

DAVID A. GOLDSTROHM, Ph.D.
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Expert in protein mass spectrometry and biochemistry, delivering project results on time and under budget.

CORE COMPETENCIES

- Spearheaded collaboration with interdisciplinary team that creatively designed mass spectrometric phosphoproteomic workflows to characterize protein post-translational modifications resulting in a novel protocol that successfully identify 262 unique phosphopeptides including 111 novel phosphorylation sites, during metabolic acidosis.
- Part of a creative and highly motivated research team that successfully characterized qualitative and quantitative changes in 1057 phosphoproteins utilizing label-free spectral counting mass spectrometric techniques, uncovering numerous key regulators of the cellular response to metabolic acidosis.
- Superb technical skills and scientific expertise with the ability to supervise and communicate effectively while contributing productively to research goals, resulting in several important protein identifications that may lead to the development of an effective GA inhibitor that is of therapeutic value in treating stroke patients.
- Using a combination of biochemistry, cellular DNA and yeast genetic manipulations, protein expression and purification techniques, and protein-protein and protein-DNA interactions studies, successfully elucidated a novel role for Mediator in post-preinitiation complex recruitment function during the transcriptional activation during oxidative stress.
- Uncovered a novel role for the transcription factor TFIIA in the regulation of gene expression during oxidative stress using an arrangement of biochemistry, yeast genetic screens and two-hybrid assays, cell-based assays, molecular biology, DNA microarrays, protein-protein and protein-DNA interaction studies, and nuclear localization studies.

RESEARCH EXPERTISE

Laboratory Techniques and Assays

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|----------------------------|----------------------------|------------------------|-----------------------|
| • Mass Spectrometry | • Peptide Characterization | • Protein Biochemistry | • Gel Electrophoresis |
| • Q-TOF-LC/MS | • Protein Characterization | • Protein Purification | • Sample Preparation |
| • LTQ RPLC-MS ⁿ | • Peptide Enrichment | • Molecular Cloning | • RT-PCR |
| • MALDI-TOF/TOF | • Protein Isolation | • Chromatin IP | • Animal Dissection |
| • Data Processing | • Amino Acid Analysis | • Yeast Two-Hybrid | • Primer Extension |
| • Database Interrogation | • Protein Fractionation | • Genetic Screens | • Tissue Culture |
| • Bioinformatics | • SDS-PAGE | • Western-blotting | • DNase I Footprint |
| • 2D-HPLC | • Genetic Mutations | • Pull-downs | • S1 Nuclease |
| • Complex Mixtures | • Cell Biology | • Co-IP | • Run-on |
| • Spectral Interpretation | • Chromatography | • Gene Knockouts | • EMSA |

Software

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|--------------|------------------------|---------------------|------------|
| • Odyssey | • Microsoft Word | • Adobe Illustrator | • SEQUEST |
| • ImageQuant | • Microsoft Excel | • Adobe Photoshop | • Scaffold |
| • iCycler | • Microsoft PowerPoint | • Mascot | • Xcalibur |

PROFESSIONAL DEVELOPMENT

Managing

- GLP-trained laboratory manager including team leader, project design, and equipment repair, 2004-2006.
- Radiation manager including departmental training, record maintenance, waste disposal, and clean up, 2003-2006.
- Hazardous waste manager including departmental training, record maintenance, waste disposal, and clean up, 2006.

Consulting

- Developed experimental protocols for a Denver, CO based biotech company, 2005.
- Performed critical data analysis and experimental design for a San Francisco, CA based biotech company, 2006.

Collaborations

- Provided critical reviews and helpful insight that aided in the publication of the manuscript "Disruption of histone deacetylase gene RPD3 accelerates PHO5 activation kinetics through inappropriate Pho84p Recycling", 2005.
- Developed experimental designs and provided useful discussion that aided in the publication of the manuscript "Histone chaperone specificity in Rtt109 activation", 2008.

- Spearheaded collaboration with proteomics core facility resulting in publication of the manuscript “Optimized workflow for confident identification of phosphopeptides using a linear ion trap mass spectrometer”, 2010.
- Performed protein purification and functional analysis aiding in the publication of the manuscript “The assembly of the preinitiation complex in eukaryotic transcription: thermodynamic and kinetic characterization”, 2006.

Teaching Assistantship

- Principles of Biochemistry and Eukaryotic Cellular Biology Lecture, 2002.
- Principles of Biochemistry and Eukaryotic Cellular Biology Lab, 2003.
- Eukaryotic Cell Biology Lecture, 2003.

Mentoring

- Trained and mentored a total of 10 graduate students and 4 undergraduate students, 2001-2010.
- Volunteer tutor for Colorado State University in biochemistry, molecular biology, and genetics, 2001-2005.
- Designed experimental protocols and managed booth to represent CSU biochemistry department at the National Western Stock Show to support community involvement with science, 2006.
- Served on numerous mock oral examination committees, 2002-2010.

EDUCATION

Postdoctoral Fellow, Biochemistry, Colorado State University, 2007-present

Advisor: Norman P. Curthoys, Ph.D.

Doctor of Philosophy, Biochemistry, Colorado State University, 2006

Advisor: Laurie A. Stargell, Ph.D.

Master of Science, Biochemistry, Colorado State University, 2002

Advisor: Laurie A. Stargell, Ph.D.

Bachelor of Arts, Biochemistry, University of Arizona, 2000

Advisor: Michael A. Wells, Ph.D.

SELECTED ORAL AND POSTER PRESENTATIONS

- Gammelgaard, D., Goldstrohm, D.A., Curthoys, N.P., and Prenni, J.E. Proteomic analysis of protein phosphorylation in the renal response to metabolic acidosis (*58th ASMS Conference on Mass Spectrometry, Salt Lake City, Utah, 2010*).
- Goldstrohm, D.A., Gammelgaard, D., Broeckling, C.D., Prenni, J.E., and Curthoys, N.P. Mass spectrometric identification of changes in protein expression and phosphorylation that regulate the renal response to metabolic acidosis (*57th ASMS Conference on Mass Spectrometry, Philadelphia, Pennsylvania, 2009*).
- Goldstrohm, D.A., and Stargell, L.A. Transcriptional activation during oxidative stress (*Keystone Symposia, Regulation of eukaryotic transcription: from chromatin to mRNA, Taos, New Mexico, 2006*).
- Goldstrohm, D.A., and Stargell, L.A. Transcriptional activation during oxidative stress (*Pingree Symposia, Colorado, 2006*).
- Goldstrohm, D.A., and Stargell, L.A. A transcriptional model for the war against oxidative stress (*Cellular and Molecular Biology Research Symposia, Fort Collins, Colorado, 2004*).
- Goldstrohm, D.A., and Stargell, L.A. Dynamic interplay of transcription factors during oxidative stress (*Graduate Research Symposia, Fort Collins, Colorado, 2006*).

SELECTED PUBLICATIONS

- Goldstrohm, D.A., Broeckling, C.D., Prenni, J.E., and Curthoys, N.P. Optimized workflow for confident identification of phosphopeptides using a linear ion trap mass spectrometer (*Submitted to Journal of Proteome Research, 2010*).
- Goldstrohm, D.A., Lee, S.K., and Stargell, L.A. Mediator plays a role in post-preinitiation complex recruitment function during transcriptional activation during oxidative stress (*Submitted to Journal of Biological Chemistry, 2010*).
- Kraemer, S.M., Goldstrohm, D.A., Berger, A., Hankey, S., Rovinsky, S.A., Moye-Rowley, S.W., and Stargell, L.A. TFIIA plays a role in the response to oxidative stress (*Eukaryotic Cell, 5(7), 1081-1090, 2006*).
- Goldstrohm, D.A., Pennington, J.E., and Wells, M.A. The role of hemolymph proline levels as a nitrogen sink during blood meal digestion by the mosquito *Aedes aegypti*. (*Journal of Insect Physiology, 49(2), 115-121, 2003*).
- Goldstrohm, D.A., and Stargell, L.A. Differing roles of Mediator subunits in the response to non-optimal growth conditions (*Manuscript in preparation*).