GLOUCESTER MARINE
GENOMICS INSTITUTE

2017 GMGI SCIENCE FORUM

SPEAKER ABSTACTS AND BIOGRAPHIES

KEYNOTE SPEAKER: STEPHEN R. PALUMBI, PhD

BIOGRAPHY:

Jane and Marshal Steel Professor of Marine Science, Department of Biology

Harold A. Miller Director, Hopkins Marine Station

Department of Biology Stanford University

Steve's research group is engaged in study of the genetics, evolution, population biology and systematics of marine species from corals to sharks to whales. A major focus of Steve's research is on the conservation and management of marine populations, the identification of seafood products available in commercial markets, and strategies for finding and protecting the world's strongest Pacific corals. Recently elected to the National Academy of Sciences, Steve is the Director of the Hopkins Marine Station, a member of the Management Committee for the Center for Ocean Solutions, a Senior Science Advisor for the Communications Partners for Science and the Sea, and a board member for several conservation organizations. His work has been used in design of the current network of marine protected areas in California, seafood labelling laws in Japan and the United States, and in numerous TV and film documentaries.

Steve's latest book for non-scientists, *The Extreme Life of the Sea*, is about the amazing species in the sea, written with Steve's son and novelist Anthony. Previous books were *The Death and Life of Monterey Bay: A Story of Revival* and *The Evolution Explosion.*

ABSTRACT:

The Use of Genetic Data for Marine Population Inferences in the Age of Genomics: The Expanded Impact of Supergenes, Selection and Genomic Architecture

TO BE PROVIDED

NINA OVERGAARD THERKILDSEN, PhD

BIOGRAPHY:

Nina Overgaard Therkildsen is an assistant professor in the Department of Natural Resources at Cornell University. She is keenly interested in developing ways to leverage genomic analysis for improving fisheries management and marine conservation. Using both contemporary and historical DNA samples, her research aims to characterize population structure in exploited species and shed light on how different populations respond to fishing pressure and other human-induced impacts. She holds a PhD in fish population genetics from the Technical University of Denmark, an MSc in biology from the University of Copenhagen, Denmark and a BA in human ecology from College of the Atlantic, ME.

ABSTRACT:

Genomic underpinnings of fisheries-induced evolution

A growing body of evidence suggests that the strong mortality fishing imposes on particular size and age groups has caused notable changes in heritable life history traits in many exploited fish stocks. Such rapid evolutionary change is of concern because it may compromise stock productivity and resilience to overfishing. In wild fish stocks, it is, however, often difficult to fully disentangle genetic from environmentally induced changes and to distinguish selection caused by fisheries from selection driven by other factors. To get a basic understanding of how fisheries selection may affect the exploited populations at the molecular level, we have returned to a seminal experiment that under highly controlled conditions demonstrated substantial evolution in growth rates and a suite of correlated traits in response to size-selective fishing over just five generations in the Atlantic silverside (*Menidia menidia*). I will present results from an exome-wide scan for genomic changes underlying these phenotypic shifts. The results provide a first look into the genomic basis for fisheries-induced evolution and shed light on what types of genetic variation and physiological pathways fisheries-selection acts on, how extensively it impacts the genome through direct and indirect effects, and how reversible the changes are once fishing stops. These insights should provide a better understanding of how fisheries-induced selection operates and what signatures we may expect in affected natural populations.

IAN BRADBURY, PhD

BIOGRAPHY:

Dr Ian Bradbury is a research scientist with the Department of Fisheries and Oceans and is the Cox Fisheries Scientist in residence at Dalhousie University. Originally from Newfoundland he completed his PhD in 2007 at Dalhousie University and started with DFO in 2010. His research uses genomic tools to inform the conservation and management of both marine and anadromous species from throughout Atlantic Canada. Specific work focuses on identifying the genomic basis of marine climate associated adaptation, developing genetic baselines for individual identification in multiple species, and quantifying the impacts of escaped farmed salmon on wild populations.

ABSTRACT:

Informing fisheries management in Atlantic Canada through the emerging field of fisheries genomics

Advances in DNA sequencing technology have fundamentally changed the field of population genetics, allowing genome-wide patterns of divergence and linkage disequilibrium to be examined on scales previous impossible. This presents huge potential for application to fisheries management, but also brings challenges both logistical and theoretical. Here I explore potential advances that the emerging field of population genomics may hold for fisheries management, focusing on the benefits, limitations, and the challenges that remain. Specifically, I will examine how a high resolution genome-wide perspective can alter our interpretation of marine population structure, contributes to our understanding of fishery associated exploitation, and enhances predictions of future stock productivity and distribution patterns. Genomic studies increasingly report cryptic diversity in exploited marine species, which is revealing a need for changes in the geographic scales of management, but also complicated by substantial variation in differentiation across the genome and among methods. Using new genomics-based descriptions of stock structure, stock specific exploitation can be resolved at spatial scales previously not possible. However, logistical challenges such as the design and assessment of informative panels of loci from huge datasets remains a source of significant bias and error. Similarly, marine genomic data integration with high resolution environmental and habitat data are allowing the prediction of future distribution patterns under marine climate change scenarios. Genomic applications in fisheries science offer the potential for significant advances to the management of marine resources, yet will require continued consideration of the logistical and theoretical limitations if potential gains are to be fully realized.

CINDY LAWLEY, PhD

BIOGRAPHY

Cindy comes from a background in Marine Science and Business Development. She holds a PhD in Biological Oceanography (Scripps Institution of Oceanography, UCSD) where she used genetic method as tools to study marine fish populations around the Channel Islands in southern California. She also holds a Master's in Evolutionary Biology (SDSU), a Bachelor's of Science and a Single Subject Teaching Credential (UCSB). Cindy has spent the last 13 years at Illumina, a company with technology that has been pivotal to driving down the cost barriers to implementing genetic tools. She has extensive experience developing genetic and genomic based solutions to improve our understanding of human health as well as production traits in agriculture species. For example, Cindy was part of the award-winning technology transfer project to develop bovine genomic products resulting in a transformation in the dairy industry through implementation of genomic selection. Her mission is to lower the barrier of entry for implementing scalable sequencing and genotyping solutions in the areas of precision breeding, wildlife conservation, fisheries, oceanography and food safety.

ABSTRACT

Discovery to deployment: use of molecular methods to improve aquaculture production

Genotyping and skim sequencing offer a low cost way to characterize genetic information across lines of interest in both plant and animal breeding programs. This is key to characterize diversity in relevant lines and build precision breeding tools to improve production in commercial agriculture and aquaculture. We will compare traditional breeding to methods of breeding that implement genomic selection and describe successes in genomic breeding focusing on livestock and aquaculture.

JOSEPH BUTTNER, PhD AND JASON BROWN, PhD

BIOGRAPHIES:

Dr. Joseph Buttner is a Professor in the Department of Biology, Outreach Specialist for the Cat Cove Marine Laboratory and Co-coordinator of the Northeastern Massachusetts Aquaculture Center at Salem State University (SSU) in Salem, MA. Dr. Joe joined SSU in 1997 after working with finfish culture in ponds, recirculating aquaculture systems and the Great Lakes. He is a *Certified Fisheries Professional*, initially in 1984; renewed in 2008 and 2014, by the American Fisheries Society and a USDA Designated Extension Contact for aquaculture in Massachusetts. A *Life Member* of the American Fisheries Society, *Charter Member* of the East Coast Shellfish Growers Association, and *Trustee* for the Massachusetts Aquaculture Association, Dr. Joe maintains membership in over a half dozen professional associations. He pursues an active research and outreach program that involves students in collaborative projects as illustrated by his authorship or co-authorship on more than 100 published articles, half peer reviewed and half for technical/lay audiences. Over $2 million in external funds have been secured to support research and students. Current research projects focus on subtidal culture of softshell clams, aquaponics in temperate latitudes, zebrafish culture, and pond culture in Liberia

supported by the Fulbright Program and U.S. State Department. As a faculty at SSU, Dr. Joe supervises and instructs students in the Aquaculture Concentration, as well as teaching courses in Biology for nonmajors, majors and graduate students.

Dr. Jason Brown is an Assistant Professor of Biology at Salem State University with a teaching focus in genetics. In his research, he uses molecular, biochemical, and imaging techniques to understand the assembly and function of cilia with a primary focus on genes implicated in human disease. Before his appointment at Salem State in 2014, he was a postdoctoral fellow funded by an NIH Individual National Research Service Award in the Department of Cell and Developmental Biology at the University of Massachusetts Medical School. Dr. Brown has co-authored 15 peer-reviewed publications, including 7 as first or co-first author. He has also mentored 14 research students, including undergraduate and master's students, some of whom have gone on to win university and national (ASCB) awards for their work. Dr. Brown is a member of Genetics Society of America, American Society for Cell Biology, and Sigma Xi, the scientific research society.

ABSTRACT:

Aquaculture in Massachusetts and Genomics

The FAO characterizes aquaculture as the aquatic equivalent of terrestrial agriculture. Aquaculture includes the farming of animals, plants and algae. It is pursued in fresh, brackish and marine waters. Level of management and exogenous energy use intensify as production occurs in open, semi-closed, or closed systems. Aquatic organisms are grown primarily for human food, but organisms are also produced and maintained for research, instruction, biotechnical, ornamental, restoration and enhancement, preservation of endangered species and other uses.

In Massachusetts many forms of aquaculture are pursued, but production of bivalve mollusks dominates as oysters, quahogs, and to a lesser degree softshell clams and blue mussels are reared in coastal, marine waters. Most production targets the gourmet market as opposed to commodity markets. Given the Commonwealth's history, tradition and demographics, other aquaculture pursuits more appropriate for Massachusetts exist including production of zebrafish for biomedical research, aquaponics for year-round sustainable production of finfish and vegetables, and gamefish for recreational angling.

The NorthEastern Massachusetts Aquaculture Center housed at Salem State University's Cat Cove Marine Laboratory (CCML) was established in 1997 to service the needs and nurture opportunities for aquaculture in northeastern Massachusetts. Since opening in April 1999, CCML has produced over 41 million softshell clams that have been distributed to more than 40 communities in Massachusetts. Activities have evolved beyond traditional aquatic husbandry to collaborative efforts that embrace and involve biotechnology such as the fledgling collaborative project with the Gloucester Marine Genomics Institute (GMGI) *A Genomic Approach for Selection of SSCs (Mya arenaria) with Enhanced Survival and Growth.* This new collaboration has not only connected GMGI with Salem State University (SSU), but has also helped more closely connect the

organismal/environmental and molecular/cell biology sides of the SSU Biology Department.

ANDREA BODNAR, PhD

BIOGRAPHY:

Andrea is a Biochemist whose research interests lie at the intersection of marine biology and human health. With experience in both academic and industry settings she brings a unique perspective to the marine sciences with a particular interest in marine biotechnology and biomedicine. Prior to joining GMGI as the Science Director, Andrea was a Senior Scientist in the Molecular Discovery Lab at the Bermuda Institute of Ocean Sciences (BIOS). At BIOS, her research program focused on using sea urchins as models to understand the cellular and molecular mechanisms underlying extreme longevity, negligible aging and naturally occurring resistance to cancer. Prior to that, Andrea held Senior Scientist positions in the Oncology Department of Hoffman-La Roche, the Department of Cell Biology and Pharmacology at Geron Corporation and the Bioprocessing Technology Institute at the National University of Singapore. She received a BSc and PhD in Biochemistry from McMaster University in Canada and conducted post-doctoral studies in the Department of Neurological Science at the University of London.

ABSTRACT:

Marine Biotechnology: Exploring the Genetic Diversity of the Sea

As the largest reservoir of biodiversity on the planet, the marine environment offers tremendous opportunity for new discoveries to advance biology and medicine. The unique biological and chemical adaptations of marine organisms have made then valuable models for biomedical research as well as sources of novel therapeutic compounds and enzymes for biotechnology applications. Marine animal models have enhanced our understanding of fundamental biological processes including many that are relevant to human health. To date there have been six Nobel Prizes awarded for research conducted using marine animals that have contributed to our understanding of cellular immunity, nerve conduction, photoreceptor function, cell division, and the process of learning and memory. Chemical adaptions of marine organisms have yielded novel and potent drugs for the treatment of human disease with nine FDA-approved marine-derived drugs currently on the market for indications such as cancer, pain and infectious disease. Advances in next-generation sequencing are providing unprecedented access to information encoded in the genomes of marine organisms, providing a sustainable and cost-effective approach to explore their biological and chemical diversity to the fullest. Gloucester Marine Genomics Institute aims to apply the most innovative genomic technologies to marine science to accelerate new discoveries that impact biomedicine and biotechnology as well as fisheries and aquaculture.

BRAM LUTTON, PhD

BIOGRAPHY:

Bram Lutton is an Associate Professor of Biology and Biotechnology who began teaching at Endicott College in 2009, following a postdoctoral fellowship at Massachusetts General Hospital and Harvard Medical School and a visiting professorship at Franklin W. Olin College of Engineering. Dr. Lutton received a Bachelors degree from Colby College, along with Masters and Doctoral degrees in Physiology from Boston University. His research is focused on evolutionary, cellular, and molecular mechanisms of reproductive endocrine-immune interactions. Dr. Lutton has supervised numerous high school and undergraduate students pursuing graduate, medical, and veterinary degrees, as well as careers in the biotechnology industry. He feels strongly about promoting discovery science and fostering interdisciplinary collaborations among colleagues; to this end he has coordinated national conference symposia focused on dismantling the barriers between investigators studying various model species from basic science and clinical perspectives since 2006. Dr. Lutton chairs the Educational Council for the Society for Integrative and Comparative Biology and is a member of the Professional Societies Alliance for Life Science Education and the Sigma Xi National Honor Society.

ABSTRACT:

The Little Skate (Leucoraja erinacea) as a model for studies of hematology and immunology.

Understanding hematopoietic stem cell (HSC) activity has been imperative to investigators who attempt to manipulate these cells for various clinical purposes. A mechanistic understanding of immune function through evolutionary time is therefore imperative for clear comprehension of the complex interactions between physiological systems. *Leucoraja erinacea* may serve a unique role in these studies as this model lacks an endosteal (bone) niche, such as that which houses mammalian bone marrow. While this mammalian compartmentalization is protective, it is an obstructive barrier for studies aiming to understand neuroendocrine-immune crosstalk. *L. erinacea* possesses unique and specialized organs, similar in function to mammalian bone marrow but composed of only stromal niche, without bone; it is within these organs that HSC are maintained. While many molecular and cellular interactions modulate HSC activation and the production of immune cells, the chemokine receptor-ligand pair, CXCR4-CXCL12, plays a crucial role in maintenance of homeostasis in bone marrow. Inhibiting this molecular tethering with clinical agents, such as Plerixafor, activates HSC and leads to mobilization of cells from the bone marrow in humans. Our lab has identified and annotated CXCR4 and CXCL12 expression in *L. erinacea* using genomic and transcriptomic sequence information, and we've found that *L. erinacea* treated with Plerixafor exhibited significant leukocyte mobilization. Moreover, we have identified for the first time the presence of secondary immune organ function in the unique hematopoietic organs of *L. erinacea* following parasitic infection. Therefore, important and novel implications exist for the *L. erinacea* model in hematological and immunological studies.

STACEY GOLDBERG

BIOGRAPHY:

Stacey R. Goldberg, originally from Maryland, is currently in the final stages as a PhD candidate at University of Prince Edward Island (UPEI), Canada in the Biomedical Science department of the Atlantic Veterinary College (AVC). She studies alongside an exceptional group of faculty, scientists and students in the Marine Natural Products Lab under the advisorship of Dr. Russell Kerr. Her career has taken a circuitous route beginning when she received her BS in Marine Biology from Towson University in Baltimore, and shortly thereafter accepted a position in a cancer research and vaccine development lab at Johns Hopkins University (JHU). She completed her MS at JHU in Biotechnology while working as a full-time employee. She then moved on to a research associate position at AERAS Global, a non-profit organization for tuberculosis vaccine development, funded mainly by the Bill and Melinda Gates Foundation. Here she did exceedingly well in the immunology department by optimizing technologies, particularly flow cytometry and FACS, for the purposes of assessing vaccine efficacy in clinical trials. As such, she was promoted to a research specialist position within a year of employment, with a few direct reports. She took the opportunity of management very seriously, and AERAS was willing to fund her requests to attend a management course. The next stage in her career was to go back to her roots by merging marine science with that of her expertise in biotechnology. She was offered an opportunity to do so with BIOS (Bermuda Institute of Ocean Sciences) working with phytoplankton, and was eager to accept it and move to the island. This position was very challenging as it was somewhat of a novel field of study for her. Yet, she was able to excel in this position as the sole flow cytometry technologist by using FACS to sort cells (microalgae) in the lab and in 'real-time' at sea. After 2 years of oceanographic research, again Stacey wanted to challenge herself further to pursue higher education in an area of study that would even more so combine fields of marine biology, biotechnology, and chemistry; this is what led her to her present studies at UPEI in marine natural products research. She received a 3-year postgraduate scholarship through NSERC (Natural Sciences and Engineering Research Council of Canada) and is currently writing her dissertation to be defended by the end of 2017.

ABSTRACT:

Cultivation of Bacteria Associated with Marine Sponges and

Genomic Mining for Novel Enzymes Involved in Halogenation of Natural Products

S. Goldberg[1], B. Haltli[1,2], H. Correa[2], R. Kerr[1,2]

[1] Department of Biomedical Sciences, Atlantic Veterinary College, Charlottetown, PEI

[2] Department of Chemistry, University of Prince Edward Island, Charlottetown, PEI

Marine sponges historically have been a major research interest for two main, and often interrelated reasons: they are reservoirs for abundant and diverse microbial communities and are rich sources of structurally diverse, pharmacologically relevant natural products. A common feature of secondary metabolites isolated from marine sponges is the presence of a halogen functional group, which in many cases is required for the biological activity. There is increasing evidence that in some cases symbiotic microbes are the true producers of secondary metabolites, rather than the invertebrate host. However, culturing novel and diverse microbes under traditional laboratory conditions remains an obstacle, thus access to their secondary metabolome is limited. The objective of this research was to first assess the cultivable bacterial consortia of four marine sponges known to contain halogenated natural products, in comparison to the surrounding seawater and sediment. By using a variety of growth media to increase diversity, a bacterial library consisting of 915 isolates was established from all sources, and reduced to a total of 112 OTUs according to 16S rRNA gene sequencing. Secondly, interspecific bacterial diversity of each sponge species versus surrounding sediment and seawater was assessed. Additionally, a total of 16 isolates from the full library were considered unclassified (putatively novel), and six of these were phylogenetically classified and described as novel species according to polyphasic analysis. Finally, in order to increase the likelihood of identifying halogenated compounds in culture, we screened the entire library of cultivated bacteria for genes involved in halogenation. Using PCR primers that were successful in identifying novel genes encoding flavin-dependent halogenases (Hentschel et al., 2012), we were able to amplify partial sequences of genes encoding halogenase enzymes in five *Streptomyces* isolates. However, we were not able to identify by UPLC-HRMS any associated halogenated metabolites in culture when using a variety of fermentation conditions, suggesting that the halogen-associated gene clusters may be cryptic in these strains. Exploring new cultivation techniques to increase microbial and in turn enzymatic diversity, as well as induction efforts to elicit production of halogenated metabolites, may be a pathway for future work.

JESSICA MARK WELCH, PhD

BIOGRAPHY:

Jessica Mark Welch is an Associate Scientist at the Marine Biological Laboratory in Woods Hole, Massachusetts. She uses genomics and fluorescence microscopy to investigate the spatial organization and function of complex natural microbiomes. Dr. Mark Welch received her Ph.D. from the Department of Molecular and Cellular Biology at Harvard University in 2001.

ABSTRACT:

Spatial Organization of Host-Associated Microbiomes at the Micron Scale

The spatial organization of complex natural microbiomes at the micron scale is almost entirely unexplored, yet it is critical to understanding the interactions of individual taxa responsible for generating the emergent properties of the community. Building on ribosomal RNA sequence analysis, we have developed a method for analyzing micron-scale spatial organization of microbiomes that we call CLASI-FISH (Combinatorial Labeling and Spectral Imaging - Fluorescence *in situ* Hybridization). Application of this method to human dental plaque revealed a complex and highly organized consortium that provides a framework for understanding the metabolic interactions and community structure of plaque. Application of the method to a gnotobiotic gut microbiome revealed a surprising degree of spatial mixing at scales from microns to hundreds of microns, challenging the view that the mucosal epithelium and the lumen of the gut are distinct and stratified compartments. The CLASI-FISH method is applicable to a wide range of host-associated and environmental microbiomes; initial evidence suggests that it can be applied, for example, to investigate the microbiomes associated with the surface of kelp and the digestive tracts of marine organisms. This method should be useful in moving toward a mechanistic understanding of the key role that host-associated microbiomes can play in the biology of their hosts.

DON ANDERSON, PhD

BIOGRAPHY:

Senior Scientist

Woods Hole Oceanographic Institution

Don Anderson is a Senior Scientist in the Biology Department of the Woods Hole Oceanographic Institution. He earned three degrees from MIT – a BS in Mechanical Engineering in 1970, and a MS (1975) and PhD in Civil and Environmental Engineering in 1977. He joined the scientific staff at WHOI in 1978. In 1993, he was awarded the Stanley W. Watson Chair for Excellence in Oceanography, in 1999 was named a NOAA Environmental Hero, and in 2006 received the Yasumoto Lifetime Achievement Award from the International Society for the Study of Harmful Algae (ISSHA). Anderson is the former director of WHOI's Coastal Ocean Institute (COI), and presently serves as Director of the Cooperative Institute for North Atlantic Research (CINAR). Anderson also serves as Director of the U.S. National Office for Harmful Algal Blooms.

Anderson's research focus is on toxic or harmful algal blooms (HABs), commonly called "red tides". His research ranges from molecular and physiological studies of growth, sexuality, and toxin production to the large-scale oceanography and ecology of the

"blooms" of these microorganisms, including numerical modeling, forecasting, and a range of monitoring and management strategies, many reliant on novel instrumentation and biosensors. Along with an active field and laboratory research program, Anderson is heavily involved in national and international program development for research, monitoring, and management of red tides, marine biotoxins, and HABs. He has testified multiple times before Congressional committees, and has been actively involved in legislation and appropriations related to HABs and hypoxia. He is also an advisor to multiple foreign countries and international aid organizations in the evaluation or creation of management programs for HABs.

Anderson is the author, co-author, or editor of over 300 scientific papers and 14 books.

ABSTRACT:

Novel insights into harmful algal bloom (HAB) dynamics using

in situ autonomous biosensors

Donald M. Anderson and Michael L. Brosnahan

Blooms of the toxic dinoflagellate *Alexandrium fundyense* cause recurrent outbreaks of paralytic shellfish poisoning (PSP) throughout the world. In our recent studies, we co-deployed two autonomous biosensors – the Environmental Sample Processor (ESP) and the Imaging FlowCytobot (IFCB) - from a specially built observatory platform. The ESP uses molecular assays to detect and analyze cells and toxins whereas the IFCB is an automated underwater microscope. These instruments have typically been deployed separately, but in 2016, were used concurrently during a major *A. fundyense* bloom for the first time. The raft also supports other sensors on an automated winch profiler that records salinity, temperature, chlorophyll, and other parameters through the full depth of the study site several times per hour. Together, these in situ technologies are providing extraordinary insights into processes underlying *A. fundyense* blooms that challenge our understanding based on culture studies. Specifically, field populations swim and migrate faster (>2X), divide faster (> 2X), produce more gametes (4X) and are more toxic (>4X) than indicated from culture experiments using local isolates. The implications of these findings are profound: 1) culture-based assessments have substantially underestimated the true growth and toxigenic potential of blooms of *Alexandrium* and presumably, other harmful algal bloom (HAB) species; and 2) our ability to understand and forecast HABs requires characterization of critical rates and behavioral patterns in natural populations, generated, whenever possible, through in situ observations. Optical and molecular technologies will play a major role in these future studies.

DAVID SHERMAN, PhD

BIOGRAPHY:

Prof. Sherman received his B.A. in chemistry at UC Santa Cruz (1978) and Ph.D. in synthetic organic chemistry at Columbia University with Gilbert Stork (1981). After working at Biogen Research Corporation, he moved to the John Innes Institute as a research scientist with Sir Prof. David A. Hopwood (1987-1990). Following 13 years at the University of Minnesota, Prof. Sherman moved to the University of Michigan and is now the Hans W. Vahlteich Professor of Medicinal Chemistry, Professor of Chemistry, and Professor of Microbiology & Immunology. Sherman's laboratory is in the U-M Life Sciences Institute where his research focuses on the discovery and analysis of bioactive natural products and their metabolic pathways from marine bacteria and fungi.

Dr. Sherman was founding Director of the Center for Chemical Genomics at the University of Michigan Life Science Institute (2004 – 2013). LSI maintains core facilities covering the areas of high throughput screening and drug discovery, structural biology and protein production with resources to support cross-disciplinary science including genetics; genomics and proteomics; molecular and cellular biology; and structural, chemical and computational biology. Sherman now serves on the advisory board for the UM Center for the Discovery of New Medicines.

Notable Awards: A. C. Cope Scholar Award (ACS), Fellow, American Association for the Advancement of Sciences (AAAS), Charles Thom Award (Society for Industrial Microbiology and Biotechnology), Distinguished Lecturer Award (American Society for Microbiology)

For more information please see: http://www.lsi.umich.edu/labs/david-sherman-lab

ABSTRACT:

"Function and Structure of the Biochemical Machines that Generate Pharmaceuticals from Diverse Microbes"

TO BE PROVIDED