# [ACF 2014 July - September Presentations](#_Toc447117146)

***[Bjorkman, Beth 1](#_Toc447117147)***

[***Brown, William 1***](#_Toc447117148)

[***DeHart, Abigail 2***](#_Toc447117149)

[***Dykstra, Michael 3***](#_Toc447117150)

[***Hogan, Joseph 3***](#_Toc447117151)

[***Hundley, Zachary 4***](#_Toc447117152)

[***LaFleur, James 5***](#_Toc447117153)

[***Moore, Eric 6***](#_Toc447117154)

[***O'Brien, Amanda 7***](#_Toc447117155)

[***Schneider, Patrick 8***](#_Toc447117156)

[***Shatsky, Adam 9***](#_Toc447117157)

[***Smith, Kathryn 9***](#_Toc447117158)

[***VanOevern, Sarah 10***](#_Toc447117159)

**ACF 2014 July - September Presentations**

**Bjorkman, Beth**

July - September FY14

Mathematical Association of America (MAA) Mathfest

"Graph Theoretic Models of Interdependent Preferences in Referendum Elections"

In referendum elections, voters are frequently required to cast votes simultaneously on multiple questions or proposals. The separability problem occurs when a voter's preferences on the outcome of one or more proposals depend on the predicted outcomes of other proposals. These kinds of interdependencies cannot be fully expressed in a simultaneous election. When voters are forced to separate issues that may be linked in their minds, the resulting election outcomes can be unsatisfactory or even paradoxical. In this talk, we will use graph theoretic models to characterize, construct, and better understand interdependent voter preferences in referendum elections. We will also explore connections between these models and prior research on the structure of interdependent multidimensional preferences. This work was completed as part of the Grand Valley State University Summer Mathematics REU.

**Brown, William**

July - September FY14

2013 Michigan Council of Teachers of Mathematics (MCTM) Annual Conference

"Adventures with Mathematics, Grades 3-5 / Adventures with Mathematics, Grades K-2 / Engaging Families in Mathematical Learning"

Adventures with Mathematics, Grades 3-5 Room A102/103 Char Beckmann, Grand Valley State University Bill Brown, Grand Valley State University Katie Smith, Grand Valley State University Megan Frame, Eastern Michigan University Upper Elementary General interest Looking for ways to engage students in mathematics in and outside of school? Adventures with Mathematics includes games, activities, and problems aligned with the CCSS. Adventures with Mathematics, Grades K-2 Room A102/103 Char Beckmann, Grand Valley State University Bill Brown, Grand Valley State University Katie Smith, Grand Valley State University Megan Frame, Eastern Michigan University Early Elementary General interest Looking for ways to engage students in mathematics in and outside of school? Adventures with Mathematics includes games, activities, and problems aligned with the CCSS. Engaging Families in Mathematics Learning Room A102/103 Char Beckmann, Grand Valley State University Bill Brown, Grand Valley State University Katie Smith, Grand Valley State University Megan Frame, Eastern Michigan University Early elementary, Upper elementary, Middle school General interest What to do when kids are out of school? Play with mathematics! We will share several engaging activities suitable for home, family math events, out on a eld day, and classrooms.

**DeHart, Abigail**

July - September FY14

2nd International Conference on Business Social Partnership: Towards Value Based Social Engagement

"Self-Interest, Sympathy, and Social Entrepreneurship"

Traditionally, economic models and theories are based on some form of rational choice theory, supposing consumers make decisions based on calculated self-interest. Historically, this has also been the assumption about classical economist Adam Smith and his work Wealth of Nations, associating both with the term homo economicus because his theory entails structuring a self-interested society in economically beneficial ways. However, this interpretation of Wealth of Nations is too narrow because it neglects a crucial element to his analysis i.e., the role of sympathy for a stable and economic order. Smiths larger humanitarian purpose was to balance concern for the poor with the reality that some degree of self-interest is essential for upward mobility. To Smith, ethics was an integral part of economics. This paper will reexamine Smiths account of the sociability of man, especially his account of the plurality of motivations in order to evaluate modern instances where traditional rationality models may not be enough, specifically when accounting for philanthropic organizations and social entrepreneurial movements. As some dissenters of rational choice theory point out, individuals do not always make rational and utility-maximizing decisions. Furthermore, because social entrepreneurs often face scenarios that are constantly changing, behavioral economics is becoming increasingly relevant and necessary when experiencing, what would be traditionally labeled, irrationalconsumer behavior. Revisiting conversations about Smiths role of sympathy as it relates to self-interest will suggest there are alternate human motivations causing us to act, and are worth examining because of their modern implications.

**Dykstra, Michael**

July - September FY14

The Sixth Annual World Molecular Imaging Congress

"Development of A Quality Control Protocol to Assess the Feasibility of Cerenkov Luminescence Imaging. A Mathematical Method to Estimate CCD Saturation of Cerenkov Luminescence Imaging"

There are approximately 40 million foreign-born persons living in the United States, accounting for 13% of the total population. Mental health practitioners are finding that some of their clients are foreign-born persons with limited English proficiency. This session lecture will provide skills for working effectively with interpreters to enhance service delivery to clients with limited English proficiency. Objectives " How to use interpreters effectively in mental health. " Challenges that may arise when working with interpreters in a mental health setting. " Training interpreters to work with mental health practitioners.

**Hogan, Joseph**

July - September FY14

2013 Southern Writers, Southern Writing Graduate Conference

"Authenticity and the"

An analysis of the character John Grady Cole, the Stoic, John Wayne-ian protagonist in Cormac McCarthys All the Pretty Horses, calls attention to the novels placement in the tradition of the American Western. However, when considering Grady Cole in relation to the genre, it becomes quite easy to overstate the extent to which the novel relies on empty cultural constructions and clichés like the rough-ridin cowboy of American cinema. This essay considers how one such reading of All the Pretty HorsesSarah Gleeson-Whites 2007 article in Southwestern American Literatureoveremphasizes the novels reliance on genre and, in so doing, wrongly ascribes to its protagonist a certain nostalgia and inauthenticity that affirms the deadness of the Old West. This essay first admits that Gleeson-Whites analysis rightly places the novel in the context of the cinematic American Western tradition, but posits that its preoccupation with intertextuality and empty cultural artifact obfuscates a central element of the text from the readers critical eye: namely, the extent to which McCarthy presents his protagonists code as entirely authentic. Accordingly, in this essay, I challenge the notion that All the Pretty Horses derives its meaning from the empty cultural construction of the Old West. Further, I examine the ways in which such a reading would undermine the novels philosophical and aesthetic significance. In all, I call for the adoption of an attitude toward the text that simultaneously accounts for the novels clear relation to the cinematic Western, but also takes seriously the authenticity of John Grady Coles thoroughly Western code, encapsulated in his dictum: There aint but one truth& the truth is what happened. It aint what come out of somebodys mouth.

**Hundley, Zachary**

July - September FY14

The 27th Annual Symposium of The Protein Society

"Factors Determining Carbapenemase Activity in the OXA Family of ß-Lactamases"

Bacterial resistance to antibiotic therapies, especially to ²-lactams is a growing health-care problem. Resistance mediated by class D ²-lactamases has been both the least studied, and most rapidly expanding in the past decade. Of particular clinical concern is the emergence of class D enzymes with the ability to hydrolyze the newest family of ²-lactams: the carbapenems. Class D ²-lactamases are extremely diverse in terms of sequence and hydrolytic profiles, and it remains unclear what factors determine multispecificity in general, and carbapenemase activity in particular. Recent studies have revealed the importance of the ²5-²6 loop in acquiring carbapenemase activity1. Here we present a combined experimental and computational study of the effects that several point mutations in the OXA-24s ²5-²6 loop have on the enzyme catalytic profile. Site-directed mutagenesis and kinetic assays indeed show significant changes in the catalytic profiles of the mutant enzymes. We have employed several computational techniques, namely sequence and motif analysis, Molecular Dynamics simulations and covariance analysis based on the Anisotropic Network Model in order to determine the impact of M223A, G224D and P227S mutations on the dynamics of the OXA-24 active site. We show here that the mutations affect the dynamics of the catalytic site, specifically the carboxylated lysine residue and its hydrogen bonding network within the binding pocket. Multiple sequence alignment and motif analysis show distinct patterns of the ²5-²6 loop sequence variation in different subgroups of OXA carbapenemases. These data will help correlate the sequence traits of OXA carbapenemases to their mechanism of substrate selection and hydrolysis. 1. De Luca et al., PNAS 2011, 108, 18424.

**LaFleur, James**

July - September FY14

The 27th Annual Symposium of The Protein Society

"Factors Determining Carbapenemase Activity in the OXA Family of ß-Lactamases"

Bacterial resistance to antibiotic therapies, especially to ²-lactams is a growing health-care problem. Resistance mediated by class D ²-lactamases has been both the least studied, and most rapidly expanding in the past decade. Of particular clinical concern is the emergence of class D enzymes with the ability to hydrolyze the newest family of ²-lactams: the carbapenems. Class D ²-lactamases are extremely diverse in terms of sequence and hydrolytic profiles, and it remains unclear what factors determine multispecificity in general, and carbapenemase activity in particular. Recent studies have revealed the importance of the ²5-²6 loop in acquiring carbapenemase activity1. Here we present a combined experimental and computational study of the effects that several point mutations in the OXA-24s ²5-²6 loop have on the enzyme catalytic profile. Site-directed mutagenesis and kinetic assays indeed show significant changes in the catalytic profiles of the mutant enzymes. We have employed several computational techniques, namely sequence and motif analysis, Molecular Dynamics simulations and covariance analysis based on the Anisotropic Network Model in order to determine the impact of M223A, G224D and P227S mutations on the dynamics of the OXA-24 active site. We show here that the mutations affect the dynamics of the catalytic site, specifically the carboxylated lysine residue and its hydrogen bonding network within the binding pocket. Multiple sequence alignment and motif analysis show distinct patterns of the ²5-²6 loop sequence variation in different subgroups of OXA carbapenemases. These data will help correlate the sequence traits of OXA carbapenemases to their mechanism of substrate selection and hydrolysis. 1. De Luca et al., PNAS 2011, 108, 18424.

**Moore, Eric**

July - September FY14

Midwest Yeast Conference 2013

"Investigating the cellular interaction of Mid1 and protein phosphatase Dis2 in in Schizosaccharomyces pombe cell division"

Investigating the cellular interaction of Mid1 and protein phosphatase Dis2 in in Schizosaccharomyces pombe cell division Author: Eric Moore and Dawn M. Clifford Hart Affiliation: Grand Valley State University, Department of Cell and Molecular Biology, Allendale, MI 49401. Cell size, in accordance with shape, are principle factors contributing to the point at which a cell enters mitosis and ultimately divides into two equivalent daughters. In tandem with synthesizing the components that are essential for cell division, a determining characteristic of the G2 phase of the cell cycle is growth. In Schizosaccharomyces pombe, a concentration gradient regulates mitotic commitment with respect to cell growth. When the cell exits the DNA replicative S phase and enters the G2 phase, it is short and the majority of cell growth and elongation has yet to occur. A distinguishing feature of S. pombe cells is that they maintain a prolonged G2 phase when compared to other replication systems. At the beginning of G2 the cell is short, and as a result, there is an overlapping concentration of the negative mitotic regulator protein Pom1. As the cell elongates throughout G2, Pom1 concentration is maintained at high levels at the cell tips and progressively lower levels across the equator. Concurrently, positive mitotic regulators Cdr2 and Mid1 are restricted to the equator of the cell where the nucleus resides. Dis2 phosphatase at the cell tips leads to Pom1 binding the cortex. As Pom1 migrates towards the center of the cell from either tip, it autophosphorylates and dissociates from the cortex. Pom1 then migrates back towards the cell tip where Dis2 dephosphorylates it and the concentration gradient is maintained as the cell elongates. This trend continues until a growth threshold is reached where Mid1 has localized to the cortical interphase nodes and sets the stage for divisional septum formation. Mid1 serves as the scaffold that recruits proteins associated with the actin contractile ring, such as IQGAP protein Rng2 and myosin II essential light chain Cdc4, among various other proteins. Mid1 dissociates from the contractile ring as Sid2, the most downstream SIN kinase, is displaced from the spindle pole body to the division site to initiate contractile ring constriction. Though these interactions of Mid1 have been elucidated, many other Mid1 protein interactions may exist within the cell. A tandem affinity purification revealed Dis2 as a potential binding partner of Mid1, an interaction which has not yet been characterized. Preliminary results affirm that Dis2 dephosphorylates Mid1 in vitro. Mid1-GFP localization exhibits broad cytoplasmic distribution in dis2” cells when visualized in vivo. The principle aim of this investigation is to further elucidate the interactions between Mid1 and Dis2 and the factors that lead to their association. Grand Valley State University, Department of Cell and Molecular Biology, Allendale, MI 49401. This research is supported by National Science Foundation RUI Award #1157997.

**O'Brien, Amanda**

July - September FY14

The 27th Annual Symposium of The Protein Society

"Mechanism of Telomerase Inhibition by Novel Non-Nucleosidic Drug Candidates"

Telomerase is a reverse transcriptase enzyme that synthesizes and adds telomeric DNA repeats to the ends of linear chromosomes. Normal somatic cells show very low telomerase activity and thus a limited capacity for proliferation. However, majority of cancer types have the ability to overexpress telomerase, which enables the cancer cells to divide uncontrollably. This makes telomerase an important anti-cancer drug target and designing an effective inhibitor of telomerase will potentially aid cancer therapy in all telomerase-expressing tumors. Here we present the results of computational modeling of interactions between the telomerase TERT domain and several non-nucleosidic drug candidates. On the basis of our protein-ligand docking simulations, domain motions, and bioinformatics analysis, we identified several different modes of drug binding to telomerase leading to inhibition of its TERT domains function via distinct mechanisms. Non-nucleosidic drugs are postulated to affect telomerase processivity. The binding modes presented here support this hypothesis, especially through involvement of the Fingers subdomain and changes in the protein dynamics. Our results will aid and inform further efforts in inhibitor design and optimization.

**Schneider, Patrick**

July - September FY14

Midwest Yeast Conference 2013

"Codifying the proteins involved in the nuclear localization of the Mid1 protein in fission yeast cell division"

The ability for Schizosaccharomyces pombe to undergo a successful round of cell division is contingent upon the regulation of protein rich punctate structures embedded within the medial regions of the yeast's cytoplasmic membrane. Cell cycle progression is directly correlated to fluctuations in the protein composition of these node-like frameworks. Mid1 is a prominent nodal protein that acts as a recruitment tool necessary to correctly assemble the contractile ring late in mitosis. During interphase, Mid1 localizes heavily within the nucleoplasm. Upon mitotic onset, a significant efflux of Mid1 from the nucleus is observed. This Mid1 emigration from the nucleus is regulated by the polo-like kinase Plo1. While this mechanism largely accounts for Mid1s cytoplasmic aggregation, little is known about the proteins involved in the extensive localization of Mid1 within the nucleus during interphase. Our ongoing research implicates Sid2 kinase as a viable candidate for such a task. Here we establish Mid1 as a substrate for Sid2 phosphorylation as well as Mid1s inability to enter the nucleus upon mutating its Sid2 consensus motifs. In addition to these phosphorylation regions, there exists a classical nuclear localization sequence within Mid1s protein domain map. Its presence suggests the use of importin proteins to import Mid1 to the nucleus directly. Fission yeast contain two importin ± genes, imp1 and cut15, which may assist in Mid1s movement. Upon establishing the importin proteins responsible for Mid1s nucleocytoplasmic transport, the phosphorylation status of Mid1 will be investigated, as it may serve as a marker that affects its binding ability with the transport molecules. Furthermore, studies using importin ± orthologs have shown that they are phosphorylated by casein kinase II. Similar assays will be done to determine if this event is consistent within S. pombe, and if the potential phosphorylation of Imp1 and Cut15 affect Mid1 localization as well as their own. By determining mechanisms involved in Mid1s voyage during the cell cycle, cogent prospects can be made about points of regulation that contribute to Mid1 protein function.

**Shatsky, Adam**

July - September FY14

Montana State University Philosophy Conference

"Why Compatibilists cannot resist Prepunishment: A Defence of Smilansky"

No Abstract.

**Smith, Kathryn**

July - September FY14

2013 Michigan Council of Teachers of Mathematics (MCTM) Annual Conference

"Adventures with Mathematics, Grades 3-5 / Adventures with Mathematics, Grades K-2 / Engaging Families in Mathematical Learning"

The Adventures in Mathematics books were created to engage students in mathematics during the summer in everyday settings, however many teachers have found uses for the activities in their classrooms. Presenting these books and activities give teachers additional resources. The Engaging Families in Mathematics Learning session includes activities and games created by my classmates and me as fun activities to be used inside or outside of the classroom to encourage students, teachers, and parents to think of their world from a mathematical lens. We don't realize how many things we do on a daily basis that involve math! We want to provide teachers with a way to help students and parents realize this. Each presentation will be a brief description of the books or projects followed by time for the attendees to participate in each activity, gain resources, and ask questions. As a presenter at the conference, I will facilitate one activity each session. From this presentation, we hope to gain feedback for improvement on the current activities and ideas for new ones. When not presenting, I will attend other presentations to gain resources and information on how to effectively teach mathematics to all students I will have in my future classroom. Specifically, I hope to gain knowledge of the Common Core State Standards and learn of ways to meet the standards and reach all of my students which I can apply in my student teaching placement at Muskegon High School in the fall.

**VanOevern, Sarah**

July - September FY14

Midwest Yeast Conference 2013

"Identification of potential cytoskeletal proteins as binding partners of Mid1 in Schizosaccharomyces pombe"

The anillin-like protein, Mid1 in Schizosaccharomyces pombe is responsible for recruiting the necessary cytoskeleton proteins to the medial plane of the cell to assemble the actin-myosin contractile ring during cytokinesis. This final step in cell division is a highly dynamic process that results in ultimate division of the cell into daughter cells. Orientating the contractile ring to the proper site of cell cleavage is vital to the equal distribution of genetic material. Mid1 contains several protein binding domains important for proper contractile ring formation, yet a complete understanding of Mid1 interactions has not been attained. To identify Mid1 binding proteins at the contractile ring, tandem affinity purification (TAP) complexes were isolated from mitotic extracts expressing TAP-tagged versions of Mid1. Using mass spectrometry for identification, several cytoskeleton proteins, such as Rho1 and Cpc2, were identified as potential binding partner of Mid1. Rho1, a small GTPase, is characterized for its role in myosin activities and actin assembly. This protein is known to be required for cytokinesis and accumulates in the equatorial region immediately before cell division. Cpc2, a RACK1 homolog, has a more global role and is implemented in translation of specific mRNAs and cytoskeleton integrity under certain stress conditions. Whether these cytoskeleton proteins physically interact with Mid1 is of important interest. Here, we hypothesis that Rho1 and Cpc2 can bind to Mid1 and may be important for both the formation of and stability of the contractile ring. This research is supported by a National Science Foundation RUI Award #1157997.