William M. Old

Curriculum Vitae

Address: Department of Molecular, Cellular and Developmental Biology
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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, Oncogenic 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

Grants and Contracts:

Active

DARPA-13-34-RTA-FP-007 PI: Old 1/01/2014 – 1/12/2020
DARPA/DOD $9,559,579 (direct), PI (Old), Co-PIs: M. Stowell, X. Liu, Y.C. Lee.
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.

Supplement to DARPA-13-34-RTA-FP-007 PI: Old 8/19/2019 – 6/12/2020
AFRL/ARO/DOD $191,981 (direct)
AFRL Technology Transition The goal of this supplement is to transition our multi-omics methods and technologies developed during the SPARTA program to labs at AFRL/DOD and perform profiling experiments for a large human cohort of PBMC lines for biomarker studies. My lab will oversee all aspects of the transition work.

DSM PI: Old 10/31/2019 – 1/31/2020
Estimated $30,000 (direct)
Target profiling and identification for bioactive lipid compounds that modulate cholesterol metabolism in human organoids. This contract will apply our new whole proteome thermal profiling methods to identify proteins that exhibited stability alterations in rats administered bioactive lipids being investigated by DSM, in human induced pluripotent stem cell derived cerebral organoids.

Completed in the last 5 years

R21 CA205912 PI: Taatjes, Role: MPI 04/01/2016 – 03/31/2019
NIH/NCI $275,000 (direct)
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. My lab conducted the phosphoproteomics work, which was a major focus of the grant.

Aquinnah Pharmaceuticals PI: Old 05/31/2018-04/20/2019
$62,500 (direct)
Identification of Novel ALS and FTD Targets
Identification and validation of novel targets of preclinical ALS drugs identified through phenotypic screening

DSM PI: Old 01/01/2018-12/31/2018
$100,000 (direct)
Target engagement and mechanism of action profiling in rat hippocampal neurons
Using our recently developed isothermal shift assay (iTSA) method, we will identify and validate novel bioactive small molecules. This contract was to apply our new whole proteome thermal profiling methods to identify proteins that exhibited stability alterations in rats administered bioactive lipids being investigated by DSM.

Syros Pharmaceuticals PI: Old & Taatjes 12/01/2016-12/31/2018
$18,480 (direct)
Phosphoproteomics and RNA-seq dissection of a pre-clinical AML drug to identify novel pathway targets.

Linda Crnic Institute Grand Challenge Grant PI: Old 04/01/2015 – 04/01/2018
$100,000/yr (direct)
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 $1,018,825 (direct)
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 MPI: Taatjes 01/01/2014 – 12/31/2015
NIH/NCI $ 239,250 (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. My role is to oversee the

metabolic labeling cell culture work, drug treatment experiments and phosphoproteomic mass spectrometry work.

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

1S10OD012300-01 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.

Publications:

Preprints

1. Ball K., Pisconti A., Grounds K., **Old W.***, Stowell M.* (2017) Unexpected Early Proteomic Changes in Alzheimer's Disease Model Mice Synaptosomes. bioRxiv. doi: 10.1101/144972. *co-corresponding authors.

Papers in review

2. Anderson, E.N., Morera, A., Kour, S., Cherry, J.D., Ramesh, N., Schwartz, J., Ebmeier, C.C., **Old, W.M.**, Gleixner, A., Donnelly, C., Stein, T., Pandey, U.B. (2019) “Traumatic injury compromises nucleocytoplasmic transport and leads to TDP-43 pathology”, *Nature Neuroscience.* (submitted).

Papers in revision

3. McClure-Begley, T.D.‡, Ebmeier, C.C., Ball, K.E., Jacobsen, J.R., Kogut, I., Bilousova, G., Klymkowsky, M.K., and **Old, W.M.** (2018). Cerebral organoid proteomics reveals signatures of dysregulated cortical development associated with human trisomy 21. *BioRxiv*. doi: 10.1101/315317. (In revision at Molecular, Cellular Proteomics).

Peer-reviewed research papers

4. Ball, K.A.*, Webb, K.J.*, Coleman, S.J., Cozzolino, K.A., Jacobsen, J., Jones, K.R., Stowell, M.H.B., and **Old, W.M.** (2020). Rapid discovery of drug target engagement by isothermal shift assay. *Communications Biology*. *equally contributing co-authors. (accepted by journal 1/20/2020).

5. Park J-D., Moon K., Miller C., Rose J., Xu F., Ebmeier C.C., Jabcobsen J.R., Mao D., **Old W.M.**, DeShazer D, Seyedsayamdost MR. (2019). Thailandenes, cryptic polyene natural products isolated from Burkholderia thailandensis using phenotype-guided transposon mutagenesis. ACS Chem Biol. 2019 Dec 9. Doi:10.1021/acschembio.9b00883.
6. Miles, M., Bhattacharjee, B., Sridhar, N., Fajrial, A.K., Ball, K., Lee, Y.C., Stowell, M., **Old, W.M.**; Ding, X., (2019). Flattening of Diluted Species Profile via Passive Geometry in a Microfluidic Device. *Micromachines 10*.
7. Kawaguchi, T., Rollins, M.G., Moinpour, M., Morera, A.A., Ebmeier, C.C., Fierro-Monti, I., **Old, W.M.**, Schwartz, J.C. (2019) "Changes to the TDP-43 and FUS interactomes induced by DNA Damage". *Journal of Proteome Research.* doi.org/10.1021/acs.jproteome.9b00575*.*
8. Morgenthaler, A.B., Kinney, W.R., Ebmeier, C.C., Walsh, C.M., Snyder, D.J., Cooper, V.S., **Old, W.M.**, Copley, S.D. (2019) "Mutations that improve efficiency of a weak-link enzyme are rare compared to adaptive mutations elsewhere in the genome". *eLIFE* 8, e53535*.*
9. Kim, J., Flood, J.J., Kristofich, M., Gidfar, C., Morgenthaler, A.B., Fuhrer, T., Sauer, U., Snyder, D., Cooper, V.S., Ebmeier, C.C., **Old, W.M.**, Copley, S.D. (2019) "Hidden resources in the E. coli genome restore PLP synthesis and robust growth after deletion of the "essential" gene pdxB". Proceedings of the National Academy of Sciences.
10. Guard S.E., Ebmeier C.C., **Old W.M.**, Label-Free Immunoprecipitation Mass Spectrometry Workflow for Large-scale Nuclear Interactome Profiling. J. Vis. Exp. (2019, Pending publication), e60432, In-press. doi:10.3791/60432.
11. Guard, S.E., Poss, Z.C., Ebmeier, C.C., Pagratis, M., Simpson, H., Taatjes, D.J., and **Old, W.M.** (2019). The nuclear interactome of DYRK1A reveals a functional role in DNA damage repair. Scientific Reports *9*, 6539.
12. Chapnick, D.A., Bunker, E., Liu, X., and **Old, W.M.** (2019). Temporal Metabolite, Ion, and Enzyme Activity Profiling Using Fluorescence Microscopy and Genetically Encoded Biosensors. Methods Mol. Biol. 1978, 343–353.
13. Fu, X., Sokolova, V., Webb, K.J., **Old, W.**, and Park, S. (2018). 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 *115*, 13246–13251.
14. Stabell, A.C., Meyerson, N.R., Gullberg, R.C., Gilchrist, A.R., Webb, K.J., **Old, W.M.**, Perera, R., and Sawyer, S.L. (2018). Dengue viruses cleave STING in humans but not in nonhuman primates, their presumed natural reservoir. ELife 7.
15. Kristofich, J., Morgenthaler, A.B., Kinney, W.R., Ebmeier, C.C., Snyder, D.J., **Old, W.M.**, Cooper, V.S., and Copley, S.D. (2018). Synonymous mutations make dramatic contributions to fitness when growth is limited by a weak-link enzyme. PLoS Genet 14, e1007615.
16. Hoyer, M.J., Chitwood, P.J., Ebmeier, C.C., Striepen, J.F., Qi, R.Z., **Old, W.M.**, and Voeltz, G.K. (2018). A Novel Class of ER Membrane Proteins Regulates ER-Associated Endosome Fission. Cell *175*, 254-265 e14.
17. Basken, J., Stuart, S.A., Kavran, A.J., Lee, T., Ebmeier, C.C., **Old, W.M.**, and Ahn, N.G. (2018). Specificity of Phosphorylation Responses to Mitogen Activated Protein (MAP) Kinase Pathway Inhibitors in Melanoma Cells. Molecular & Cellular Proteomics *17*, 550–564.
18. 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., and Taatjes, D.J. (2017). Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. Cell Reports 20, 1173–1186.
19. Carrieri, D., Lombardi, T., Paddock, T., Cano, M., Goodney, G.A., Nag, A., **Old, W.**, Maness, P.C., Seibert, M., Ghirardi, M., and Yu, J.P. (2017). 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 21, 64–75.

20. Adams, D.J., Nemkov, T.G., Mayer, J.P., **Old, W.M.**, and Stowell, M.H.B. (2017). Identification of the primary peptide contaminant that inhibits fibrillation and toxicity in synthetic amyloid-beta42. PloS One 12, e0182804.
21. 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.**, and Taatjes, D.J. (2016). Identification of Mediator Kinase Substrates in Human Cells using Cortistatin A and Quantitative Phosphoproteomics. Cell Reports 15, 436–450.
22. Kershner, J.P., Yu McLoughlin, S., Kim, J., Morgenthaler, A., Ebmeier, C.C., **Old, W.M.**, and Copley, S.D. (2016). A Synonymous Mutation Upstream of the Gene Encoding a Weak-Link Enzyme Causes an Ultrasensitive Response in Growth Rate. Journal of Bacteriology 198, 2853–2863.
23. Volkov, V.A., Grissom, P.M., Arzhanik, V.K., Zaytsev, A.V., Renganathan, K., McClure-Begley, T., **Old, W.M.**, Ahn, N., and McIntosh, J.R. (2015). Centromere protein F includes two sites that couple efficiently to depolymerizing microtubules. The Journal of Cell Biology 209, 813–828.
24. Stuart, S.A., Houel, S., Lee, T., Wang, N., **Old, W.M.**, and Ahn, N.G. (2015). A Phosphoproteomic Comparison of B-RAFV600E and MKK1/2 Inhibitors in Melanoma Cells. Molecular & Cellular Proteomics : MCP 14, 1599–1615.
25. Nichols, C.M., **Old, W.M.**, Lineberger, W.C., and Bierbaum, V.M. (2015). Gas-phase acidities of nitrated azoles as determined by the extended kinetic method and computations. The Journal of Physical Chemistry. A 119, 395–402.
26. Marholz, L.J., Chang, L., **Old, W.M.**, and Wang, X. (2015). Development of substrate-selective probes for affinity pulldown of histone demethylases. ACS Chemical Biology *10*, 129–137.
27. Long, J., Tokhunts, R., **Old, W.M.**, Houel, S., Rodgriguez-Blanco, J., Singh, S., Schilling, N., J. Capobianco A, Ahn, N.G., and Robbins, D.J. (2015). Identification of a family of fatty-acid-speciated sonic hedgehog proteins, whose members display differential biological properties. Cell Reports 10, 1280–1287.
28. Lee, T., Wang, N., Houel, S., Couts, K., **Old, W.**, and Ahn, N. (2015). Dosage and temporal thresholds in microRNA proteomics. Molecular & Cellular Proteomics : MCP *14*, 289–302.
29. Brown, R.*, Stuart, S.A., Houel, S., Ahn, N.G., and **Old, W.M.** (2015). Large-Scale Examination of Factors Influencing Phosphopeptide Neutral Loss during Collision Induced Dissociation. Journal of the American Society for Mass Spectrometry *26*, 1128–1142.
30. Subramanian, V., Dubini, A., Astling, D.P., Laurens, L.M., **Old, W.M.**, Grossman, A.R., Posewitz, M.C., and Seibert, M. (2014). Profiling Chlamydomonas Metabolism under Dark, Anoxic H2-Producing Conditions Using a Combined Proteomic, Transcriptomic, and Metabolomic Approach. Journal of Proteome Research 13, 5431–5451.
31. Avena, J.S., Burns, S., Yu, Z., Ebmeier, C.C., **Old, W.M.**, Jaspersen, S.L., and Winey, M. (2014). Licensing of yeast centrosome duplication requires phosphoregulation of sfi1. PLoS Genetics 10, e1004666.
32. Ponicsan, S.L., Houel, S., **Old, W.M.**, Ahn, N.G., Goodrich, J.A., and Kugel, J.F. (2013). The non-coding B2 RNA binds to the DNA cleft and active-site region of RNA polymerase II. Journal of Molecular Biology 425, 3625–3638.
33. Peden, E.A., Boehm, M., Mulder, D.W., Davis, R., **Old, W.M.**, King, P.W., Ghirardi, M.L., and Dubini, A. (2013). Identification of global ferredoxin interaction networks in Chlamydomonas reinhardtii. The Journal of Biological Chemistry 288, 35192–35209.
34. Yen, C.Y., Houel, S., Ahn, N.G., and **Old, W.M.** (2011). Spectrum-to-spectrum searching using a proteome-wide spectral library. Molecular & Cellular Proteomics : MCP 10, M111 007666.
35. Meyer-Arendt, K., **Old, W.M.**, Houel, S., Renganathan, K., Eichelberger, B., Resing, K.A., and Ahn, N.G. (2011). IsoformResolver: A peptide-centric algorithm for protein inference. Journal of Proteome Research 10, 3060–3075.
36. Chatterjea, S.M., Resing, K.A., **Old, W.**, Nirunsuksiri, W., and Fleckman, P. (2011). Optimization of filaggrin expression and processing in cultured rat keratinocytes. Journal of Dermatological Science 61, 51–59.

37. Houel, S., Abernathy, R., Renganathan, K., Meyer-Arendt, K., Ahn, N.G., and **Old, W.M.** (2010). Quantifying the impact of chimera MS/MS spectra on peptide identification in large-scale proteomics studies. Journal of Proteome Research 9, 4152–4160.
38. Yen, C.Y., Meyer-Arendt, K., Eichelberger, B., Sun, S., Houel, S., **Old, W.M.**, Knight, R., Ahn, N.G., Hunter, L.E., and Resing, K.A. (2009). A simulated MS/MS library for spectrum-to-spectrum searching in large scale identification of proteins. Molecular & Cellular Proteomics : MCP 8, 857–869.
39. Xu, Q., Zhu, S., Wang, W., Zhang, X., **Old, W.**, Ahn, N., and Liu, X. (2009). Regulation of kinetochore recruitment of two essential mitotic spindle checkpoint proteins by Mps1 phosphorylation. Molecular Biology of the Cell 20, 10–20.
40. Wang, W., Yang, Y., Gao, Y., Xu, Q., Wang, F., Zhu, S., **Old, W.**, Resing, K., Ahn, N., Lei, M., and Liu, X. (2009). Structural and mechanistic insights into Mps1 kinase activation. Journal of Cellular and Molecular Medicine 13, 1679–1694.
41. **Old, W.M.**, Shabb, J.B., Houel, S., Wang, H., Couts, 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., and Ahn, N.G. (2009). Functional proteomics identifies targets of phosphorylation by B-Raf signaling in melanoma. Molecular Cell 34, 115–131.
42. Holinger, E.P., **Old, W.M.**, Giddings, T.H., Wong, C., Yates, J.R., and Winey, M. (2009). Budding yeast centrosome duplication requires stabilization of Spc29 via Mps1-mediated phosphorylation. The Journal of Biological Chemistry 284, 12949–12955.
43. *Witze, E.S., ***Old, W.M.**, Resing, K.A., and Ahn, N.G. (2007). Mapping protein post-translational modifications with mass spectrometry. Nature Methods 4, 798–806. *equally contributing co-first authors.
44. Sun, S., Meyer-Arendt, K., Eichelberger, B., Brown, R., Yen, C.Y., **Old, W.M.**, Pierce, K., Cios, K.J., Ahn, N.G., and Resing, K.A. (2007). Improved validation of peptide MS/MS assignments using spectral intensity prediction. Molecular & Cellular Proteomics : MCP 6, 1–17.
45. Mattison, C.P., **Old, W.M.**, Steiner, E., Huneycutt, B.J., Resing, K.A., Ahn, N.G., and Winey, M. (2007). Mps1 activation loop autophosphorylation enhances kinase activity. The Journal of Biological Chemistry 282, 30553–30561.
46. Ahn, N.G., Shabb, J.B., **Old, W.M.**, and Resing, K.A. (2007). Achieving in-depth proteomics profiling by mass spectrometry. ACS Chemical Biology 2, 39–52.
47. 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., and Ahn, N.G. (2006). Analysis of membrane proteins from human chronic myelogenous leukemia cells: comparison of extraction methods for multidimensional LC-MS/MS. Journal of Proteome Research 5, 709–719.
48. **Old, W.M.**, Meyer-Arendt, K., Aveline-Wolf, L., Pierce, K.G., Mendoza, A., Sevinsky, J.R., Resing, K.A., and Ahn, N.G. (2005). Comparison of label-free methods for quantifying human proteins by shotgun proteomics. Molecular & Cellular Proteomics : MCP 4, 1487–1502.
49. Russell, S.A., **Old, W.**, Resing, K.A., and Hunter, L. (2004). Proteomic informatics. International Review of Neurobiology 61, 127–157.
50. 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., and Ahn, N.G. (2004). Improving reproducibility and sensitivity in identifying human proteins by shotgun proteomics. Analytical Chemistry 76, 3556–3568.
51. Conant, G.C., Plimpton, S.J., **Old, W.**, Wagner, A., Fain, P.R., Pacheco, T.R., and Heffelfinger, G. (2003). Parallel Genehunter: implementation of a linkage analysis package for distributed-memory architectures. Journal of Parallel and Distributed Computing 63, 674–682.
52. Pacheco, T.R., Bellus, G.A., Oreskovich, N.M., Talbert, J., **Old, W.**, and Fain, P.R. (2002). Exclusion of candidate genes and loci for multiple lentigines syndrome. The Journal of Investigative Dermatology 119, 535–538.

53. 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., and Spritz, R.A. (2002). Mapping of an autoimmunity susceptibility locus (AIS1) to chromosome 1p31.3-p32.2. Human Molecular Genetics 11, 661–667.
54. 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., and Willardson, B.M. (2001). Modulation of the G protein regulator phosducin by Ca2+/calmodulin-dependent protein kinase II phosphorylation and 14-3-3 protein binding. The Journal of Biological Chemistry 276, 23805–23815.

A complete list of publications can be found here:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1FGvfcAUNub/bibliography/40138006/public/?sort=date&direction=descending

Commercial ventures:

- Valene Biosciences, LLC. (04/2019) Co-founder with M. Stowell, J. Mayer & B. Worrell. Valene is an early stage company aimed at commercializing a new platform technology for drug discovery based on fluxional shapeshifting cyclic peptides.
- Bioloomics, LLC. Co-founder with X. Liu and D. Chapnick. BioLoomics is an R&D biotech company commercializing a new technology developed by our DARPA funded project (PI: Old). This platform is based on fluorescence biosensor arrays and high-content microscopy that enables parallel reporting of hundreds of biochemical pathways in living cells for fast automated screening of on and off target drug responses in cell culture model systems. Currently, this technology is protected as a provisional patent (Application No. 62/599,551) titled, 'Synthetic Fluorescent Protein Biosensors and Use Thereof in Drug Screening Methods'.

Patents, Patent Applications & Invention Disclosures:

1. **Old, W.M.,** Thompson, D.R., (2007) United States Patent 7279679 "Methods and systems for peak detection and quantitation."
2. Thompson, D.R., **Old, W.M.**, Gines, D.L., (2008) United States Patent 7457708 "Methods and devices for identifying related ions from chromatographic mass spectral datasets containing overlapping components."
3. Bertness, Kristine A., Brubaker, M.D., **Old, W.M.**, (2016) United States Patent 9460921 "Nanowire Article and Processes for Making and Using the Same."
4. **Old, W.**; Chapnick, D. A.*, McClure-Begley, T. D., Gong, T., Worrell, B. T.*, Ebmeier, C. C.*, Bowman, C. N., (2016) United States Patent Application WO2016057936A1 "Crosslinking compounds for effective and efficient cross-linking and identification of intermolecular and intramolecular interactions of proteins, peptides, and nucleic acids".
5. **Old, W.**, Stowell M.H., Lee, Y.C., Chapnick, D.A., McClure-Begley, T.D., Liu, X., Ball, K., Bhattacharjee, B. (2019) PCT International Application No. 16/419,054. "Microfluidic Devices and Methods for Cellular Thermal Shift Assays." Filed May 22, 2019.
6. Liu, X., Chapnick, D., **Old, W.**, McClure-Begley, T., and Bunker, E. (2018) PCT Application No. PCT/US18/65673. "Synthetic fluorescent protein biosensors and use thereof in drug screening methods."
7. Liu, X., **Old, W.**, Chapnick, D. (2019) PCT Application No. PCT/US18/65673. ''Novel Systems and Methods for the Therapeutic Use of Cannabinoids or Cannabinoid Analogs to Increase the Lipid Order of Cholesterol Containing Cell Membranes."
8. **Old, W.**, Stowell, M., Worrell, B. (2019) Invention Disclosure, CU Boulder, 07/15/2019 "Shape Shifting Cyclic Peptides (SSCPs) as a Platform for the Discovery of Novel Therapeutics".

Teaching

Fall 2019 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 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 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.

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 Ahn 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 Ahn to develop the course and material.

Teaching: guest lectures

Fall 2018, MCDB 5230 (3) Graduate Core 1, 4 lectures, Oct 9-19. Cancer signaling and protein kinase regulation.

Fall 2016 Sept 14, 1hr lecture, Responsible Conduct of Research (Dale Mood). Guest lecture on mentoring.

Fall 2015 Oct 22, MCDB3333, 1hr lecture: 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, 1hr lecture, Mass Spectrometry and Chromatography (Jose Jimenez). A mass spec course focused on fundamentals. I gave a guest lecture on biological applications 11/8/2011.

Seminars and Lectures

2019

- 6/4/2019, June 4, 67th ASMS Conference on Mass Spectrometry, Atlanta, GA, June 4, *"Illuminating the druggable proteome: deconvolution of drug action by multi-omics, thermal profiling and high-content screening"*
- 9/19/2019 CU MCDB, Boulder, CO *"Illuminating molecular interaction networks with chemical proteomics"*

2018

- 8/15/2018, Crnic Supergroup, Boulder, CO "Emerging Functions of Nuclear DYRK1A"
- 11/19/2018, Edgewood Chemical and Biological Center, Aberdeen Proving Ground, MD "*SPARTA Project: Subcellular Pan-omics for Rapid Threat Assessment*" **(invited)**

2017

- 4/19/2017, DARPA Rapid Threat Assessment (RTA) Review Meeting, Arlington, VA **(invited)**
- 12/12/2017, George Washington University, Washington, DC, "*Systems pharmacology reveals cannabidiol disruption of cholesterol biosynthesis and trafficking*" **(invited)**
- 2/17/16 Crnic Supergroup

2016

- 2/17/16 Crnic Supergroup, CU Anschutz, *"Correcting growth defects in a human cerebral organoid model of Down Syndrome"*
- 3/15/2016 US HUPO Meeting, Lightning Talk, Mar. 15, 2016, Boston, MA, "*How does an extra copy of chromosome 21 affect human brain development and cognition?"*
- 5/4/2016, DARPA Rapid Threat Assessment (RTA) 6 Month Review Meeting, Arlington, VA **(invited)**. Attending: Scientists from Vanderbilt, GWU, govt. scientists from NIH, FDA, DOD.
- 10/12/2016, DARPA Rapid Threat Assessment PI Review Meeting, Arlington, VA **(invited).** "*Systems biology of Bendamustine cancer therapeutic reveals hexose drug interaction mechanism". Attending: Scientists from Vanderbilt, GWU, govt. scientists from NIH, FDA, DOD.*

2015

- 2/11/2015, DARPA BiT Meeting, San Francisco, CA **(invited)**
- 5/20/2015, Linda Crnic Institute Supergroup, CU Anschutz, Denver, CO
- 9/22/2015, DARPA Rapid Threat Assessment (RTA) Period 1 Kickoff Meeting, Arlington, VA **(invited).** Attending: Scientists from Vanderbilt, GWU, govt. scientists from FDA, DOD.
- 10/8/2015, MCDB Departmental Retreat Seminar, Vail, CO, Oct. 8, 2015

2014

- 1/14/14 National Institutes of Standards (NIST), Boulder, CO **(invited)**
- 2/6/2014, DARPA Rapid Threat Assessment Kick-Off Meeting, Arlington, VA **(invited).** Attending: Scientists from Vanderbilt, GWU, govt. scientists from NIH, FDA, DOD.
- 3/3/2014, Dept. of MCD Biology, CU Boulder, Boulder, CO

2013

- 4/29/2013, JSCBB Mini Symposium, Boulder, CO
- 8/12/2013, SRI International, Harrisonburg, VA **(invited)**

2012

- Netherlands NVMS – BSMS International Congress on Mass Spectrometry Rolduc, March 28-30, 2012 **(invited)**

2010

- UND North Dakota Feb 2010 **(invited)**
- 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) **(invited)**

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

Popular press

2015 Our work as presented by Dr. Tristan McClure-Begley in my lab at the Neuroscience 2015 meeting was picked up by the popular scientific press (The Scientist): Probing Down Syndrome with Mini Brains Researchers create cerebral organoids using induced pluripotent stem cells from patient skin cells and characterize protein-expression changes linked to cognitive impairment. By Bob Grant | October 20, 2015 http://www.the-scientist.com/?articles.view/articleNo/44284/title/Probing-Down-Syndrome-with-Mini-Brains/