Hunter N. B. Moseley, Associate Professor

CC434 Roach Building, 800 Rose Street, Lexington, KY 40536-0093 • hunter.moseley@uky.edu • http://bioinformatics.cesb.uky.edu

Broad Research Interests	Develop computational methods for analyzing and interpreting biological and biophysical data that leverage relevant information from public scientific databases, integrate system-wide analysis across omics-level datasets, and enable new understanding of biological systems and disease processes.

Research Experience	
2013-present	**Head of a Biophysical Informatics & Systems Biochemistry Lab, University of Kentucky**
	Associate Professor, Department of Molecular & Cellular Biochemistry, University of Kentucky
2008-2013	Assistant Professor, Department of Chemistry, University of Louisville
1998-2008	Postdoc to Research Assistant Prof, Bioinformaticist, Ctr. Adv. Biotechnology & Medicine, Rutgers Univ.

Education	
1992-1998	**Ph.D. Biochemistry and Molecular Genetics, N. Rama Krishna (advisor)**
	University of Alabama at Birmingham, Birmingham, AL
1988-1992	**B.A. Chemistry, Computer Science, and Mathematics triple major; Biology minor**
	Huntingdon College, Montgomery, AL

Major Research Projects

- Metabolomics data analysis and moiety modeling using SIRM data, Univ of Louisville.
- Automated protein resonance assignments of solid state NMR data, Univ of Louisville.
- **AutoAssign package for automated protein NMR resonance assignments**, Rutgers Univ.
- **AVS - NMR assignment validation tools used by BioMagResBank on all submissions**, Rutgers Univ.
- **CORCEMA - NOESY and TrNOESY analysis program, U.S. patent 5,668,734**, UAB

Professional Activities

- Co-authored 34 publications with an "h" index of 18.
- **Informatics Core Director, Resource Ctr for Stable Isotope-Resolved Metabolomics,Univ.of Kentucky**
- **Informatics Director, Center for Environmental and Systems Biochemistry, Univ. of Kentucky**
- **Associate Member, Northeast Structural Genomics Consortium**
- Review Editor, *Frontiers in Molecular Sciences - Metabolomics*
- **Program Committee, UT-KBRIN Bioinformatics Summit**
- Peer-reviewed grant proposals for NSF and manuscripts for *J Biomol NMR, J Mag Reson, PNAS, Protein Sci, Bioinformatics, J Struct Funct Genomics, CEJB, RECOMB, Rap Com MS, Anal Chem*
- **Given 32 oral presentations at various conferences, workshops, and universities.**

Teaching Experience	
2015-present	**Instructor for biochemistry course BCH-401G-Honors, University of Kentucky**
2009-2013	**Instructor for biochemistry courses (CHEM 445, CHEM 547, CHEM 647), University of Louisville**
2008-2013	Coordinator of Chemistry Dept Graduate Seminar Program (CHEM 695), University of Louisville
2007-2008	Coordinator for CABM Summer Undergraduate Internship Program, Rutgers Univ.

Honors and Awards	
2015	UK College of Education Teacher Who Made A Difference Honoree
2013	**NSF CAREER Award**
2012	**Kentucky Academy of Science Outstanding Early Career Award**
2011	**UofL Faculty Favorite Award (nominated by students for excellence in teaching)**
2010	**Kentuckiana Metroversity Award for Instructional Development (regional multi-university award)**
2008	University of Louisville Faculty Learning Community on Critical Thinking
1999-2001	**NSF Postdoctoral Research Fellowship in Biological Informatics**
1998	**UAB Samuel B. Barker Annual Award for Excellence in Graduate Studies, Doctoral Level,** (top university doctoral award; awarded to only one student per year)
1996	**UAB Department of Biochemistry & Molecular Genetics McKibben Award (top dept. doctoral award)**
1988-1992	4-Year Full Tuition Bellingraph Scholarship, Huntingdon College

Recent Research Support

- NIH: 1U24DK097215-01A1 *Resource Center for Stable Isotope-Resolved Metabolomics* Higashi/Fan/Lane/Moseley(PIs) - $6,188,893 (direct); Duration: 09/11/2013-08/31/2018; Role: PI ($881,220)
- NSF 1252893 *CAREER:Developing Biochemoinformatics Tools for Large Scale Metabolomics…* Moseley(PI) - $760,657 (direct); Duration: 07/01/2013 to 6/30/2018; Role: PI ($760,657)
- NIH:1P01CA163223-01A1 *Systems Biochemistry in Lung Cancer…* Fan/Lane/Yan(PIs) - $6,144,152 (direct); Duration: 03/01/2013-2/28/2018; Role:Co-I ($553,602)
- NIH:1R01ES022191-01 *Integrated Chemoselective & Informatics Platform for Large-Scale Metabolomics* Fan/Higashi/Moseley/Nantz(PIs) - $1,482,460 (direct); Duration: 9/26/2012-06/30/2017; Role: PI ($324,298)

Activities	
1994-2013	Certified Moniteur Fencing Instructor, Louisville Fencing Center, Bucks County Acad. of Fencing, & BFC
1998	President and co-founder of the Birmingham Fencing Club (BFC), Birmingham, Alabama.

Synergistic Activities (5 top activities)

1) The PI is actively recruiting, exposing, and training graduate, undergraduate and high school students with bioinformatics-based research projects. In the last 5 years, the PI's lab has included 6 graduate students (including 2 woman), 33 undergraduate students (including 7 women), and 11 high school students (including 3 woman) from a wide range of disciplines including chemistry, biochemistry, biology, mathematics, physics, computer science & engineering, business, chemical engineering, and biomedical engineering.

2) The PI has joined a wonderful and very fruitful collaboration with Drs. Teresa Fan, Andrew Lane, and Rick Higashi under the auspices of the University of Kentucky Resource Center for Stable Isotope-Resolved Metabolomics. I bring needed bioinformatics expertise into an already established mix of sample generation from cells/tissue/animals, sample handling, NMR analytical, mass spec analytical, and metabolic expertises. This collaboration has already led to many joint publications where everyone's expertises are applied to complex metabolomics projects.

3) The PI has actively participated in five different summer undergraduate research programs including: i) UofL Chemistry & Structural Biology REU, ii) NCI R25 Cancer Education Program, iii) UofL Summer Research Opportunity Program, iv) KBRIN-Sponsored Summer Research Opportunities for Kentucky Undergraduate Students, and v) CABM Summer Undergraduate Internship Program (Rutgers Univ). The PI has mentored students in the first 4 programs. The PI coordinated the CABM Summer Undergraduate Internship Program in 2007 and 2008. In addition, the PI accepted a high school student Daniel Levine into the 2007 seminar series component as a trial expansion of the program. The PI then established a relationship with a science and engineering magnet high school in the area for the high school student expansion of this summer program in 2008.

4) The PI has been granted IRB approval to evaluate the effectiveness of scaffolded explicit revision methodologies in his yearly taught course, CHEM 445 – Survey of Biochemistry. Valuable data has already been collected, analyzed, and submitted for publication which demonstrates the effectiveness of using explicit revision within multiple student assessment instruments used in the course.

5) While at Rutgers University, the PI developed and maintained the AutoAssign software package for automated protein resonance assignments of solution NMR data, especially for the Northeast Structural Genomics Consortium. Nearly 300 academic (free) and commercial labs have licensed AutoAssign and the program is cited in twice as many Protein Data Bank and Biological Magnetic Resonance Data Bank (BMRB) entries as all other automated assignment programs combined. The PI also developed the Assignment Validation Suite (AVS) for validating protein resonance assignments. AVS was the first outside assignment validation tool adopted by the Biological Magnetic Resonance Bank (BMRB), which they use on all submitted entries. The PI maintains AVS for the BMRB.

Publications

- Current "h" index is 18 as per J. E. Hirsch's definition for quantifying an individual's scientific research output (physics/0508025 v5 09/29/2005).

34) Sen Yao, Robert M. Flight, Eric C. Rouchka, and **Hunter N.B. Moseley**. "A less biased analysis of metalloproteins reveals novel zinc coordination geometries" *Proteins* (accepted). doi:10.1002/prot.24834

33) Andrew N. Lane, Sengodagounder Arumugam, Pawel K. Lorkiewicz, Richard M. Higashi, Sébastien Laulhé, Michael H. Nantz, **Hunter N.B. Moseley**, and Teresa W.-M. Fan. "Chemoselective detection and discrimination of carbonyl-containing compounds in metabolite mixtures by 1H-detected 15N NMR" *Magnetic Resonance in Chemistry* 53, 337 (2015).

32) Abdallah M. Eteleeb, **Hunter N.B. Moseley**, and Eric C. Rouchka. "A Comparison of Combined P-value Methods for Gene Differential Expression Using RNA-Seq Data" *BCB'14: Proceedings of the 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics*, pp417-425. doi:10.1145/2649387.2649421 (2014).

31) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, and **Hunter N.B. Moseley**. "Development of Large-Scale Metabolite Identification Methods for Metabolomics" *Frontiers in Genetics*, 5, 237 (2014). Citations: 3 (Google Scholar)

30) Richard M. Higashi, Teresa W-M. Fan, Pawel K. Lorkiewicz, **Hunter N.B. Moseley**, Andrew N. Lane. "Stable Isotope Labeled Tracers for Metabolic Pathway Elucidation by GC-MS and FT-MS" *Mass Spectrometry in Metabolomics: Methods in Molecular Biology*, vol 1198, 147, editor D. Raftery. Humana Press (2014).

29) William J. Carreer, Robert M. Flight, and **Hunter N.B. Moseley**. "A computational framework for high-throughput isotopic natural abundance correction of omics-level ultra-high resolution FT-MS datasets" *Metabolites*, 3, 853-866 (2013). Citations: 2 (Google Scholar)

28) **Hunter N.B. Moseley**. "Error Analysis and Propagation in Metabolomics Data Analysis" *Comp Struct Biotech J*, 4, e201301006 (2013). Citations: 6 (Google Scholar)

27) Eric C. Rouchka, Robert M. Flight, and **Hunter N.B. Moseley**. "Proceedings of the Eleventh Annual UT-ORNL-KBRIN Bioinformatics Summit 2012" *BMC Bioinformatics*, 13, A1 (2012).

26) Teresa W-M. Fan, Pawel Lorkiewicz, Katherine Sellers, **Hunter N.B. Moseley**, Richard M. Higashi, and Andrew N. Lane. "Stable isotope-resolved metabolomics and applications to drug development" *Pharmacology & Therapeutics*, 133, 366 (2012). Citations: 45 (Google Scholar)

25) **Hunter N.B. Moseley**, Andrew N. Lane, Alex C. Belshoff, Richard M. Higashi, and Teresa W-M. Fan. "A novel method for deconvoluting metabolic subunits from mass isotopologues in stable isotope resolved metabolomic experiments under non steady-state conditions: application to the biosynthesis of UDP-GlcNAc" *BMC Biology*, 9, 37 (2011). Citations: 28 (Google Scholar)

24) **Hunter N.B. Moseley**, Richard M. Higashi, Teresa W-M. Fan, and Andrew N. Lane. "Metabolic Modeling of Converging Metabolic Pathways: Analysis of Non-Steady State Stable Isotope-Resolve Metabolism of UDP-GlcNAc and UDP-GalNAc" *BIOINFORMATICS 2011 – Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms*. Ed. Marco Pellegrini, Ana Fred, Joaquim Filipe, and Hugo Gamboa. SciTePress, Portugal, 108-115 (2011). Citations: 3 (Google Scholar)

23) **Hunter N.B. Moseley**, Lindsay J. Sperling, and Chad M. Rienstra. "Automated Protein Resonance Assignments of Magic Angle Spinning Solid-State NMR Spectra of β1 Immunoglobulin Binding Domain of Protein G (GB1)" *J Biomol NMR*, 48, 123-128 (2010). Citations: 12 (Google Scholar)

22) **Hunter N.B. Moseley**. "Correcting for the Effects of Natural Abundance in Stable Isotope Resolved Metabolomics Experiments Involving Ultra-High Resolution Mass Spectrometry." *BMC Bioinformatics* 11, 139-144 (2010). Citations: 15 (Google Scholar)

21) Andrew N. Lane, Teresa W-M. Fan, Zhengzhi Xie, **Hunter N.B. Moseley**, and Richard M. Higashi. "Stable isotope analysis of lipid biosynthesis by high resolution mass spectrometry and NMR." *Anal. Chim. Acta*. 651, 201-208 (2009). Citations: 27 (Google Scholar)

20) Gregory J. Kornhaber, David Snyder, **Hunter N.B. Moseley**, and Gaetano T. Montelione. "Identification of Zinc-Ligated Cysteine Residues Based on $^{13}C\alpha$ and $^{13}C\beta$ Chemical Shift Data." *J Biomol NMR*, 34, 259-269 (2006). Citations: 51 (Google Scholar)

19) Michael Baran, **Hunter N.B. Moseley**, James M. Aramini, Marvin J. Bayro, Daniel Monleon, Jessica Lau, and Gaetano T. Montelione. "SPINS: A Laboratory Information Management System for Organizing and Archiving Intermediate and Final Results from NMR Protein Structure Determinations." *Proteins: Struct Funct Bioinformatics*, 62,843-851 (2006). Citations: 12 (Google Scholar)

18) Yuanpeng J. Huang, **Hunter N.B. Moseley**, Michael C. Baran, Cheryl Arrowsmith, Robert Powers, Roberto Tejero, Thomas Szyperski, and Gaetano T. Montelione. "An integrated platform for automated analysis of protein NMR structures." *Meth Enzymology* 394, 111-141 (2005). Citations: 56 (Google Scholar)

17) Michael C. Baran, Janet Y. Huang, **Hunter N.B. Moseley**, and Gaetano T. Montelione. "Automated Analysis of Protein NMR Assignments and Structures." *Chemical Reviews* 104, 3541-3556 (2004). Citations: 88 (Google Scholar)

16) **Hunter N.B. Moseley**, Nadeem Riaz, James M. Aramini, Thomas Szyperski, and Gaetano T. Montelione. "A Generalized Approach to Automated NMR Peak List Editing: Application to Reduced Dimensionality Triple Resonance Spectra." *J Magn Reson* 170, 263-277 (2004). Citations: 40 (Google Scholar)

15) **Hunter N.B. Moseley**, Gurmukh Sahota, and Gaetano T. Montelione, "Assignment Validation Software Suite for the Evaluation and Presentation of Protein Resonance Assignment Data." *J Biomol NMR* 28, 341-355 (2004). **Citations: 84 (Google Scholar)**

14) Deyou Zheng, Yuanpeng J. Huang, **Hunter N.B. Moseley**, Rong Xiao, James Aramini, G.V.T. Swapna, and Gaetano T. Montelione, "Automated protein fold determination using a minimal NMR constraint strategy." *Protein Science* 12, 1232-1246 (2003). **Citations: 58 (Google Scholar)**

13) Michael Baran, **Hunter N.B. Moseley**, Gurmukh Sahota, and Gaetano T. Montelione, "SPINS: Standardized Protein NMR Storage. A data dictionary and object-oriented relational database for archiving protein NMR spectra." *J Biomol NMR* 24, 113-121 (2002). Citations: 20 (Google Scholar)

12) Daniel Monleon, Kimberly Colson, **Hunter N.B. Moseley**, Clemens Anklin, Robert Oswald, Thomas A. Szyperski, and Gaetano T. Montelione, "Rapid Analysis of Protein Backbone Resonance Assignments Using Cryogenic Probes, Distributed Linux-based Computing, and Automated Spectral Analysis." *J Struct Func Genomics* 2, 93-101 (2002). Citations: 33 (Google Scholar)

11) Thomas Szyperski, Deok C. Yeh, Dinesh K. Sukumaran, **Hunter N.B. Moseley**, and Gaetano T. Montelione. "Reduced-dimensionality NMR Spectroscopy for High-Throughput Protein Resonance Assignment: Implementation and Automated Analysis." *Proc Natl Acad Sci USA* 99, 8009-8014 (2002). **Citations: 163 (Google Scholar)**

10) **Hunter N.B. Moseley**, Daniel Monleon, and Gaetano T. Montelione, "Automatic Determination of Protein Backbone Resonance Assignments from Triple Resonance NMR Data." *Meth Enzymology* 339, 91 (2001). **Citations: 149 (Google Scholar)**

9) **Hunter N.B. Moseley** and Gaetano T. Montelione. "Automated analysis of NMR assignments and structures for proteins." *Curr Opin Struct Biol* 9, 635-642 (1999). **Citations: 188 (Google Scholar)**

8) N. Rama Krishna and **Hunter N.B. Moseley**. "Complete Relaxation and Conformational Exchange Matrix Analysis of NOESY Spectra of Reversibly Forming Ligand-Receptor Complexes: Application to Transferred NOESY," in "Structure Computation and Dynamics in Protein NMR." *Biological Mag Resonan* Vol 17, editors: N. R. Krishna and L.J. Berliner, Plenum Press, New York (1999). Citations: 3 (Google Scholar)

7) **Hunter N.B. Moseley**. "Implementation and Application of Complete Relaxation and Conformational Exchange Matrix Analysis of NOESY Spectra." **dissertation** (1998). Citations: 1 (Google Scholar)

6) **Hunter N.B. Moseley**, Weontae Lee, Cheryl H. Arrowsmith, and N. Rama Krishna. "Quantitative Determination of Conformational, Dynamic, and Kinetic Parameters of a Ligand-Protein/DNA Complex from a CORCEMA Analysis of Intermolecular Transferred NOESY." *Biochemistry* 36, 5293 (1997). Citations: 27 (Google Scholar)

5) Ernest V. Curto, **Hunter N.B. Moseley**, and N. Rama Krishna. "CORCEMA evaluation of the potential role of intermolecular transferred NOESY in the characterization of ligand-receptor complexes." *J Comp-Aided Molec Design* 10, 361 (1996). Citations: 17 (Google Scholar)

4) **Hunter N.B. Moseley**, Ernest V. Curto, and N. Rama Krishna. "Complete Relaxation and Conformational Exchange Matrix (CORCEMA) Analysis of NOESY Spectra of Interacting Systems: Two-dimensional Transferred NOESY." *J Magn Reson* B108, 243 (1995). **Citations: 92 (Google Scholar)**

3) Patricia L. Jackson, **Hunter N.B. Moseley**, and N. Rama Krishna. "Relative Effects of Protein-Mediated and Ligand-Mediated Spin-Diffusion Pathways on Transferred NOESY, and Implications on the Accuracy of the Bound Ligand Conformation." *J Magn Reson* B107, 289 (1995). Citations: 22 (ISI)

2) Curtis C. Maier, **Hunter N.B. Moseley**, Shan-Ren Zhou, John N. Whitaker, and J. Edwin Blalock. "Identification of Interactive Determinants on Idiotypic-Anti-idiotypic Antibodies through Comparison of Their Hydropathic Profiles." *Immunomethods* 5, 107 (1994). Citations: 25 (Google Scholar)

1) Rick L. Davies and **Hunter N.B. Moseley**. "Student Roots: Square root algorithm in Forth." *Forth Dimensions* 8, 8-9 (1987). Citations: 0 (unknown)

Oral Presentations

33) "Teaching Critical Thinking in STEM Disciplines", **STEM Teaching Enhancement Workshop & Forum**, Lexington, KY (2015).

32) "Biomedical Informatics at the University of Kentucky", **10th Annual CCTS Spring Conference**, Lexington, KY (2015).

31) "Resource Center for Stable Isotope Resolved Metabolomics:Tracing Networks & Pools," **NIH Common Fund Annual Meeting – Metabolomics**, Triangle, NH (2014).

30) "Natural Abundance Correction and Moeity Modeling in FTMS Data," **RCSIRM Workshop**, Lexington, KY (2014).

29) "Development of Large-Scale Metabolite Identification Methods for Metabolomics," **UT-KBRIN Bioinformatics Summit**, Cadiz, KY (2014).

28) "An Informatics and Modeling Platform for Stable Isotope-Resolved Metabolomics." **55th Experimental Nuclear Magnetic Resonance Conference**, Boston, MA (2014).

27) "Defining and Cultivating Critical Thinking Among Your Students." **University of Kentucky**, Lexington, KY (2014).

26) "What is Critical Thinking?" **University of Kentucky**, Lexington, KY (2013).

25) "Applications of Stable Isotope-Resolved Metabolomics: From Bench to Bedside." **University of Kentucky**, Lexington, KY (2013).

24) "Scaffolded Explicit Revision as a Practical Framework to Promote Effective Student Effort in Content-Rich Courses." **2013 I2A Institute: Sharing the Impact of Critical Thinking**, Louisville, KY (2013).

23) "Scaffolded Explicit Revision as a Practical Framework to Promote Effective Student Effort." **2013 Kentucky Innovations Conference**, Lexington, KY (2013).

22) "Scaffolded Explicit Revision as a Practical Framework to Promote Effective Student Effort in Content-Rich Courses." **2013 Celebration of Teaching & Learning: Teaching in Harmony with the Brain: Applying Learning Science in Today's Classroom and Beyond**, Louisville, KY (2013).

21) "Metabolic Modeling of Converging Metabolic Pathways. Analysis of Non-Steady State Stable Isotope-Resolved Metabolomics of UDP-GlcNAc and UDP-GalNAc." **IUPUI**, Indianapolis, IN (2012).

20) "Scaffolded Explicit Revision as a Practical Framework to Promote Effective Student Effort in Content-Rich Science Courses." **2012 Ideas to Action (I2A) Institute: Critical Thinking Innovation**, Louisville, KY (2012).

19) "Metabolic Modeling of Converging Metabolic Pathways. Analysis of Non-Steady State Stable Isotope-Resolved Metabolomics of UDP-GlcNAc and UDP-GalNAc." **The 25th Anniversary CABM Symposium**, Ctr. Adv. Biotech & Med., Rutgers University & UMDNJ., Piscataway, NJ (2011).

18) "Metabolic Modeling of Converging Metabolic Pathways. Analysis of Non-Steady State Stable Isotope-Resolved Metabolomics of UDP-GlcNAc and UDP-GalNAc." **BIOINFORMATICS 2011**, Rome, Italy (2011).

17) "Metabolic Modeling of Converging Metabolic Pathways. Analysis of Non-Steady State Stable Isotope-Resolved Metabolomics of UDP-GlcNAc and UDP-GalNAc." **Metabolomics Network Annual Meeting**, NIH Campus, Bethesda, MD (2010).

16) "Metabolic Modeling of Converging Metabolic Pathways. Analysis of Non-Steady State Stable Isotope-Resolved Metabolomics of UDP-GlcNAc and UDP-GalNAc." **Huntingdon College**, Montgomery, AL (2010).

15) "Stable isotope-resolved metabolomics analysis of UDP-GlcNAc & UDP-GalNAc: Computational resolution and modeling of their converging biosynthetic pathways." **239th American Chemical Society National Meeting and Exposition**, San Francisco, CA (2010).

14) "Stable Isotope Resolved Metabolomics (SIRM) of UDP-GlcNAc and UDP-GalNAc Metabolism in Prostate Cancer." **5th Annual Metabolomics Society International Conference, Edmonton, Alberta. Canada** (2009).

13) "Automated Analysis of RD and GFT NMR data with Pattern Picker." **Protein Structure Initiative NMR Workshop, Rutgers University** (2008).

12) "Automated NMR Analysis for Structural Genomics: From FIDS to Resonance Assignments and then to Structure." **Huntingdon College**, Montgomery, AL (2008).

11) "Automated Analysis from FIDs to Resonance Assignments Using GFT Data," **CCPN-NESG Workshop on Automated and Interactive NMR Data Analysis, Rutgers University** (2007).

10) "Automated Analysis from FIDs to Resonance Assignments Using GFT Data," **ESF Exploratory Workshop: Experimental and Computational Aspects of High-Throughput Protein NMR, European Science Foundation, Goteburg University, Sweden** (2006).

9) "NMR Automation: From FIDs to Resonance Assignments and then to Structure," **Biomolecular NMR Workshop, BioMagRes Databank, University of Wisconsin-Madison**, Madison, WI (2006).

8) "Automation of the NMR Structure Determination Process for Structural Genomics," **University of Copenhagen, Denmark** (2005).

7) "Current Methods in NMR Structure Determination", **DIMACS Working Group on New Algorithms for Inferring Molecular Structure from Distance Restraints, Rutgers University** (2004).

6) "Automation of the NMR Structure Determination Process for Structural Genomics," **NJ ACS NMR Topical Group**, Woodbridge, NJ (2003).

5) "Automated Protein Assignments and Structure Determination," **BioNMR Workshop, University of Alabama at Huntsville**, Huntsville, AL (2003).

4) "Automatic Determination of Protein NMR Assignments using AutoAssign and AutoPeak," **Biomolecular NMR Workshop, BioMagRes Databank, University of Wisconsin-Madison**, Madison, WI (2002).

3) "Current Methods in Automated Assignment and Automated Structure Determination," **Workshop 2000: NMR Methods for Biomolecular Structures, National Laboratory of Protein Engineering and Plant Genetic Engineering, Peking University**, Beijing, China (2000).

2) "Automated Analysis of Protein NMR Spectra: Development for Structural Genomics and Structure-Based Drug Design," **Cambridge Healthtech Institute's 2nd International Conference on NMR Technologies** (1999).

1) "Automated Analysis of Protein NMR Spectra: Development for Structural Genomics," **Intersections of Structural Biology & Genomics Symposium, Cornell Theory Center** (1999).

Poster Presentations

58) Tamas L. Nagy, Stacy R. Webb, Rebecca E. Dutch, Hunter Moseley. "Characterization of the Structural Constraints of Viral Type I Fusion Proteins", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

57) Sen Yao, Robert M. Flight, Eric C. Rouchka, Hunter N.B. Moseley. "A less biased analysis of metalloproteins reveals novel zinc coordination geometries", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

56) Andrey Smelter, Indraneel Reddy, Eric C. Rouchka, and Hunter N.B. Moseley. "Automated Assignment of Magic-Angle-Spinning Solid-State Protein NMR Spectra", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

55) Eugene W. Hinderer and Hunter N.B. Moseley. "Extracting subcellular localization from Gene Ontology", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

54) David R Henderson and Hunter N.B. Moseley. "Automated, iterative and scored assignment of metabolites via [1H]-NMR Spectral Peak Lists", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

53) William A. McCollam, Joshua M. Mitchell, and Hunter N.B. Moseley. "A graph database atom-resolved implementation of KEGG metabolic pathways", 14th Annual UT-KBRIN Bioinformatics Summit, Paris Landing, TN (2015).

52) Joshua M. Mitchell, Teresa W.-M. Fan, Andrew N. Lane, and Hunter N.B. Moseley. "Development and in silico Evaluation of Large-Scale Metabolite Identification Methods Using Functional Group Detection for Metabolomics", 249th American Chemical Society National Meeting & Exposition, Denver, Colorado (2015).

51) Joshua M. Mitchell, Teresa W.-M. Fan, Andrew N. Lane, and Hunter N.B. Moseley. "Development and in silico Evaluation of Large-Scale Metabolite Identification Methods Using Functional Group Detection for Metabolomics", American Society for Biochemistry and Molecular Biology Annual Meeting, Boston, Massachusetts (2015).

50) Stacy R. Webb, Tamas Nagy, Hunter N.B. Moseley, Mike Fried, & Rebecca E. Dutch. "Fusion protein TM-TM interactions: Modulators of pre-fusion protein stability", Physical Virology Gordon Research Conference, Ventura, California (2015).

49) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, Richard M. Higashi, and Hunter N.B. Moseley. "Development of Large-Scale Metabolite Identification Methods for Metabolomics", NIH Common Fund Annual Meeting – Metabolomics, Triangle, NH (2014).

48) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, Richard M. Higashi, and Hunter N.B. Moseley. "Development of Large-Scale Metabolite Identification Methods for Metabolomics", International Conference of the Metabolomics Society, Tsuruoka, Japan (2014).

47) Andrew N. Lane, Sengodagounder Arumugam, Pawel Lorkiewicz, Richard Higashi, Sebastien Laulhe, Michael Nantz, Hunter N.B. Moseley, Teresa W.-M. Fan. "Chemoselective detection of carbonyl compounds in metabolite mixtures by NMR", Markey Cancer Center Research Day, Lexington, KY (2014).

46) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, Richard M. Higashi, and Hunter N.B. Moseley. "Development of Large-Scale Metabolite Identification Methods for Metabolomics", Markey Cancer Center Research Day, Lexington, KY (2014).

45) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, Richard M. Higashi, and Hunter N.B. Moseley. "Development of Large-Scale Metabolite Identification Methods for Metabolomics", Bluegrass Biophysicla Symposium, Lexington, KY (2014).

44) Tamas L. Nagy, Rebecca E. Dutch, Hunter Moseley. "Investigating the Expanding Role of Transmembrane Domains in Enveloped Virus Entry." 13th Annual UT-KBRIN Bioinformatics Summit, Cadiz, KY (2014).

43) Sen Yao, Robert M. Flight, Hunter N.B. Moseley. "Coordination Characterization of Zinc Metalloproteins." 13th Annual UT-KBRIN Bioinformatics Summit, Cadiz, KY (2014).

42) Joshua M. Mitchell, Teresa W-.M. Fan, Andrew N. Lane, Richard M. Higashi, and Hunter N.B. Moseley. "Development of Large-Scale Metabolite Identification Methods for Metabolomics." 13th Annual UT-KBRIN Bioinformatics Summit, Cadiz, KY (2014).

41) Tamas Nagy, Rebecca E. Dutch, and Hunter N.B. Moseley. "Investigating the Expanding Role of Transmembrane Domains in Enveloped Virus Entry." National Conference on Undergraduate Research, Lexington, KY (2014).

40) Hunter N.B. Moseley. "Scaffolded Explicit Revision as a Practical Framework to Promote Effective Student Effort in Content-Rich Courses." 2013 I2A Institute: Sharing the Impact of Critical Thinking, Louisville, KY (2013).

39) Sen Yao, Tim D. Cook, and Hunter N.B. Moseley. "Coordination Characterization of Zinc Metalloproteins", UT-ORNL-KBRIN Bioinformatics Summit, Buchanan, TN (2013).

38) Joshua M. Mitchell and Hunter N.B. Moseley. "Computational Tools for the Identification of Detectable Uncharacterized Derivatized Metabolites within the Context of Known Metabolic Networks", UT-ORNL-KBRIN Bioinformatics Summit, Buchanan, TN (2013).

37) Pawel K. Lorkiewicz, Richard M. Higashi, Stephanie J. Mattingly, Michael H. Nantz, Hunter N. B. Moseley, Andrew N. Lane, Teresa W-M. Fan. "Chemoselective capture of carbonyl-containing metabolites for stable isotope resolved

metabolomic analysis of crude cell extracts by FTICR-MS", The Institute for Molecular Diversity & Drug Design (IMD³) 15th Annual Symposium, Louisville, KY (2013).

36) Andrew N. Lane, Sengodagounder Arumugam, Pawel Lorkiewicz, Richard M. Higashi, Sebastien Laulhe, Michael Nantz, Hunter N.B. Moseley, and Teresa W-M. Fan. "Chemoselective detection of carbonyl compounds in metabolite mixtures by NMR", Keystone Symposium: Frontiers of NMR in Biology, Snowbird, UT (2013).

35) Joshua M. Mitchell and Hunter N.B. Moseley. "Computational tools for the identification of detectable uncharacterized derivatized metabolites within the context of known metabolic networks", James Graham Brown Cancer Center 11th Annual Retreat, Louisville, Kentucky (2012).

34) Andrew N. Lane, Sengodagounder Arumugam, Pawel Lorkiewicz, Richard M. Higashi, Sebastien Laulhe, Michael Nantz, Hunter N.B. Moseley, and Teresa W-M. Fan. "Chemoselective detection of carbonyl compounds in metabolite mixtures by NMR", James Graham Brown Cancer Center 11th Annual Retreat, Louisville, KY (2012).

33) Alex Belshoff, Michael Bousamra, Teresa W-M. Fan, Richard M. Higashi, Andrew N. Lane, and Hunter N.B. Moseley. "Sodium Selenite alters metabolic pathways involved in UDP-GlcNAc synthesis in human lung cancer models", James Graham Brown Cancer Center 11th Annual Retreat, Louisville, KY (2012).

32) Eugene W. Hinderer and Hunter N.B. Moseley. "Retrieval of Enzyme Category and Subcellular Localization for Use in Metabolic Network Analysis", Kentucky Academy of Science Annual Meeting, Richmond, Kentucky (2012). **1st place undergraduate poster award.**

31) Alex Belshoff, Michael Bousamra, Teresa W-M. Fan, Richard M. Higashi, Andrew N. Lane, and Hunter N.B. Moseley. "Sodium Selenite alters metabolic pathways involved in UDP-GlcNAc synthesis in human lung cancer models", Research Louisville, Louisville, KY (2012).

30) Joshua M. Mitchell and Hunter N.B. Moseley. "Developing computational tools for metabolite identification in ultra-high resolution mass spectrometry data," Research Louisville, Louisville, Kentucky (2012). **2nd place undergraduate poster award.**

29) Joshua M. Mitchell and Hunter N.B. Moseley. "Developing computational tools for metabolite identification in ultra-high resolution mass spectrometry data," University of Louisville Undergraduate Research Symposium, Louisville, Kentucky (2012).

28) Sen Yao, Timothy D. Cook, Hunter N.B. Moseley. "Coordination characterization and function annotation trends of zinc metalloproteins," 11th Annual UT-ORNL-KBRIN Bioinformatics Summit, Louisville, Kentucky (2012).

27) Joshua M. Mitchell and Hunter N.B. Moseley. "Developing computational tools for metabolite identification in ultra-high resolution mass spectrometry data," 11th Annual UT-ORNL-KBRIN Bioinformatics Summit, Louisville, Kentucky (2012).

26) William J. Carreer and Hunter N.B. Moseley. "Correcting for the effects of natural abundance in stable isotope resolved metabolomics experiments involving multiple simultaneous isotopic labels and ultra-high resolution mass spectrometry," 11th Annual UT-ORNL-KBRIN Bioinformatics Summit, Louisville, Kentucky (2012).

25) Joshua M. Mitchell, Rima R. Patel, Rodney Folz Jr, Andrew McCollam, and Hunter N.B. Moseley. "Developing Computational Tools for Molecular Comparison and Metabolic Placement of Detectable Uncharacterized Metabolites," James Graham Brown Cancer Center 10th Annual Retreat, Louisville,KY (2011).

24) Anne Le, Max Hamaker, Joseph Barbi, Haixia Zhang, Lisa J. Zimmerman, Daniel C. Liebler, Robbert J.C. Slebos, Hunter Moseley, Richard M. Higashi, Andrew Lane, Teresa W. M. Fan and Chi V. Dang. "Myc induction of hypoxic glutamine metabolism and a glucose-independent TCA cycle in human B lymphocytes," AACR Metabolism and Cancer Conference, Baltimore, MD (2011)

23) Alex Belshoff, Andrew N. Lane, Hunter N.B. Moseley, Michael Bousamra, Richard M. Higashi, and Teresa W-M. Fan. "An Investigation of UDP-GlcNAc Synthesis in Human Lung Cancer with Perturbations by Selenium Compound Treatment", Research Louisville, Louisville, KY (2011).

22) Hunter N. B. Moseley, Lindsay J. Sperling, and Chad M. Rienstra. "Development of automated protein resonance assignment methods for magic angle spinning solid-state NMR," **Gordon Research Conference: Computational Aspects of Biomolecular NMR**, Lucca, Italy (2011).

21) Hunter N. B. Moseley, Lindsay J. Sperling, and Chad M. Rienstra. "Development of automated protein resonance assignment methods for magic angle spinning solid-state NMR," 10th Annual UT-ORNL-KBRIN Bioinformatics Summit, Memphis, Tennessee (2011).

20) Patrick Mullaney, Abigail Hoskins, and Hunter N.B. Moseley. "A Faster, More Efficient Library for Interfacing with the BMRB," 10th Annual UT-ORNL-KBRIN Bioinformatics Summit, Memphis, Tennessee (2011).

19) Tim D. Cook, Yao Sen, and Hunter N.B. Moseley. "Developing Computational Tools to Study Zinc's Functional Role in Proteins," Posters-at-the-Capitol, Lexington, Kentucky (2011).

18) Joshua M. Mitchell, Rima R. Patel, Rodney Folz Jr., and Hunter N.B. Moseley. "Developing Computational tools for Metabolite Molecular Comparison and Search," Posters-at-the-Capitol, Lexington, Kentucky (2011).

17) Hunter N.M. Moseley, Alex C. Belshoff, Richard M. Higashi, Teresa W-M. Fan, Andrew N. Lane. "Stable Isotope Resolved Metabolomics (SIRM) of UDP-GlcNAc and UDP-GalNAc Metabolism in Prostate Cancer," James Graham Brown Cancer Center 9th Annual Retreat, Louisville,KY (2010).

16) Hunter N.B. Moseley, N. Riaz, J.M. Aramini, T.A. Szyperski, and G.T. Montelione. "NMR Automation: From FIDS to Resonance Assignments using Peak Pattern Recognition of GFT NMR Data," **Gordon Research Conference: Computational Aspects of Biomolecular NMR**, Aussois, France (2006).

15) Hunter N.B. Moseley, Y.J. Huang, M.C. Baran, G. Sahota, D.A. Snyder, N. Riaz, D. Monleon, M. Bayro, J.M. Aramini, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "From Spectra to Resonance Assignments to Structure: Efforts in Automation of Protein NMR Data Analysis," Intl. Conf. on Structural Genomics, Washington, DC (2004).

14) Hunter N.B. Moseley, N. Riaz, J.M. Aramini, T.A. Szyperski, and G.T. Montelione. "A Generalized Approach to Automated NMR Peak List Editing: Application to Reduced Dimensionality Triple Resonance Spectra," **Gordon Research Conference: Computational Aspects of Biomolecular NMR**, Ventura, CA (2004).

13) Hunter N.B. Moseley, G. Sahota, M. Kiriyeva, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "AutoPeak/AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," Keystone Conference: Frontiers of NMR in Molecular Biology VIII, 130, Taos, NM (2003).

12) Hunter N.B. Moseley, G. Sahota, M. Kiriyeva, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," 43rd Exp. NMR Conf., Asilomar, CA (2002).

11) Hunter N.B. Moseley, G. Sahota, M. Kiriyeva, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," Keystone Conference: Structural Genomics: From Gene Sequence to Function, Breckenridge, Colorado (2002).

10) Hunter N.B. Moseley, G. Sahota, M. Kiriyeva, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," **Gordon Research Conference: Computational Aspects of Biomolecular NMR**, Lucca, Italy (2001).

9) Hunter N.B. Moseley, G. Sahota, M. Kiriyeva, G.V.T. Swapna, T.A. Szyperski, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," Keystone Symposium: Frontiers of NMR in Molecular Biology VII (2001).

8) Hunter N.B. Moseley, D.E. Zimmerman, G. Sahota, M. Kiriyeva, C.A. Kulikowski, G. Armhold, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," 41st Exp. NMR Conf., Asilomar, CA (2000).

7) Hunter N.B. Moseley, D.E. Zimmerman, C.A. Kulikowski, G. Armhold, and G.T. Montelione. "AutoAssign: An Expert System for Automated Analysis of Protein Resonance Assignments," 40th Exp. NMR Conf., Asilomar, CA (1999).

6) Hunter N.B. Moseley, K. Scheffler, N.R. Krishna, and T. Peters. 6th Annual F. L. Suddath Memorial Symposium, Atlanta, GA (1998). **1st place graduate student poster award.**

5) Hunter N.B. Moseley, W. Lee, C.H. Arrowsmith, and N.R. Krishna. 38th Exp. NMR Conf., Orlando, FL (1997).

4) Hunter N.B. Moseley and N.R. Krishna. 4th Annual F L. Suddath Memorial Symposium, Atlanta, GA (1996). **2nd place graduate student poster award.**

3) Hunter N.B. Moseley, E.V. Curto, and N.R. Krishna. "Complete Relaxation and Conformational Exchange Matrix (CORCEMA) Analysis of NOESY Spectra: Applications to Transferred NOESY and Protein Folding Studies," *Biophysical Journal* 68, A421 (1995).

2) Hunter N.B. Moseley, E.V. Curto, and N.R. Krishna. An International Symposium: NMR as a Structural Tool for Macromolecules, Indianapolis, IN (1994).

1) Hunter N.B. Moseley, E.V. Curto, and N.R. Krishna. 35th Exp. NMR Conf., Asilomar, CA (1994).