

William M. Old
Curriculum Vitae

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Education and Employment:

1992: B.S. Chemistry, University of Texas, Austin
2000: Ph.D. Biochemistry, CU Boulder, with Dr. Natalie Ahn
2000-2002 Post-doc. CU Health Sciences, Denver, with Dr. Richard Spritz and Dr. Larry Hunter, Bayesian methods for protein identification and linkage mapping.
2002-2003 Internship, Agilent Labs, Fort Collins, CO. Computational proteomics.
2003-2009 Post-doc, CU Boulder, with Dr. Kathryn Resing, Study of dysregulated kinase signaling in melanoma

Academic Positions:

2009-2014 Manager & Director, W.M. Keck Biomolecular Mass Spectrometry Facility, Department of Chemistry & Biochemistry, Univ. of Colorado Boulder
2009-2014 Research Assistant Professor, Department of Chemistry and Biochemistry, CU Boulder
08/2014-present Assistant Professor, Molecular, Cellular and Developmental Biology, CU Boulder

Funding:

Active

DARPA-13-34-RTA-FP-007 PI: Old 1/01/2014 – 12/31/2018
DARPA/DOD \$14,578,359 total

SPARTA: Subcellular Pan-Omics for Advanced Rapid Threat Assessment The goal of this project is to develop a system for identifying the molecular mechanisms mediating cellular responses to any drug, threat agent, or biological signal, based on mass spectrometry based profiling of global protein, RNA and metabolite responses to cellular perturbations. Note: A no-cost extension of the cooperative agreement extended the funding period from 1/20/2019 to 12/31/2019.

R21 CA205912 PI: Taatjes, Role: MPI 04/01/2016 – 03/31/2019
NIH/NCI \$381,822 (total)

Mediator Kinases and AML Cell Proliferation The goal of this project is to identify the protein kinases that phosphorylate mediator complexes and drive acute myeloid leukemia cell proliferation.

Completed in the last 5 years

Linda Crnic Institute Grand Challenge Grant PI: Old 04/01/2015 – 04/01/2018
\$100,000/yr

The Role of Dysregulated DYRK1A Signaling in Trisomy 21 Neuronal Abnormalities The goal of this project is determine the role of aberrant DYRK1A signaling on the neurodevelopmental defects in Down Syndrome.

R01 CA155453-01 PI: Old 09/01/2011 – 11/30/2016
NCI/NIH \$1,571,815 total

A New Model of Peptide Fragmentation for Improved Protein Identification and Targeted Biomarker Profiling The goal of this application is to develop more accurate and sensitive methods for large-scale biomarker profiling and protein identification, based on a kinetic model of gas-phase peptide fragmentation.

R21 CA175448-01A1 PI: Old 01/01/2014 – 12/31/2015
NIH/NCI \$ 275,000 (direct)

Comprehensive Identification of CDK8 Kinase Targets Using SILAC Phosphoproteomics The goal of this project is to identify the substrates of the CDK8 kinase using proteomic profiling of genetic and pharmacological perturbations of CDK8 activity in human cancer cell lines.

CU Molecular Oncology Program Grant PI: Old 9/29/2015
\$ 7,800 (total)

Mechanism of salinomycin sensitivity in cancer stem cell populations The goal of this grant is to identify genes that contribute to drug resistance in cancer, using a reverse genetic shRNA screen.

1S100D012300-01 PI: Knight, Role: co-PI 4/22/2013 – 04/21/2015
NIH \$1,900,000 (direct)

A HIGH-MEMORY SUPERCOMPUTER FOR PROTEOMICS, TEXT MINING AND MICROBIOME RESEARCH The goal of this project was to build a next generation supercomputer for collaborative large-scale biological research at University of Colorado and the Biofrontiers institute.

DARPA-13-37-TA1 PI: Gill, Role: co-PI 04/01/2014 – 09/30/2014
DARPA/DOD \$189,535 (direct)

Title: Colorado BioFab MTO Living Foundries: 1000 Molecules The goal of this project is to engineer microbes as biosynthetic platforms for synthesizing molecules of human interest.

CIRES Innovative Research Program PI: Copley, Role: co-PI 04/30/2014 – 09/01/2015
CU/CIRES \$25,000

Development of an unbiased method for identifying regulatory proteins bound to DNA in vivo: Finding the needle in the haystack. The goal of this project is to develop a method to identify transcription factor complexes that are recruited to any specific DNA element in bacteria.

Patents:

1. **Old, William M.**, Thompson, Dean R., United States Patent 7279679 (2007) "Methods and systems for peak detection and quantitation."
2. Thompson, Dean R., **Old, William M.**, Gines, David Lee, United States Patent 7457708 (2008) "Methods and devices for identifying related ions from chromatographic mass spectral datasets containing overlapping components."
3. **Old, William M.**, McClure-Begley, T., Gong, T., Worrell, B., Chapnick, D., Begovic, E., Bowman, C., Technology Provisional Patent (CU3663B), "Linkers for Protein Interaction Profiling and Methods of Making and Using the Same."
4. Bertness, Kristine A., Brubaker, M.D., **Old, William M.**, United States Patent 9460921 (2016) "Nanowire Article and Processes for Making and Using the Same."

Publications:Preprints

1. Guard S.E., Poss Z.C., Ebmeier C.C., Pagratis M., Taatjes D.J., **Old W.M.** The nuclear interactome of DYRK1A reveals a functional role in DNA damage repair. *bioRxiv*. 2018. doi: 10.1101/432757.
2. McClure-Begley T.D., Ebmeier C.C., Ball K.E., Jacobsen J.R., Kogut I., Bilousova G., Klymkowsky M.K., **Old W.M.** Cerebral organoid proteomics reveals signatures of dysregulated cortical development associated with human trisomy 21. *bioRxiv*. 2018. doi: 10.1101/315317.
3. Ball K., Pisconti A., Grounds K., **Old W.**, Stowell M. Unexpected Early Proteomic Changes in Alzheimer's Disease Model Mice Synaptosomes. *bioRxiv*. 2017. doi: 10.1101/144972.

Peer-reviewed research papers

1. Fu X., Sokolova V., Webb K.J., **Old W.**, Park S. Ubiquitin-dependent switch during assembly of the proteasomal ATPases mediated by Not4 ubiquitin ligase. *Proceedings of the National Academy of Sciences of the United States of America*. 2018;115(52):13246-51. doi: 10.1073/pnas.1805353115. PubMed PMID: 30530678; PMCID: PMC6310792.
2. Stabell A.C., Meyerson N.R., Gullberg R.C., Gilchrist A.R., Webb K.J., **Old W.M.**, Perera R., Sawyer S.L. Dengue viruses cleave STING in humans but not in nonhuman primates, their presumed natural reservoir. *eLife*. 2018;7. doi: 10.7554/eLife.31919. PubMed PMID: 29557779; PMCID: PMC5860865.
3. Kristofich J., Morgenthaler A.B., Kinney W.R., Ebmeier C.C., Snyder D.J., **Old W.M.**, Cooper V.S., Copley S.D. Synonymous mutations make dramatic contributions to fitness when growth is limited by a weak-link enzyme. *PLoS Genet*. 2018;14(8):e1007615. doi: 10.1371/journal.pgen.1007615. PubMed PMID: 30148850; PMCID: PMC6128649.
4. Hoyer M.J., Chitwood P.J., Ebmeier C.C., Striepen J.F., Qi R.Z., **Old W.M.**, Voeltz G.K. A Novel Class of ER Membrane Proteins Regulates ER-Associated Endosome Fission. *Cell*. 2018;175(1):254-65 e14. doi: 10.1016/j.cell.2018.08.030. PubMed PMID: 30220460.
5. Basken J., Stuart S.A., Kavran A.J., Lee T., Ebmeier C.C., **Old W.M.**, Ahn N.G. Specificity of Phosphorylation Responses to Mitogen Activated Protein (MAP) Kinase Pathway Inhibitors in Melanoma Cells. *Molecular & cellular proteomics : MCP*. 2018;17(4):550-64. doi: 10.1074/mcp.RA117.000335. PubMed PMID: 29255136; PMCID: PMC5880111.
6. Ebmeier C.C., Erickson B., Allen B.L., Allen M.A., Kim H., Fong N., Jacobsen J.R., Liang K., Shilatifard A., Dowell R.D., **Old W.M.**, Bentley D.L., Taatjes D.J. Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. *Cell reports*. 2017;20(5):1173-86. doi: 10.1016/j.celrep.2017.07.021.
7. Carrieri D., Lombardi T., Paddock T., Cano M., Goodney G.A., Nag A., **Old W.**, Maness P.C., Seibert M., Ghirardi M., Yu J.P. Transcriptome and proteome analysis of nitrogen starvation responses in *Synechocystis* 6803 Delta glgC, a mutant incapable of glycogen storage. *Algal Research-Biomass Biofuels and Bioproducts*. 2017;21:64-75. doi: 10.1016/j.algal.2016.11.003. PubMed PMID: WOS:000396365500009.
8. Adams D.J., Nemkov T.G., Mayer J.P., **Old W.M.**, Stowell M.H.B. Identification of the primary peptide contaminant that inhibits fibrillation and toxicity in synthetic amyloid-beta42. *PloS one*. 2017;12(8):e0182804. doi: 10.1371/journal.pone.0182804. PubMed PMID: 28792968; PMCID: PMC5549942.
9. Poss Z.C., Ebmeier C.C., Odell A.T., Tangpeerachaikul A., Lee T., Pelish H.E., Shair M.D., Dowell R.D., **Old W.M.**, Taatjes D.J. Identification of Mediator Kinase Substrates in Human Cells using Cortistatin A and Quantitative Phosphoproteomics. *Cell reports*. 2016;15(2):436-50. doi: 10.1016/j.celrep.2016.03.030. PubMed PMID: 27050516; PMCID: PMC4833653.
10. Kershner J.P., Yu McLoughlin S., Kim J., Morgenthaler A., Ebmeier C.C., **Old W.M.**, Copley S.D. A Synonymous Mutation Upstream of the Gene Encoding a Weak-Link Enzyme Causes an Ultrasensitive Response in Growth Rate. *Journal of bacteriology*. 2016;198(20):2853-63. doi: 10.1128/JB.00262-16. PubMed PMID: 27501982; PMCID: PMC5038006.

11. Volkov V.A., Grissom P.M., Arzhanik V.K., Zaytsev A.V., Renganathan K., McClure-Begley T., **Old W.M.**, Ahn N., McIntosh J.R. Centromere protein F includes two sites that couple efficiently to depolymerizing microtubules. *The Journal of cell biology*. 2015;209(6):813-28. doi: 10.1083/jcb.201408083. PubMed PMID: 26101217; PMCID: PMC4477864.
12. Stuart S.A., Houel S., Lee T., Wang N., **Old W.M.**, Ahn N.G. A Phosphoproteomic Comparison of B-RAFV600E and MKK1/2 Inhibitors in Melanoma Cells. *Molecular & cellular proteomics : MCP*. 2015;14(6):1599-615. doi: 10.1074/mcp.M114.047233. PubMed PMID: 25850435; PMCID: PMC4458723.
13. Nichols C.M., **Old W.M.**, Lineberger W.C., Bierbaum V.M. Gas-phase acidities of nitrated azoles as determined by the extended kinetic method and computations. *The journal of physical chemistry A*. 2015;119(2):395-402. doi: 10.1021/jp5110533. PubMed PMID: 25521708.
14. Marholz L.J., Chang L., **Old W.M.**, Wang X. Development of substrate-selective probes for affinity pulldown of histone demethylases. *ACS chemical biology*. 2015;10(1):129-37. doi: 10.1021/cb5006867. PubMed PMID: 25335116; PMCID: 4301071.
15. Long J., Tokhunts R., **Old W.M.**, Houel S., Rodriguez-Blanco J., Singh S., Schilling N., A J.C., Ahn N.G., Robbins D.J. Identification of a family of fatty-acid-speciated sonic hedgehog proteins, whose members display differential biological properties. *Cell reports*. 2015;10(8):1280-7. doi: 10.1016/j.celrep.2015.01.058. PubMed PMID: 25732819; PMCID: PMC4350664.
16. Lee T., Wang N., Houel S., Coutts K., **Old W.**, Ahn N. Dosage and temporal thresholds in microRNA proteomics. *Molecular & cellular proteomics : MCP*. 2015;14(2):289-302. doi: 10.1074/mcp.M114.043851. PubMed PMID: 25467838; PMCID: PMC4350026.
17. Brown R., Stuart S.A., Houel S., Ahn N.G., **Old W.M.** Large-Scale Examination of Factors Influencing Phosphopeptide Neutral Loss during Collision Induced Dissociation. *Journal of the American Society for Mass Spectrometry*. 2015;26(7):1128-42. doi: 10.1007/s13361-015-1109-y. PubMed PMID: 25851653; PMCID: PMC4509682.
18. Subramanian V., Dubini A., Astling D.P., Laurens L.M., **Old W.M.**, Grossman A.R., Posewitz M.C., Seibert M. Profiling Chlamydomonas Metabolism under Dark, Anoxic H₂-Producing Conditions Using a Combined Proteomic, Transcriptomic, and Metabolomic Approach. *Journal of proteome research*. 2014;13(12):5431-51. doi: 10.1021/pr500342j. PubMed PMID: 25333711.
19. Avena J.S., Burns S., Yu Z., Ebmeier C.C., **Old W.M.**, Jaspersen S.L., Winey M. Licensing of yeast centrosome duplication requires phosphoregulation of *sf11*. *PLoS Genet*. 2014;10(10):e1004666. doi: 10.1371/journal.pgen.1004666. PubMed PMID: 25340401; PMCID: PMC4207612.
20. Ponicsan S.L., Houel S., **Old W.M.**, Ahn N.G., Goodrich J.A., Kugel J.F. The non-coding B2 RNA binds to the DNA cleft and active-site region of RNA polymerase II. *Journal of molecular biology*. 2013;425(19):3625-38. doi: 10.1016/j.jmb.2013.01.035. PubMed PMID: 23416138; PMCID: 3672349.
21. Peden E.A., Boehm M., Mulder D.W., Davis R., **Old W.M.**, King P.W., Ghirardi M.L., Dubini A. Identification of global ferredoxin interaction networks in *Chlamydomonas reinhardtii*. *The Journal of biological chemistry*. 2013;288(49):35192-209. doi: 10.1074/jbc.M113.483727. PubMed PMID: 24100040; PMCID: 3853270.
22. Yen C.Y., Houel S., Ahn N.G., **Old W.M.** Spectrum-to-spectrum searching using a proteome-wide spectral library. *Molecular & cellular proteomics : MCP*. 2011;10(7):M111 007666. doi: 10.1074/mcp.M111.007666. PubMed PMID: 21532008; PMCID: PMC3134071.
23. Meyer-Arendt K., **Old W.M.**, Houel S., Renganathan K., Eichelberger B., Resing K.A., Ahn N.G. IsoformResolver: A peptide-centric algorithm for protein inference. *Journal of proteome research*. 2011;10(7):3060-75. doi: 10.1021/pr200039p. PubMed PMID: 21599010; PMCID: PMC3167374.
24. Chatterjea S.M., Resing K.A., **Old W.**, Nirunsuksiri W., Fleckman P. Optimization of filaggrin expression and processing in cultured rat keratinocytes. *Journal of dermatological science*. 2011;61(1):51-9. doi: 10.1016/j.jdermsci.2010.11.003. PubMed PMID: 21146962; PMCID: PMC3031422.
25. Houel S., Abernathy R., Renganathan K., Meyer-Arendt K., Ahn N.G., **Old W.M.** Quantifying the impact of chimera MS/MS spectra on peptide identification in large-scale proteomics studies. *Journal*

- of proteome research. 2010;9(8):4152-60. doi: 10.1021/pr1003856. PubMed PMID: 20578722; PMCID: PMC3221600.
26. Yen C.Y., Meyer-Arendt K., Eichelberger B., Sun S., Houel S., **Old W.M.**, Knight R., Ahn N.G., Hunter L.E., Resing K.A. A simulated MS/MS library for spectrum-to-spectrum searching in large scale identification of proteins. *Molecular & cellular proteomics : MCP*. 2009;8(4):857-69. doi: 10.1074/mcp.M800384-MCP200. PubMed PMID: 19106086; PMCID: 2667364.
 27. Xu Q., Zhu S., Wang W., Zhang X., **Old W.**, Ahn N., Liu X. Regulation of kinetochore recruitment of two essential mitotic spindle checkpoint proteins by Mps1 phosphorylation. *Molecular biology of the cell*. 2009;20(1):10-20. doi: 10.1091/mbc.E08-03-0324. PubMed PMID: 18923149; PMCID: PMC2613107.
 28. Wang W., Yang Y., Gao Y., Xu Q., Wang F., Zhu S., **Old W.**, Resing K., Ahn N., Lei M., Liu X. Structural and mechanistic insights into Mps1 kinase activation. *Journal of cellular and molecular medicine*. 2009;13(8B):1679-94. doi: 10.1111/j.1582-4934.2008.00605.x. PubMed PMID: 19120698; PMCID: PMC2829362.
 29. **Old W.M.**, Shabb J.B., Houel S., Wang H., Coutts K.L., Yen C.Y., Litman E.S., Croy C.H., Meyer-Arendt K., Miranda J.G., Brown R.A., Witze E.S., Schweppe R.E., Resing K.A., Ahn N.G. Functional proteomics identifies targets of phosphorylation by B-Raf signaling in melanoma. *Molecular cell*. 2009;34(1):115-31. doi: 10.1016/j.molcel.2009.03.007. PubMed PMID: 19362540; PMCID: 2735263.
 30. Holinger E.P., **Old W.M.**, Giddings T.H., Jr., Wong C., Yates J.R., 3rd, Winey M. Budding yeast centrosome duplication requires stabilization of Spc29 via Mps1-mediated phosphorylation. *The Journal of biological chemistry*. 2009;284(19):12949-55. doi: 10.1074/jbc.M900088200. PubMed PMID: 19269975; PMCID: PMC2676026.
 31. *Witze E.S., ***Old W.M.**, Resing K.A., Ahn N.G. Mapping protein post-translational modifications with mass spectrometry. *Nature methods*. 2007;4(10):798-806. doi: 10.1038/nmeth1100. PubMed PMID: 17901869. *Co-first authors
 32. Sun S., Meyer-Arendt K., Eichelberger B., Brown R., Yen C.Y., **Old W.M.**, Pierce K., Cios K.J., Ahn N.G., Resing K.A. Improved validation of peptide MS/MS assignments using spectral intensity prediction. *Molecular & cellular proteomics : MCP*. 2007;6(1):1-17. doi: 10.1074/mcp.M600320-MCP200. PubMed PMID: 17018520.
 33. Mattison C.P., **Old W.M.**, Steiner E., Huneycutt B.J., Resing K.A., Ahn N.G., Winey M. Mps1 activation loop autophosphorylation enhances kinase activity. *The Journal of biological chemistry*. 2007;282(42):30553-61. doi: 10.1074/jbc.M707063200. PubMed PMID: 17728254.
 34. Ahn N.G., Shabb J.B., **Old W.M.**, Resing K.A. Achieving in-depth proteomics profiling by mass spectrometry. *ACS chemical biology*. 2007;2(1):39-52. doi: 10.1021/cb600357d. PubMed PMID: 17243782.
 35. Ruth M.C., **Old W.M.**, Emrick M.A., Meyer-Arendt K., Aveline-Wolf L.D., Pierce K.G., Mendoza A.M., Sevinsky J.R., Hamady M., Knight R.D., Resing K.A., Ahn N.G. Analysis of membrane proteins from human chronic myelogenous leukemia cells: comparison of extraction methods for multidimensional LC-MS/MS. *Journal of proteome research*. 2006;5(3):709-19. doi: 10.1021/pr050313z. PubMed PMID: 16512687.
 36. **Old W.M.**, Meyer-Arendt K., Aveline-Wolf L., Pierce K.G., Mendoza A., Sevinsky J.R., Resing K.A., Ahn N.G. Comparison of label-free methods for quantifying human proteins by shotgun proteomics. *Molecular & cellular proteomics : MCP*. 2005;4(10):1487-502. doi: 10.1074/mcp.M500084-MCP200. PubMed PMID: 15979981.
 37. Russell S.A., **Old W.**, Resing K.A., Hunter L. Proteomic informatics. *International review of neurobiology*. 2004;61:127-57. doi: 10.1016/S0074-7742(04)61006-3. PubMed PMID: 15482814.
 38. Resing K.A., Meyer-Arendt K., Mendoza A.M., Aveline-Wolf L.D., Jonscher K.R., Pierce K.G., **Old W.M.**, Cheung H.T., Russell S., Wattawa J.L., Goehle G.R., Knight R.D., Ahn N.G. Improving reproducibility and sensitivity in identifying human proteins by shotgun proteomics. *Analytical chemistry*. 2004;76(13):3556-68. doi: 10.1021/ac035229m. PubMed PMID: 15228325.
 39. Conant G.C., Plimpton S.J., **Old W.**, Wagner A., Fain P.R., Pacheco T.R., Heffelfinger G. Parallel GeneHunter: implementation of a linkage analysis package for distributed-memory architectures.

Journal of Parallel and Distributed Computing. 2003;63(7):674-82. doi:
[https://doi.org/10.1016/S0743-7315\(03\)00080-7](https://doi.org/10.1016/S0743-7315(03)00080-7).

40. Pacheco T.R., Bellus G.A., Oreskovich N.M., Talbert J., **Old W.**, Fain P.R. Exclusion of candidate genes and loci for multiple lentiginos syndrome. The Journal of investigative dermatology. 2002;119(2):535-8. doi: 10.1046/j.1523-1747.2002.18203.x. PubMed PMID: 12190883.
41. Alkhateeb A., Stetler G.L., **Old W.**, Talbert J., Uhlhorn C., Taylor M., Fox A., Miller C., Dills D.G., Ridgway E.C., Bennett D.C., Fain P.R., Spritz R.A. Mapping of an autoimmunity susceptibility locus (AIS1) to chromosome 1p31.3-p32.2. Human molecular genetics. 2002;11(6):661-7. PubMed PMID: 11912181.
42. Thulin C.D., Savage J.R., McLaughlin J.N., Truscott S.M., **Old W.M.**, Ahn N.G., Resing K.A., Hamm H.E., Bitensky M.W., Willardson B.M. Modulation of the G protein regulator phosphodiesterase by Ca²⁺/calmodulin-dependent protein kinase II phosphorylation and 14-3-3 protein binding. The Journal of biological chemistry. 2001;276(26):23805-15. doi: 10.1074/jbc.M101482200. PubMed PMID: 11331285.
43. McMillen D.A., **Old W.M.**, Bleibaum J.L., Nicolet C.M., Resing K.R., Sarath G., Yadav S.P. Job compensation in the biotechnology core laboratory. Nature biotechnology. 2000;18(6):686-9. doi: 10.1038/76553. PubMed PMID: 10835613.

Teaching and Mentoring Activities

Teaching: formal courses

Fall 2018 MCDB 2150, Principles of Genetics, 3 credits, 170 students. This is an introductory course on the principles of genetics, with an emphasis on human genetics.

Fall 2018, MCDB Graduate Core, 4 lectures, Oct 9-19. Signaling and protein kinase regulation.

Fall 2017 MCDB 2150, Principles of Genetics, 3 credits, 153 students. This is an introductory course on the principles of genetics, with an emphasis on human genetics.

Fall 2016 MCDB 3990, Introduction to Systems Biology, 3 credits. 11 students. My long term goal is to develop this course to introduce students to emerging interdisciplinary approaches in biology: computation, mathematical modeling, big data and experimental technologies used in proteomics, transcriptomics and metabolomics. This gives students a survey of many new aspects of biological research they probably haven't been exposed to and are used extensively in industry and big pharma. I emphasize training in practical hands-on statistics and visualization techniques that the students are likely to use, whether in academia, industry or government research.

Fall 2015 MCDB 3990, Introduction to Systems Biology, 3 credits. 9 students. I developed this course, that was started and taught one semester by Dr. Mike Klymkowsky. This is essentially a new course I've developed for upper division biology undergraduates, in which they learn mathematical modeling, data-driven modeling and experimental methods in large scale biology. FCQ Course overall 5.3. FCQ Instr overall 5.4.

Spring 2013 CHEM 5811, Advanced Methods in Protein Sequencing and Analysis, 3 credit hrs, ~11 graduate students. I co-taught this course with Natalie Ahn, preparing, teaching and grading the labs and working with Natalie to develop the course and material.

Spring 2009 CHEM 5811, Advanced Methods in Protein Sequencing and Analysis, 3 credit hrs, 7 graduate students. I co-taught this course with Natalie Ahn, preparing, teaching and grading the labs and working with Natalie to develop the course and material.

Teaching: guest lectures

Fall 2016 Sept 14, Responsible Conduct of Research (Dale Mood). Guest lecture on mentoring.

Fall 2015 Oct 22, MCDB3333: Biomedical Discoveries and Innovations (Ravinder Singh). Gave a guest lecture on mass spectrometry based proteomics as a tool to understand biological systems.

Fall 2011 CHEM 5181, Mass Spectrometry and Chromatography (Jose Jimenez). A mass spec course focused on fundamentals. I gave a guest lecture on biological applications 11/8/2011.

Invited talks and seminars

- 2018 Crnic Supergroup talk, Aug. 15, Boulder, CO
- 2017 Crnic Supergroup talk,
- 2016 US HUPO Meeting, Lightning Talk, Mar. 15, 2016, Boston, MA
- 2015 DARPA BiT Meeting, Feb 11, 2015, San Francisco, CA
Linda Crnic Institute Supergroup, May 20, 2015, CU Anschutz, Denver, CO
MCDB Departmental Retreat Seminar, Vail, CO, Oct. 8, 2015
- 2014 National Institutes of Standards (NIST), Jan. 1, 2014, Boulder, CO
DARPA Rapid Threat Assessment Kick-Off Meeting, Feb. 6, 2014, Arlington, VA
Dept. of MCD Biology, CU Boulder, Mar. 3, 2014, Boulder, CO
- 2013 JSCBB Mini Symposium, July 29, 2013, Boulder, CO
SRI International, August 12, 2013, Harrisonburg, VA
- 2012 Netherlands NVMS – BSMS International Congress on Mass Spectrometry
Rolduc, March 28-30, 2012
- 2010 UND North Dakota Feb 2010
US Human Proteome Organization Meeting Mar. 9, 2010, Denver, CO
58th Annual Meeting for the American Society of Mass Spectrometry, May 25, 2010, Salt Lake City, UT
Clinical Proteomic Technologies for Cancer (NCI/CPTAC) Sept. 8, 2010 Bethesda, MD
- 2009 Enzyme Mechanisms 2009 Meeting, Jan. 5, 2009, Tucson, AZ
GlaxoSmithKline, Jan. 14, 2009, Upper Merion, PA
US Human Proteome Organization Meeting Feb. 25, 2009, San Diego, CA
Annual Symposium of the Functional Genomics Consortium at Kansas State University, March 4, 2009, Manhattan, KS
International Mass Spectrometry Conference, Bremen Germany, Sept. 3, 2009
Department of Biochemistry and Molecular Biology, University of Georgia, Sept. 11, 2009
Clinical Proteomic Technologies for Cancer 2009 Annual Meeting, Bethesda MD, Oct. 5
University of Colorado Denver (Kirk Hansen)
- 2008 Endocrine Society Annual Meeting June 17, 2008, San Francisco, CA
Ninth Principal Investigators (PI) Meeting for the Innovative Molecular Analysis Technologies (IMAT) Program, October 26-28, 2008, Cambridge, MA
- 2007 Association of Biomolecular Resource Facilities 2007, Tampa, FL
University of Nebraska Medical Center Sept. 17, 2007, Omaha, NE