

## CURRICULUM VITAE

### **Nathan A. Yates, Ph.D.**

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### **Education:**

B.S. Allegheny College, Meadville, PA. Enrolled 1984 – 1988. Major in Chemistry.

Ph.D. University of Florida, Department of Chemistry, Gainesville, FL. Enrolled 1988 – 1993.  
Concentration in Analytical Chemistry.

### **Positions Held:**

- 1987 – 1988 Summer intern in the atmospheric chemistry lab of Dr. Allen Fried, National Institute of Science and Technology, Gaithersburg, MD
- 1988 – 1993 Graduate student in the laboratory of Dr. Richard A. Yost, University of Florida, Gainesville, FL
- 1989 – 1990 Industrial co-op student in the Research and Development Labs at Finnigan Corporation, San Jose CA
- 1993 – 1995 Postdoctoral Fellow in the laboratory of Dr. Donald F. Hunt, Department of Chemistry, University of Virginia, Charlottesville, VA
- 1995 – 2001 Sr. Research Chemist, Department of Molecular Design and Diversity, Merck Research Laboratories, Merck & Co. Inc., Rahway, NJ
- 2001 – 2004 Research Fellow, Department of Medicinal Chemistry, Merck Research Laboratories, Merck & Co. Inc., Rahway, NJ
- 2004 – 2010 Sr. Research Fellow, Molecular Profiling Department, Merck Research Laboratories, Merck & Co. Inc., Rahway, NJ
- 2010 – 2011 Scientific Director, Exploratory and Translations Science Department, Merck Research Laboratories, Merck & Co. Inc., Rahway, NJ
- 2011 – pres. Associate Professor, Department of Cell Biology, University of Pittsburgh School of Medicine, Pittsburgh, PA
- 2011 – pres. Director, Biomedical Mass Spectrometry Center, University of Pittsburgh School of the Health Sciences, Pittsburgh, PA

2011 – pres. Director, Cancer Proteomics Facility, University of Pittsburgh Cancer Institute, Pittsburgh, PA

**Professional Societies:**

1988 – pres. American Chemical Society  
 1992 – pres. American Society for Mass Spectrometry  
 2006 – 2009 The Association for Biomolecular Resource Facilities  
 2011 – 2012 United States Human Proteomics Organization

**Professional Service:**

2001 – 2004 *ad hoc* grant reviewer, NIH CSR S10 Shared Instrumentation Grant Program  
 2001 – pres. *ad hoc* reviewer for Analytical Chemistry  
 2002 – pres. *ad hoc* reviewer for Journal of the American Society for Mass Spectrometry  
 2004 *ad hoc* grant reviewer, NIH CSR S10 High End Instrumentation Grants Program  
 2004 – pres. *ad hoc* reviewer for Journal of Proteomics Research  
 2005 – 2006 Program Committee Member, The American Society for Mass Spectrometry  
 2006 Chair, Biomarkers for Drug Safety and Efficacy Oral Session, 54th ASMS Conference on Mass Spectrometry  
 2006 – 2007 *ad hoc* grant reviewer, NIH CSR S10 Shared Instrumentation Grant Program  
 2007 *ad hoc* reviewer for Proceedings of the National Academy of Science USA  
 2007 – 2008 Chair, Proteomics Research Group, Association of Biomolecular Resource Facilities  
 2008 – 2009 Chair, Merck Technology Coordinating Committee, Merck Research Laboratory  
 2009 Chair, Blue Sky Innovation Challenge, Merck Research Laboratory  
 2010 Discussion leader, Protein Based Biomarkers Oral Session, 12th Annual Symposium on Chemical and Pharmaceutical Structure Analysis  
 2010 – 2011 *ad hoc* grant reviewer, NIH CSR S10 Shared Instrumentation Grant Program  
 2010 – 2011 Board of Directors, US Human Proteome Organization  
 2011 *ad hoc* grant reviewer, NIH CSR S10 High End Instrumentation Grants Program  
 2011 Chair, Systems Biology/Cellular Pathway Oral Session, 59th ASMS Conference on Mass Spectrometry  
 2013 – 2015 Participant, NIH – Data Storage Repository Workshop  
 2015 *ad hoc* grant reviewer, NIH Biomedical Technology Research Resource (P41)

**Awards and Honors:**

1991 Kenan Analytical Chemistry Award, Union Carbide  
 1993 Shell Fellowship in Analytical Chemistry  
 1994 STA / NSF Fellowship Science and Technology Agency of Japan (declined)  
 2006 New Jersey Early Career Award in Mass Spectrometry, North Jersey American Chemical Society, Mass Spectrometry Discussion Group  
 2010 Distinguished Analytical Scientist Award, Chemical and Pharmaceutical Science Association

**Invited Lectures:**

06/03/1991 “Ion Trap” Future Leaders in Mass Spectrometry Seminar, 39th ASMS Conference on Mass Spectrometry, Nashville, TN

- 04/11/1995 “Quadrupole Ion Trap Mass Spectrometry: Instrumentation and Methods for Peptide Sequence Analysis”, Washington-Baltimore Mass Spectrometry Discussion Group, Rockville, MD
- 03/22/1998 “Ion Trap Applications in Combinatorial Chemistry” 49th Pittsburgh Conference and Exposition on Analytical Chemistry and Applied Spectroscopy, New Orleans, LA
- 01/17/1991 “A Rapid Screening Method for Evaluating Combinatorial Mixtures Based on Cross-Correlation of Measured and Predicted Electrospray Ionization Mass Spectra” East Tennessee Mass Spectrometry Discussion Group, Oak Ridge National Laboratory, Oak Ridge, TN
- 05/20/2000 “A Rapid Screening Method for Evaluating Combinatorial Mixtures Based on Cross-Correlation of Measured and Predicted Electrospray Ionization Mass Spectra” 33rd Middle Atlantic Regional ACS Meeting, Newark DE
- 04/03/2003 “Application of a Hybrid Linear Ion Trap / Fourier Transform Mass Spectrometer for Biomarker Discovery” National Institute of Health, Bethesda MD
- 06/07/2004 “End-to-End Data Analysis of Label Free Biomarker Experiments: Both Cross-Sectional and Longitudinal Designs” 54th ASMS Conference on Mass Spectrometry, Seattle WA
- 12/11/2004 “Application of Hybrid Linear Ion Trap / Fourier Transform Mass Spectrometry for Comparative Protein Profiling” Montreal Mass Spectrometry Discussion Group, Montreal, CA
- 02/10/2005 “LC-MS Profiling - New Capabilities for Quantitative Proteomics” 6th Iglers MS Tage, Iglers Austria
- 10/23/2006 “Protein-Based Biomarker Discovery - Concepts to Tools to Applications” 9th Annual Symposium on Chemical and Pharmaceutical Structure Analysis, Princeton NJ
- 01/14/2007 “Identification of Peptidase Substrates in Human Plasma by FTMS Based Differential Mass Spectrometry” Delaware Valley Mass Spectrometry Discussion Group, Villanova, PA
- 05/12/2007 “Exploratory Proteomics Studies Show Promise for Alzheimer's Disease” Merck Technology Symposium, Long Branch, NJ
- 06/01/2007 “Proteomics: From Basic Research to the Clinic” Thermo Fisher Scientific Users Meeting, 55th ASMS Conference on Mass Spectrometry, Indianapolis, IN
- 11/10/2007 “Proteomics: From Basic Research to the Clinic” Skirball Institute Structural Biology Seminar Series, New York University, NY
- 10/19/2008 “Differential Mass Spectrometry: Instruments, Analyses, and Applications” 11th Annual Symposium on Chemical and Pharmaceutical Structure Analysis, Langhorne, PA
- 02/16/2010 “High-Resolution ORBITrap-ETD for Characterization of Intact HDL Proteins” Advances in Molecular Mechanisms of Atherosclerosis symposium, Banff, Alberta CA
- 10/14/2010 “The development of a multi-column nanoHPLC system for enhanced productivity” New Objective Users Meeting, 13th Annual Symposium on Chemical and Pharmaceutical Structure Analysis, Langhorne, PA
- 12/08/2010 “Differential mass spectrometry identifies candidate markers for Alzheimer's Disease in humans” Greater Boston Area Mass Spectrometry Discussion Group, Cambridge MA

- 04/12/2013 “Application of an Unbiased Proteomic Platform for the Identification of Protein Markers in Cerebrospinal Fluid” Translational Neuroscience Program Seminar Series, Pittsburgh PA
- 04/21/2013 “The Proteomics Telescope - How Mass Spectrometry Is Changing Our View of the Proteome” Fudan University, Shanghai, China
- 04/22/2013 “Introduction to Differential Mass Spectrometry, Protein / Peptide Characterization and Quantitation Workshop” Shanghai Institute of Material Medica, Shanghai, China
- 12/11/2013 “The Proteomics Telescope – How Mass Spectrometry Is Changing Our View of the Proteome” LNBio - IV Proteomics Workshop, CNPEM Tutorial Lecture, Campinas Brazil
- 12/12/2013 “Differential Mass Spectrometry – Pharmaceutical Applications of Quantitative Proteomics” LNBio - IV Proteomics Workshop, CNPEM Tutorial Lecture, Campinas Brazil
- 03/05/2014 “Bridging the Gap Between Nanospray and Clinical Analysis: New Approaches for Automated Proteomics” Pittcon 2014, Chicago, IL
- 04/28/2014 “CHORUS: A Community-based Solution for the Storage, Analysis, and Exchange of Mass Spectrometry Data and Information” US HUPO 10th Annual Conference 2014, Seattle, WA
- 06/17/2014 “HighDef Proteomics – Advancing Differential Mass Spectrometry through Great Industry Partnerships” New Objective ASMS Breakfast, Baltimore MD
- 06/18/2014 “CHORUS: A Community-based Solution for the Storage, Analysis, and Exchange of Mass Spectrometry Data and Information” ASMS Workshop, Baltimore MD
- 08/25/2014 “MS in the Cloud” International Mass Spectrometry Conference, Geneva, Switzerland
- 09/19/2014 “ReThinking and ReCreating Scientific Data Analysis: Mass Spectrometry Moves Big Data to the Cloud” 2014 Cell Biology Retreat, Pittsburgh PA
- 10/01/2014 “Automated Multi-dimensional Multi-channel LC/LC-MS/MS For Increased Dynamic Range” CPSA 2014 USA Innovators Lecture, Langhorne, PA
- 10/01/2014 “Re-Thinking and Re-Creating the Modern Scientific Data Analysis Paradigm: Mass Spectrometry Moves Big Data to the Cloud” CPSA 2014 USA Thermo Fisher Lunch and Roundtable, Langhorne, PA
- 10/07/2014 “ReThinking and ReCreating Scientific Data Analysis: Mass Spectrometry Moves Big Data to the Cloud” Magee Women’s Research Institute, Pittsburgh PA
- 10/17/2014 “CHORUS: A Community-based Solution for the Storage, Analysis, and Exchange of Mass Spectrometry Data and Information” Presentation at Thermo Fisher, San Jose CA
- 10/29/2014 “Re-Thinking and Re-Creating the Modern Scientific Data Analysis Paradigm: Mass Spectrometry Moves Big Data to the Cloud” ACS Central Eastern Regional Meeting, Green Tree, PA
- 02/05/2015 “Proteomic Applications of Differential Mass Spectrometry From Basic Research to the Clinic” Presentation to Novartis Analytical Science Institute, Basel Switzerland
- 02/05/2015 “CHORUS - a Community Solution for the Storage, Visualization, Sharing, and Analysis of Mass Spectrometry Data” Presentation to Novartis Analytical Science Institute, Basel Switzerland

- 03/09/2015 “Software and Cloud-Based Applications for the Clinical Laboratory” Pittcon 2015, New Orleans, LA
- 04/12/2015 “Breaking the Megapixel Boundary with Multi-Dimensional Proteomic Analysis” Multi-Chromatographic Separation and Identification for Glyco-proteomics Tsinghua University, Shanghai, China
- 04/13/2015 “Continuous MUDPIT – Automated and Flexible Multi-Dimensional LC System for Comprehensive Proteomic Analysis” National Facility for Protein Science Shanghai (NCPSS), Shanghai, China
- 04/16/2015 “Mass Spectrometry Looks to Cloud Computing for Data Permanence and Re-Analysis” Pharmaceutical Structure Analysis Meeting, Shanghai, China
- 06/05/2015 “Identifying Proteins to which Small-Molecule Probes and Drugs Bind” Presentation to Merck Research Laboratories, Rahway NJ
- 06/26/2015 “The Proteomics Telescope - How Differential Mass Spectrometry Is Changing Our View of the Proteome” Senior Vice Chancellor's Research Seminar, Pittsburgh, PA
- 08/04/2015 “Differential Mass Spectrometry – Proteomics Applications in Basic, Translational, and Clinical Research” CPSA Brazil, São Paulo, Brazil
- 09/21/2015 “Development and Application of Differential Mass Spectrometry As An Enabling Technology For Biomarker Discovery and Drug Development” ISPROF 2015, Caparica-Lisbon, Portugal
- 10/06/2015 “Simplifying Complex Workflows for Larger Scale and Speed” CPSA 2015 USA, Langhorne, PA
- 10/29/2015 “Proteomic Profiling via Label Free Differential Mass Spectrometry” Sanofi US, Cambridge, MA
- 11/11/2015 “Elucidation of Proteins that Bind Small Molecule Drugs via Chemical Proteins” Drug Discovery Institute, External Advisory Board, Pittsburgh, PA
- 11/23/2015 “Differential Mass Spectrometry – An Enabling Technology For Biomarker Discovery and Drug Development” Albert Einstein College of Medicine, Bronx, NY
- 12/03/2015 “Discovering Drug-Protein Interactions by Proteomics” MBSB Seminar, University of Pittsburgh, Pittsburgh, PA
- 12/10/2015 “Differential Mass Spectrometry – An Enabling Technology For Biomarker Discovery and Drug Development” University of South Alabama Mitchell Cancer Institute, Mobile, AL
- 3/23/2016 “MS Bioinformatics in the Cloud: CHORUS and Beyond” CPSA Metabolomics, Gainesville, FL
- 4/17/2016 “Development and Application of Differential Mass Spectrometry as an Enabling Technology for Biomarker Discovery and Drug Development” 1<sup>st</sup> PHOENIX Mini-Symposium on Frontiers of Proteomics, Beijing, China
- 5/18/2016 “Emerging Issues and Needs with Personalized Healthcare: Pittsburgh Pirates and Performance Analytics” Mozaic Solutions Annual Meeting, Pittsburgh PA
- 5/20/2016 “High-Resolution Mass Spectrometry Discovering Molecular Profiles in Previously Un-Analyzed Data” CPSA Analytics, Pittsburgh, PA
- 6/5/2016 “Benefits of Larger Studies in Discovery Proteomics” New Objective ASMS Users Meeting, San Antonio, TX

**Research Funding Information:**Current Grants

1. P30 CA047904 24 (Davidson) 08/01/2010 – 07/31/2020  
NIH/NCI  
Cancer Center Support Grant (Cancer Biomarkers Facility)  
The major goals of this project are to develop and apply mass spectrometry based proteomics for the discovery and translation of cancer biomarkers.  
Role: Co-investigator
2. 1 P01 AG043376-01A1 (Robbins) 07/01/2013 – 06/30/2018  
NIH/NIA  
Cell Autonomous and Non-Autonomous Mechanisms of Aging  
Dr. Yates will direct all proteomic approaches to identify factors secreted by senescent cells, stem cells and circulating factors for all three projects.  
Role: Core Leader / Co-investigator
3. 2 R01MH071533-11 (Sweet) 04/01/2014 – 03/31/2019  
NIH  
Plasticity of Auditory Cortical Circuits in Schizophrenia  
The purpose of this application is to apply modern quantitative proteomic techniques to the analysis of post-mortem brain tissue from subjects with schizophrenia.  
Role: Co-investigator
4. 1 R01AR065445-01 (Huard) 04/01/2014 – 03/31/2019  
NIH  
Bone Abnormalities & Healing Defect in Muscular Dystrophy  
This proposal aims to determine the nature of skeletal system defects and characterize whether the progressive bone histopathology observed in a mouse model of muscular dystrophy is driven by stem cell abnormalities. Dr. Yates will direct the proteomic analyses of a series of stem cell pools.  
Role: Co-investigator
5. P50 AG05133 (Sweet) 04/01/2015 – 03/31/2020  
NIA  
Alzheimer's Disease Research Center
6. R01 DE024728 (Johnson) 01/01/2016 – 12/30/2020  
NIH  
Implications of Procaspase-8 mutations in oral squamous cell

Expired Grants (listed chronologically)

1. R21 EB017184 (Isenberg) 04/01/2014 – 03/31/2016

NIH

Bioengineering Tracheas through Targeting Activated CD47

This proposal will investigate newly-identified signaling pathways and the role that they play in limiting cellular and tissue regeneration, engraftment and tracheal angiogenesis.

Role: Co-investigator

2. 1 S10 OD018071-01 (Yates) 07/01/2014 – 06/30/2015

NIH

Request for triple quadrupole mass spectrometer for the University of Pittsburgh

The purpose of this application is to obtain a shared instrument for metabolite analysis.

Role: Principal Investigator

### Courses taught:

- 2002 – 2005 Peptide Sequencing and Protein Identification by  $\mu$ LC/MS/MS Ion Trap Mass Spectrometry, Chemical and Pharmaceutical Structure Analysis (2-day short course)
- 2004 – 2007 Quadrupole Ion Trap Mass Spectrometry, American Society of Mass Spectrometry (2-day short course)
- 2008 – 2013 Case Studies in Quantitative Proteomics, American Society of Mass Spectrometry. (2-day short course)
- 2010 Proteomics, Concepts in Biotechnology and Genomics. Master's in Business and Science: Biotechnology and Genomics Track, Rutgers University (invited lecture)
- 2010 Proteomics: Technology and Applications, B.S. / M.S. Biotech Program at Kean University (invited lecture).
- 2010 – 2013 Applications of Proteomics to the Clinical Labs: Applications to the Clinical Laboratory (2-day short course)
- 2013 – 2015 Basics of Personalized Medicine, MSCMP 3790, University of Pittsburgh School of Medicine, (invited lecture).
- 2013 – 2015 Chemical Separations, Chem 2220, University of Pittsburgh, (invited lecture).
- 2013 – 2015 Structural Biophysics, University of Pittsburgh and Carnegie Mellon University, (two invited lectures).
- 2014 Drug Discovery, University of Pittsburgh, School of Medicine (invited lecture).

### Advisory or supervisory responsibilities:

- 1995 – 2011 Supervised masters and doctoral level chemists, bioanalytical chemists, statisticians, computer scientists, project managers and administrative staff at Merck and Co. Inc., Rahway NJ.
- 2011 – pres. Directed staff scientists, technicians, and administrative staff in the Biomedical Mass Spectrometry Center at the University of Pittsburgh, Pittsburgh PA.
- 2011 – pres. Supervised graduate students and post-doctoral fellows at the University of Pittsburgh, Pittsburgh PA.

**Trainees/Advisees:**

| <u>Years supervised</u> | <u>Name</u>                 | <u>Subsequent (or current) position</u>       |
|-------------------------|-----------------------------|---|
| 2007 – 2010             | Nykia Walker, M.S.          | Graduate Student, Kean University             |
| 2013 – pres.            | Matthew MacDonald, Ph.D.    | Assistant Professor, University of Pittsburgh |
| 2013 – pres.            | Melanie Grubisha, M.D.Ph.D. | Resident, University of Pittsburgh            |
| 2013 – 2015             | Jamil Alhassan, B.S.        | Medical Student, University of Pittsburgh     |
| 2014 – pres.            | Harris Bell-Temin Ph.D.     | Postdoc., University of Pittsburgh            |
| 2015 – pres.            | Christina King, M.S.        | Graduate Student, University of Pittsburgh    |

Individual Fellowships awarded to trainees:

1. NIH K01 MH107756-01 to Matthew MacDonald (co-mentor)  
Title: ATP1A3 Induced Alterations to Glutamate Signaling Protein Networks in Schizophrenia

**PUBLICATIONS****Peer-reviewed Original Research Articles:**

1. Fried A, Nunnermacker L, Cadoff B, Sams R, Yates N, Dorko W, Dickerson R, Winstead E. Reference No2 Calibration System for Ground-Based Intercomparisons during Nasas Gte/Cite-2 Mission. *J Geophys Res-Atmos.* 1990 Jun 20;95(D7):10139-46. PubMed PMID: WOS:A1990DM73600029. English.
2. Kim RM, Manna M, Hutchins SM, Griffin PR, Yates NA, Bernick AM, Chapman KT. Dendrimer-supported combinatorial chemistry. *Proceedings of the National Academy of Sciences of the United States of America.* 1996 Sep 17;93(19):10012-7. PubMed PMID: 11607705. Pubmed Central PMCID: 38327.
3. Esser CK, Kevin NJ, Yates NA, Chapman KT. Solid-phase synthesis of a N-carboxyalkyl tripeptide combinatorial library. *Bioorg Med Chem Lett.* 1997 Oct 21;7(20):2639-44. PubMed PMID: WOS:A1997YF10500017. English.
4. Yates N, Wislocki D, Roberts A, Berk S, Klatt T, Shen DM, Willoughby C, Rosauer K, Chapman K, Griffin P. Mass spectrometry screening of combinatorial mixtures, correlation of measured and predicted electrospray ionization spectra. *Analytical chemistry.* 2001 Jul 1;73(13):2941-51. PubMed PMID: WOS:000169660100027. English.
5. Guan Z, Yates NA, Bakhtiar R. Detection and characterization of methionine oxidation in peptides by collision-induced dissociation and electron capture dissociation. *Journal of the American Society for Mass Spectrometry.* 2003 Jun;14(6):605-13. PubMed PMID: 12781462.
6. Mehl JT, Cummings JJ, Rohde E, Yates NN. Automated protein identification using atmospheric-pressure matrix-assisted laser desorption/ionization. *Rapid Commun Mass Sp.* 2003;17(14):1600-10. PubMed PMID: WOS:000184039400012. English.



7. Wiener MC, Sachs JR, Deyanova EG, Yates NA. Differential mass spectrometry: a label-free LC-MS method for finding significant differences in complex peptide and protein mixtures. *Analytical chemistry*. 2004 Oct 15;76(20):6085-96. PubMed PMID: 15481957.
8. Paweletz CP, Wiener MC, Sachs JR, Meurer R, Wu MS, Wong KK, Yates NA, Hendrickson RC. Surface enhanced laser desorption ionization spectrometry reveals biomarkers for drug treatment but not dose. *Proteomics*. 2006 Apr;6(7):2101-7. PubMed PMID: 16518871.
9. Bunger MK, Cargile BJ, Sevinsky JR, Deyanova E, Yates NA, Hendrickson RC, Stephenson JL, Jr. Detection and validation of non-synonymous coding SNPs from orthogonal analysis of shotgun proteomics data. *Journal of proteome research*. 2007 Jun;6(6):2331-40. PubMed PMID: 17488105.
10. Meng F, Wiener MC, Sachs JR, Burns C, Verma P, Paweletz CP, Mazur MT, Deyanova EG, Yates NA, Hendrickson RC. Quantitative analysis of complex peptide mixtures using FTMS and differential mass spectrometry. *Journal of the American Society for Mass Spectrometry*. 2007 Feb;18(2):226-33. PubMed PMID: 17070068.
11. Turck CW, Falick AM, Kowalak JA, Lane WS, Lilley KS, Phinney BS, Weintraub ST, Witkowska HE, Yates NA, Association of Biomolecular Resource Facilities Proteomics Research G. The Association of Biomolecular Resource Facilities Proteomics Research Group 2006 study: relative protein quantitation. *Molecular & cellular proteomics : MCP*. 2007 Aug;6(8):1291-8. PubMed PMID: 17513294.
12. Yates NA, Deyanova EG, Geissler W, Wiener MC, Sachs JR, Wong KK, Thornberry NA, Roy RS, Settlage RE, Hendrickson RC. Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry. *Int J Mass Spectrom*. 2007 Jan 1;259(1-3):174-83. PubMed PMID: WOS:000243180300022. English.
13. Lee AY, Paweletz CP, Pollock RM, Settlage RE, Cruz JC, Secrist JP, Miller TA, Stanton MG, Kral AM, Ozerova ND, Meng F, Yates NA, Richon V, Hendrickson RC. Quantitative analysis of histone deacetylase-1 selective histone modifications by differential mass spectrometry. *Journal of proteome research*. 2008 Dec;7(12):5177-86. PubMed PMID: 19367703.
14. Sevinsky JR, Cargile BJ, Bunger MK, Meng F, Yates NA, Hendrickson RC, Stephenson JL, Jr. Whole genome searching with shotgun proteomic data: applications for genome annotation. *Journal of proteome research*. 2008 Jan;7(1):80-8. PubMed PMID: 18062665.
15. Zhao X, Deyanova EG, Lubbers LS, Zafian P, Li JJ, Liaw A, Song Q, Du Y, Settlage RE, Hickey GJ, Yates NA, Hendrickson RC. Differential mass spectrometry of rat plasma reveals proteins that are responsive to 17beta-estradiol and a selective estrogen receptor modulator PPT. *Journal of proteome research*. 2008 Oct;7(10):4373-83. PubMed PMID: 18785765.
16. Mazur MT, Cardasis HL, Spellman DS, Liaw A, Yates NA, Hendrickson RC. Quantitative analysis of intact apolipoproteins in human HDL by top-down differential mass spectrometry. *Proceedings of the National Academy of Sciences of the United States of America*. 2010 Apr 27;107(17):7728-33. PubMed PMID: 20388904. Pubmed Central PMCID: 2867874.
17. Paweletz CP, Wiener MC, Bondarenko AY, Yates NA, Song Q, Liaw A, Lee AY, Hunt BT, Henle ES, Meng F, Sleph HF, Holahan M, Sankaranarayanan S, Simon AJ, Settlage RE, Sachs JR, Shearman M, Sachs AB, Cook JJ, Hendrickson RC. Application of an end-to-end biomarker discovery platform to

- identify target engagement markers in cerebrospinal fluid by high resolution differential mass spectrometry. *Journal of proteome research*. 2010 Mar 5;9(3):1392-401. PubMed PMID: 20095649.
18. Sietsema KE, Meng F, Yates NA, Hendrickson RC, Liaw A, Song Q, Brass EP, Ulrich RG. Potential biomarkers of muscle injury after eccentric exercise. *Biomarkers : biochemical indicators of exposure, response, and susceptibility to chemicals*. 2010 May;15(3):249-58. PubMed PMID: 20028270.
  19. Zhao X, Southwick K, Cardasis HL, Du Y, Lassman ME, Xie D, El-Sherbeini M, Geissler WM, Pryor KD, Verras A, Garcia-Calvo M, Shen DM, Yates NA, Pinto S, Hendrickson RC. Peptidomic profiling of human cerebrospinal fluid identifies YPRPIHPA as a novel substrate for prolylcarboxypeptidase. *Proteomics*. 2010 Aug;10(15):2882-6. PubMed PMID: 20517885.
  20. Chen F, Lam R, Shaywitz D, Hendrickson RC, Opiteck GJ, Wishengrad D, Liaw A, Song Q, Stewart AJ, Cummings CE, Beals C, Yarasheski KE, Reicin A, Ruddy M, Hu X, Yates NA, Menetski J, Herman GA. Evaluation of early biomarkers of muscle anabolic response to testosterone. *Journal of cachexia, sarcopenia and muscle*. 2011 Mar;2(1):45-56. PubMed PMID: 21475673. Pubmed Central PMCID: 3063869.
  21. Falick AM, Lane WS, Lilley KS, MacCoss MJ, Phinney BS, Sherman NE, Weintraub ST, Witkowska HE, Yates NA. ABRF-PRG07: advanced quantitative proteomics study. *Journal of biomolecular techniques : JBT*. 2011 Apr;22(1):21-6. PubMed PMID: 21455478. Pubmed Central PMCID: 3059538.
  22. Friedman DB, Andacht TM, Bunger MK, Chien AS, Hawke DH, Krijgsveld J, Lane WS, Lilley KS, MacCoss MJ, Moritz RL, Settlege RE, Sherman NE, Weintraub ST, Witkowska HE, Yates NA, Turck CW. The ABRF Proteomics Research Group studies: educational exercises for qualitative and quantitative proteomic analyses. *Proteomics*. 2011 Apr;11(8):1371-81. PubMed PMID: 21394914.
  23. Conway JP, Johns DG, Wang SP, Walker ND, McAvoy TA, Zhou H, Zhao X, Previs SF, Roddy TP, Hubbard BK, Yates NA, Hendrickson RC. Measuring H(2)(18)O tracer incorporation on a QQQ-MS platform provides a rapid, transferable screening tool for relative protein synthesis. *Journal of proteome research*. 2012 Mar 2;11(3):1591-7. PubMed PMID: 22289114.
  24. Lee AY, Yates NA, Ichetovkin M, Deyanova E, Southwick K, Fisher TS, Wang W, Loderstedt J, Walker N, Zhou H, Zhao X, Sparrow CP, Hubbard BK, Rader DJ, Sitlani A, Millar JS, Hendrickson RC. Measurement of fractional synthetic rates of multiple protein analytes by triple quadrupole mass spectrometry. *Clinical chemistry*. 2012 Mar;58(3):619-27. PubMed PMID: 22249652.
  25. Wang W, Walker ND, Zhu LJ, Wu W, Ge L, Gutstein DE, Yates NA, Hendrickson RC, Ogletree ML, Cleary M, Opiteck GJ, Chen Z. Quantification of circulating D-dimer by peptide immunoaffinity enrichment and tandem mass spectrometry. *Analytical chemistry*. 2012 Aug 7;84(15):6891-8. PubMed PMID: 22788854.
  26. Huang F, Zeng X, Kim W, Balasubramani M, Fortian A, Gygi SP, Yates NA, Sorkin A. Lysine 63-linked polyubiquitination is required for EGF receptor degradation. *Proceedings of the National Academy of Sciences of the United States of America*. 2013 Sep 24;110(39):15722-7. PubMed PMID: 24019463. Pubmed Central PMCID: 3785728.
  27. Antony ML, Lee J, Hahm ER, Kim SH, Marcus AI, Kumari V, Ji X, Yang Z, Vowell CL, Wipf P, Uechi GT, Yates NA, Romero G, Sarkar SN, Singh SV. Growth arrest by the antitumor steroidal

- lactone withaferin A in human breast cancer cells is associated with down-regulation and covalent binding at cysteine 303 of beta-tubulin. *The Journal of biological chemistry*. 2014 Jan 17;289(3):1852-65. PubMed PMID: 24297176. Pubmed Central PMCID: 3894360.
28. Chappell DL, Lee AY, Castro-Perez J, Zhou H, Roddy TP, Lassman ME, Shankar SS, Yates NA, Wang W, Laterza OF. An ultrasensitive method for the quantitation of active and inactive GLP-1 in human plasma via immunoaffinity LC-MS/MS. *Bioanalysis*. 2014 Jan;6(1):33-42. PubMed PMID: 24341493.
  29. Wang W, Choi BK, Li W, Lao Z, Lee AY, Souza SC, Yates NA, Kowalski T, Poci A, Cohen LH. Quantification of intact and truncated stromal cell-derived factor-1alpha in circulation by immunoaffinity enrichment and tandem mass spectrometry. *Journal of the American Society for Mass Spectrometry*. 2014 Apr;25(4):614-25. PubMed PMID: 24500701.
  30. Miedel MT, Zeng X, Yates NA, Silverman GA, Luke CJ. Isolation of serpin-interacting proteins in *C. elegans* using protein affinity purification. *Methods*. 2014 Aug 1;68(3):536-41. PubMed PMID: 24798811. Pubmed Central PMCID: 4113314.
  31. Strickler AG, Vasquez JG, Yates N, Ho J. Potential diagnostic significance of HSP90, ACS/TMS1, and L-plastin in the identification of melanoma. *Melanoma research*. 2014 Sep 4. PubMed PMID: 25191796.
  32. Fang Q, Inanc B, Schamus S, Wang XH, Wei L, Brown AR, Svilar D, Sugrue KF, Goellner EM, Zeng X, Yates NA, Lan L, Vens C, Sobol RW. HSP90 regulates DNA repair via the interaction between XRCC1 and DNA polymerase beta. *Nature communications*. 2014;5:5513. PubMed PMID: 25423885. Pubmed Central PMCID: 4246423.
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