

BIOGRAPHICAL SKETCH

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| | | | |
|---|------------------------------------|---------|----------------|
| NAME Philip C. Andrews | POSITION TITLE Professor | | |
| eRA COMMONS USER NAME (credential, e.g., agency login) andrewsp | | | |
| EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i> | | | |
| INSTITUTION AND LOCATION | DEGREE <i>(if applicable)</i> | YEAR(s) | FIELD OF STUDY |
| Georgia Institute of Technology, Atlanta, GA | B.S. | 1973 | Chemistry |
| Purdue University, West Lafayette, IN | Ph.D. | 1977 | Biochemistry |
| Purdue University, West Lafayette, IN | Postdoc | 1978-87 | Biochemistry |

A. Positions and Honors

Positions and Employment

- 1973–1975 Analyst for Indiana State Chemist, West Lafayette, IN
- 1976 Teaching Assistant, Department of Biochemistry, Purdue University, West Lafayette, IN
- 1976–1978 Research Assistant, Department of Biochemistry, Purdue University, West Lafayette, IN
- 1978–1987 Research Associate, Department of Biochemistry, Purdue University, West Lafayette, IN
- 1978–1990 Assistant Research Scientist, Dept. of Biochemistry, Purdue University, West Lafayette, IN
- 1988–1990 Director of the Laboratory for Macromolecular Structure, Purdue University, West Lafayette, IN
- 1990–1996 Associate Professor, Dept. of Biological Chemistry, University of Michigan, Ann Arbor, MI
- 1990–2001 Director of the Protein Structure Facility, University of Michigan, Ann Arbor, MI
- 1996–2004 Professor and Research Professor, Dept. of Biol. Chem., University of Michigan, Ann Arbor, MI
- 2001–2009 Director of the Michigan Proteome Consortium, Ann Arbor, MI
- 2002-2008 Instructor, Proteomics Workshop, Cold Spring Harbor Laboratory
- 2003-2009 Director of the National Resource for Pathways & Proteomics, University of Michigan
- 2004-present Professor of Biological Chemistry, University of Michigan, Ann Arbor, MI

B. Selected peer-reviewed publications (in chronological order)

92. Walker AK, Rymar G, Andrews PC: Mass spectrometric imaging of immobilized pH gradient gels and creation of "virtual" two-dimensional gels. *Electrophoresis* 22: 933-45, 2001.
93. Phadke, N.D., Molloy, M.P., Steinhoff, S.A., Ulintz, P.J., Andrews, P.C., Maddock, J.R Analysis of the outer membrane proteome of *Caulobacter crescentus* by two-dimensional electrophoresis and mass spectrometry. *Proteomics* 1: 705-720, 2001.
94. Loo, R.R., Cavalcoli, J.D., VanBogelen, R.A., Mitchell, C., Loo, J.A., Moldover, B., and Andrews, P.C. Virtual 2D gel electrophoresis: Visualization and analysis of the *E. coli* proteome by mass spectrometry. *Anal. Chemistry* 73: 4063-4070, 2001.
95. Molloy, M. P. and Andrews, P.C. Phosphopeptide derivatization signatures to identify serine and threonine phosphorylated peptides by mass spectrometry. *Anal Chem.* 73: 5387-94, 2001.
96. Molloy, M.P., Phadke, N.D., Chen, H., Tyldesley, R., Garfin, D.E., Maddock, J.M., Andrews, P.C. Profiling the alkaline membrane proteome of *Caulobacter crescentus* with two-dimensional electrophoresis and mass spectrometry. *Proteomics* 2: 899-910, 2002.
97. Ge Y, Molloy MP, Chamberlain JS, Andrews PC. Proteomic analysis of mdx skeletal muscle: Great reduction of adenylate kinase 1 expression and enzymatic activity. *Proteomics*.3:1895-903, 2003.
98. Ge Y, Molloy MP, Chamberlain JS, Andrews PC. Differential expression of the skeletal muscle proteome in mdx mice at different ages. *Electrophoresis.* 25:2576-85, 2004.
100. Chen X, Li C, Izumi T, Ernst SA, Andrews PC, Williams JA. Rab27b localizes to zymogen granules and regulates pancreatic acinar exocytosis. *Biochem Biophys Res Commun.* 2004 Oct 29; 323(4): 1157-62.

101. Yamada K, Strahler JR, Andrews PC, Matthews RG. Regulation of human methylenetetrahydrofolate reductase by phosphorylation. *Proc Natl Acad Sci U S A*. 102: 10454-10459, 2005.
102. Misek DE, Kuick R, Wang H, Galchev V, Deng B, Zhao R, Tra J, Pisano MR, Amunugama R, Allen D, Walker AK, Strahler JR, Andrews PC, Omenn GS, Hanash SM: A wide range of protein isoforms in serum and plasma uncovered by a quantitative intact protein analysis system. *Proteomics*. 5: 3343-3352, 2005.
103. Omenn GS, States DJ, Adamski M, Blackwell TW, Menon R, Hermjakob H, Apweiler R, Haab BB, Simpson RJ, Eddes JS, Kapp EA, Moritz RL, Chan DW, Rai AJ, Admon A, Aebersold R, Eng J, Hancock WS, Hefta SA, Meyer H, Paik YK, Yoo JS, Ping P, Pounds J, Adkins J, Qian X, Wang R, Wasinger V, Wu CY, Zhao X, Zeng R, Archakov A, Tsugita A, Beer I, Pandey A, Pisano M, Andrews P, Tammen H, Speicher DW, Hanash SM. Overview of the HUPO Plasma Proteome Project: results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. *Proteomics*. 2005 Aug;5(13):3226-45.
104. Keshamouni, V.G., Michailidi, G., Grasso, C.S., Anthwal, S., Strahler, J.R., Walker, A., Arenberg, D.A., Reddy, R.C., Akulapalli, S., Thannickal, V.J., Standiford, T. J., Andrews, P.C. and Omenn, G.S.: Differential Protein Expression Profiling by iTRAQ-2DLC-MS/MS Reveals a Metastatic Phenotype in TGF-induced Epithelial-Mesenchymal Transitions in Human Lung Cancer Cells. *Journal of Proteome Research*. J Proteome Res. 2006 May;5(5):1143-54.
105. Falkner J, Andrews P. Fast tandem mass spectra-based protein identification regardless of the number of spectra or potential modifications examined. *Bioinformatics*. 2005 May 15; 21(10):2177-84.
106. Ulintz PJ, Zhu J, Qin ZS, Andrews PC. Improved classification of mass spectrometry database search results using newer machine learning approaches. *Mol Cell Proteomics*. 2006 Mar;5(3):497-509. Epub 2005 Nov 30.
107. Falkner JA, Falkner JW, Andrews PC. ProteomeCommons.org JAF: reference information and tools for proteomics. *Bioinformatics*. 2006 Mar 1;22(5):632-3. Epub 2006 Jan 24.
108. Ostrom, PH, Gandhi, H, Strahler, JR, Walker, AK, Andrews, PC, Leykam, J, Stafford, TW, Kelly, RK, Walker, DN, Buckley, M and Humpula, J.: Unraveling the sequence and structure of the protein osteocalcin from a 42 ka fossil horse. *Geochimica et Cosmochimica Acta*. (in press)
109. Garcia BA, Joshi S, Thomas CE, Chitta RK, Diaz RL, Busby SA, Andrews PC, Ogorzalek Loo RR, Shabanowitz J, Kelleher NL, Mizzen CA, Allis CD, Hunt DF. Comprehensive Phosphoprotein Analysis of Linker Histone H1 from *Tetrahymena thermophila*. *Mol Cell Proteomics*. 2006 Sep;5(9):1593-1609. Epub 2006 Jul 10. PMID: 16835217
110. Ulintz PJ, Zhu J, Qin ZS, Andrews PC. Improved classification of mass spectrometry database search results using newer machine learning approaches. *Mol Cell Proteomics*. 2006 Mar;5(3):497-509. Epub 2005 Nov 30. PMID: 16321970
111. Jagtap P, Michailidis G, Zielke R, Walker AK, Patel N, Strahler JR, Driks A, Andrews PC, Maddock JR. Early events of *Bacillus anthracis* germination identified by time-course quantitative proteomics. *Proteomics*. 2006 Oct;6(19):5199-211. PMID: 16927434
112. Jiang M, Datta K, Walker A, Strahler J, Bagamasbad P, Andrews PC, Maddock JR. The *Escherichia coli* GTPase CgtAE Is Involved in Late Steps of Large Ribosome Assembly. *J Bacteriol*. 2006 Oct;188(19):6757-70. PMID: 17337586
113. Kozarova A, Sliskovic I, Mutus B, Vacratsis PO, Simon ES, Andrews PC. Identification of Redox Sensitive Thiols of Protein Disulfide Isomerase Using Isotope Coded Affinity Technology and Mass Spectrometry. *J Am Soc Mass Spectrom*. 2007 Feb;18(2):260-9 PMID: 17074504
114. Falkner JA, Falkner JW, Andrews PC. ProteomeCommons.org IO Framework: reading and writing multiple proteomics data formats. *Bioinformatics*. 2007 Jan 15;23(2):262-3. PMID: 17121776.
115. Falkner JA, Kachman M, Veine DM, Walker A, Strahler JR, Andrews PC. Validated MALDI-TOF/TOF Mass Spectra for Protein Standards. *J Am Soc Mass Spectrom*. 2007 May;18(5):850-5. PMID 17329120.
116. Jiang M, Sullivan SM, Walker AK, Strahler JR, Andrews PC, Maddock JR. Identification of novel *Escherichia coli* ribosome-associated proteins using isobaric tags and multidimensional protein identification techniques. *J Bacteriol*. 2007 May;189(9):3434-44. PMID: 17337586.
117. Jayapandian M, Chapman A, Tarcea VG, Yu C, Elkiss A, Ianni A, Liu B, Nandi A, Santos C, Andrews P, Athey B, States D, Jagadish HV. Michigan Molecular Interactions (MiMI): putting the jigsaw puzzle together. *Nucleic Acids Res*. 2007 Jan;35(Database issue):D566-71. Epub 2006 Nov 27.

118. Parrish JR, Yu J, Liu G, Hines JA, Chan JE, Mangiola BA, Zhang H, Pacifico S, Fotouhi F, Dirita VJ, Ideker T, Andrews P, Finley RL Jr. A proteome-wide protein interaction map for *Campylobacter jejuni*. *Genome Biol.* 2007 Jul 5;8(7):R130 PMID: 17615063
119. Mathivanan S, et al. Human Proteinpedia enables sharing of human protein data. *Nat Biotechnol.* 2008 Feb;26(2):164-7. PMID: 18259167
120. Leichert LI, Gehrke F, Gudiseva HV, Blackwell T, Ilbert M, Walker AK, Strahler JR, Andrews PC, Jakob U. Quantifying changes in the thiol redox proteome upon oxidative stress in vivo. *Proc Natl Acad Sci U S A.* 2008 Feb 14. PMID: 18287020
121. Ulintz PJ, Bodenmiller B, Andrews PC, Aebersold R, Nesvizhskii AI. Investigating MS2/MS3 matching statistics: a model for coupling consecutive stage mass spectrometry data for increased peptide identification confidence. *Mol Cell Proteomics.* 2008 Jan; 7(1):71-87. Epub 2007 Sep 13. PMID: 17872894.
122. Chen X, Ulintz PJ, Simon ES, Williams JA, Andrews PC. Global topology analysis of pancreatic zymogen granule membrane proteins. *Mol Cell Proteomics.* 2008 Aug 4. [Epub ahead of print] PMID: 18682380
123. Christensen JB, Byrd SA, Walker AK, Strahler JR, Andrews PC, Imperiale MJ. Presence of the adenovirus IVa2 protein at a single vertex of the mature virion. *J Virol.* 2008 Sep; 82(18):9086-93. Epub 2008 Jul 9. PMID: 18614642.
124. Falkner JA, Hill JA, Andrews PC. Proteomics FASTA archive and reference resource. *Proteomics.* 2008 May; 8(9):1756-7. PMID: 18442177.
125. Yocum AK, Gratsch TE, Leff N, Strahler JR, Hunter CL, Walker AK, Michailidis G, Omenn GS, O'Shea KS, Andrews PC. Coupled global and targeted proteomics of human embryonic stem cells during induced differentiation. PMID: 19072539
126. Chen X, Andrews PC. Purification and proteomics analysis of pancreatic zymogen granule membranes. *Methods Mol Biol.* 2008;432:275-87. PMID: 19153703
127. Simon ES, Young M, Chan A, Bao ZQ, Andrews PC. Improved enrichment strategies for phosphorylated peptides on titanium dioxide using methyl esterification and pH gradient elution. *Anal Biochem.* 2008 Jun 15;377(2):234-42. Epub 2008 Mar 22. PMID: 18396144
128. Falkner JA, Falkner JW, Yocum AK, Andrews PC. A Spectral Clustering Approach to MS/MS Identification of Post-Translational Modifications. *J Proteome Res.* 2008 Sep 19. [Epub ahead of print] PMID: 18800783
129. Keshamouni VG, Jagtap P, Michailidis G, Strahler JR, Kuick R, Reka AK, Papoulias P, Krishnapuram R, Srirangam A, Standiford TJ, Andrews PC, Omenn GS. Temporal quantitative proteomics by iTRAQ 2D-LC-MS/MS and corresponding mRNA expression analysis identify post-transcriptional modulation of actin-cytoskeleton regulators during TGF-beta-Induced epithelial-mesenchymal transition. *J Proteome Res.* 2009 Jan;8(1):35-47. PMID: 19118450
130. Ulintz PJ, Yocum AK, Bodenmiller B, Aebersold R, Andrews PC, Nesvizhskii AI. Comparison of MS(2)-only, MSA, and MS(2)/MS(3) methodologies for phosphopeptide identification. *J Proteome Res.* 2009 Feb;8(2):887-99. PMID: 19072539
131. Abdullah NM, Kachman M, Walker A, Hawley AE, Wroblewski SK, Myers DD, Strahler JR, Andrews PC, Michailidis GC, Ramacciotti E, Henke PK, Wakefield TW. Microparticle surface protein are associated with experimental venous thrombosis: a preliminary study. *Clin Appl Thromb Hemost.* 2009 Mar-Apr;15(2):201-8. PMID: 19028772
132. Rodriguez H, Snyder M, Uhlén M, Andrews P, Beavis R, Borchers C, Chalkley RJ, Cho SY, Cottingham K, Dunn M, Dylag T, Edgar R, Hare P, Heck AJ, Hirsch RF, Kennedy K, Kolar P, Kraus HJ, Mallick P, Nesvizhskii A, Ping P, Pontén F, Yang L, Yates JR, Stein SE, Hermjakob H, Kinsinger CR, Apweiler R. Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles. *J Proteome Res.* 2009 May 19. [Epub ahead of print]. PMID: 19344107
133. Bell AW, Deutsch EW, et al., A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. *Nat Methods.* 2009 May 17. [Epub ahead of print]. PMID: 19448641

C. Research Support

Ongoing Research Support

P41-RR18627 Andrews (PI)
NCRR

09/30/03 - 08/31/08 (NCXT)

Integrated Technologies for Pathway Mapping: National Resource for Proteomics & Pathways (NRPP).
The pertinent goals of this center are to develop new approaches to mapping organellar architecture and mapping signal transduction pathways through phosphoproteome analysis.
Role: Director

P30 DK034933 Owyang (PI)
National Institutes of Health

12/01/05 - 11/30/10

Michigan Gastrointestinal Peptide Research Center
The objective of the proteomics core of the MGPRC is to provide cutting-edge service support for center members.
Role: Core Director

No designated grant number Andrews (PI)
CTA Catalytic Funds:

06/01/09 – 05/31/09 (NCTX)

A Michigan Proteome Informatics Resource
Develop a portal for a computational resource for proteomics researchers in the state of Michigan
Role: Director

Recently Completed:

Grant# GR-687 Omenn (PI)
State of Michigan/MEDC
Proteome Alliance for Cancer

09/01/05 - 08/31/08 (NCXT)

The Andrews component of this project is quantitative MS/MS analysis for cancer biomarker analysis and an understanding of the mechanism of cancer. The aims of the project are: (1) improve extent, quantitation, and reproducibility of proteomic analyses with newly emerging technologies; (2) apply emerging technologies to proteome analyses of specific cancers and cancer models.
Role: Co-Investigator

P30 AR4831 Fox (PI)
National Institutes of Health

09/01/01 - 07/31/08

University of Michigan Rheumatic Diseases Core Center
The objective of this project is to support basic science core services and pilot projects in rheumatic disease research (replaced Biomedical Research Division of MAMDC).
Center grant for the Arthritis Center. No direct costs targeted to Andrews.
Role: Consultant