BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Nathan A. Yates	Associate Professor Department of Cell Biology
eRA COMMONS USER NAME (credential, e.g., agency login) NYATES	Scientific Director Biomedical Mass Spectrometry Center

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Allegheny College, Meadville PA	BS	06/88	Chemistry
University of Florida, Gainesville FL	PhD	05/93	Analytical Chemistry
University of Virginia, Charlottesville VA	Postdoctoral	11/95	Bio-analytical Chemistry

A. Personal Statement

My 25 plus years of experience with mass spectrometry have afforded me numerous opportunities to advance academic, government, and industrial science through the development and application of new molecular analysis methods. I received my bio-analytical training in the laboratories of Professors Richard A. Yost and Donald F. Hunt. Professor Yost invented the triple quadrupole mass spectrometer and demonstrated the use of selected reaction monitor for ultra-trace level analysis. Professor Hunt is a pioneer in the development and application of biological mass spectrometry and my work in his laboratory contributed to adoption of ion trap mass spectrometry as a new disruptive technology for proteomics. As a Scientific Director at Merck & Co., Inc., I led a large industrialized mass spectrometry laboratory in the Department of Exploratory and Translational Sciences that was responsible for the discovery and translation of new biomarker assays. During my tenure at Merck, I invented Differential Mass Spectrometry (dMS), an efficient MS based strategy for comparing complex biological systems that permits un-biased analysis of all ions detected in full scan mass spectra, not just ions that have corresponding tandem mass spectra and peptide sequences. The dMS platform has been used to discover protein-based biomarkers for Alzheimer's disease, diabetes, and cancer. In collaboration with Rosetta Biosoftware, I commercialized the dMS approach as part of the Elucidator™ proteomics analysis suite that was later acquired by Microsoft Corporation. At the University of Pittsburgh, I am an Associate Professor in the Department of Cell Biology. My research continues to focus on innovative laboratory techniques and data analysis methods for the analysis of biologically relevant proteins. One practical output of my research has been the development of quantitative translational assays for clinic, including the measurement of GLP-1 in human plasma, the intact measurement of D-Dimer, and the kinetic analysis of Apo lipoproteins related to atherosclerosis. In collaboration with public and private partners, I have also developed a global cloud computing solution that is used by the top mass spectrometry laboratories around the world. The CHORUS platform enables mass spectrometry discoveries to be shared and communicated around the world by making large scale comparisons of mass spectrometry data easy. I am active in the scientific community as a regular member of NIH shared instrument grant study sections, a short course instructor at the ASMS annual meeting, and a former chair of the ABRF proteomics research group. As the Scientific Director of the Biomedical Mass Spectrometry (BioMS) Center I enjoy collaborating with scientists from other fields and advancing new methods for measuring biology.

B. Positions and Employment

1986,1987	Summer Internship, National Institute of Science and Technology
1988-1993	Research Assistant, University of Florida, Professor Richard A. Yost
1990	Graduate Co-op Student, Finnigan Corporation
1990	Visiting Scientist, Kennedy Space Flight Center
1993-1995	Postdoctoral Fellowship, University of Virginia, Professor Donald F. Hunt
1995-2001	Senior Research Chemist, Molecular Design and Diversity Dept., Merck & Co., Inc.
2001-2004	Research Fellow, Department of Medicinal Chemistry, Merck & Co., Inc.
2004-2010	Senior Research Fellow, Molecular Profiling Department, Merck & Co. Inc.
2011	Scientific Director, Exploratory and Translations Science Department, Merck & Co., Inc.
2011-present	Associate Professor, Department of Cell Biology, University of Pittsburgh
2011-present	Scientific Director, Biomedical Mass Spectrometry Center, University of Pittsburgh

Awards and honors

1991 Kenan Analytical Chemistry Award, Union Carbide; 1993 Shell Fellowship in Chemistry; 1994 STA/NSF Fellowship, Science and Technology Agency of Japan (declined); 2006 New Jersey Early Career Award in Mass Spectrometry, New Jersey ACS; 2012 Chemical and Pharmaceutical Structure Analysis - Distinguished Analytical Scientist.

Patents

1991: Method of operating an ion trap mass spectrometer to determine the resonant frequency of trapped ions, **Yates NA**, Bradshaw SC, Yost RA, Tucker DB, *U.S. Pat. No.* 5,128,542

2004: Mass spectrometry data analysis techniques, Sachs JR, Wiener MC, **Yates NA**, *U.S. Pat. No.* 6,906,320

C. Selected Peer-reviewed Publications (in reverse chronological order)

1. Strickler AG, Vasquez JG, **Yates N**, Ho J. Potential diagnostic significance of HSP90, ACS/TMS1, and L-plastin in the identification of melanoma. Melanoma Res. 2014 Dec;24(6):535-44. PubMed PMID: 25191796.

2. Fang Q, Inanc B, Schamus S, Wang XH, Wei L, **Yates NA** et al. HSP90 regulates DNA repair via the interaction between XRCC1 and DNA polymerase β. Nat Commun. 2014 Nov 26;5:5513. PubMed PMID: 25423885.
3. MacDonald ML, Ding Y, Newman J, Hemby S, Penzes P, **Yates NA** et al. Altered Glutamate Protein Co-Expression Network Topology Linked to Spine Loss in the Auditory Cortex of Schizophrenia. Biol Psychiatry. 2014 Nov 26;PubMed PMID: 25433904.
4. 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.
5. Wang W, Choi BK, Li W, Lao Z, Lee AY, Souza SC, **Yates NA**, Kowalski T, Pocai A, Cohen LH. Quantification of Intact and Truncated Stromal Cell-Derived Factor 1α in Circulation by Immunoaffinity Enrichment and Tandem Mass Spectrometry. J Am Soc Mass Spectrom. 2014 Feb 6; 25(4): 614-25. PMID: 24500701. PMCID: not applicable.

6. 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 β-Tubulin. J Biol Chem. 2014 Jan 17;289(3):1852-65. PMID: 24297176. PMCID: PMC3894360.

7. 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. Proc Natl Acad Sci USA. 2013 Sep 24;110(39):15722-7. PMID: 24019463. PMCID: PMC3785728. PMCID: PMC3785728.

8. 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. Anal Chem. 2012 Aug 7;84(15):6891-8. PMID: 22788854. PMCID: not applicable.

9. 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. Clin Chem. 2012 Mar;58(3):619-27. PMID: 22249652. PMCID: not applicable.

10. 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 H218O Tracer Incorporation on a QQQ-MS Platform Provides a Rapid, Transferable Screening Tool for Relative Protein Synthesis. J Proteome Res. 2012 Mar 2;11(3):1591-7. PMID: 22289114. PMCID: not applicable.

11. Friedman DB, Andacht TM, Bunger MK, Chien AS, Hawke DH, Krijgsveld J, Lane WS, Lilley KS, MacCoss MJ, Moritz RL, Settlage 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. PMID: 21394914. PMCID: not applicable.

12. 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. Proc Natl Acad Sci USA. 2010 Apr 27;107(17):7728-33. PMID: 20388904. PMCID: PMC2867874.

13. 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. J Proteome Res. 2010 Mar 5;9(3):1392-401. PMID: 20095649. PMCID: not applicable.

14. 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. J Proteome Res. 2008 Dec 5;7(12):5177-86. PMID: 19367703. PMCID: not applicable.

15. Turck CW, Falick AM, Kowalak JA, Lane WS, Lilley KS, Phinney BS, Weintraub ST, Witkowska HE, **Yates NA.** The Association of Biomolecular Resource Facilities Proteomics Research Group 2006 study: relative protein quantitation. Mol Cell Proteomics. 2007 Aug;6(8):1291-8. PMID: 17513294. PMCID: not applicable.

16. **Yates NA**, Deyanova EG, Geissler WM, 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):174-83. DOI 10.1016/j.ijms.2006.09.020

17. 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. Anal Chem. 2004 Sep 17;76(20):6085-96. PMID: 15481957. PMCID: not applicable.

18. 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. J Am Soc Mass Spectrom. 2007 Feb;18(2):226-33. PMID: 17070068. PMCID: not applicable.

19. Kim RM, Manna M, Hutchins SM, Griffin PR, **Yates NA**, Bernick AM, Chapman KT. Dendrimer-supported combinatorial chemistry. Proc Natl Acad Sci USA. 1996 Sep 17;93(19):10012-7. PMID: 11607705. PMCID: PMC38327.

F. Research Support

ACTIVE

P30 CA047904 24 (Davidson) **08/01/2010 – 07/31/2015**
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

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: Co-investigator

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

1 S10 OD018071-01 (Yates) **04/01/2014 – 03/31/2015**
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

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

1 R01AR065445-01 (Huard) **04/01/2016 – 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

PENDING

P50 AG05133 (Sweet) **04/01/2015 – 03/31/2020**
NIA
Alzheimer's Disease Research Center
This proposal aims to determine the Neuropathology of Psychosis in AD Dr. Yates will direct the proteomic analyses, apply novel data analysis methods, and assist in the publication and communication of results.
Role: Co-investigator