tan, Kai Yang, Yuxin Li, Timothy I. Shaw, Yanyan Wang, Daniel Bastardo Blanco, **Xusheng Wang**, Ji-Hoon Cho, Sherri Rankin, Cliff Guy, Junmin Peng and Hongbo Chi. Integrative proteomics and phosphoproteomics profiling reveals dynamic signaling networks

- and mTORC1-dependent mitochondrial function in T cell activation. *Immunity*. 2017; DOI: 10.1016/j.immuni.2017.02.010
24. Drew R. Jones, **Xusheng Wang**, Timothy Shaw, Ji-Hoon Cho, Junmin Peng. Multiplexed quantification of metabolites with MISSILE. *Metabolomics (Los Angel)*. 2017; 7(189): 2153-0769.
 25. Mingming Niu, Ji-Hoon Cho, Kiran Kodali, Vishwajeeth R. Pagala, Anthony A. High, Hong Wang, Zhiping Wu, Yuxin Li, Wenjian Bi, Hui Zhang, **Xusheng Wang**, Wei Zou, Junmin Peng. Extensive peptide fractionation and ion-based interference detection enable accurate quantification by isobaric labeling and mass spectrometry. *Analytical Chemistry*. 2017; 89 (5): 2956–2963
 26. **Xusheng Wang**, Ashutosh K. Pandey, Megan K. Mulligan, Evan G. Williams, Khyobeni Mozhui, Zhengsheng Li, Virginija Jovaisaite, L. Darryl Quarles, Zhousheng Xiao, Jinsong Huang, John A. Capra, Zugen Chen, William L. Taylor, Lisa Bastarache, Katherine S. Pollard, Daniel C. Ciobanu, Alexander O. Reznik, Artem V. Tishkov, Igor B. Zhulin, Junmin Peng, Stanley F. Nelson, Joshua C. Denny, Johan Auwerx, Lu Lu, Robert W. Williams. Joint mouse-human phenome-wide association to test gene function and disease risk. *Nature Communications*. 2016; 7:10464.
 27. Yuxin Li, **Xusheng Wang**, Ji-Hoon Cho, Timothy Shaw, Zhiping Wu, Bing Bai, Hong Wang, Suiping Zhou, Thomas Beach, Gang Wu, Jinghui Zhang, Junmin Peng. JUMPg: an Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. *Journal of Proteome Research*. 2016; 15:2309–2320.
 28. Mark Hatley, Jason Hanna, Matthew Garcia, Jonathan Go, David Finkelstein, Kiran Kodali, Vishwajeeth Pagala, **Xusheng Wang**, Junmin Peng. PAX7 is a required target for microRNA-206 induced differentiation of fusion-negative rhabdomyosarcoma. *Cell Death & Disease*. 2016; 7(6), e2256.
 29. Haiyan Tan, Zhiping Wu, Hong Wang, Bing Bai, Yuxin Li, **Xusheng Wang**, Bo Zhai, Thomas G Beach, Junmin Peng. Refined phosphopeptide enrichment by phosphate additive and the analysis of human brain phosphoproteome. *Proteomics*. 2015; doi: 10.1002/pmic.201400171.
 30. Joseph Leo Mertz, Haiyan Tan, Vishwajeeth Pagala, Bing Bai, Ping-Chung Chen, Yuxin Li, Ji-Hoon Cho, Timothy I. Shaw, **Xusheng Wang** and Junmin Peng. Sequential elution interactome analysis of the Mind bomb 1 ubiquitin ligase reveals a novel role in dendritic spine outgrowth. *Molecular & Cellular Proteomics*. 2015; doi: 10.1074/mcp.M114.045898.
 31. Arora, Kavisha, Chandrima Sinha, Weiqiang Zhang, Chang Suk Moon, Aixia Ren, Sunitha Yarlagadda, Wolfgang R. Dostmann, Adebawale Adebisi, Yael Haberman, Lee A. Denson, **Xusheng Wang**, Anjaparavanda P. Naren. Altered cGMP dynamics at the plasma membrane contribute to diarrhea in ulcerative colitis. *American Journal of Pathology*. 2015; 185: 2790-2804.
 32. **Xusheng Wang**, Yuxin Li, Zhiping Wu, Junmin Peng. JUMP: A Tag-based Database Search Engine for Peptide Identification with High Sensitivity and Specificity. *Molecular & Cellular Proteomics*. 2014; 13(12):3663-3673.
 33. Aixia Ren, Changsuk Moon, Weiqiang Zhang, Chandrima Sinha, Sunitha Yarlagadda, Kavisha Arora, **Xusheng Wang**, Junming Yue, Kaushik Parthasarathi, Rick Heil-Chapdelaine, Gabor Tigyi and Anjaparavanda P. Naren. Asymmetrical macromolecular complex formation of LPA2 receptor mediates gradient sensing in fibroblasts. *Journal of Biological Chemistry*. 2014; M114. 595512.

34. Ashutosh K Pandey, Lu Lu, **Xusheng Wang**, Ramin Homayouni, Robert W Williams. Functionally enigmatic genes: a case study of the brain ignorome. *PLoS One*. 2014; doi: 10.1371/journal.pone.0088889.
35. Hong Wang, Yanling Yang, Yuxin Li, Bing Bai, **Xusheng Wang**, Haiyan Tan, Tao Liu, Thomas G Beach, Junmin Peng, Zhiping Wu. Systematic optimization of long gradient chromatography mass spectrometry for deep analysis of brain proteome. *Journal of Proteome Research*. 2014; dx.doi.org/10.1021/pr500882h.
36. Leslie C. Jellen, Lu Lu, **Xusheng Wang**, Erica L. Unger, Christopher J. Earley, Richard P. Allen, Robert W Williams, and Byron C. Jones. Iron deficiency alters expression of dopamine-related genes in the ventral midbrain in mice. *Neuroscience*. 2013; 252:13-23.
37. Bai, Bing, Chadwick M. Hales, Ping-Chung Chen, Yair Gozal, Eric B. Dammer, Jason J. Fritz, **Xusheng Wang**, Qiangwei Xia, Duc M. Duong, Craig Street, Gloria Cantero, Dongmei Cheng, Drew R. Jones, Zhiping Wu, Yuxin Li, Ian Diner, Craig J. Heilman, Howard D. Rees, Hao Wu, Li Lin, Keith E. Szulwach, Marla Gearing, Elliott J. Mufson, David A. Bennett, Thomas J. Montine, Nicholas T. Seyfried, Thomas S. Wingo, Yi E. Sun, Peng Jin, John Hanfelt, Donna M. Willcock, Allan Levey, James J. Lah, Junmin Peng. U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. *Proceedings of the National Academy of Sciences*. 2013; 110:16562-16567.
38. **Xusheng Wang**, Khyobeni Mozhui, Zhengsheng Li, Megan K Mulligan, Jesse F Ingels, Roderick T Hori, Hao Chen, Melloni N Cook, Robert W Williams, Lu Lu. A promoter polymorphism in the *Per3* gene is associated with alcohol and stress response. *Translational Psychiatry*. 2012.2(e73): doi:10.1038/tp.2011.71.
39. Leslie C. Jellen, Erica L. Unger, Lu Lu, Robert W. Williams, Sarah Rousseau, **Xusheng Wang**, Christopher J. Earley, Richard P. Allen, Michael F. Miles, Byron C. Jones. Systems genetic analysis of the effects of iron deficiency in mouse brain. *Neurogenetics*. 2012; 13(2):147-157.
40. Chan Hyun Na, Drew R. Jones, Yanling Yang, **Xusheng Wang**, Yanji Xu, Junmin Peng. Synaptic protein ubiquitination in rat brain revealed by antibody-based ubiquitome analysis. *Journal of Proteome Research*. 2012; 11(9):4722-4732.
41. Zhihong Zhu, Chenhao Zhang, **Xusheng Wang**, Melloni N. Cook, Robert Williams, Lu Lu, Jun Zhu. Dissecting anxiety-related QTLs in mice by univariate and multivariate mapping. *Chinese Science Bulletin*. 2012; 57(21): 2727-2732.
42. Jesse D. Ziebarth, Melloni N. Cook, **Xusheng Wang**, Robert W. Williams, Lu Lu, Yan Cui. Treatment-and population-dependent activity patterns of behavioral and expression QTLs. *PloS One*. 2012; 7(2): e31805. doi:10.1371.
43. Megan K. Mulligan, **Xusheng Wang**, Adrienne L. Adler, Khyobeni Mozhui, Lu Lu, Robert W. Williams. Complex control of GABA (A) receptor subunit mRNA expression: variation, covariation, and genetic regulation. *PloS One*. 2012; 7(4): e34586. doi:10.1371.
44. Autumn M. McKnite, Maria Elisa Perez-Munoz, Lu Lu, Evan G. Williams, Simon Brewer, P  n  lope A. Andreux, John W. M. Bastiaansen, **Xusheng Wang**, Stephen D. Kachman, Johan Auwerx, Robert W. Williams, Andrew K. Benson, Daniel A. Peterson, Daniel C. Ciobanu. Murine gut microbiota is defined by host genetics and modulates variation of metabolic traits. *PloS One*. 2012; 7(6): e39191. doi:10.1371.
45. Hong Lu, **Xusheng Wang**, Matthew Pullen, Huaijin Guan, Hui Chen, Shwetapadma Sahu, Bing Zhang, Hao Chen, Robert W. Williams, Eldon E. Geisert, Lu Lu, Monica M. Jablonski.

- Genetic dissection of the Gpnmb network in the eye. *Investigative Ophthalmology & Visual Science*, 2011. doi: 10.1167/iovs.10-6493.
46. Patrizia Porcu, Todd K. O'Buckley, Soomin C. Song, Jo Lynne Harenza, Lu Lu, **Xusheng Wang**, Robert W. Williams, Michael F. Miles, A. Leslie Morrow. Genetic analysis of the neurosteroid deoxycorticosterone and its relation to alcohol phenotypes: identification of QTLs and downstream gene regulation. *PLoS One*, 2011.6(4): e18405.
 47. Khyobeni Mozhui, **Xusheng Wang**, Jingchun Chen, Megan M Mulligan, Jesse Ingles, Xiangning Chen, Lu Lu, Robert W Williams. Genetic regulation of *Nrx1* expression: an integrative cross-species analysis of schizophrenia candidate genes. *Translational Psychiatry*. 2011.1(e25): doi:10.1038/tp.2011.24.
 48. **Xusheng Wang**, Ying Chen, Xiaodong Wang, Jun Zhu, Lu Lu. Genetic regulatory network analysis for App based on genetical genomics approach, *Experimental Aging Research*. 2010. 36(1): 79-93.
 49. Daniel C. Ciobanu, Lu Lu, Khyobeni Mozhui, **Xusheng Wang**, Manjunatha Jagalur, John A. Morris, William L. Taylor, Klaus Dietz, Perikles Simon, Robert W. Williams. Detection, validation, and downstream analysis of allelic variation in gene expression. *Genetics*, 2010. 184(1): 119-128.
 50. **Xusheng Wang**, Richa Agarwala, John A Capra, Zugen Chen, Deanna M Church, Daniel C Ciobanu, Zhengsheng Li, Lu Lu, Khyobeni Mozhui, Megan K Mulligan, Stanley F Nelson, Katherine S Pollard, Williams L Taylor, Donald B Thomason, Robert W Williams. High-throughput sequencing of the DBA/2J mouse genome. *BMC Bioinformatics*, 2010. 11(Suppl 4): O7.
 51. Zhengsheng Li, Megan K. Mulligan, **Xusheng Wang**, Michael F. Miles, Lu Lu, Robert W. Williams. A transposon in *Comt* generates mRNA variants and causes widespread expression and behavioral differences among Mice. *PLoS One*, 2010. 5(8): e12181.
 52. Jiasheng Wu, Yanhong Zhao, **Xusheng Wang**. Bioinformatic analysis of myb protein family in *Oryza sativa* L.ssp.*japonica*. *Journal of South China Agriculture University*. 2009. 30(4): 43-48.
 53. Jiajuan Dai*, **Xusheng Wang*** (co-firth author), Ying Chen, Xiaodong Wang, Jun Zhu, Lu Lu. Expression QTL and genetic regulatory network analysis reveals that *Gabra2* is involved in the stress response. *Stress*. 2009; 12(6): 499-506.
 54. Qin Shen*, **Xusheng Wang*** (co-firth author), Ying Chen, Lingli Xu, Xiaodong Wang, Jun Zhu, Lu Lu. Expression QTL and regulatory network analysis of microtubule-associated protein tau gene. *Parkinsonism Related Disorder*. 2009; 15(7):525-531.
 55. Eldon E. Geisert, Lu Lu, Natalie E. Freeman-Anderson, **Xusheng Wang**, Weikuan Gu, Yan Jiao, Robert W. Williams. Large-scale variation in gene expression in the mouse eye: Covariance with ocular and retinal traits. *Molecular Vision*. 2009; 15:1730-1763.
 56. Alice Gerrits, Yang Li, Bruno M. Tesson, Leonid V. Bystrykh, Ellen Weersing, Albertina Ausema, Bert Dontje, **Xusheng Wang**, Rainer Breitling, Ritsert C. Jansen, Gerald de Haan, Expression quantitative trait loci are highly sensitive to cellular differentiation state. *PLoS Genetics*. 2009; 5(10): p. e1000692.
 57. **Xusheng Wang**, Minghua Zhang, Jun Zhu, Shu Geng. Spectral prediction of *Phytophthora infestans* infection on tomatoes using artificial neural network (ANN). *International Journal of Remote Sensing*. 2008; 29:1693-1706.

58. Khyobeni Mozhui, Daniel C. Ciobanu, Thomas Schikorski, **Xusheng Wang**, Lu Lu, Robert W. Williams. Dissection of a QTL hotspot on mouse distal chromosome 1 that modulates neurobehavioral phenotypes and gene expression. *PLoS Genetics*. 2008, 4(11): e1000260.
59. Jiasheng Wu, Yanhong Zhao, **Xusheng Wang**. Bioinformatic Analysis of MYB Protein Family in *Oryza sativa* L.ssp.*japonica*. *Journal of South China Agriculture University*. 2009. 30(4): 43-48.
60. **Xusheng Wang**, Ying Chen, Xiaodong Wang, Lu Lu. Advance in study of gene expression (eQTL). *Life Science*. 2009; 1: 38-43.
61. Jiasheng Wu, **Xusheng Wang**. Methods of bioinformatic analysis for candidate genes underlying quantitative trait loci (QTLs). *Journal of Zhejiang Forestry College*. 2008; 25:104-108.
62. Lu Lu, Lai Wei, Jeremy L Peirce, **Xusheng Wang**, Jianhua Zhou, Ramin Homayouni, Robert W Williams, David C Airey. Using gene expression databases for classical trait QTL candidate gene discovery in the BXD recombinant inbred genetic reference population: Mouse forebrain weight. *BMC Genomics*. 2008, 9: 444.
63. **Xusheng Wang**, Hongbo Zhu, Gulei Jin, Weiren Wu, Jun Zhu. Genome-scaled identification and analysis of LEA genes in rice (*Oryza sativa* L.). *Plant Science*. 2007; 172(2): 414-420.
64. Dong-liang Yu, **Xusheng Wang**, Fei Xu, Yan Fu. Bioinformatics identification and analysis for Box C/D SnoRNAs in silkworm genome. *Scientia Agricultura Sinica*. 2007; 40(1):196-203.
65. Tianxia Xiao, Xiangqian Zhao, **Xusheng Wang**, Weiren Wu, Jun Zhu. Examination and evaluation of PCR-based RGA markers in rice. *Journal of Zhejiang University*. 2007; 33(1):51-55.
66. Mahmood Qaisar, Zheng Ping, Wu Donglei, **Wang Xusheng**, Yousaf Hayat, Ul-Islam Ejaz, Hassan Muhammad Jaffar, Jilani Ghulam, Azim Rashid. Prediction of anoxic sulfide biooxidation under various HRTs using artificial neural networks. *Biomed Environ Sci* 2007;20:398-403.
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69. Yusong Xu, **Xusheng Wang**, Hubin Wang, Chenfu Lou. Cloning and genomic organization of a novel zinc finger protein gene from silkworm, *Bombyx mori*. *Canye Kexue*. 2005; 30(4):343-347.
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71. **Xusheng Wang**, Jun Zhu, Locedie Mansueto, Richard Bruskiewich. Identification of candidate genes for drought stress tolerance in rice by the integration of a genetic (QTL) map with the rice genome physical map. *Journal Zhejiang University Science (B)*. 2005; 6B(5):382-388.
72. Gulei Jin, **XuSheng Wang**, Jun Zhu. Bioinformatic analysis of the 14-3-3 gene family in rice. *ACTA Genetica Sinica*. 2005; 32(7):726-732.

73. Zhongzhong Chen, **Xusheng Wang**, Jun Zhu. Analysis of SSRs polymorphism by genome-scale comparing between indica and japonica. *Chinese Journal of Rice Science*. 2005; 19(4):303-307.
74. Dongliang Yu, Boxiong Zhong, Yan Fu, **Xusheng Wang**. Comparison of ESTs and SNPs from posterior silk gland of silkworm *Bombyx mori* between the strain P50 and C108. *Canye Kexue*. 2005; 31(4): 434-438.
75. Richard M. Bruskiwich, Alexander B. Cosico, William Eusebio, Arlet M. Portugal, Luralyn M. Ramos, Ma. Teresa Reyes, May Ann B. Sallan, Victor Jun M. Ulat, **Xusheng Wang**, Kenneth L. McNally, Ruairaidh Sackville Hamilton, Christopher Graham McLaren. Linking genotype to phenotype: the International Rice Information System (IRIS). *Bioinformatics*. 2003; 19 Suppl1:i63-65.

Citation of Publication in Google Scholar

<https://scholar.google.com/citations?user=eM3dr7qAAAAJ&hl=en>

BOOK CHAPTER

Vishwajeeth R. Pagala, Anthony A. High, **Xusheng Wang**, Haiyan Tan, Kiran Kodali, Ashutosh Mishra, Kanisha Kavdia, Yanji Xu, Zhiping Wu, and Junmin Peng. Quantitative Protein Analysis by Mass Spectrometry. *Protein-Protein Interactions Methods in Molecular Biology*. (2015). Volume 1278, 2015, pp 281-305.

PATENT

Weiren Wu, Yongquan Lu, **Xusheng Wang**. Development of amplified consensus genetic markers in gramineae. (No. CN1769492)

GRANTS

CURRENT

NIH/NIAID R01

04/01/2022 - 03/30/2027

Title: Validation of a novel tau clearance mechanism

Total: \$500,000.00 (UND)

Goals: The goal is to examine a novel mechanistic link between oxidative stress and OTULIN activity via ABL1 during the progression of tauopathy.

Role: Co-I

NIH/NINDS R01

09/01/2021 – 08/31/2026

1.2 calendar MO

(Na)

Total: \$221,941 (UND)

Region-Specific Vulnerability Of The Lewy Body Dementia's Brain

Goals: The goal of this project is to understand the LBD pathogenesis mechanism, we must identify the proteome and transcriptome changes of multiple cell types and regions that comprise the brain.

Role: Co-I

UND VPR Seed Program

04/01/2021 - 03/30/2023

1 calendar MO

(Wang)

Total: \$150,000

*Artificial Intelligence (AI)-based Multi-omics
Data Integration for Alzheimer's Disease*

Goals: The goal is to provide an AI framework for disease outcome prediction, and ultimately patients will benefit from better prognosis and predictions based on their multi-omics profiles in the precision medicine era.
Role: PI

NIH/NIA RF1AG057181 Sub-award 04/01/2020 - 03/30/2022 0.6 Calendar MO
(Bu) Total: \$100,000 (UND)

Impact of ApoE2 on Aging-related Conditions

Goals: The goal of this project is to understand the molecular and cellular mechanisms by which the $\epsilon 2$ allele of the apolipoprotein E gene (APOE2) protects against Alzheimer's disease (AD), promotes healthy brain aging, and increases longevity, thereby informing the development of therapeutic strategies for AD and other aging-related conditions.

Role: co-I

NIH DaCCoTA 09/01/2021 - 08/31/2022 2.4 calendar MO
Feasibility Grant Total: \$56,000

*Integrated systems biology approach to
diabetic microvascular complications*

Goals: The goal is to identify chromatin structures maintained in cfDNA and to develop a powerful and robust AI-based prediction model for cancer diagnosis.

Role: PI

COMPLETED

University of North Dakota (UND) COBRE 10/01/2019 – 06/30/2020 0.6 Calendar MO
Epigenomics and Development and Disease, Total: \$30,000
Pilot Grant

Allele-Specific and Imprinted Expression of Mouse Brain Proteome

Goals: The goal of the proposal is to understand allele-specific and imprinted protein expression by profiling mouse brain proteome.

Role: PI

NIH/NIDA P30 (1P30DA044223-01) 09/01/2019 – 06/30/2021 0.6 Calendar MO
Pilot Grant Total: \$50,000

Genetic Regulation of the Rat Brain Proteome

Goals: The goal of this study is to understand genetic regulation of protein expression by profiling brain proteome of the HXB/BXH recombinant inbred (RI) rat panel.

Role: Project PI

UND COBRE HPI 04/01/2020 – 03/31/2021 0.6 Calendar MO
Pilot Grant (UND000021452) Total: \$32,000

Genetic Regulation of Host Proteome in Response to Salmonella Typhimurium Infection in Mice

Goals: The goal of the proposal is to understand genetic regulation of host protein expression in response to Salmonella Typhimurium infection in mouse.

Role: PI

ND EPSCoR STEM 10/01/2020 - 05/01/2021 0.6 calendar MO

*Predicting Clinical Outcomes of Alzheimer's
Disease Using Deep Learning Approach*

Total: \$5,000

Goals: The overarching goal of this project is to predict disease outcomes by combining multi-omic data and artificial neural network.

Role: PI

**UND College of Arts & Science
Collaborative Research Funding** 09/01/2020 - 08/31/2021 0.6 calendar MO
From Big Data to Precision Medicine

for Alzheimer's Disease

Total: \$20,000

Goals: The overarching goal of this project is to predict AD risk proteins by using multi-omics data obtained from existing molecular profiling studies, to determine the structural information of AD risk proteins, and to communicate up-to-date scientific findings to the general public.

Role: PI

PENDING

NSF CAREER

05/01/2022 – 04/30/2027

CAREER: Systems Proteomics Approach
to Bridging the Genome-to-Phenome Gap

Total: \$807,794.00

Goals: Our long-term goal is to construct signal transduction networks to bridge the genome-to-phenome relationship.

Role: PI

NIH/NIDA P30

07/01/2022 - 06/30/2027

Title: NIDA P30 Core Center of Excellence
in Omics, Systems Genetics, and the Addictome

Total: \$1,225,776.00 (UND)

Goals: The goal is to generate quantitative omic data for the Hybrid Rat Diversity Panel (HRDP), which include proteomic and metabolomic data using mass spectrometry (MS)-based technologies, DNA methylation data using microarrays, chromatin accessibility data with ATAC-seq, and transcript data by Iso-Seq.

Role: Core Lead

DoD Investigator Initiated Research Award

07/01/2022 - 06/30/2027

Title: Diet and high intensity interval training to treat
peripheral neuropathy in prediabetes and the metabolic syndrome

Total: \$737,822.00 (UND)

Goals: The goal is to identify the best MetS intervention, among DR, HIIT, and DR/HIIT, for treating PN in an animal model simulating the real lifestyle trajectories of military personnel and veterans.

Role: Co-I

NIH/NIDA R01

07/01/2022 - 06/30/2027

Title: Identification of Gene Variants Mediating the
Behavioral and Physiological Response to THC

Total: \$1,007,976.24 (UND)

Goals: The goal is to identify and validate genetic modulators of acute physiological responses to THC.

Role: Co-I