ASM Intermountain Branch Meeting
April 13, 2019

8:30 – 9:00 **Registration** / Poster Set-up / Continental Breakfast

9:00 – 10:00 **Opening Session (2254 CONF CENTER)**
Welcome
Keynote Address
Dr. John S. Parkinson "*Dissecting the Three-Protein Brain of E. coli*"

10:00 – 11:00 **Oral Presentations 1** 2265 CONF Center. (10 min talks for graduate students / 8 min talks for undergraduates)

Session 1A. 2265 CONF Center

Landon Barlow	Borrelia burgdorferi Biofilm: An Investigation Into Growth and Control of an Alzheimer's Disease-Associated Bacterium
Daphne Skordas	Microbiota composition trends among high-risk ASD individuals
Blake Hirschi	Different compositions of Staphylococcus Aureus Biofilms Facilitate Antibiotic Resistance Gene Transfer at Different Rates
Deborah Johnson	Combating vaccine hesitancy with personal experience: A social and educational intervention
J. Porter Hunt	Bacterial cell-free protein synthesis biosensors for clinical and environmental applications

Session 1B 2267 CONF Center

Claudia Tellez Freitas	CD5 co-receptor influences T cell metabolism, gut microbiota and cognitive behavior
Kelsey Bennion	The where, what, and why of HPRT in cancer: Its presence, mechanism, and target potential
Eliza Bitter	Thymidine Kinase 1 surface expression in human breast cell lines and its correlation to cellular invasion
John Carter	Overcoming Transgene Silencing Via Manipulation of Nucleosome Positioning
Daniel Arens	Characterizing novel pathways at the pivotal point for controlling the balance between respiration and lipid biosynthesis in yeast

11:00 – 11:30 **Poster Presentations I.** (In the hallways of the Conference Center)
Even-numbered posters will be presented

11:30 – 12:15 **Lunch. (2260 Conference Center)**

12:15- 1:15 **Oral Presentations 2** (10 min talks for graduate students / 8 min talks for undergraduates)

Session 2A 2265 CONF Center

Matthew B. Crook	Bioinformatic Analysis of the Genome of Rhizobium sp. IRBG74
Alex Benedict	Medicago-Sinorhizobium symbiotic outcome as determined by peptide-peptidase interactions
Kirsten Butcher	Mechanisms for Soil Moisture Effects on Microbial Carbon Use Efficiency
Jacob McWhorter	Characterization of Some Extended-Spectrum Beta-Lactamase-positive Coliforms Isolated from Environmental Samples of Utah Valley
Rachel Hughes	The variable influence of the microbiota on Drosophila melanogaster traits
Marley Madsen	Bacterial community composition of slot canyon rock pools and open rock pools of the Colorado Plateau

Session 2B 2267 CONF Center

Israel Guerrero	A Humanized Mouse Model Alternative for Chikungunya Virus Infection
Daniel William Thompson	Phighting Phytopathogens with Phage
Trever Thurgood	A Case Study of Phage Therapy in Response to Multi-Antibiotic-Resistant Bacterial Infections
David Bates	Neutralization of proximal-end bias from in-vitro reconstituted nucleosomes through read recovery
Averi McFarland	Hyperactivation of the Mn-dependent phosphoglucomutase PGM boosts capsule biosynthesis in *Streptococcus pneumoniae*

1:15 – 2:00 **Poster Presentation 2.** (In the hallways of the Conference Center)
Odd-numbered posters will be presented

2:00 – 2:30 **Closing Session**
Awards
Business

Pages

Poster Assignments / Authors / Titles **2 – 4**

Oral Presentations – Abstracts **5 – 11**

Poster Presentations – Abstracts **12 – 41**

Poster Number	Authors	Poster Title:
1	Cambree King	The Relationship Between Histone Modifications and Nucleosome Sequence Motifs
2	Davis Garner	The Limits of DNA Influence on Chromatin Organization
3	Andrew Nelson	The Role of Autoinduction in Extract Preparation for Cell-Free Protein Synthesis
4	Ashley Smith	Non starter lactic acid bacteria growth in cheese
5	Austin Watts	The Role of Auxin in Growth Promotion of Rice by Rhizobium sp. IRBG74
6	Craig Oberg	Effect of Ozone Treatment on Staphylococcus Survival in Athletic Locker and Training Rooms
7	J. McKayla Crump	Phosphate-solubilizing bacteria isolated from the roots of a tomato plant (Solanum lycopersicum.)
8	Ella Johnson, Lexie Jones	Understanding the Micrococcin Biosynthetic Pathway
9	Keilen Kelly	Determining intracellular phosphate sequestration using Ppx to quantify polyphosphate
10	Kye Davis Boyd, Connor Boyd, Jared Hamula, Tyler Joseph Alger, Christina Keshek	Novel Protein Interaction Screen with Bacteriophage
11	Kyson Jensen	Bacterial Adaptations to Stressful Environments
12	Mason Burningham	Optimization of Microbial Fuel Cells
13	Riley James Hansen	Gluten's Impact on the Microbiome of the Human G.I. Tract
14	Sarah Driggs	Two component system RstB/RstA
15	Steven Brugger	Analysis of known APOE and depression SNPs in patients with multiple sclerosis
16	Charles R. Roll	Effect of Parkinson's Disease on expression of dopamine D2 receptors in peripheral blood leukocytes
17	Edwin Jesus Velazquez	Monoclonal antibodies against the tumor proliferation biomarker thymidine kinase 1 and its use for the treatment of cancer
18	Maxwell Drummond Drummond	The Ability of Rice Bran to Modulate the Mucosal Immune Response
19	Rachel Johnson	Anti-TK1 Antibodies as Potential Immunotherapy for Targeting Cancer Cells
20	Alma Kaneshiro	Quantification of Staphylococcus Aureas Biofilm Clearance
21	Brady Wahlstrom	Characterization of Hemolytic Activity of Probiotic Lactobacilli
22	Daniel Sandberg	The Effect of Probiotics On the Healthy Human Gut Microbiome
23	Joshua Gee	The role of the brain-eating amoeba Naegleria fowleri CD59-like protein in human infections
24	Joshua T. Calder	A novel trimeric autotransporter lipoprotein may be a component of the extracellular matrix of Yersinia pseudotuberculosis contributing to biofilm cohesiveness.
25	Kade Pachner	A Survey of Coccidiosis in Utah's Wild Turkey Population
26	Aurora Rodriguez KatherineAllen	Characterization of diversity in T-4 like Bacteriophages.
27	Nicholas Christman	Enhancing the antimicrobial ability of Gallium with Bacterial Siderophores
28	Tyler Henderson	Examination of cAMP secretion in Mycobacterium smegmatis
29	Alisa Knowles	Analysis of Differential Gene Expression in Halomonas-Inoculated Alfalfa Grown in the Presence of Salt
30	Brent Nielsen	Characterization of salt-tolerant bacteria isolated from three halophytes that exhibit growth promotion capabilities with alfalfa grown under saline conditions

31	Brinton Michael Moe Colin Michael Laura Uricoechea Tyler Frederick Hanis Tyson A Stoker Dylan Elton Samuel Alejandro Flor Tyler Divis	Discovering Antibiotic Resistant Genes in Bacteriophages
32	Bryson Carrier	Who Brought the Microbes? Investigating the Source of Fecal Veneer on Rock Climbing Holds
33	Carson Walker	Food Preference Determined by Genetic Predisposition for Familiar Microbiota Rather Than Rearing Conditions in Drosophila
34	Isaac A Trost	Evaluating Lotus japonicus as an alternative host for Rhizobium pusense IRBG74
35	Khin Pyae	Microbial adaptation to high-nickel soils
36	Annena Jane Lundgren	Overcoming Nucleosome Position Dependent Gene Silencing Via Positioning Manipulation
37	Ashlin Cowger	Bioaerosols associated with evaporative cooler use in low-income homes in the semi-arid climate of Utah County, Utah, USA
38	Colleen Newey	PAS Kinase as a Potential Therapeutic Target for Metabolic Diseases
39	Emily Dawn-Shellman Hales	Restoring Transgene GFP Expression via RNAi Knockdown of Gene Silencing Elements
40	Jacob Mark Miller	The Impact of Multiple Sclerosis Disease Status and Subtype on Hematologic Profile
41	Jeremy Beales	Contribution of Known Risk Variants to Multiple Sclerosis Age of Onset
42	Jordan Barnett	Asparaginase Cancer Treatment Biosensor
43	Megan Rimmasch	Automating the extraction of multiple sclerosis treatment data for pharmacogenetic studies
44	Nancy Wilson	Catching Your Attention The Effect of Textual Presentation Format on Reader Understanding of New Concepts
45	Sarah Ricks	In Vitro Transcription from Reconstituted Chromatin Reported by RNA Mango
46	Serena Seychelle Young	Predicting Catabolic Pathways in Lactobacillus wasatchensis using Metabolic Modeling
47	Tanner Call	The Gut Microbiome as a Driver of Host Dietary Preference in Drosophila melanogaster
48	Albin Taylor Rhen Davis Rochelle Gaertner	RNA Sequencing of Enterobacteriaceae Bacteriophages to Determine Gene Functions
49	Aurora Rodriguez, Emilee Lynn Carr, Rochelle Gaertner	Isolation and Characterization of Novel but Ubiquitous Family of Serratia Phages
50	Austen Nathaniel Gleave Emilee Lynn Carr	Characterization of 18 Bacteriophage Families Based on Distinct Protein Profile
51	Braden Brundage, Joshua Michael Findley, Weston Larson	PCR analysis of widespread human fecal samples to identify common bacteriophage.
52	Emily Cluff, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	Host Range Analysis of Sinorhizobium Phages Reveals New Avenues for Studying Phage Receptor Binding
53	Joshua D. Chamberlain, Kurt J. Ellis, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris	Phages Infect, But Not All Phages Infect Absolutely. Or Something Like That.

	O'Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Daniel Arens, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	
54	Hailey Olsen, Morgan Weatherred, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Sam Weeks, Daniel Arens, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	The Genome of Squally, A Novel T4-like Sinorhizobium meliloti Phage.
55	Karina Tovar Laura Uricoechea	Bacterial Killers: Infection of Unwanted Gut Bacteria
56	Michelle Lauren Nishiguchi	Pick Your Poison: Bactericidal Cocktails
57	Nicholas Carter	Discovery of Highly Conserved Protein Groups in Families of Bacteriophages
58	Tanner Johns	Finding and assessing the lytic nature of phages that target Yokenella regensburgei
59	Trever Thurgood	A Case Study of Phage Therapy in Response to Multi-Antibiotic-Resistant Bacterial Infections
60	Dillon Donaghy	Reduction of Plasmodium falciparum in Human Whole Blood Product Using Riboflavin and UV Light
61	Dalton Karlinsey	Testing the effect of Viral Protein R (Vpr) on the progression of HIV-1 to AID
62	Rachel Palmer	Prospective Biomarkers in Endometrial Cancer
63	Michael Tene	Testing a New Disinfection Tool
64	Michael Tene	Surface Sampling Methods
65	Josie Tueller	Flow Cytometry Education: A semester long course
66	Allen Weinert	Chemokine receptor CCBP2-V41A and its role in inflammation and Alzheimer's disease
67	Hailey Wilcox	Bacterial Effect of Fruit Fly Lifespan
68	Stephen Funk	The yjbB gene controls phosphate import in E. coli
69	Rachel Erickson	Comparing Thymidine kinase 1 differences in human breast cell lines and its relationship to cellular invasion
70	Kiara Whitley	Helper T cells and T cell signaling

Oral Presentations - ABSTRACTS

Landon Barlow	Borrelia burgdorferi Biofilm: An Investigation Into Growth and Control of an Alzheimer's Disease-Associated Bacterium
	A strong correlation between the bacterial family Spirochaetaceae and the pathogenicity of Alzheimer's Disease (AD) exists. Spirochetes have an affinity for neural tissue and readily reside on the brain where they grow, not as free-floating planktonic cells, but as biofilms: communities of aggregated cells that provide added resistance to antimicrobial agents. Though microorganisms naturally exist as biofilms, they have primarily been studied in the planktonic state and the clinical importance of biofilms is often underestimated. The body responds to *B. burgdorferi* biofilms on the brain by recruiting Amyloid-Beta (AB) in an attempt to neutralize the bacterium. AB is unable to penetrate the biofilm and begins to accumulate on the brain, ultimately initiating degeneration of the neurocircuitry. This study aims to successfully grow *B. burgdorferi* biofilms and investigate the inhibitory properties of antibiotics in biofilm formation. *B. burgdorferi* will be cultivated over various periods of time, using one of two media: modified BSK-1914 media with 6% rabbit serum, and modified RPMI- 1640 media with 6% rabbit serum. The biofilms are exposed by removing the planktonic cells and then are treated with XTT/Menadione assay for cell viability. The most effective time length and media for biofilm growth will be determined. That Procedure will then be used to cultivate biofilms that are subject to various antibiotics. Spectrometry of the XTT/Menadione assays will be the primary method used to determine cell viability and the inhibitory effects of antibiotic treatments. Future work into the investigation of combination therapy, a process of using several medications and modalities such as Low Level Light Therapy, Low Frequency Ultrasound, and Extracorporeal Shockwave Therapy will be pursued. The results of this work could provide expanded knowledge of inhibition of *B. burgdorferi* biofilm growth and one day lead to increased understanding of the pathogenicity and treatment of AD.
Daphne Skordas	Microbiota composition trends among high-risk ASD individuals
	Approximately one in every one hundred children is diagnosed with autism or ASD. This disorder often impairs social interactions and affects various other mental functions, depending on the severity. Recent research has identified a connection between an autism diagnosis and an altered gut microbiota. Using this information as a basis, we examined the relative abundances of various bacterial species in search of patterns characteristic of an autistic individual's microbiota. The subjects of this study were 38 children up to age 24 months, each of which has an older sibling. Half of these older siblings have a confirmed autism diagnosis, and the other half are considered neurotypical. The children from each group were age and gender matched to reduce the influence of covariates. The parents of these children collected fecal samples from their child's diaper, which were picked up by lab members and stored for further processing. DNA was extracted from each sample, amplified, then subjected to 16S sequencing to identify the bacterial species present. Raw sequencing data was processed and analyzed using QIIME, a bioinformatics tool specifically designed to determine taxonomic identities by comparison to reference sequences. Using the QIIME data, we determined that the bacterial species *B. fragilis* is differentially abundant in siblings of neurotypical children. It is likely that a lower abundance of *B. fragilis* associated with the ASD phenotype. Other studies have demonstrated that *B. fragilis* can be used as a treatment for ASD-like phenotypes in mouse models, but it could also be used as a biomarker for autism. It may be possible to determine which of these children will develop autism or ASD by comparing their gut microbiota to the microbiota of known ASD and non-ASD individuals. Current methods of autism diagnosis can be subjective and difficult to perform before age 2, often requiring further assessments. This study has the potential to improve the way autism is diagnosed in young children. By developing our methods into a clinical procedure, it could be used to test individuals more effectively and earlier than the existing assessments discussed previously.
Blake Hirschi	Different compositions of Staphylococcus Aureus Biofilms Facilitate Antibiotic Resistance Gene Transfer at Different Rates
	Staphylococcus aureus (SA) is both a commensal human colonizer and a major cause of global disease. We have been involved in SA analysis since 2013 in order to contribute to the current conversation revolving around SA as an important human pathogen. The work we have been doing has helped to shed light on the source of prevalence of antibiotic resistance in SA, its ability to produce biofilm and how these things contribute to its success as a human pathogen. In particular, the work to better characterize the production of biofilms is ongoing in order for us to understand its role in the overall virulence of SA. We have found that certain strains of SA have tendencies to make biofilms out of different materials. We are investigating whether or not specific compositions of biofilms contribute to gene transfer more readily than others. We have collected livestock associated (LA) SA isolates from the surfaces of local meat as well as strains of SA from volunteer's nares and have characterized the biofilm composition and antibiotic resistance of each of these strains. We intend to co-inoculate a LA staph strain and a human associated strain and observed the gene transfer events in regards to the differing biofilm compositions. We hypothesize that if we co-culture two strains of SA, both resistant to different antibiotics in a biofilm composed mainly of extracellular DNA then we will see a higher rate of gene transfer than a biofilm composed of polysaccharide because strains with tendencies to add DNA to the surrounding matrix may also demonstrate the ability to pick up DNA.

Deborah Johnson	Combating vaccine hesitancy with personal experience: A social and educational intervention
	Vaccine hesitancy is 'a delay in acceptance or refusal of vaccination despite availability of vaccination services' (WHO-SAGE). The World Health Organization (WHO) named vaccine hesitancy as one of the top ten threats to global health in 2019 along with items like climate change, limited primary care access and antibiotic resistance. In Utah County, only 86.9% of children who entered kindergarten in 2017-2018 were adequately immunized making this a serious local concern. Confronting vaccine hesitancy is a fraught and nuanced issue. For example, correcting erroneous assumptions about potential health and safety risks often creates a "backfire effect" where vaccine hesitant parents further entrench their beliefs. However, parents respond more positively to entreaties about the dangers of vaccine-preventable diseases. As such, we asked college students in three courses to interview family or community members that had experienced either a vaccine preventable disease (VPD) or an autoimmune disease. Students (n=425) were assessed for their vaccine attitudes before and after the intervention. Vaccine hesitant students (n=56, 13%) significantly improved their vaccine attitude scores through either interviewing a community member who experienced a VPD or by receiving vaccine specific instruction in class. 28/56 vaccine hesitant students became pro-vaccine. Therefore, emphasizing the risks of VPD rather than the safety of vaccines may increase the likelihood that the rising generation vaccinates their children.
J. Porter Hunt	Bacterial cell-free protein synthesis biosensors for clinical and environmental applications
	Living cells have been engineered into biosensors for an impressive array of analytes ranging from medical and environmental to industrial compounds. These sensors generally sustain several key limitations, which include long and complicated culturing procedures, the risk of infecting the environment with synthetic organisms, and the inability to generate a signal in the presence of cytotoxic analytes or sample matrices. These limitations can largely be overcome with biosensors engineered from cell-free protein synthesis (CFPS) platforms. We have recently employed *E. coli* CFPS to detect estrogenic and thyrogenic compounds. These tests can be completed in less than 60 minutes, function in the presence of environmental samples, raw sewage, and human blood or urine, and can be dried onto paper to generate a portable indicator. Additionally, we have developed a rapid and inexpensive bacterial CFPS asparaginase test for potentially monitoring patients with acute lymphocytic leukemia, and a rapid bacterial CFPS test for serum glutamine. This work demonstrates the exciting potential of bacterial cell-free protein synthesis as a clinical and an environmental sensing tool.

Claudia Tellez Freitas	CD5 co-receptor influences T cell metabolism, gut microbiota and cognitive behavior
	T cells are key players in the adaptive immune response and undergo metabolic changes upon activation. CD5 is a co-receptor found on T cells and plays a significant role in regulating T cell thymic development, intracellular signaling and cytokine production. Previous studies have found that naïve T cells with high CD5 expression (CD5hi) have increased TCR signal strength and enhances immune response to foreign peptide in the periphery. Additionally, we have reported that CD5hi naïve T cells have higher calcium mobilization and improved T cell activation compared to CD5lo T cells. Calcium influx levels can modulate and influence metabolic changes in T cells. Thus, we hypothesized that CD5hi, CD5lo and CD5 deficient T cells have different bioenergetic demands that affect metabolic pathways and T cell activation. We evaluated the effects of CD5 levels on metabolism using CD5 deficient mice vs wild type controls and found CD5 deficient T cells had significant differences in metabolic function. In addition, we observed that gut microbiota from CD5KO mice was different from CD5WT mice suggesting an influence of the CD5 co-receptor in the microbial community. Recently published work has described a connection between increased T cell metabolism, gut microbiota and altered cognitive function in PD-1 deficient mice. We have also found significant differences between CD5 deficient and wild type mice in marble burying rates, elevated plus and open field activity. These behavioral test results suggest CD5 deficient mice have altered cognitive function and higher levels of anxiety. Thus, CD5 deficiency alters T cell metabolism, gut microbiota and cognitive function.
Kelsey Bennion	The where, what, and why of HPRT in cancer: Its presence, mechanism, and target potential
	Although the role of Hypoxanthine-guanine phosphoribosyltransferase (HPRT) as a housekeeping gene is well established, the other roles of HPRT in tumor proliferation are less known. As cancer is the result of uncontrolled cell proliferation and salvage pathway enzymes play an important role in cell proliferation, we examined the role of overall HPRT expression in tumor growth. Past publications show increased overall expression of HPRT as well as increased surface expression of HPRT on Raji, SW-620, HT-29, HCC 1806, and DU145 cancer cell lines. These findings motivated us to understand the purpose, and potential evolutionary advantage, of overall elevated HPRT in tumor proliferation. UV mass spectrometry revealed that Raji $HPRT^{-/-}$ cell lysate had significantly lower guanosine and adenosine levels compared to the Raji $HPRT^{WT}$ cell lysate. As adenosine is a potent anti-inflammatory agent, these results suggest that HPRT has an anti-inflammatory immune function through its regulation of guanosine and adenosine in the tumor microenvironment. Elevated HPRT would increase guanosine and adenosine production, decrease immune infiltration, and perpetuate tumor growth. Understanding the role of HPRT in tumor proliferation necessarily begets the use of HPRT as a therapeutic target.

	As HPRT is on the surface of several cancer cell lines and not on the surface of healthy cells, we investigated the use of surface HPRT as a therapeutic target. To study the cytotoxic-inducing effects of an HPRT antibody, we performed antibody dependent cell mediated cytotoxicity (ADCC) experiments on PC3 and DU145 prostate cancer cells. In all previous experiments, we observed a significant association between HPRT and the surface of DU145 cells, but found no HPRT presence on the surface of PC3 cells. In the ADCC experiments, DU145 cells treated with HPRT antibody experienced significantly higher cell death (4.5ug, p-value < 0.0001; 6ug, p-value = 0.028; 8ug, p-value = 0.025) compared to control wells while PC3 cells treated with HPRT antibody experienced insignificant cell death (4.5ug, p-value = 0.33; 6ug, p-value = 0.35; 8ug, p-value = 0.99) compared to control wells. Due to the increased cytotoxic-inducing effect of the HPRT antibody, a panel of HPRT antibodies are actively being developed and will be used in a monoclonal antibody treatment as well as in a CAR construct. This study expands current knowledge of the role of HPRT in tumor growth and supports the use of HPRT as a future target in cancer immunotherapy.
Eliza Bitter	Thymidine Kinase 1 surface expression in human breast cell lines and its correlation to cellular invasion
	The purpose of this study is to determine the role of Thymidine Kinase 1 (TK1) in the cellular invasion of breast cancer cells in vitro. TK1 is a cytosolic DNA salvage pathway enzyme responsible for the conversion of thymidine to thymidine monophosphate; it is known to increase during G1/S phase of the cell cycle and is significantly elevated in the serum of multiple cancer patients including breast, lung, and colon. As such, TK1 has been implicated as a useful biomarker for cancer prognosis and patient monitoring. In addition to TK1 upregulation in cancer serum, recent findings have shown that TK1 also localizes to the surface membrane (mTK1) of ALL, AML, and colon cancer cells in patients. However, minimal studies have determined if mTK1 is an indicator of invasion potential. In addition, the function and timing of TK1 expression on the cellular surface has not been determined. We hypothesized that levels of mTK1 correlate to the invasive capacity of the cell. In addition, we hypothesize that the expression of TK1 on the surface of cancer cells is not dependent on the proliferative state of the cells. When comparing the TK1 cytosolic expression in metastatic cancer cell lines to primary cancer cell lines through RNA-seq, we found that there was a trend of overall elevation in metastatic cell lines (n = 39) when compared to primary cell lines (n = 31). This expression was extremely irregular between cell lines and TK1 showed significant variability between samples. To evaluate TK1 in a specific subset of cancer, a microarray of ductal and lobular carcinoma with matched metastatic and adjacent normal was stained for TK1 levels. Similar to bioinformatic data, metastatic samples showed significantly higher levels of TK1 when compared to primary and normal tissue (p = .0001). We then tested several breast cancer cell lines (primary: HCC 1806, HCC 1937, JIMT-1 MB 157 and BT549; metastatic: T47D, MCF7, ZR751, and MDA-MB-231) for mTK1 levels. We found significant TK1 expression in all cell lines tested when compared to controls; the highest overall expression was in primary breast cancer cell lines by about 30% (p = .0001). The highest individual expression was in primary breast cell line MB 157 (98.0, p = .0001) and the lowest individual expression in MDA-MB-231 metastatic breast cancer cells (47.2%; p = .01). Lastly, the baseline invasion comparing selected cell lines from metastatic and primary groups showed that metastatic cell line MDA-MB-231 had the highest invasion potential (p = .0001) and JIMT-1 had the lowest invasion potential (p = .0002). When correlating cell invasion to mTK1 levels, this indicates that there may be a negative correlation to invasion potential.
John Carter	Overcoming Transgene Silencing Via Manipulation of Nucleosome Positioning
	By the end of April 2003, the human genome had been sequenced. It meant the beginning of a new era free of genetic disease, healed by the power of gene therapy. The more science tried to tinker with transgenes the more it became apparent that we were still lacking knowledge of what controlled genes. This new field of science was called epigenetics. As the field of epigenetics has grown, areas of specialization have developed. One such area is chromatin architecture. Chromatin is a complex of DNA and protein macromolecules. The fundamental component of chromatin is the nucleosome. Nucleosome position dictates the accessibility of DNA to transcription factors, thus affecting gene expression. The position of a nucleosome is influenced by the DNA sequence and competition with DNA-binding proteins. Several sequences have been found to increase the likelihood of DNA-histone binding, including the Widom 601 sequence. Which has been shown to position nucleosomes *in vitro* as well as *in vivo*. By inserting the 601 sequence into transgenetic constructs we can dictate where nucleosomes will form which will allow us to manipulate the accessibility of genetic elements. Being able to manipulate gene expression, will lead to the promised era thought to be here when the human genome was first sequenced. Micro injection into *C. elegans* of DNA constructs consisting of GFP under the Unc-54 enhancer and Myo-2 promoter with several arrangements of nucleosome positioning sequences was carried out. GFP expression was categorized. To ascertain nucleosome position MNase-seq was conducted. MNase digests the DNA between histones in a relatively non-specific manner. The histones in the nucleosomes are then digested. The nucleosome core DNA can then be sequenced. By using selective hybridization with a biotin labeled DNA probe we can enrich for the transgenic elements and look at nucleosome positions at a specific locus. The genetic output of this experiment showed that GFP was silenced in all constructs. However, the molecular assay showed the 601 sequence did position Nucleosomes. While the nucleosome positioning was not able to overcome the genetic silencing this research did show that the 601 sequence is able to position nucleosomes. Light has also been shed on how nucleosome

	positioning can be manipulated as we did see a decrease in nucleosomes being position on the Unc-54 enhancer element.
Daniel Arens	Characterizing novel pathways at the pivotal point for controlling the balance between respiration and lipid biosynthesis in yeast
	Protein kinases play a major role in cellular functions by phosphorylating other proteins and in the realm of glucose metabolism PAS kinase (PASK) plays an integral role. When PASK function is disrupted the dysregulation of glucose can cause issues with lipid biosynthesis, cellular growth, and respiration, which ultimately contribute to metabolic disorder. Recently, our lab identified a PASK substrate, Centromere Binding Factor 1 (CBF1), that has been shown to negatively regulate lipid biosynthesis and positively regulate respiration in yeast. Recently, our lab discovered several target proteins that could recover the respiration defect of CBF1-deficient yeast when overexpressed. None of these target genes were previously known to regulate respiration, therefore we assayed corresponding knockout strains in Seahorse Respiration Assays. One strain which lacks the uncharacterized yeast protein Pears and Lemons (PAL1) decreased respiration, this is consistent with the increased growth seen on respiratory carbon sources when it's overexpressed. Preliminary mass spectrometry results have identified several proteins with altered expression in multiple strains from our respiration assays. Various interacting partners of PAL1 have also been identified including TAR1, which can be found in the mitochondria and is associated with respiratory metabolism. These studies have identified and provided initial characterization of novel proteins that regulate that central, essential metabolic process of respiration. In addition, they highlight the unexplored nature of this process.

Matthew B. Crook	Bioinformatic Analysis of the Genome of Rhizobium sp. IRBG74
	Rhizobium sp. IRBG74 was isolated from root nodules of a tropical legume, *Sesbania cannabina*, by researchers at the International Rice Research Institute (IRRI) in the Philippines in the mid-1990s. IRRI agronomists later demonstrated that when *Rhizobium* sp. IRBG74 was used as an inoculant, the growth and yield of rice was improved. The genome of *Rhizobium* sp. IRBG74 was sequenced in 2013. I have performed various bioinformatics analyses to 1. understand the relationship between *Rhizobium* sp. IRBG74 and other rhizobia; 2. discover features of *Rhizobium* sp. IRBG74 that could contribute to its ability to interact with and benefit its two very different hosts (a grass and a legume); 3. understand aspects of the basic biology of *Rhizobium* sp. IRBG74; and 4. identify features of the *Rhizobium* sp. IRBG74 genome that could affect genetic analysis of this bacterium.
Alex Benedict	Medicago-Sinorhizobium symbiotic outcome as determined by peptide-peptidase interactions
	In nutrient-limited soils, exchange of resources between organisms can be essential for robust growth. Symbiosis between the legume, *Medicago truncatula,* and soil bacteria, *Sinorhizobium meliloti*, can benefit both species through the exchange of fixed carbon for fixed nitrogen. Chemical signaling between the two species initiates rhizobial infection of plant tissue where there is an abundance of fixed carbon available to the bacteria. When inside the plant, a portion of the rhizobia are endocytosed into a root nodule cell where, surrounded by plant membrane, they are exposed to an arsenal of plant-derived Nodule-specific Cysteine Rich (NCR) peptides. These NCR peptides elicit permanent physiological changes on the bacteria that ultimately enslave them to the plant. In this state, they begin fixing atmospheric nitrogen for their host. Bacterial peptidases that interfere with host peptides can facilitate their survival and/or enable them to enact a more parasitic role in their hosts. We have screened through 1/3 of *S. meliloti's* ~140 core genome-encoded peptidases and found 3 so far which, when over-expressed, have a negative impact on nitrogen fixation and plant health. One of these peptidases, Smc00451, degrades several NCR peptides *in vitro*. These findings demonstrate the importance of peptide-peptidase interactions in determining symbiotic outcome.
Kirsten Butcher	Mechanisms for Soil Moisture Effects on Microbial Carbon Use Efficiency
	Microbial carbon use efficiency (CUE) plays a pivotal role in regulating microbially-mediated carbon and nitrogen transformation rates in the soil, but little is understood about how CUE is impacted by edaphic properties, like soil moisture availability. The purpose of this research is to evaluate the relative importance of water potential and water content in controlling CUE of soil microbial communities. Moist soil incubations were used to assess the impact of both water potential and water content on CUE, and soil slurries were used to assess the impact of water potential alone on CUE. Assimilation and respiration rates in moist soils resembled optimum curves across the water potential gradient, reaching a maximum rate around -0.15 MPa, before declining as measured water potential values surpassed 0.0 MPa. Conversely, assimilation and respiration rates in soil slurries showed linear and exponential declines, respectively, with increasing water potential. Calculated values of CUE in moist soils demonstrated no significant relationship with water potential and averaged 0.24, whereas slurries demonstrated a significant exponential increase in CUE as water potential increased, with a maximum of 0.74 at -0.01 MPa. Results of this study indicated that water content (substrate diffusional limitation) exerts more control over CUE than water potential (dehydration effects) across all water potentials assessed,

	with at least 51% of the decline in CUE attributed to diffusional limitations at the lowest water potential measured.
Jacob McWhorter	Characterization of Some Extended-Spectrum Beta-Lactamase-positive Coliforms Isolated from Environmental Samples of Utah Valley
	Background: The CDC has listed extended-spectrum beta-lactamase (ESBL)- producing pathogenic bacteria asserious public health threats. We previously identified such bacteria in the gut of Utah birds and waste water samples. Here we characterized some of the isolates for the presence of small plasmids and the antibiotic resistance genes CTX, GES, SHV, TEM, and VEB. Materials and method: Raw and posttreatment sewage water samples were collected from wastewater treatment facility of Orem. The samples were serially diluted and then plated on Hardy Chrome ESBL agar plates and MacConkey Agar plates. The plates were incubated at 37° C overnight and then at room temperature for up to 48 hours and colony forming units (CFU) were counted. Selected isolated colonies were biochemically characterized. Plasmid DNA extracted using alkaline lysis protocol was resolved in 0.8 % agarose gels (before or after treated by S1 nuclease) to detect small plasmids. Large plasmid detection using pulsed field gel electrophoresis is currently underway. PCR was conducted using bacterial DNA as template and primers specific for the antibiotic resistance genes CTX, GES, SHV, TEM, and VEB. Results: ESBL-positive colonies grew only from raw sewage water, not from processed water collected at the release point. Comparison of bacterial growth on ESBL and MacConkey Agar plates indicated that about 0.4-4.0% of the coliforms were ESBL-producing. The resistant bacterial counts varied from 1.88 x104-7.20x104 CFU/ml. The predominant coliform species included Escherichia coli, Klebsiella pneumoniae, and Citrobacter sp. Small plasmids were found in about 20% of the ESBL-positive colonies examined so far. About one-third of the ESBL-producing isolates were positive for the GES gene, three-fourth of the isolates were positive for the TEM gene, about one sixth of the isolates were positive for the CTX and SHV genes, and none of the tested isolates was positive for the VEBgene. Conclusions: ESBL-producing coliforms are abundantly and persistently present in the raw sewage of Utah. Many of the ESBL-producing isolates carry one or more of the four common antibiotic resistance genes. This report warrants further investigations on the genomic characteristics of the multidrug-resistant coliforms and to identify the sources of the ESBL-producing enteric bacteria in the Utah Valley.
Rachel Hughes	The variable influence of the microbiota on Drosophila melanogaster traits
	Associated microorganisms ('microbiota') engage in complex interactions with their hosts that influence animal behaviors and adaptive traits. Here we focus on how the microbiota influence traits in *Drosophila melanogaster*. *D. melanogaster* is an established model for understanding how organisms adopt different trait patterns in different geographies. For example, *D. melanogaster* in the eastern United States are locally adapted across a latitudinal cline; low latitude populations invest in early reproduction ('fast') whereas high latitude populations favor somatic maintenance ('slow'). We previously showed that the *Drosophila* microbiota, which is dominated by lactic acid (LAB) and acetic acid (AAB) bacteria, also varies with latitude; and that species from the different bacterial orders can dictate the fast-slow strategy of female wild *D. melanogaster*. We sought to explore how other factors such as reproductive tract bacteria and host sex might vary these established influences of the microbiota on the host. Stress tolerance and lifespan are known to vary with *D. melanogaster* sex. *Wolbachia* persist in *D. melanogaster* populations and influence host survival and biology. Therefore, to test if *Wolbachia* and host sex mediate variation in host response to the microbiota, we conducted a preliminary pilot study with small N. To test this hypothesis, we reared *D. melanogaster* either bacteria-free or with different microbial communities that mimic latitude-specific microbiome swaps. We then measured the starvation resistance of both male and female flies; and the development rate of flies in replicate vials for each treatment. Consistent with our past findings, female *D. melanogaster* starvation resistance was heavily influenced by microbial composition, as indicated by microbial treatment masking the impact of host genotype on locally adapted traits. Conversely, host genotype influenced the starvation resistance of male flies more strongly than the microbiota, such that different fly genotypes reared with different microbial communities did not display overlapping phenotypes. Under bacteria-free conditions, the presence of *Wolbachia* reverse the locally adapted responses independent of the microbiota. Taken together, our results suggest that variation in both *Wolbachia* infection and host sex fundamentally alter how the microbiota influences host traits, and justify future studies with larger N to reproduce the observed phenomena.
Marley Madsen	Bacterial community composition of slot canyon rock pools and open rock pools of the Colorado Plateau
	Desert rock pools are unique freshwater ecosystems that experience regular desiccation and flooding cycles. Desert rock pools can be found on the exposed surface of rocky outcrops, hereafter termed "open rock pools", and in narrow slot canyons. Slot canyon rock pools are similar to open rock pools, but are subject to different environmental conditions due to the morphology of the canyons in which they are located. My research investigates the bacterial communities of open rock pools and slot canyon rock pools of the Colorado Plateau using environmental DNA (eDNA) collected from the soil. It tests differences in alpha- and beta-diversity and identifies differentially abundant bacterial phyla that are indicators for each habitat type. Slot canyons are almost completely unexplored within the biological sciences, and my research is the first investigation of its kind within these extraordinary environments.

Israel Guerrero	A Humanized Mouse Model Alternative for Chikungunya Virus Infection
	Chikungunya virus (CHIKV) is an alphavirus that can be transmitted to humans by mosquitoes. Symptoms include rash, high fever and, its hallmark, severe arthritis that can last for years. Previous primate and mouse models have successfully mimicked the acute phase of Chikungunya infection, but have only achieved partial success in modeling the chronic symptoms of the disease. Clinical reports also show a particular profile of pro- and anti-inflammatory cytokines during both phases of CHIKV infection in human patients. Our previous research has shown that CHIKV infection in human cells results in a higher production of infectious virus and drastic different cytokine profiles from human and murine CHIKV infected monocytes. TNF and CCL2 are upregulated in CHIKV-infected human cells, which may play a role in macrophage recruitment and systemic inflammation. In contrast, CHIKV-infected mouse cells showed an upregulation of IL-6, which may contribute to the anti-inflammatory activity by inhibiting TNF and IL-10. CHIKV-associated polyarthritis has been unattainable in murine models, thwarting further understanding of the initial virus dissemination to the joints and the persistence of viral RNA in the joints. We infected Balb/c mice which have RAG1$^{-/-}$ γc$^{-/-}$ gene knockouts and observed the disease progression. Joint inflammation and viremia levels correlate to previous IFN-knockout models peaking at day 8 and drastically reducing the viral load and joint inflammation at day 15. We also analyzed through Immunohistochemistry CHIKV presence and macrophage infiltration in brain, liver, muscle and joint tissue. Macrophages have been one of the suspected cells to contribute to the systemic spread of CHIKV. We have shown that CHIKV replicates its genome more efficiently in human macrophages compared to murine macrophages. Also, we have explored the cytokine profile in CHIKV-infected human and mouse macrophages. Our RAG1$^{-/-}$ γc$^{-/-}$ mouse study has shown that CHIKV infection is viable in this immunocompromised model and that engraftment with human immune cells may provide answers to better understand CHIKV's pathogenesis in humans. Macrophages have been one of the suspected cells to contribute to the systemic spread of CHIKV. We have shown that CHIKV replicates its genome more efficiently in human macrophages compared to murine macrophages. Also, we have explored the cytokine profile in CHIKV-infected human and mouse macrophages. Our results suggest that CHIKV benefits from a species-specific interaction within the host cell, by achieving more production of infectious virus in human cells, possibly due to contrasting cytokine profiles between the two species. Preliminary data from our murine model study shows great promise in further results with a humanized murine model were the infected human macrophages could be part of a complex viral replication strategy that CHIKV uses to spread through its host.
Daniel William Thompson	Phighting Phytopathogens with Phage
	Erwinia amylovora is a gram negative phytopathogen which infects plants of the *Rosaceae* family. The primary mode of infection for this bacterium is through the blossoms of the plant and quickly spreads deeper into the plants system. This infection causes necrosis in the plant tissue called fire blight and is responsible for millions of dollars in agricultural loss in the United States. Current methods of treatment for this infection utilize an over-spray of antibiotics on the plants, but the growing concern of the rise in antibiotic resistant strains is leading to the need for other, more effective, methods of treatment. The recent emphasis in bacteriophage research has provided a potential method of treatment using phage cocktails to treat the infection. Five years of USDA approved field testing of one such cocktail named Fire Quencher has effectively shown the success of using phage cocktails on infected plants.
Trever Thurgood	A Case Study of Phage Therapy in Response to Multi-Antibiotic-Resistant Bacterial Infections
	Bacillus anthracis is a pathogenic member of the *Bacillus cereus* group, a small group of pathogenic and non-pathogenic *Bacillus* species. *B. anthracis* is a Gram-positive, spore-forming bacteria capable of causing serious infection in man and animal. *B. anthracis,* more commonly known as anthrax, has been studied for over a century by biologists and is commonly known for its potential use a bioweapon. While there have been no known bioterrorist attacks for almost two decades, the pathogen has been known to cause disease in humans and livestock from infected soil, its natural ecological niche. Once infected, unless intervention occurs quickly after onset of symptoms, anthrax has a high mortality rate for each of its three forms of infection: cutaneous, gastrointestinal and inhalation (20%, 50% and >80%, respectively). To date, only a dozen phages have been isolated against *B. anthracis*, none of which have been shown to infect any pathogenic strains of *B. anthracis.* In 2017, our lab isolated 23 bacteriophages on *B. anthracis* strain Sterne and sequenced all 23. While none of these phages were completely novel, preliminary results have shown that representative phages from 3 different phylogenetic groupings can infect a variety of pathogenic anthrax strains, the first bacteriophages ever reported to do so. Here, we explore the genomic content of these phages that allow for infection of their host bacteria and expanded host range. Furthermore, these phages will be the first published organisms that could serve as potential therapeutic treatments for anthrax infections.
David Bates	Neutralization of proximal-end bias from in-vitro reconstituted nucleosomes through read recovery
	Understanding chromatin, the combination of DNA and protein, is fundamental to areas such as gene expression and development. The most basic unit of chromatin is the nucleosome, which

	consists of a histone octamer wrapped by DNA ~1.7 times. The histone octamer is comprised of two proteins each of H2A, H2B, H3, and H4. It has been demonstrated that nucleosomes have certain preferences in the DNA sequences they tend to form on. Such preferences include an enrichment of A/T dinucleotides approximately every 10 bp, enrichment of G and C nucleotides at the dyad, and also a depletion of A or T homopolymeric runs. *In vitro* nucleosome reconstitutions have an additional preference, or bias, that has been observed: enrichment on the proximal ends of linear DNA. This preference can substantially bias data. We have developed a novel computer program that greatly reduces the bias resulting from proximal end nucleosome formation. Using similar libraries with different known ends of fragmented DNA, we are able to compare nucleosome reads and recover those that would typically have been thrown out due to proximity to the end of DNA. We provide evidence that such a method greatly reduces the bias in the final library of reads as measured by k-mer usage before and after the comparison and recovery process.
Averi McFarland	Hyperactivation of the Mn-dependent phosphoglucomutase PGM boosts capsule biosynthesis in *Streptococcus pneumoniae*
	Capsular polysaccharide (CPS) is essential for virulence of numerous pathogenic bacteria, including the human upper respiratory pathogen *Streptococcus pneumoniae*. During initial colonization of *S. pneumoniae*, the CPS must be thin enough to allow adherence, but during disease progression, the CPS must be thick enough to resist host defenses such as phagocytosis. The mechanism of how CPS production is regulated is not clear. Our data show that manganese (Mn) perturbations affect CPS thickness. Since Mn-dependent enzymes are particularly susceptible to hyperactivation or mismetallation, we hypothesize that CPS biosynthesis might be modulated by a Mn-dependent enzyme, possibly the phosphatase CpsB and/or the phosphoglucomutase Pgm. CpsB is proposed to function as a regulatory enzyme by limiting CpsD activity, while Pgm provides key precursor sugars for CPS biosynthesis. Using a metal- free mag-fura-2 competition assay, we show that apo-CpsB and -Pgm proteins can bind up to 2 Mn2+ ions. Activation of CpsB during Mn stress does not promote aberrant dephosphorylation of CpsD. In contrast, increasing Mn concentrations, but not other metal ions, enhances the specific activity of Pgm. We propose a role for Mn in regulating CPS production via activation of the key Mn-dependent enzyme Pgm.

POSTER ABSTRACTS

Poster Number	Authors	Poster Title:
1	Cambree King	The Relationship Between Histone Modifications and Nucleosome Sequence Motifs
		Our goal is to understand how nucleosome positioning is affected by histone modifications. Nucleosomes consist of an octamer of core histone proteins wrapped by DNA 1.7 times. Four different proteins make up the histone octamer; two proteins each of H2A, H2B, H3 and H4. Certain modifications of histones, such as methylation and acetylation, are correlated with changes in gene expression. Generally, positioning of nucleosomes shows sequence preference for high G/C content at the dyad flanked by alternating periodicities of A/T dinucleotides and G/C dinucleotides approximately every 5 bp. The alternating regions coordinate with the DNA helix allowing A/T dinucleotides to face in towards the octamer in the minor groove and G/C dinucleotides to face in towards the octamer in the major groove. Knowing the stated positioning preferences, we want to understand how histone modifications affect positioning preferences further. Previously, we chose five different lysines on H3 and modified them with methylation or acetylation. We allowed them to form nucleosomes *in vitro* with sheared genomic DNA. We used high-throughput sequencing to examine and identify the nucleosomal DNA for short DNA motifs unique to each modification compared to an unmodified control. To determine if these DNA motif preferences were an artifact of the code written to analyze the sequencing data, we have designed a competitive binding assay for nucleosomes using modified H3. Understanding how nucleosome sequence preferences are affected by histone modifications will ultimately enable us to better engineer DNA constructs for future use in medicine and industry.
2	Davis Garner	The Limits of DNA Influence on Chromatin Organization
		Essentially all nuclear DNA is compacted by nucleosomes, which affect protein accessibility to the DNA and therefore play a critical role in gene expression and silencing. Nucleosome positions can be rearranged by chromatin remodeling complexes to allow or restrict transcription factors access to the DNA. Nucleosome positions are also influenced by the inherent DNA sequence that they sit on. Various genome studies show that nucleosomes favor positions that allow thermodynamically favorable bending of the DNA as well as regions of transcriptional importance. To identify the limits of DNA influence on nucleosome positioning, we used high throughput sequencing techniques to map and compare nucleosome positions in two C. elegans strains. We also sequenced one transgenic line with GFP fused histones to see if the GFP fusion influences nucleosome positioning. Our results will determine how influential single nucleotides are on the positioning and occupancy of nucleosomes, as well as if GFP-fused histones show a significant difference in positioning. The analysis we produce will show the extent that DNA sequence influences chromatin organization in vivo.
3	Andrew Nelson	The Role of Autoinduction in Extract Preparation for Cell-Free Protein Synthesis
		Cell-free Protein Synthesis (CFPS) has been shown to be an effective alternative to traditional means of recombinant protein synthesis. A key part of this CFPS is the preparation of a cell extract, the necessary machinery that a cell uses for the creation of proteins. This is generally a time-consuming, tedious process, requiring frequent measurements and monitoring of the cell culture to know when to induce the cells. Autoinduction, a method which induces the culture inherently, has been shown to be equally effective at inducing cells. This technology has the potential to significantly reduce the amount of hands-on time needed for protein expression. However, to our knowledge, the effects of this approach on extract preparation for a cell-free system have not yet been elucidated. Here, we demonstrate the successful use of autoinduction media in cell extract preparation in both BL21* DE3 E. Coli and ClearColi, the latter being a genetically engineered, endotoxin-free E. Coli strain that requires an especially long culture time.
4	Ashley Smith	Non starter lactic acid bacteria growth in cheese
		Non-starter lactic acid bacteria (NSLAB) growth in cheese can impact the quality of the finished product. Our objective was to correlate the growth of NSLAB in aging cheese with the detection of *Lactobacillus wasatchensis*, a NSLAB known to cause gas defects. Two batches of Cheddar cheese were made in a facility with *Lb. wasatchensis* contamination and aged for between 5-48 weeks. Starter lactic acid bacteria (SLAB) and NSLAB organism were quantified weekly on M17+Lactose agar aerobically, and MRS-ribose agar anaerobically, respectively. Over 5-weeks the SLAB remained at

		about 10^8 cfu g^{-1}, while NSLAB increased from below detection to 10^8 cfu g^{-1}. DNA was extracted directly from the aging cheese at regular intervals. DNA yields ranged from 445 ng g^{-1} to 2.2 µg g^{-1} cheese. *Lb. wasatchensis* was detected by PCR with species specific primers at 3 and 13 weeks of aging when NSLAB were 10^6 cfu g^{-1} and 10^7 cfu g^{-1}, respectively. *Lb. wasatchensis* appears accumulate as cheese made at this facility ages. Further work to develop more sensitive detection techniques, including microbiome analysis, will allow us to better understand and control the growth dynamics of this organism.
5	Austin Watts	The Role of Auxin in Growth Promotion of Rice by Rhizobium sp. IRBG74
		Auxin is a known growth hormone for plants and many plant-beneficial bacteria are known to produce it. It has previously been shown that Rhizobium sp. IRBG74 promotes growth of rice, but the mechanism is unknown. We hypothesized that Rhizobium sp. IRBG74 accomplishes this by production and secretion of auxin. To address this hypothesis, we first performed a bioinformatic analysis to identify putative auxin biosynthesis genes in the genome of IRBG74 using BLAST with known auxin biosynthesis genes as queries. To test whether the genes identified by BLAST play a role in promoting growth of rice, we are making in-frame deletions of each one. Briefly, we use overlap-extension PCR to create and stitch together deletion fragments and then we clone these fragments into the sacB deletion vector pJQ200SK. The target genes are then disrupted by homologous recombination and then deintegration is selected for with sucrose. After this is done we test the mutant to verify the deletion occurred by PCR. Once the deletion mutants are verified, each one is tested on rice seedlings and compared to wild-type IRBG74. Rice growth is quantified by shoot dry weight and by root branching, as measured using ImageJ.
6	Craig Oberg	Effect of Ozone Treatment on Staphylococcus Survival in Athletic Locker and Training Rooms
		Staphylococcus aureus is a common human-borne bacterium found in 40% of the population, primarily in their nasal passages. This bacterium, a common cause of in-hospital postoperative infections, can also be found in the athletic community, residing on uniforms, training table, playing fields, practice mats and even team mates. Outbreaks of *S. aureus* within athletic teams is not uncommon. In sports venues, ozone has been used to sterilize swimming pools, athletic equipment, and other surfaces prone to bacterial contamination. This research was conducted to determine if a commercial ozone generator was effective is killing *S. aureus* in a locker room. Petri dishes (TSA) inoculated with a nonpathogenic strain of *S. aureus* were put in strategic locations (in triplicate) in WSU training and locker rooms. Lids were removed from the inoculated petri plates and three ozone generators, one for the training room and one for each of the two locker rooms were turned on for a set time. In trial one, they were on for 120 minutes for the two football locker rooms and 90 minutes for the training room, while in trial two they were all on for 180 minutes. Additionally, uninoculated control plates were placed in each room as a test for air borne contaminants that might fall on the plates during the experimental protocol. Three hours after ozone infusion, petri dishes were carefully collected, then incubated for 48 h at 37°C. Following incubation, the number of *S. aureus* colonies on each plate were recorded. Two hours into the run cycle, ozone measurements were made using an Ozone Monitor InDevR Model 205. Results for trial one showed an overall *S. aureus* reduction of 78.7 $\pm$ 8.3%, while trial two showed an increase in the overall reduction to 93 $\pm$ 1.8%. There was a modest correlation between *S. aureus* survival and distance from the ozone generator in trial one (R^2= 63). Average ozone readings increased from a background of 17 ppb to 1042 ppb at ground level and 1344 ppb 1.5 m above ground level at 2 h of ozone generation. These results show that ozone can reduce *S. aureus* in locker rooms and that increasing the run time from 2 h (recommended by manufacturer) to 3 h significantly decreases survival rates.
7	J. McKayla Crump	Phosphate-solubilizing bacteria isolated from the roots of a tomato plant (Solanum lycopersicum.)
		Found in the rhizosphere, phosphate-solubilizing bacteria (PSB) make inorganic phosphate available to plants. Our purpose was to characterize PSB isolates from the bulk soil, rhizosphere, and rhizoplane of a tomato plant (*Solanum lycopersicum.*) Samples were placed in distilled water, shaken, serially-diluted, and plated on Pikovskayas Agar, a selective medium for isolating PSB. A single isolate from each environment was taken and characterized. Staining and motility testing showed these isolates to be Gram-negative, motile bacilli. 16S rRNA gene sequencing revealed these to be putative *Burkholderia* (Betaproteobacteria) strains.These PSB successfully utilized a wide range of carbon sources, including galactose, fructose, and mannose, as demonstrated using BIOLOG GEN III plates. Surprisingly, these PSB were naturally

		resistant to range of antibiotics, including triple sulfa, penicillin, and tetracycline. Isolation, cultivation, and other assays were conducted at 30ºC. The isolation and characterization of PSB furthers our understanding of the properties of plant growth-stimulating bacteria.
8	Ella Johnson, Lexie Jones	Understanding the Micrococcin Biosynthetic Pathway
		Post-translational modifications (PTMs) are chemical modifications that occur on a peptide that increases protein diversity within the cell. We are using the micrococcin model system, which has been altered to be expressed in *E. coli,* to investigate PTM structure and selection criteria. The micrococcin precursor peptide, TclE, undergoes over 20 PTMs, and some of the enzymes' recognition sites are often far from the site of modification (alloselectivity). Our project focuses on the structural features of the compounds involved in the first step of the micrococcin biosynthetic pathway: scaffold protein TclI which binds to the PTM enzymes TclJ and TclN and the precursor peptide TclE in order to modify cysteines into thiozoles on TclE. We are using a combination of plasmid modifications, bacterial two-hybrid systems, and nickel pull-down assays to determine the recognition sites of these compounds, with the future goal of establishing a system for modifying peptides with engineered PTMs.
9	Keilen Kelly	Determining intracellular phosphate sequestration using Ppx to quantify polyphosphate
		Inorganic phosphate is a necessary molecule for maintaining the structure and metabolism of cells. A minimum amount of phosphate is required to sustain these processes, but too much phosphate can also be toxic. Escherichia coli has developed a complex system of importers, exporters, and metabolic enzymes to keep intracellular phosphate at optimal levels. The Pit, Pst, and Pho families of proteins are known to be involved in phosphate transport and its regulation. YjbB is another promising candidate for a phosphate exporter used by E. coli. It is thought that high concentrations of internal phosphate can be dealt with without the use of exporters by sequestering it as polyphosphate. Ppk and Ppx are the enzymes used to synthesize polyphosphate from ATP and degrade it. We are interested in understanding how phosphate sequestration by Ppk and Ppx affects or is affected by phosphate export. To quantify polyphosphate in strains missing one or more genes involved with phosphate homeostasis, we purify polyphosphate from cell cultures and use Ppx from *Saccharomyces cerevisiae* to break polyphosphate into inorganic phosphate. Phosphate is then quantified with a standard assay kit. Using these measurements, we have studied the effects of mutations on polyphosphate storage. This poster presents recent data regarding the roles of Ppk, Ppx, YjbB, and other proteins in phosphate homeostasis under conditions of high intracellular levels of phosphate.
10	Kye Davis Boyd, Connor Boyd, Jared Hamula, Tyler Joseph Alger, Christina Keshek	Novel Protein Interaction Screen with Bacteriophage
		Bacteriophages (phages) are studied as an alternative approach to address the antibiotic-resistant bacteria epidemic, which is expected to be the leading cause of death by 2050. There are approximately 10^{32} phages on our planet with diverse and understudied genomes, and serratia phages have shown to be genetically unique compared to other phages based on their blast hits on NCBI. This study aims to show that the phage's unknown protein functions can be extrapolated by the novel proteins' interactions with the serratia (host) proteins. In this study, the functions of hypothetical proteins from six novel serratia phages were determined by conducting a bacterial 2-hybrid assay. During the procedure, the protein of interest and a protein of a known function are introduced to a solution of hydrolyzed adenylate cyclase, which will anneal to both proteins and produce cyclic adenosine monophosphate (cAMP), if the proteins are able to interact. These phages were isolated in the BYU Life Science labs, sequenced, and annotated using DNA Master and NCBI protein blasts. Herein are contained the observed protein interactions and the putative functions of the serratia phage proteins.
11	Kyson Jensen	Bacterial Adaptations to Stressful Environments
		Microbes are master adapters. They are found in nearly every possible landscape and environment throughout the world. They are able to overcome 'stressors' or environments and conditions which are less suitable for life. Stressors include: heat, acidity, toxic chemicals, oxidation, salinity, etc. Our goal is to observe these adaptations to stressors, learn how bacteria adapt, and observe if there are any fitness trade-offs in adapting to these stressors. For this project we have decided to use a symbiotic bacterial strain, *Mesorhizobium*, which is found on the roots of *A. wrangelianus*, a legume. This legume can survive on

		soil with both high concentrations of Ni and low concentrations of Ni, which makes it quick and easy to acquire closely related bacteria from both soil types. To identify probable genes, which give these bacterial strains the ability to grow in high Ni environments, we will take Ni tolerant strains, preform transposon mutagenesis, coupled with deep sequencing which will allow us to identify mutations that disrupt Ni tolerance. We theorize that the genes responsible for allowing these strains to adapt to these harsh environments encode for efflux proteins, or sequestration proteins. The efflux proteins could export the excess Ni out of the cell, while the sequestration proteins could act as a sponge and soak up the excess Ni. Genes responsible for oxidative stress enzymes or other variant enzymes could also be responsible.
12	Mason Burningham	Optimization of Microbial Fuel Cells
		Microbial fuel cells, or biobatteries, are systems that harness the capacity of some microorganisms to produce an electrical current as they undergo metabolism. These organisms are commonly found in soil samples rich in organic materials. These systems have a wide variety of potential uses as a source of electrical power over long periods of time. These batteries are inexpensive while remaining environmentally friendly. The hypothesis was that simple biobatteries could be constructed that performed as well as more complex systems described in the literature. We investigated the parameters under which biobatteries would produce the greatest electrical potential, comparing several factors. Both the physical structure of the batteries and the environmental parameters were investigated. Through this testing we were able to attain electrical potentials greater than 1000 mV, with some individual cases nearly reaching 1200 mV, which is the theoretical maximum voltage attainable from this system. Notably, the highest reported potential we have found in the literature was roughly 700 mV. The batteries remained functional over the course of over one year with little to no maintenance, although the electrical potential did decrease. Additional research into increasing output could be necessary for practical viability.
13	Riley James Hansen	Gluten's Impact on the Microbiome of the Human G.I. Tract
		The human microbiome is the community of microbes associated with the human body. Disruption and imbalances in these microbiomes can cause diverse symptoms from depression to eczema. Celiac Disease (CD) is characterized by an immune response in the small intestine that is triggered by the protein gluten, found in wheat. Previous studies have identified microbial dysbiosis in patients with CD. To better understand how these dysbiosis can affect the disease itself we will exam the microbiome diversity and composition in CD patients and healthy individuals on gluten-free diets. This will help identify what microbiome changes are associated with CD compared to those that are caused by the CD patients lack of gluten in their diet. The microbial populations of three different groups will be analyzed: 1. those diagnosed with CD and on a gluten-free diet, 2. those who do not have CD and are on a gluten-free diet, and 3. those who do not have CD and are not on a specific diet. The dietary and disease influences on the microbiome of the gastrointestinal tract will be analyzed via a single stool sample collected from each study subject. Microbial DNA was extracted using the QIAamp PowerFecal DNA kit following manufacturer's specifications (Qiagen) V3/V4 region of 16s rRNA will be sequenced using the 600 cycle v3 MiSeq kit (Illumina) The results of the analysis will be compared to existing microbial genome databases to determine the composition of microbes present in the study groups.
14	Sarah Driggs	Two component system RstB/RstA
		Two component systems (TCS) are essential to bacterial survival. Through TCS, bacteria are able to regulate gene expression in response to environmental changes and stressors. In *E. coli*, the PhoB/PhoR TCS has been well studied and is responsible for regulating phosphate homeostasis. While performing RNA seq on *E. coli* grown in various phosphate concentrations, we observed another TCS, RstB/RstA, that was upregulated in high phosphate concentrations. This TCS is known to regulate magnesium and calcium homeostasis, an essential part of the PhoB/PhoR complex. To understand more about this newly researched system, we performed a series of growth curves and saw a growth deficiency in the ΔRrstA strain, and no growth deficiency in the ΔRrstB strain. To confirm this growth deficiency and the results for other strains in the RNA seq, we performed a spot plating assay of the different deletion strains, along with transformed pstSCAB mutants grown in selective ampicillin media and observed the results.
15	Steven Brugger	Analysis of known APOE and depression SNPs in patients with multiple sclerosis
		Multiple Sclerosis (MS) is a debilitating disease characterized by the demyelination of the axons of the central nervous system. Although symptomatic manifestations of MS are unique to each patient, previous studies have demonstrated that up to 50% of MS patients will experience clinically significant depression at some point in their life. This

		correspondence warranted an investigation into a potential genetic link between MS and depression. Certain *APOE* variants have been reported to be linked to depressive affect in MS patients, which this study aimed to replicate. We also examined the relationship between MS and a collection of SNPs recently identified as being significantly associated with depression in the general population. This study was performed by dividing an EHR population of MS patients into three groups: MS patients with billing codes for depression at any point in their medical record (n=270), at least one year before their MS diagnosis (n=31), and at least one year after their MS diagnosis (n=154). Controls were defined as patients with MS but no billing codes for depression (n=968). Genome-wide association analyses did not identify any significant SNPs within each of these categories. Logistic regression analyses with both *APOE* and other depressive SNPs failed to reach statistical significance for association between MS and depression, although moderate significance was discovered with one known depression SNP on chromosome 1 (rs1432639, p = 0.058). We were unable to replicate the results linking known *APOE* SNPs to depression in MS patients, nor were we able to identify any associations between reported depression SNPs in the general population and MS in our patients.
16	Charles R. Roll	Effect of Parkinson's Disease on expression of dopamine D2 receptors in peripheral blood leukocytes
		Parkinson's Disease (PD) is a progressive neurological disorder characterized by degeneration of dopamine (DA)- producing neurons in the substantia nigra area of the midbrain. The death of these neurons causes DA levels in the nigrostriatal system to decline, which is characterized by deficits in the initiation of movement and in cognitive abilities. Often, PD is not diagnosed until there is considerable DA depletion. With earlier detection, PD patients could receive treatment and support in order to slow the progression of the disease. Recently, we have reported an increase in blood plasma DA levels and downregulation of specific leukocyte D2Rs in individuals with restless leg syndrome (RLS), also a DA-dependent disorder. The objective of this study, similar to the RLS study, was to evaluate blood catecholamine levels and expression of leukocytes D2Rs. We hypothesize that persons with PD will have decreased expression of D2R receptors on specific subpopulations of leukocytes. This study may help with early detection of PD, as well as important treatment information in persons suffering from PD.
17	Edwin Jesus Velazquez	Monoclonal antibodies against the tumor proliferation biomarker thymidine kinase 1 and its use for the treatment of cancer
		Thymidine Kinase 1 (TK1) a serum tumor proliferation biomarker is up-regulated in malignant tissues and can be found on the cell membrane of several cancer types. Despite the strong correlation of TK1 levels with cancer progression, there are currently no TK1-based therapeutics being tested in the clinical setting. Furthermore, the current availability of anti TK1 antibodies for diagnostic purposes is limited in number and epitope selection. In this study we have generated and evaluated a panel of high-affinity monoclonal antibodies to detect and quantify TK1. In addition, we have tested their potential as cancer immunotherapeutic agents. The antibodies were evaluated for their ability to bind TK1 using Western blot, Enzyme-Linked Immunosorbent Assay (ELISA) and flow cytometry. Western blot data showed specific binding of the antibodies to the TK1 protein as well as multiple forms of TK1 in recombinant human TK1 and serum samples from cancer patients. Through indirect ELISA, we identified 3B2E11, 9C10, 7D1, 2E8, 1B12 as the most sensitive antibodies with limits of detection (LOD) within the picomolar range. Clone 3B2E11 showed to be the most sensitive antibody with an LOD of 10.73 pg/ml. In addition, the antibodies showed capacity to work in sandwich ELISA (LOD = 0.93 ng/ml, clones 3B2E11 and 2E8). Three of the TK1 antibodies (clones 8G2, 3B4 and 5F7G11) showed consistent binding to different cancer cell lines, lung (95.6%), prostate (72.2%), breast (49.1%) and colon (41.1%) in flow cytometry. No significant binding was detected on normal lymphocytes. The clones 8G2 and 3B4 were selected for antibody-dependent cell-mediated cytotoxicity (ADCC). A significant increase in killing of A549 lung cancer cells was observed compared to isotype controls (About 80% increase with clone 8G2B and a 70% increase with clone 3B4). The antibodies developed have the capacity for detection and quantification of TK1 in serum and detection of TK1 surface expression on the membrane of cancer cells. Moreover, our *in vitro* ADCC experiments provide evidence that membrane associated TK1 is a potential immunotherapeutic target for the development of TK1-based therapeutics for the treatment of cancer.
18	Maxwell Drummond Drummond	The Ability of Rice Bran to Modulate the Mucosal Immune Response
		The mucosal immune system's intimate relationship with billions of commensal bacteria provides a unique approach for modulating mucosal immune responses. Probiotic bacteria can outcompete pathogenic bacteria and secrete a variety of antimicrobial compounds. It has also been determined that probiotic bacteria can enhance innate and humoral immune responses. Increases in overall levels of secretory IgA have been

		observed in mice orally dosed with *Lactobacillus acidophilus*. Probiotic bacteria have also demonstrated the ability to increase phagocytic activity, macrophage recruitment, and pro-inflammatory cytokine production. Probiotics experience an increase in intestinal abundance when metabolites known as prebiotics are introduced. Prebiotics can also lead to the acidification of the colonic lumen, since probiotic bacteria produce short-chain fatty acids when they ferment certain prebiotic metabolites. This acidification can further reduce the prevalence of pathogens and increase the motor activity of colonic epithelial cells. Rice is a widely consumed staple food across the globe. Often, when rice is processed the outer layers are removed, including a layer known as the bran. It has been demonstrated that rice bran contains a multitude of prebiotic metabolites, antioxidants, and other nutrients. The objective of this study is to determine how rice bran can modulate the mucosal immune response of infants in nutrient poor environments. This has been determined by analyzing the level of secretory IgA found in the stool of infants fed with rice bran. The IgA was quantified with an enzyme-linked immunosorbent assay performed on infantile fecal supernatants from Mali and Nicaragua.
19	Rachel Johnson	Anti-TK1 Antibodies as Potential Immunotherapy for Targeting Cancer Cells
		One promising strategy for the development of effective cancer immunotherapies relies on cancer specific antibodies. Thus, identification of cancer specific antibodies is a key component of the development of cancer immunotherapies, including Chimeric Antigen Receptor (CAR) T cell therapy. The use of antibody-based immunotherapy can eliminate certain dangers associated with other cancer therapies, such as chemotherapy, due to the high specificity of antibodies to target cancer cells. We have isolated a panel of antibodies that bind to the cancer-specific antigen thymidine kinase 1 (TK1), and are characterizing their function to determine if they can be used safely and effectively for cancer cell targeting. Nine TK1-specific antibodies were isolated using a yeast display system and will be evaluated for TK-1 specificity and cancer cell cytotoxicity in vitro. Affinity for and specificity to cell-expressed TK1 will be tested using flow cytometry with both cancer and normal cells. Upon confirmation of specificity to cancer-bound TK1, we will determine the cytotoxicity of our antibody panel by measuring antibody dependent cell cytotoxicity (ADCC) of both cancer and normal cells. We hypothesize that these antibodies will be effective in targeting TK1 expressing cancer cells, and can be used in immunotherapeutic platforms such as CAR T cell therapy in the future.
20	Alma Kaneshiro	Quantification of Staphylococcus Aureas Biofilm Clearance
		Antibiotic resistance is of great concern in the medical community, with bacterial resistance increasing proportional to their use. Staphylococcus aureus, such as methicillin resistant S. aureus (MRSA), can cause fatal infections. Problems due to this resistance are compounded when the infecting bacteria form a biofilm, thick sticky layers of bacterial secretions, which are difficult for antibiotics to penetrate. Biofilm formation is common in hospital settings on stents, catheters, and IV lines. Biofilms make antibiotic treatment risky due to incomplete killing—the most resistant survive exposure. There is evidence that bacteriophage can break up biofilms, possibly making them more susceptible to antibiotics. We induced a S. aureus biofilm formation using chemicals that mimic a skin wound. Using bacteriophage K, we inoculated the biofilm and observed clearance. Samples of cell pellets and liquid supernatant were collected, and DNA was extracted. Real-time PCR was used to quantify the levels of bacteriophage K replication, representing clearance of the bacteria. This research can be used to find efficient ways to treat an infection caused by a S. aureus biofilm. Bacteriophage used in combination with antibiotics may be able to better clear a biofilm infection and reduce antibiotic resistance risk due to more complete infection clearance.
21	Brady Wahlstrom	Characterization of Hemolytic Activity of Probiotic Lactobacilli
		Probiotic lactobacilli (PLBs) are valued for their supposed health promoting aspects. However, we observed that seven PLBs, identified as either *Lactobacillus rhamnosus* or *Lactobacillus plantarum,* caused beta hemolysis when grown on sheep blood agar (SBA), a characteristic of pathogens. This study's goal was to characterize this hemolysis. To test hemolytic properties, two species of probiotic lactobacilli were grown at 25, 30, and 37 ^{o}C, aerobically and anaerobically, by plating four different volumes (5, 10, 25, 50 uL) of a 24 hour culture on SBA. After 4 days of incubation at these temperatures, beta hemolysis was observed on the two larger samples for each organism under anaerobic conditions, with stronger hemolysis occurring at higher temperatures. Under aerobic conditions we saw yellow opaque alterations on the SBA but not full beta hemolysis. The PLBs were also grown in broth for 2 and 6 days, filter sterilized to obtain cell free culture supernatants (CFCSs). These were plated on SBA and incubated for 24 hours. All five CFCSs of the PLBs caused yellow-opaque alterations of the SBA, with day 6 CFCSs causing larger alterations than day 2 CFCSs. The pH of CFCSs was adjusted to pH 6 and non-cultured broth to 3.5. These

		were tested along with the original CFCSs (pH 3.4-3.5) on SBA. All pH 3.4-3.5 CFCSs caused a yellow-opaque alteration of the SBA, while pH 6 did not. In contrast, non-cultured broth of either pH did not alter the SBA. These data indicate that the yellow alteration of the blood is due to a metabolite of the lactobacilli and is pH dependent. In order to test the heat labile nature of the CFCS metabolites, they were autoclaved and plated on SBA. The heated CFCSs caused a yellow-opaque alteration of SBA indicating these metabolites were heat stable. Further biochemical characterization of the metabolites included attempts to separate the active component(s) by molecular weight filtration, methanol extraction and sensitivity to catalase. Our evidence suggested H2O2 was one of the yellowing agents. Interestingly, the active CFCS products were never able to cause beta hemolysis similar to that caused by lactobacilli colonies growing on sheep blood agar.
22	Daniel Sandberg	The Effect of Probiotics On the Healthy Human Gut Microbiome
		Over several years, probiotic use has increased notably, as have the number of over-the-counter probiotic products available to consumers. Many consumers use probiotics for preventative purposes rather than to treat specific illnesses. The influence of probiotics on the healthy human gut microbiome has not been extensively studied, and many questions remain regarding the influence of probiotic supplementation on existing gut flora. We examined the effect of a commercial probiotic on the composition, and diversity, of gut flora in healthy adults using V3/V4 16S rRNA gene sequencing. We enrolled thirty participants and randomly assigned them to probiotic (n=15) or placebo (n=15) groups. Over the course of the study we collected three stool samples to generate baseline, probiotic/placebo effect, and return to baseline measurements. The probiotic/placebo effect samples were collected after taking a probiotic/placebo tablet for 30 days, and the return to baseline sample was collected after stopping taking the probiotic/placebo tablet for 30 days. From the resulting samples (n=88, two samples were lost to attrition) we extracted DNA from the stool samples using the QIAamp PowerFecal DNA Kit (QIAGEN), quantified the DNA using QuantiFluor® ONE dsDNA System (Promega), and generated the V3/V4 16S rRNA library following Illumina protocols. DNA was sequenced using 500-cycle MiSeq Reagent Kit v2 (Illumina). Analysis was completed using QIIME on the Nephele platform from the National Institute of Allergy and Infectious Diseases (NIAID) Office of Cyber Infrastructure and Computational Biology (OCICB). No significant difference in gut community diversity between probiotic and placebo groups was observed. Intake of a single species probiotic in health individuals does not improve microbial GI diversity above baseline levels.
23	Joshua Gee	The role of the brain-eating amoeba Naegleria fowleri CD59-like protein in human infections
		Naegleria fowleri is a free-living amoeba that is also capable of causing fatal human infections of the central nervous system. Commonly known as the “brain-eating amoeba”, *N. fowleri* is the causative agent of an extremely rare and fatal infection, primary amoebic meningoencephalitis. *N.fowleri* is dangerously lethal in the fact that it rapidly deteriorates the brain and is most often diagnosed at death. It is believed that *N. fowleri* CD59-like complement regulatory protein is important in the infection process. This protein is thought to play a protective role in resistance to lytic cell death caused by complement, an immune system component. The CD59-like protein thus results in the amoeba becoming camouflaged by the host's native immune system. Inhibition of this protein is a novel step toward treatment of infection. An established and successful approach to treating infectious organisms is to use antibodies that target and interrupt the function of outer membrane proteins involved in the infection process.The goal of this research is to evaluate the hypothesis that human anti-CD59 antibodies can neutralize the amoeba’s CD59-like protein in the presence of complement, which would normally lyse the cells. To do this, we established an experimental infection model using human cells (HeLa cervical cancer cells) grown to confluence in a monolayer, which are used to analyze the levels of infection caused by *N. fowleri*. Infections are performed after treating the amoeba with complement, in the presence or absence of anti-CD59 antibody. This reveals the level of protection against complement that is provided by the *N. fowleri* CD59-like protein. This model mimics the natural infection of *N. fowleri*, and will provide a greater understanding of its pathogenesis.
24	Joshua T. Calder	A novel trimeric autotransporter lipoprotein may be a component of the extracellular matrix of Yersinia pseudotuberculosis contributing to biofilm cohesiveness.
		Yersinia pseudotuberculosis (*Yptb*) forms biofilms in order to grow in challenging environments. Biofilm formation plays a key role in the success of *Yptb*, allowing the bacterium enhanced survival when faced with desiccation, temperature variation, predation, or lack of nutrients. The strength and cohesiveness of Yersinia biofilms has previously been solely attributed to an extracellular polysaccharide matrix encoded by the *hms* genes. The recently discovered BarA-UvrY two-component regulatory system

		controls the stability of the biofilm formed in *Yptb.* Mutations in the *uvrY* or *csrB* genes cause increased biofilm stability, although these mutants show only slightly increased levels of extracellular polysaccharide. Proteomic analysis of the mutants reveals much higher levels of a putative trimeric autotransporter lipoprotein, encoded by the YPTB2394 gene. This suggests that the lipoprotein may form part of the extracellular matrix. To investigate a possible protein component of the biofilm, we treated wild-type and *csrB* mutant *Yptb* biofilms with proteinase K. This destabilized biofilms, whereas DNase had little to no significant effect on stability. Overexpression of the YPTB2394 gene in wild-type *Yptb* results in a significant strengthening of the biofilm, similar to the *csrB* or *uvrY* mutant biofilms. Further experimentation is needed to confirm the localization of the YPTB2394 protein in the extracellular matrix of *Yptb*. Upon completion of this project, current research into biofilms will be advanced by identifying the first protein to be a component of the biofilm extracellular matrix in *Yersinia pseudotuberculosis*.
25	Kade Pachner	A Survey of Coccidiosis in Utah's Wild Turkey Population
		Coccidiosis, caused by parasites of the genus Eimeria poses a significant threat to the poultry industry. This single celled intestinal parasite commonly infects the gastrointestinal tract of chickens and turkeys, resulting in millions of dollars of revenue loss to farmers. Coccidiosis in turkeys is commonly caused by five different species of Eimeria parasites. It is unclear how common these parasites are in populations of wild turkeys. Wild turkeys were historically found in the state of Utah; however, by the time of European settlement in the 1800s, there were no remaining wild turkeys in the state. Reintroduction efforts, starting in the 1980's have been very successful and wild turkeys are now common throughout much of Utah. Currently there are no published reports describing prevalence or distribution of Eimeria species that may infect Utah's wild turkey population. In this study. We sampled birds from various flocks of wild turkeys throughout Utah to determine carriage of Eimeria parasites. Using microscopic as well as molecular techniques we have identified at least three distinct species of Eimeria parasites in wild populations of birds.
26	Aurora Rodriguez Katherine Allen	Characterization of diversity in T-4 like Bacteriophages.
		Phages are the most abundant and diverse biological entity on the planet. Bacteriophages have not only played an important role in microbial evolution and are a potential response antibiotic resistant microbial infections. Therefore, research is being done to understand their genome, paying particular attention to conserved proteins within phage phamilies. This scientific endeavor will focus on identifying conserved genes in the T4-like phage phamily, phages we have isolated that mimic the first phage isolated, T4. The goal is to distinguish the differences that exist in their structural genes to understand their shared features, and the diversity of hosts that is present in this phamily. We isolated, sequenced, and annotated the genome of bacteriophages that shared similarities with the T4 phage. Further analysis with dot plot and a phamerater map revealed contrasting features, as well as conserved proteins found among the phamily. The previously mentioned procedures allowed us to scrutinize the T4 like phage phamily in detail, which demonstrated how a vast amount of diversity can be present within the same bacteriophage phamily. These series of experiments will identify highly conserved proteins within the T4-like phage phamily that could act as evidence for microbial evolution. Furthermore, the advances that have been made to greater understand the T4 like phage phamily will become influential as we attempt to increase our knowledge of the microbial world.
27	Nicholas Christman	Enhancing the antimicrobial ability of Gallium with Bacterial Siderophores
		Iron is an essential element for bacteria. Many bacteria compete for iron by making siderophores, which are small molecules with an extremely high affinity for iron and which are imported through specific receptors. Gallium is antimicrobial because it displaces iron atoms in bacterial cells and is being explored as a potential therapeutic for antibiotic-resistant bacteria. Since gallium cannot participate in redox reactions, this causes growth inhibition or death of the cell. However, the susceptibility of diverse *Escherichia coli* to gallium compounds has not been thoroughly investigated. We have tested many extraintestinal pathogenic *E. coli* (ExPEC) strains and have found a wide range of susceptibility to gallium nitrate among these isolates. Some strains, including strain A27, appear completely resistant to gallium nitrate. We hypothesized that this resistance might be overcome by linking gallium to ExPEC-specific siderophores. Gallium-siderophore complexes would be actively imported through siderophore receptor and transport mechanisms. Strain A27 produces both aerobactin and salmochelin siderophores. We stimulated siderophore production in strain A27 by growing it in media that has a very low iron content (.009 ppm) and confirmed the presence of siderophores in the supernatant by using CAS dye assay. Gallium solutions were then prepared using

		these supernatants as well as control supernatants that did not contain siderophores. The gallium-siderophore combination was then tested for its ability to inhibit growth of strain A27. Unlike the control, the combination of siderophores and gallium caused inhibition of growth at 50 ug/ml gallium. This result indicates that the gallium-siderophore combination made resistant cells much more susceptible to gallium. Future work will involve purification of individual salmochelin or aerobactin siderophores from supernatants and testing whether the siderophore receptors are necessary for import of gallium-siderophore complexes.
28	Tyler Henderson	Examination of cAMP secretion in Mycobacterium smegmatis
		Cyclic adenosine monophosphate (cAMP) is a secondary messenger molecule found in almost all cells which allows them to recognize and respond to changing stimuli in their environment. These second messenger molecules are produced by adenylate cyclase (AC) enzymes. A human cell contains nine ACs, whereas *Mycobacterium tuberculosis*, the causative agent of tuberculosis, contains 15 ACs, many more than typical bacterial cells which only contain one. The question in the field is why is cAMP so important to *M. tuberculosis*, that it contains 15 enzymes to make it. Recent research indicates that cAMP is secreted by M. tuberculosis into host macrophages, allowing them to survive and cause disease inside the human host. Our goal is to better understand the mechanism of cAMP secretion in mycobacterial species by identifying environments and proteins important to cAMP secretion. *M. smegmatis*, a nonpathogenic surrogate for *M. tuberculosis*, was grown in specific environments that may be encountered by the pathogen in the body, as well as environments that tuberculosis cells encounter outside of the body. Environments included: 0.5% albumin, 0.005% oleic acid, 10% OADC, 0.2% glucose, Sauton's media, and TSB. We then used a commercial ELISA to measure the amounts of secreted and intracellular cAMP per 10^6 cells. Data were analyzed using an unpaired t-test. Addition of OADC caused a 2.4x reduction in secreted cAMP levels that was not observed when albumin or oleic acid were used individually ($p=0.0074$). We will also measure the secreted and intracellular cAMP using a *M. smegmatis* mutant library containing 1000 isolated colonies generated through transposon mutagenesis using ΦMycoMarT7 vector and Tn5 transposon. This will allow for identification of proteins necessary for cAMP secretion.
29	Alisa Knowles	Analysis of Differential Gene Expression in Halomonas-Inoculated Alfalfa Grown in the Presence of Salt
		Increasing soil salinity is a growing global issue, as it disrupts ecosystems and hinders crop yield. Some plants have adapted to grow in high salinity, but most crops are very sensitive to salt. Bacteria in the plant microbiome can influence how plants grow and respond to environmental stresses. Several species of salt-tolerant rhizobacteria (soil bacteria associated with plant roots) have been shown to aid plant growth despite high salt concentrations. Dr.Nielsen's laboratory at BYU has isolated several rhizobacterial species associated with local native salt-tolerant plants, and have found two that stimulate alfalfa growth in the presence of salt. We have been studying the plant growth promoting mechanisms of one of these isolates, *Halomonas.* We are using alfalfa plants to measure the expression levels of several salt-tolerance related genes that we suspected to be upregulated or downregulated in inoculated plants in comparison with uninoculated plants. Our study will lead to identification of genes that contribute to the response of the plant to salinity stress. These bacterial inoculants will benefit agriculture in areas affected by high salinity.
30	Cardon Porter, Morgan Westdyke, Eun Song, and Brent L. Nielsen	Characterization of salt-tolerant bacteria isolated from three halophytes that exhibit growth promotion capabilities with alfalfa grown under saline conditions
		Halophytes have adapted to grow in salty soils, with many species present in the western U.S. However, little is known about the microbiomes associated with these plants. We have isolated bacteria growing in the rhizosphere and as endophytes associated with Sarcoconia utahensis, Salicornia rubra, and Allenrolfea occidentalis, three native Utah halophytes. DNA sequencing of the bacteria identified species from several genera, including Halomonas, Planococcus, Kuchneria, Bacillus, Virgibacillus, and Pseudomonas. Each isolate was tested for maximum salt tolerance, optimal temperature for growth, biofilm formation, pigment production and other colony characteristics, phosphate solubilizaiton, siderophore production, and phylogenic relationships. Isolates have been tested as inoculants for plant growth stimulation of alfalfa in the presence of 1% NaCl in the watering solution. Halomonas, Planococcus and Kuchneria isolates stimulate growth of alfalfa in the presence of salt. This concentration of salt significantly inhibits growth and development of uninoculated alfalfa and rice plants. When used as inoculum Halomonas is recovered as an endophyte from the inoculated alfalfa plants, indicating the ability to become established within non-host plants. These isolates have considerable promise as inocula for enhancing growth of alfalfa and other crops in salty soil.

31	Brinton Moe Colin Michael Laura Uricoechea Tyler Hanis Tyson Stoker Dylan Elton Samuel Flor Tyler Divis	Discovering Antibiotic Resistant Genes in Bacteriophages
		By the year 2050, antibiotic-resistant infections are projected to kill 10 million people a year. In an effort to prevent this, scientists are developing new ways to fight bacteria with antibiotic-resistance. One of these methods is the use of naturally occurring prokaryotic viruses—bacteriophages—that are capable of infecting specific bacterial hosts. There has yet to be a documented case of a bacteriophage carrying an antibiotic-resistant gene. Bacteriophages have been shown to carry toxins, biofilm producing proteins, and other potentially dangerous proteins. We hypothesize that with over 80% of bacteriophage genes yet unidentified, it is likely that at least some of these genes also code for antibiotic resistance proteins. Eight bacteriophages, two of which are completely novel, were examined for antibiotic resistance genes. After isolation of the bacteriophage DNA, the phage genome was fragmented through sonication and cloned into a vector for protein expression. These random sequences are then inserted into bacteria through a process called transformation, and grown on antibiotic plates with a control culture of untransformed bacteria. Any growth of plasmid-containing bacteria on the antibiotic plates confirms the presence of antibiotic resistant genes in the original bacteriophage genome. These findings will influence future research on the development, preparation, and correct procedure for bacteriophage therapy used to fight antibiotic resistant bacterial infections, as well as the first documented case of bacteriophages carrying antibiotic-resistant gene products.
32	Bryson Carrier	Who Brought the Microbes? Investigating the Source of Fecal Veneer on Rock Climbing Holds
		Rock climbers face many dangers on the wall, but exposure to pathogens from feces is one overlooked risk. A past study surveying the microbiome of indoor rock-climbing walls identified a number of fecal-associated microorganisms, termed a “fecal veneer” [1], but failed to address where these microbes originated. While many climbers use specific shoes, many gyms that cater to beginners allow street shoes to be used on the wall. These shoes are worn in many environments which might provide a source of fecal matter such as bathrooms and sidewalks. To determine where the fecal veneer is transplanted from and develop a protocol to prevent the transfer of fecal microbes onto the walls, we examined the Utah Valley University indoor climbing gym while allowing standard and sanitized-only street shoes. Data collection and sampling occurred in 2 phases: regular policy of allowing street shoes and sanitized shoes only. Prior to sampling, there was an initial sanitizing of all climbing surfaces, floor, and seats, which commenced with a 3% bleach solution. Baseline samples for each phase were obtained at ground holds from 10 different routes the morning after sanitization. Following 4 days of climbing, samples were taken following the same procedure. Phase 2 was conducted identically except all climbers and employees had to remove or sanitize their street shoes before passing a certain point before entering the climbing facility. DNA was extracted from all swabs and the presence of indicators of general fecal contamination as well as human-specific feces were examined using PCR to elucidate the source of the fecal veneer present on rock walls under the two treatments. While a past study has examined the microbiome, this is the first study to determine the likely source of fecal-associated microbes on rock climbing holds, and thus address the health risk posed by this contamination. Additionally, by providing the climbing gym with a protocol and determining the difference that protocol has on the presence of fecal microorganisms, we are able to not only identify a potential problem, but also provide a solution to help keep climbers safe, at least from microbes, on the wall. REFERENCES: Brauer, S. L., Vuono, D., Carmichael, M. J., Pepe-Ranney, C., Strom, A., Rabinowitz, E., . . . Zinder, S. H. (2014). Microbial Sequencing Analyses Suggest the Presence of a Fecal Veneer on Indoor Climbing Wall Holds. Current Microbiology, 681-689.
33	Carson Walker	Food Preference Determined by Genetic Predisposition for Familiar Microbiota Rather Than Rearing Conditions in Drosophila
		Recently, the association between D. melanogaster and their associated microorganisms (‘microbiota’) has emerged as a model to better dissect host-microbe interactions. Many of these studies focus on a host of noticeable changes in behavior and appearance of both the fly and the bacteria. For example, fruit flies are influenced by an overwhelming genetic instinct to choose specific bacteria types in foods based on their environmental challenges. One understudied area is how bacterial colonization can

		influence host feeding preferences in a feedback loop that reinforces the establishment of particular microbial types in the animal. In this study we test the hypothesis that host genotype override microbial influences for feeding preference by comparing diet choices in flies reared with different sets of microbes. Our preliminary work supports this idea by showing that, in flies that naturally bear different abundances of specific bacterial types, diets inoculated with those bacteria were preferred even if the flies were reared bacteria-free. In the months leading up to this presentation we will continue to compare the influences of bacterial familiarity and genetic predisposition by repeating these experiments and adding new fly and bacterial genotypes to the trials. In each trial, we will inoculate a certain fly genotype with a bacteria type unlike its genetically preferred type, then we will reintroduce it to the genetically preferred bacteria and determine the force of the genetic predisposition. Together, these results will illustrate that the genetic influence on decisions of the D. melanogaster are stronger than the influence of the organism's personal experiences.
34	Isaac A Trost	Evaluating Lotus japonicus as an alternative host for Rhizobium pusense IRBG74
		Bacteria often associate with plants in a symbiotic relationship, which can help the plant host to achieve maximum growth and compete with surrounding plants in its ecosystem. One group of plants, known as legumes, form root nodules that contain nitrogen-fixing bacteria in order to increase their chances of survival. Nitrogen is an important nutrient for the plant due to its use in nucleic acids and proteins. *Rhizobium pusense* IRBG74 is a nitrogen-fixing bacterium that was isolated from the root nodules of *Sesbania cannabina*. However, conducting experiments with *Sesbania cannabina* is difficult because it requires tropical growing conditions and takes two months to form root nodules. Furthermore, *Sesbania cannabina* is a tree that is native to Southeast Asia, so obtaining and producing seed is difficult. We tested a related legume, *Lotus japonicus*, to see if it can serve as a suitable alternative host for *Rhizobium pusense* IRBG74. *Lotus japonicus* would be a more convenient model of legume to use for experiments with *Rhizobium pusense* IRBG74 because it forms root nodules more quickly and it can be kept at temperate growing conditions. *Lotus japonicus* is a small forb and it is widely used in root nodulation research, so obtaining and producing seeds is also much simpler. We tested various *nod* mutants of *Rhizobium pusense* IRBG74 for their ability to nodulate *Lotus japonicus* Gifu B-129 and compared with them with results of nodulation experiments using the original host, *Sesbania cannabina*.
35	Khin Pyae	Microbial adaptation to high-nickel soils
		The Earth's landscapes have been going through a remarkable journey of environmental changes affected either by nature or by human interventions. Environmental changes on the Earth's surface may present the soil-dwelling microbes with various challenges including desiccation, heat, salinity, oxidation, pollution, and an increase of toxic compounds in soil stoichiometry. Understanding the genetic and physiological basis of adaptation to environmental stressors is essential for explaining the microbial biodiversity. Tolerance to stressors such as high-metal concentration can be enabled by a variety of mechanisms including efflux transporters, sequestration, and variant enzyme production. Often, as a species adapt, "fitness trade-off" can occur where improved fitness in one environment decreases fitness in another. To study molecular response to stress in *Mesorhizobium*, we are comparing several strains isolated from high-Ni and low-Ni soils. Our preliminary data suggests that the tolerance to high-Ni concentration is accompanied by growth dependency on the intermediate levels of nickel. In preliminary experiments, we isolated spontaneous Ni-hyper-tolerant mutant Mesorhizobium which will be analyzed using GWAS and Tn-seq to identify genes and mechanisms responsible for the acquired Ni-tolerance.
36	Annena Jane Lundgren	Overcoming Nucleosome Position Dependent Gene Silencing Via Positioning Manipulation
		We are investigating the effect of nucleosome positioning on gene expression. As the basic organizational unit of chromatin, nucleosomes consist of DNA wrapped around a histone octamer and can restrict access to genetic material. They exist throughout the genome, often in highly positioned and phased patterns around transcriptionally active genes. Nucleosome positions can be manipulated using specific 'positioning' sequences of DNA. The Widom 601 sequence is one of the most widely-used in vitro positioning sequences due to its consistent positioning accuracy. In order to test nucleosome positioning sequences in living organisms, we are using the Widom 601 sequences to alter nucleosome positioning which should enable us to see GFP expression under the control of the unc-54 enhancer in *C. elegans*. We will gather evidence to elucidate the effect that nucleosome positioning has on gene silencing and on how manipulation of nucleosome positioning could be used to enhance or repress gene expression, with hopes of finding applications for gene therapy and other novel treatments.
37	Ashlin Cowger	Bioaerosols associated with evaporative cooler use in low-income homes in the semi-arid climate of Utah County, Utah, USA
		Asthma is the leading chronic illness in children in the United States. Since children in the U.S. spend most of their time indoors there is an increased need to understand key sources of daily asthma triggers in the home. Bacterial endotoxin, dust mite allergens and β-D-glucan have been shown to be potent inducers of asthma attacks, and high

		levels in the homes can trigger attacks in those diagnosed with asthma. We aim to better understand the risks to those with asthma that might be associated with evaporative cooler (EC) use in low-income homes. ECs are often promoted for their low energy consumption. Because of their lower cost, they are more widely used in low-income homes. ECs use evaporation to cool the air, which leads to higher indoor relative humidity. This may create an ecological niche for house dust mites in semi-arid climates where they are normally absent. EC sump water also provides an ideal environment for bacteria and fungi to grow, possibly resulting in EC loading the air with more potential asthma triggers than central air conditioning. We sampled low-income homes around Utah county with central air and evaporative cooling and tested them for the presence of dust mite allergens, β-D-glucan and endotoxin. There were significantly higher levels of endotoxins and β-(1→3)-D-glucans in the EC homes compared to the AC homes, with no significant differences in dust mite allergen levels. These findings suggest that in semi-arid environments, dust mite antigen levels are not as dependent upon EC or AC as are endotoxin and β-(1→3)-D-glucan levels.
38	Colleen Newey	PAS Kinase as a Potential Therapeutic Target for Metabolic Diseases
		Diabetes is currently the 6th leading cause of death worldwide. According to the Global Burden of Disease Study, in April of 2016 approximately 422 million people lived with diabetes and the global monetary cost of diabetes was 825 billion dollars per year and is growing. Better treatments are clearly needed. Diabetes is a disease with symptoms of high blood glucose and high triglyceride levels, caused by poor regulation of insulin. PAS (Per-Arnt-Sim) kinase is a protein kinase known to regulate glucose, insulin and triglyceride levels in mice placed on a high fat diet, suggesting it as a new therapeutic target for diabetes (Hao et al, 2007, Borter et al., 2007, Semplici et al., 2016). Our goal is to more fully understand the phenotypes associated with PAS kinase. We have studied the PAS kinase related phenotypes in mice placed on a high fat high sugar diet, which more closely approaches the Western diet. We have observed significant differences in the triglyceride as was seen on the high fat diet, and have identified specific triglycerides regulated by PAS kinase. These include primarily saturated triglycerides. In addition, we have quantified the metabolic rate of various cells from the PAS kinase and wild type mice. Muscle and liver cells isolated from the PAS kinase-deficient mice display increased respiration. We have also observed this increased respiration in yeast cells, suggesting conserved function. Taken together, our results suggest that PAS kinase controls glucose at a key point in glucose partitioning, the junction of triglyceride biosynthesis versus respiration. Our results suggest PAS kinase as a therapeutic target for the treatment of high triglycerides and metabolic diseases. Combined with previous results that implicate PAS kinase in the direct regulation of insulin, PAS kinase appears to be an attractive therapeutic target for diabetes.
39	Emily Dawn-Shellman Hales	Restoring Transgene GFP Expression via RNAi Knockdown of Gene Silencing Elements
		The mechanisms of transgene silencing in *C. elegans* are poorly understood despite the importance of the nematode as a model for genetic research. Integration of a transgene into the genome led to the expression of GFP in both the body wall and pharyngeal muscle cells of *C. elegans* as expected. However, subsequent generations stopped expressing body wall GFP. Using RNAi, we target genes responsible for gene silencing (including several chromatin remodelers). We hypothesize that knockdown of these genes will restore expression of body wall GFP and give insight into the mechanisms of *C. elegans* transgene silencing.
40	Jacob Mark Miller	The Impact of Multiple Sclerosis Disease Status and Subtype on Hematologic Profile
		Background: Multiple sclerosis (MS) is a complex disease of the central nervous system in which the myelin sheaths of the nerve cells in the brain and spinal cord are damaged. Because presentation of the disease varies widely between patients, several subtypes of MS have been defined based on patterns of its progression: relapsing remitting multiple sclerosis (RRMS), secondary progressive multiple sclerosis (SPMS), and primary progressive multiple sclerosis (PPMS). There are currently no predictive biomarkers for MS disease course. **Objective**: To characterize differences in hematologic profile both between MS cases and controls and between RRMS/SPMS and PPMS patients. **Methods**: Patient laboratory values for Caucasian and African-American MS patients were retrieved from Vanderbilt University Medical Center's Synthetic Derivative (SD). Logistic regression analysis was performed in R (version 3.1.3). Each of the 36 lab tests was analyzed separately as an independent variable. For the case-control analysis, patient median value for the given lab test was used to predict MS disease status. For the subtype analysis, patient median value for the given lab test was used to predict MS subtype. Sex and patient age were included as covariates in all analyses. Separate analyses were performed for the Caucasian and African-American groups.

		Results: In the preliminary case-control analysis, four lab tests reached significance (*P*-value < 0.001) in both the Caucasian and African-American groups after Bonferroni correction. An additional six tests reached significance in just one group. In the subtype analysis, no tests were significant in both groups, but eight tests were nominally significant in one of the two groups. **Conclusion**: This study provides evidence for differences in hematologic profiles both between MS cases and controls and between patients with different MS subtypes. Further studies that control for medication use are warranted.
41	Jeremy Beales	Contribution of Known Risk Variants to Multiple Sclerosis Age of Onset
		Background: Multiple sclerosis (MS) is an immune-mediated chronic disease of the central nervous system (CNS) characterized by inflammation and axonal demyelination. There are over 2 million individuals living with MS worldwide. Previous studies have identified approximately 200 genetic risk variants associated with the disease located outside of the major histocompatibility complex (MHC) region. Age of disease onset (AOO) is an important contributing factor to the clinical course of the disease. **Objectives**: We aimed to quantify the impact of known non-MHC MS risk loci on AOO and use them to estimate AOO narrow-sense heritability. **Methods**: To quantify the impact of these 200 variants on AOO, we used PRSice (v1.25) to calculate a genetic risk score (GRS) for a cohort of non-Hispanic white MS patients taken from the Vanderbilt University Medical Center Synthetic Derivative (SD). Using sex and body mass index (BMI) as covariates, the genetic risk score was used to predict AOO in a linear regression model using preliminary genetic data. Narrow-sense heritability was estimated using GCTA (v1.92.0). **Results**: In the linear regression, the GRS approached significance (*P*-value: 0.08), with increased genetic risk corresponding to earlier AOO (β = -254.73, 95% confidence interval: -540.0 – 30.1). Narrow-sense heritability was estimated to be 0.06 (*P*-value: 0.016). **Conclusion**: Our findings suggest that known non-MHC MS risk loci contribute to AOO and warrant further investigation. We plan to perform an identical analysis on a larger dataset and will incorporate MS subtype as a covariate to account for possible confounding.
42	Jordan Barnett	Asparaginase Cancer Treatment Biosensor
		In this research, techniques using cell free protein synthesis (CFPS) were used to detect the concentration present of Asparaginase (ASNase). The detection of ASNase is important in the clinical world for monitoring treatments for Acute Lymphocytic Leukemia (ALL), which is a blood cancer that starts in the bone marrow. In order to replicate, the cancer cell must uptake Asparagine (ASN) from the bloodstream, as it is unable to produce this amino acid on its own. In addition to other treatments, patients are treated with ASNase to deplete the blood of the patient of ASN, thus hindering the replication of the cancer cells. The ability to monitor ASNase level in the blood of the patient plays a key role in adjusting and administering the treatment of ASNase to the patient. The CFPS assay used in this research shows how a sample of serum from a patient could be diluted and tested to determine concentration of ASNase present. This robust and quick detection method provides an effective and relatively cheap biosensor that could be modified and used clinically to monitor ASNase treatments of ALL patients.
43	Megan Rimmasch	Automating the extraction of multiple sclerosis treatment data for pharmacogenetic studies
		Background: Disease-modifying treatments for multiple sclerosis (MS) are associated with a number of adverse drug reactions (ADRs), including hepatic and cardiac damage. Attempts to use pharmacogenetic analysis to identify genetic factors associated with such ADRs are complicated by the relative rarity of some ADRs. Using large databases of electronic health records (EHRs) represents one potential approach to overcoming this challenge. This approach necessitates the ability to reliably extract treatment timelines from these records. Unfortunately, manually reviewing thousands of EHRs to acquire sufficient data for a comprehensive ADR analysis is time-consuming and impractical. However, by automating the extraction process, we can create a large, longitudinal treatment database to be used in future studies.

		Objective: Our objective is to develop an algorithm to extract MS treatment data, beginning with glatiramer acetate, to create a large-scale database of information from EHRs. This database will be used in downstream pharmacogenetic studies. Methods: Records referencing glatiramer acetate from MS patients were retrieved from the Vanderbilt University Medical Center Synthetic Derivative, a deidentified version of the EHR, and used to develop the extraction algorithm in Python. Regular expressions were developed to match language patterns used by clinicians to indicate a beginning, continuation, or end of a treatment period. The algorithm employs these regular expressions to classify EHR medication references, generating a timeline of treatment events for patients. This timeline can guide ADR extraction in future studies. Results: We tested the performance of the algorithm using a training dataset of 1,000 manually reviewed and classified records using five metrics to measure performance for "start", "stop", and "continue" classes. For the "start" category we saw a 96% accuracy, 87% sensitivity, 97% specificity, 85% precision, and an F-measure of 86%. For the "stop" category there was a 91% accuracy, 95% sensitivity, 89% specificity, 79% precision, and an F-measure of 79%. For the "continue" category there was a 91% accuracy, 86% sensitivity, 97% specificity, 97% precision, and an F-measure of 91%.
44	Nancy Wilson	Catching Your Attention The Effect of Textual Presentation Format on Reader Understanding of New Concepts
		Informal investigations show that students often make decisions about their major based on their experience with a single textbook in a single class; students choosing career paths outside of the life sciences often cite the difficulty of understanding the vocabulary as presented in an academic context. We wish, therefore, to understand which text presentation formats best promote reader comprehension and retention of new concepts. In future, we hope to provide recommendations which will allow academic publishers, particularly in the life sciences, to present materials in a way that better engages learners and promotes their interest in this important field of study. Preliminary results suggest that publishers should, whenever possible, couch new concepts in a graphic. When graphic representations are not possible, conveying new concepts through implicit analogy appears to be the best vehicle for reader comprehension of new ideas.
45	Sarah Ricks	In Vitro Transcription from Reconstituted Chromatin Reported by RNA Mango
		We are interested in chromatin architecture at the nucleosome level and its effect on gene expression. Nucleosomes consist of protein complexes called histone octamers which are wrapped ~1.7 times by 147 base pairs of DNA. A nucleosome core particle further consists of a nucleosome and an adjacent short region of unbound DNA, called linker DNA, which can vary in length between adjacent nucleosomes. Canonically, each histone octamer contains two copies of each of the following histone proteins: H2A, H2B, H3 and H4. Higher order chromatin structure involves multiple nucleosome core particles. The tails of these histone proteins can be covalently modified in a number of ways, including methylation and acetylation, which correlate with levels of gene expression. There are also various non-canonical histone protein variants, which may also influence gene expression and play a role in development and cell stages. We have designed an *in vitro* transcription assay that will enable us to conduct experiments designed to identify effects of histone modifications or histone variants on transcription of reconstituted chromatin. We have designed a DNA sequence of approximately 1500 base pairs containing the binding site for a potent transcription factor, the adenovirus type II major late promoter, five 601 sequences (nucleosome preferred positioning sequences) separated by linker regions containing nucleosome semi-repelling regions, and ending with the RNA Mango gene. RNA Mango is a RNA aptamer which will fluoresce following successful transcription of the entire sequence. The necessary proteins for this *in vitro* transcription will be provided by nuclear extract. The pairing of transcription from reconstituted chromatin template reported by an RNA aptamer is a novel direction, and allows for further experiments on how histone modifications or variants alter transcription.
46	Serena Seychelle Young	Predicting Catabolic Pathways in Lactobacillus wasatchensis using Metabolic Modeling
		Lactobacillus wasatchensis, an obligate heterofermentative nonstarter lactic acid bacteria can cause late gas production and splits and cracks in Cheddar cheese. Our goal was to identify potential sources of 6-carbon sugar-compounds that may be present in cheese and cause release of CO_2 when converted to a 5-carbon sugar and utilized by *Lb. wasatchensis* for energy production. Previous studies did not explain late gas production in cheese when no galactose was present. Potential relevant metabolic pathways were determined based upon the genome of *Lb. wasatchensis* WDC04. The genome sequence was exported from the NCBI Genbank database, then metabolic modeling was performed using Knowledgebase Predictive Biology software to map the genes present for various metabolic pathways. Based upon data output from a flux balance analysis, it was confirmed that *Lb. wasatchensis* contains a complete pentose

		phosphate pathway (PPP), while pathways for glycolysis, tricarboxylic acid, and galactose metabolism were incomplete. To confirm these predictions and to look for alternative carbon metabolic pathways, we tested five strains of *Lb. wasatchensis* (CGL02, DH3, LD13, SH05, WDC04) in carbohydrate restricted MRS (CR-MRS) broth in micro-well plates supplemented with 7% oxyrase and 0.5% of either ribose, lactose, galactose, or N-acetylglucosamine (NAG). Growth occurred with ribose but was negligible when lactose, galactose, or NAG were the only carbohydrate present. The metabolic modeling also predicted additional carbohydrates that might be utilized by *Lb. wasatchensis* including gluconate which is the oxidized form of glucose. Gluconate contains 6 carbons and *Lb. wasatchensis* contains the genes for it to be converted to ribose-5-P using phosphogluconate dehydrogenase by a decarboxylating step, producing CO_2 in a similar way to galactose, when used as an energy source for the PPP. When inoculated into CR-MRS containing 0.5% sodium gluconate, four of the *Lb. wasatchensis* strains grew, confirming utilization of gluconate. Presence of gluconate in cheese thus becomes another risk factor for unwanted gas production and formation of splits and cracks in cheese.
47	Tanner Call	The Gut Microbiome as a Driver of Host Dietary Preference in Drosophila melanogaster
		The "gut microbiome", or the combination of microorganisms that colonize the interior of the GI tract of all macro-organisms, plays a significant role in host health and physiology. It has been hypothesized that host feeding behaviors are manipulated by microbiota (Alcock et al., 2014). Wong et al. recently reported that Drosophila melanogaster, or fruit flies, knowingly forage beneficial microbes but neglected to measure how gut microbiota act to change fly dietary preference alone (2017). In this study we use D. melanogaster to test if the microbiome has a causal influence on dietary preferences of a model animal host. To quantify dietary preference, modified by the gut microbiome, we assay a single genotype of fly, inoculated with a controlled microbiota, using an automated feeding assay. To manipulate the microbiota, we separately inoculate bleach-sterilized D. melanogaster eggs with each of two representative species of bacteria normally found in flies, Acetobacter and Lactobacillus. As a control, flies are reared without bacteria or with both species, representing a microbial community. Then, to test if the microbiota impacts feeding preferences based on nutritional content of the diet, we expose the flies to diets bearing 100%, 75%, 50%, or 25% of normal concentrations of glucose and yeast in two separate experiments. Each experiment targets one of the two variables, while keeping the other constant. We then compare the measured D. melanogaster preferences when the flies are mono-associated or bacteria-free. The bacteria-free treatments expose the natural host genetic preference; and the different monoassociations the influence of the different bacteria. Differences in feeding preference are assessed by combining three quantitative measures of feeding rate - frequency, duration, and interval between eating periods – into a single preference index. Preference indices of flies (10 flies per condition in each of three separate experiments) are compared using linear models and ANOVA to define the impact of the gut microbiota on host feeding preference. These results will help us understand how different members of the microbiota can influence animal feeding behaviors. Literature Cited Alcock J, Maley CC, Aktipis CA. Is eating behavior manipulated by the gastrointestinal microbiota? Evolutionary pressures and potential mechanisms. Bioessays. 2014;36(10):940-9. Wong AC, Wang QP, Morimoto J, et al. Gut Microbiota Modifies Olfactory-Guided Microbial Preferences and Foraging Decisions in . Curr Biol. 2017;27(15):2397-2404.e4.
48	Albin Taylor Rhen Davis Rochelle Gaertner	RNA Sequencing of Enterobacteriaceae Bacteriophages to Determine Gene Functions
		Bacteriophages (phage) are a widely researched entity: a prokaryotic virus that infects and lyses their bacterial host. The purpose of this procedure is to verify predicted proteins, relative transcription expression levels, and determine variances between expected and observed gene expression. This is done by analyzing the information acquired from the sequencing of mRNA transcripts, extracted from bacterial hosts infected with bacteriophage. The goal is to discover the method of infection, assimilation of genetic material, transcription, the release of progeny, etc. related to the specific bacteriophage of *Enterobacteriaceae* bacteria. Because RNA does not always encode for proteins, a study of RNA transcription levels provides insight into phage lifecycles that a protein-based study cannot. Furthermore, phage early, middle and late genes play similar roles in infections. Therefore, by identifying our phage's early, middle and late genes transcripts, we can assign putative functions. To this end, the data was obtained by the inoculation of host cells with bacteriophage and the subsequent sequencing of cDNA created by reverse transcription of RNA transcripts taken at predetermined time points following inoculation. In this study we use a collection of

		phages from different “phamilies”, some completely novel, to further characterize their infection mechanisms. Our analysis of RNAseq data from novel phage infections has elucidated the early, middle and late genes of these previously unstudied phages and will provide a foundation for future study.
49	Aurora Rodriguez, Emilee Lynn Carr, Rochelle Gaertner	Isolation and Characterization of Novel but Ubiquitous Family of Serratia Phages
		Phages are the most abundant and diverse biological entity on the planet. Bacteriophages have not only played an important role in microbial evolution and are a potential response antibiotic resistant microbial infections. Therefore, research is being done to understand their genome, paying particular attention to conserved proteins within phage phamilies. This scientific endeavor will focus on identifying conserved genes in the T4-like phage phamily, phages we have isolated that mimic the first phage isolated, T4. The goal is to distinguish the differences that exist in their structural genes to understand their shared features, and the diversity of hosts that is present in this phamily. We isolated, sequenced, and annotated the genome of bacteriophages that shared similarities with the T4 phage. Further analysis with dot plot and a phamerater map revealed contrasting features, as well as conserved proteins found among the phamily. The previously mentioned procedures allowed us to scrutinize the T4 like phage phamily in detail, which demonstrated how a vast amount of diversity can be present within the same bacteriophage phamily. These series of experiments will identify highly conserved proteins within the T4-like phage phamily that could act as evidence for microbial evolution. Furthermore, the advances that have been made to greater understand the T4 like phage phamily will become influential as we attempt to increase our knowledge of the microbial world.
50	Austen Nathaniel Gleave Emilee Lynn Carr	Characterization of 18 Bacteriophage Families Based on Distinct Protein Profile
		Each year, 50,000 people die in Europe and the USA alone as the result of multidrug resistant bacterial infections. As a result of this reduced efficiency of antibiotics, alternatives for curing these infections are being researched with the frontrunner being the use of bacteriophages to lyse the bacteria. This study worked to discover and characterize new phage families and the proteins that differentiate them. In Dr. Julianne H. Grose’s laboratory, bacteriophages to fight this antibiotic resistance epidemic were isolated, sequenced, annotated, and grouped into families based on similar morphology and common host bacteria. The families were compared based on protein function and interesting occurrences like the differences between *Serratia marcescens* phage families were investigated. Within the 78 phages isolated, there were 18 unique families. Inside each phage family, there were unique conserved proteins that allows that differentiate that family from the others. Before they can be used to cure antibiotic resistant bacterial strains in humans, bacteriophages must be fully understood and with this research, science is one step closer to saving lives through phage therapy.
51	Braden Brundage, Joshua Michael Findley, Weston Larson	PCR analysis of widespread human fecal samples to identify common bacteriophage.
		Bacteriophages (Phages) are viruses that infect bacteria and are the most abundant and diverse biological entities on earth. Although they are diverse, there can be similarities between phages. Phages with genomes of 50% similarity or more constitute groups called phage “phamilies”. Due to their genome similarities, these phages tend to have similar hosts and functional proteins. Phages are found in great diversity in the human body (phageome) with only one known phage to be common between all humans (crAssphage–cross-assembly phage). We hypothesize that there are more phages which can be found in the majority of the human population. Because of the unique composition of DNA sequences within phamilies, we elected to identify a gene product highly conserved within each phamily that, if found, would suggest the presence of phages belonging to that phamily. We conducted Polymerase Chain Reaction (PCR) tests seeking to find and amplify these identifying gene products from human sewage samples collected from different locations. Herein, we present the findings of our PCR tests.
52	Emily Cluff, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Braeden Davies, Emily Doxey, David	Host Range Analysis of Sinorhizobium Phages Reveals New Avenues for Studying Phage Receptor Binding

	Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	
		Bacteriophages are viruses that infect bacteria by binding to host cell surface receptors. Different phages bind to different receptors, creating a range of host cells that the various phages are able to infect. Determining host range for a suite of phages is the basis of this study. We evaluated the host range of 9 newly-isolated phages and 9 previously-isolated phages by examining the infection of 36 strains of *Sinorhizobium meliloti,* the alpha-proteobacterium symbiont of legumes, such as *Medicago* sp. We employed spot assays to determine infectivity of each stain of *S. meliloti*. Infection varied widely, but no phage was able to infect all 36 strains. On average, the phages infected 70.61% of the bacterial strains tested. Clustering analysis of phage infectivity using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) demonstrated two distinct clusters of phages. Similar analysis of bacterial strains showed three clusters of bacterial strains infected by the phages in the study. This study increases our knowledge of binding specificity and suggests avenues for further research of *Sinorhizobium* phage biology.
53	Joshua D. Chamberlain, Kurt J. Ellis, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Daniel Arens, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	Phages Infect, But Not All Phages Infect Absolutely. Or Something Like That.
		Even though phage infection is very specific for the host bacterium infected, not all phages infect every strain of host bacteria equally well. As has been already demonstrated for phages infecting *Sinorhizobium meliloti* strain 1021, phages employ RopA and LPS to infect bacteria. We used 6 *S. meliloti* phages to examine plaquing efficiency on 6 additional strains of *S. meliloti,* including a ropA and an lpsB mutant, to determine plaquing efficiency. Plaquing efficiency was calculated as the apparent phage titer on each bacterial strain divided by the phage titer on *S. meliloti* strain 1021. Our analysis demonstrates that some bacteria infect at rates less than, equal to, or higher than that of *S. meliloti* strain 1021. We attribute these differences in plaquing

		efficiency to naturally occurring variations in strains of *S. meliloti*. Our data suggest that mechanisms other than either LPS or RopA proteins may be involved in phage infection.
54	Hailey Olsen, Morgan Weatherred, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Sam Weeks, Daniel Arens, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	The Genome of Squally, A Novel T4-like Sinorhizobium meliloti Phage.
		Sinorhizobium meliloti is a nitrogen-fixing alphaproteobacterium that infects legumes such as *Medicago sp*. Phages that infect *S. meliloti* have been studied for many years. However, only about 15 *Sinorhizobium* bacteriophage genomes have been sequenced and reported in GenBank. This study adds the genome of *S. meliloti* phage Squally to that body of information. Bacteriophage Squally was isolated from soil using *S. meliloti* strain 1021. We have sequenced and annotated the genome of phage Squally and compared it to the genomes of other *Sinorhizobium phages.* We have determined that it is similar to N3 and M12. Squally has a genome of 205,781 bp with a GC content of 49.1%. It has 409 open reading frames, of which 24.6% have putative functions, 72.2% no known function, and 3.2% had no BLAST hit. This study illustrates that phage diversity is underestimated due to a paucity of sequenced and annotated bacteriophage genomes.
55	Karina Tovar Laura Uricoechea	Bacterial Killers: Infection of Unwanted Gut Bacteria
		In the United States, one in three adults suffers from obesity, and many with this disorder struggle to lose weight by means of diet and exercise. Recent studies have revealed a link between the human gut microbiota and obesity. One mechanism by which gut bacteria can promote obesity is if they release endotoxins such as lipopolysaccharide (LPS), which can trigger a systemic inflammatory response that interferes with insulin signaling and promotes obesity. Given this knowledge, a treatment that focuses on the destruction of harmful species of gut bacteria is a potential method of treating obesity. Bacteriophages are viruses that infect and can kill bacteria, and each phage has a range of bacterial hosts it can infect. Some phages have a broad host range, while others infect only a species or even strain of bacteria. In the development of phage-based treatments, a narrow host range is usually desirable in order to avoid off-target effects. In this study, 37 phages that target 8 different LPS-producing bacteria have been isolated. The goal of this work was to test each phage against all 8 bacteria to determine its host range. The host-range tests were performed by taking 5 ul of each phage lysate and dropping it within assigned segments on agar plates that were inoculated with the 8 potential host bacteria. If the droplet of phage cleared the bacteria in that zone, it was inferred that the phage infected and killed that specific bacterial host. We found some phages with multiple hosts, while others were highly specific. These results illustrate the importance of doing thorough host-range testing on phages that are intended for therapeutic purposes.
56		
57	Nicholas Carter	Discovery of Highly Conserved Protein Groups in Families of Bacteriophages
		Each year, 50,000 people die in Europe and the USA alone as the result of multidrug resistant bacterial infections. As a result of this reduced efficiency of antibiotics,

		alternatives for curing these infections are being researched with the frontrunner being the use of bacteriophages to lyse the bacteria. This study worked to discover and characterize new phage families and the proteins that differentiate them. In Dr. Julianne H. Grose's laboratory, bacteriophages to fight this antibiotic resistance epidemic were isolated, sequenced, annotated, and grouped into families based on similar morphology and common host bacteria. The families were compared based on protein function and interesting occurrences like the differences between *Serratia marcescens* phage families were investigated. Within the 78 phages isolated, there were 18 unique families. Inside each phage family, there were unique conserved proteins that allows that differentiate that family from the others. Before they can be used to cure antibiotic resistant bacterial strains in humans, bacteriophages must be fully understood and with this research, science is one step closer to saving lives through phage therapy.
58	Tanner Johns	Finding and assessing the lytic nature of phages that target Yokenella regensburgei
		Yokenella regensburgei is an opportunistic pathogen that is most often associated with infections in immunocompromised patients1,2. Phage therapy for *Y. regensburgei* infections would be a useful alternative to general antibiotic treatments3, because it would avoid adverse side effects like killing beneficial gut bacteria4. The purpose of this study was to determine if multiple lytic phages that target *Y. regensburgei* could be isolated from wastewater samples from distant locations. Untreated wastewater samples were collected from several cities. Phage isolation was accomplished by plating a mixture of untreated sewage with liquid *Y. regensburgei* culture. The isolated phage was purified by repeatedly picking a plaque from the plate, incubating it with *Y. regensburgei*, and plating it. After three rounds of purification, a high titer culture of purified phage was grown. In order to effectively kill their target bacteria, the phages in a therapeutic treatment must be lytic. Lytic activity assay of the isolated phages was therefore assessed by incubating 1 ml of 107 cfu/ml *Y. regensburgei* with 1 ml of 109 pfu/ml phage in 50 ml of LB broth. A sample was taken from the culture and plated by serial dilutions to track the concentration of bacteria in the mixture at hours 0, 3, 6, 9, 12, and 24 after addition of the phage. We successfully isolated lytic bacteriophages that target *Y. regensburgei* from six distant geographical locations. The lytic activity assay showed that each of the phages we isolated was initially lytic because the concentration of *Y. regensburgei* in the mixture dropped drastically within the first three hours. In every case, however, the bacterial culture recovered, suggesting either that the bacteria developed resistance, or that the phage entered the lysogenic cycle. This work has demonstrated that phages that target *Y. regensburgei* can be isolated from the environment and could potentially be used to develop a phage therapy for opportunistic *Y. regensburgei* infections. More research is required, however, to determine whether the recovery of *Y. regensburgei* after infection in the lytic activity assay was due to the evolution of resistance by bacteria or whether the phages entered the lysogenic cycle, allowing their bacterial hosts to recover. Either could impact the success of a phage therapy.
59	Trever Thurgood	First Bacteriophages Reported to Infect Pathogenic Bacillus anthracis
		Bacillus anthracis is a pathogenic member of the *Bacillus cereus* group, a small group of pathogenic and non-pathogenic *Bacillus* species. *B. anthracis* is a Gram-positive, spore-forming bacteria capable of causing serious infection in man and animal. *B. anthracis,* more commonly known as anthrax, has been studied for over a century by biologists and is commonly known for its potential use a bioweapon. While there have been no known bioterrorist attacks for almost two decades, the pathogen has been known to cause disease in humans and livestock from infected soil, its natural ecological niche. Once infected, unless intervention occurs quickly after onset of symptoms, anthrax has a high mortality rate for each of its three forms of infection: cutaneous, gastrointestinal and inhalation (20%, 50% and >80%, respectively). To date, only a dozen phages have been isolated against *B. anthracis*, none of which have been shown to infect any pathogenic strains of *B. anthracis.* In 2017, our lab isolated 23 bacteriophages on *B. anthracis* strain Sterne and sequenced all 23. While none of these phages were completely novel, preliminary results have shown that representative phages from 3 different phylogenetic groupings can infect a variety of pathogenic anthrax strains, the first bacteriophages ever reported to do so. Here, we explore the genomic content of these phages that allow for infection of their host bacteria and expanded host range. Furthermore, these phages will be the first published organisms that could serve as potential therapeutic treatments for anthrax infections.
60	Dillon Donaghy	Reduction of Plasmodium falciparum in Human Whole Blood Product Using Riboflavin and UV Light
		Many countries in Sub-Saharan Africa rely on the use of whole blood (WB) for emergency treatment for severe anemia secondary to blood loss or malaria. Many of the areas where this is done have very high prevalence of blood-borne pathogens such as malaria, and blood safety measures taken to prevent infection by these pathogens is insufficient. Pathogen reduction technology (PRT) applied to WB could improve the

		safety of blood products significantly. WB product from donors was infected with *Plasmodium falciparum in vitro*. This blood product was then treated with riboflavin and exposed to UV light in order to inactivate *P. falciparum* replication. Pre- and Post-treatment samples were taken from the infected blood product and were cultured for 21 and 12 days respectively. Pre-treatment samples showed parasite growth at 10^{-4} dilution and post-treatment samples showed no parasite growth. It was also found that this PRT did not significantly impact the cell quality of WB units, showing that the WB product would still be effective for clinical use when placed in cold storage for up to 21 days. The use of PRT to treat human WB product prevented the growth of *P. falciparum* in a significant manner, demonstrating its potential for use in controlling transfusion-transmissible disease in Sub-Saharan Africa where malaria is especially prevalent.
61	Dalton Karlinsey	Testing the effect of Viral Protein R (Vpr) on the progression of HIV-1 to AID
		The Viral Protein R (Vpr) of HIV may influence progression to AIDS, as well as play an important role in other aspects of HIV's virulence. The goal of our project is to better ascertain the role that Vpr plays in HIV's progression to AIDS. Previous studies have associated certain mutations in the Vpr gene of clinical HIV NL4-3 isolates with a significantly increased (R36W) or decreased (R77Q) rate of disease progression. [1] Using a Vpr-null as a control, we will recreate the results of this experiment, and also test the progression and replicability of R36W and R77Q mutants in the more common, JR-CSF strain. We expect that our positive controls, (Wild type, R36W) will replicate and kill cells at a normal or enhanced rate, our null mutants will have no replication in some cell types, but normal replication in others, and our experimental group (R77Q) will be able to replicate, but at a reduced rate. These data will also help us to plan and conduct similar experiments in an in vivo humanized mouse model sometime in the future. Through these experiments, we hope to establish a clear link between Vpr expression and progression of HIV to AIDS.
62	Rachel Palmer	Prospective Biomarkers in Endometrial Cancer
		As endometrial cancer becomes more prevalent, so does the need for discovery of diagnostic biomarkers associated with it. Because obesity has been identified as the most significant risk factor, many of the currently used biomarkers are related more to obesity than to cancer development. In order to identify malignant biomarkers for early detection based on cell proliferation, four genes were chosen for evaluation. In other cancer types, Jagged2 (JAG2), Aurora Kinase A (AURKA), Phosphoglycerate Kinase 1 (PGK1), and Hypoxanthine Guanine Phosphoribosyltransferase (HPRT1) have been identified as having diagnostic potential, but these genes have not het been analyzed in endometrial cancer. Using data obtained from The Cancer Genome Atlas (TCGA), we compared expression of the four selected genes in malignant versus normal tissue in 589 patients. AURKA, JAG2, HPRT1, and PGK1 all showed elevated levels of expression in the malignant tissue compared to the normal samples in each of the genes. AURKA demonstrated the highest elevation (p-value = 1.2×10^{-21}) while JAG2 showed the smallest increase (p-value = 4.6×10^{-3}). The differential expression between normal and malignant tissue suggests diagnostic biomarker potential due to the upregulation of these genes. Evaluation of protein expression by immunohistochemistry staining of normal and malignant tissue from a separate cohort showed higher levels of protein in the malignant tumor, confirming the analysis of the gene expression data. Additionally, HPRT1 and PGK demonstrated a stepwise elevation in protein expression relating significantly to cancer grade, indication potential as possible biomarkers for tumor aggressiveness. Overall patient survival was evaluated by comparing the highest 20% of biomarker expression with the lowest 20% of biomarker expression to determine if these genes had an impact on survival rats over 100 months. Despite their elevated gene expression, PGK1 (p-value = 0.589) and JAG2 (p-value = 0.46) showed insignificant differences between high and low biomarker expression. However, there was a statistically significant decrease in overall patient survival in the patients with the highest AURKA expression ($p < .0001$). Patients with high expressing HPRT1 showed similar results (p-value = .041), demonstrating the potential usefulness of these two genes as both diagnostic and prognostic biomarkers. Differential gene expression was observed in all four genes, indicating that these biomarkers show promise as diagnostic tools for the identification and classification of endometrial cancer.
63	Michael Tene	Testing a New Disinfection Tool
		Campus custodians purchased a new disinfection device, a Protexus Electrostatic Spraying System. We were asked to test the manufacturer's claims. The manufacturer claims that the chlorine solution (active ingredient sodium dichloro-s-triazinetrion) disinfects surfaces, and an electrostatic charge provides an "attractive force 15 times greater than gravity" allowing for "360 degree application" of the mist produced by the unit. The device itself is a gun-like apparatus that produces a mist of the solution that spreads over a surface, and applies the "electrostatic charge" to the mist. The

		hypotheses examined were in regard to the effectiveness of the chlorine disinfectant, as well as whether the electrostatic effect allows disinfection of inverted surfaces. We tested the device against *Staphylococcus aureus* and *Bacillus cereus* by applying 1.5 seconds of activation of the mist to approximately 6 x 102 cells in a 3.2cm square, and then sampled using RODAC plates. Against *S. aureus*, the manufacturer's recommended 528 ppm was 100% lethal but did not have a significant effect on endospore-forming *B. cereus*, there was no difference between treatments using the electrostatic effect and those not using the electrostatic effect. In addition, despite manufacturer's claims, there was no decrease to the cells on the underside of a surface treated by the mist. This has lead us to believe that while the chlorine solution itself is very effective, the electrostatic aspect does not appear to have any effect, bringing into question the cost effectiveness of the mister as opposed to spray bottles. Additional investigations will compare the effectiveness of this chlorine disinfectant with other disinfectants available to the custodial staff.
64	Michael Tene	Surface Sampling Methods
		The students in Microbiological Procedures are required to perform independent projects designed to test a hypothesis and apply statistical analysis. Over the years, many students have chosen to compare surface contamination using RODAC plates. In order to expand their experiences with surface testing, a lab exercise was designed to allow each student to compare results using RODAC plates, swabs, and 3M Post-it Durable Filing Tabs (tape). The main hypothesis being tested was that students would gain experience with different surface testing methods and be able to compare the methods in terms of ease of use, accuracy, precision, and appropriate application. Pre- and post-tests were used to evaluate students' knowledge of these enumeration methods, in addition to their statistical backgrounds. Dilutions of *Staphylococcus aureus* were spread onto 3.2 cm square areas on aluminum foil. Plastic and glass surfaces were tested, but aluminum foil worked well and is readily available. Comparisons made between the methods revealed that recoveries were highest with the RODAC plates, but even those were typically less than 20%. While RODAC plates were easiest to use, aseptic preparation of the plates could be a challenge. Using the tape was most awkward, largely due to handling the tape while sampling the surface and then inoculating agar plates, although students felt that using the tape to sample surfaces would become easier and more consistent with practice. While not as awkward as the tape, swabs required a consistency in handling (sterile swabs moistened in 3 mL saline, surface swabbed, swab vortexed in the saline for 15 seconds, spread plates inoculated from the saline) in order to reduce variance in the resultant colony counts. Overall, this exercise was deemed a success based on the pre- and post-test scores, lab reports, and use of swabs or tape for surface sampling in independent projects.
65	Josie Tueller	Flow Cytometry Education: A semester long course
		Flow cytometry is a versatile and high throughput technique for biological tests. It requires a high level of skill to operate machines and understand results. Most users learn the skills through trial and error, and many machines are underutilized. We report a course teaching flow cytometry skills to undergraduate and graduate students. This course is unique in being a full semester course, and its design to teach both technical and analytical skills related to flow cytometry. Students reported large increases in their confidence levels from the beginning to the end of the semester. This provides a resource for others who may want to implement a similar course.
66	Allen Weinert	Chemokine receptor CCBP2-V41A and its role in inflammation and Alzheimer's disease
		The leading cause of dementia in elderly patients is Alzheimer's disease (AD), a degenerating and fatal neurodegenerative condition. AD is a proteopathic disease caused by extensive accumulation of amyloid beta plaques and neurofibrillary tangles. A recent genome-wide association study analyzing 59 AD-associated cerebrospinal fluid (CSF) samples statistically associated chemokine receptor mutant CCBP2-V41A with increased CSF protein levels of the proinflammatory chemokine CCL2. CCBP2 is a known binding partner of CCL2. We hypothesize that CCBP2- V41A receptor alters CSF levels of CCL2 and that raised CCL2 levels alters immune cell function, resulting in amyloid beta deposition in the brain
67	Hailey Wilcox	Bacterial Effect of Fruit Fly Lifespan
		Drosophila melanogaster is a model for studying animal aging, and experiments in *Drosophila* have helped expand our understanding of lifespan-extension. For example, animals fed on a calorie- or methionine-restricted diet display increased longevity compared to full-fed controls. The basis for microbial influence on lifespan has also been a topic of recent interest, although the molecular mechanisms for these influences are not well established. To better understand how associated microorganisms are related to *D. melanogaster* lifespan we screened the lifespan influence of 41 strains of genome-sequenced bacteria and performed metagenome-wide association to identify bacterial genes that are predicted to influence fruit fly longevity. An analysis of the most

		significant genes identified cysteine and methionine metabolism as the sole significantly enriched pathway among the top significant hits. To confirm these predictions, we measured the influence on *Drosophila* lifespan of bacteria bearing mutations in methionine metabolism genes. The results supported that numerous bacterial methionine metabolism genes influence *D. melanogaster* longevity. To better understand how these genetic influences are related to nutrient cycling in the fly we measured the metabolomes of aging flies and their diets. In young flies the bacterial mutants influenced the levels of numerous metabolites, including those in glucose and methionine metabolism. In old flies a smaller set of metabolites were influenced, including methionine. We propose a model where bacteria that function as methionine sinks tend to promote lifespan; whereas if the bacteria are sources of methionine fly longevity is restricted. We are currently collecting additional metabolite data on aging flies reared with additional mutants to test this idea.
68	Stephen Funk	The yjbB gene controls phosphate import in E. coli
		Introduction: Phosphate homeostasis in *E. coli* is controlled by a complex interaction of enzymes, among which are *PitA* and *PitB*. These two membrane-bound symporters utilize the proton motive force to pump metal/phosphate complexes into and out of the cell, enabling the bacterium to live in low- or high-phosphate environments. Prior evidence had seemed to suggest that the *PitAB* system worked in tandem with another gene—*yjbB*—to regulate the amount of phosphate in the cell. However, it was uncertain whether the protein encoded by *yjbB* worked as a phosphate transporter or was involved in producing or utilizing polyphosphate (thereby associating the gene with genes *PpK* and *PpX*). *YjbB*'s role in regulating other phosphate-control genes was also uncertain. **Purpose**: The function of *yjbB* in phosphate homeostasis in *E. coli*, especially with relation to the *PitAB* system, was investigated. **Methods**: *E. coli* bacterial strain MG1655 was transduced to delete the *PitA* or *PitB* genes, or both. All 4 mutant strains and the wild-type were then transduced with Δ*yjbB::kan* to create 4 kanamycin-resistant *yjbB* mutants. Similar treatment was done to *PpK* and *PpX* mutants to create 6 *yjbB* mutants. All 14 strains were measured comparatively using growth curves and efficiency of plating assays. The experiments were repeated several times, both with and without constitutive SCAB transcription. **Results**: The *yjbB* deletion mutants consistently underperformed their non-deleted counterparts in fitness assays. This held true over several trials, using several different repeat transductants, in low-, medium-, and high-phosphate growth media. **Discussion**: The fact that *yjbB* was vital to the bacteria's health in any level of phosphate concentration suggests a duel importer/exporter role. As polyphosphate is only created to aid fitness in high levels of phosphate, it is unlikely that *yjbB* acts as a phosphate condensing enzyme or as a polyphosphatase. It is still uncertain to what extent *yjbB* helps regulate the PhoU regulon; further experiments with PhoU deletions could give more insights.
69	Rachel Erickson	Comparing Thymidine kinase 1 differences in human breast cell lines and its relationship to cellular invasion
		The purpose of this study is to investigate the role of thymidine kinase 1 (TK1) in invasion of breast cancer cells. TK1 is a salvage pathway enzyme that converts thymidine to thymidine monophosphate to be used in DNA synthesis and repair. TK1 is cell cycle dependent, and cytosolic levels of TK1 increase during the G1/S phase. It has also been observed that TK1 levels are elevated in the serum of patients with many different types of cancer. Studies have shown the use of TK1 as a biomarker to track cancer prognosis and patient response to treatment. Recently, it has been observed that TK1 also localizes to the cell membrane; although the mechanism, function, and timing of this process is not fully known. Due to TK1 involvement in cell proliferation, we hypothesize that membrane TK1 (mTK1) levels could be used as an indicator for invasion potential of breast cancer cells. When observing TK1 levels in various primary (n = 31) and metastatic (n = 39) cancer cell lines, RNA-seq shows that cytosolic levels of TK1 are elevated in the metastatic cells, although there was significant variability between samples and cancer types. To investigate a specific subset of cancer, we performed immunohistochemistry to stain ductal and lobular carcinoma tissue and compared to primary and normal tissue, the level of TK1 was elevated in the metastatic tissue (p = .0001). However, using flow cytometry, we tested various breast cancer cell lines (primary: HCC 1806, HCC 1937, JIMT-1 MB 157 and BT549; metastatic: T47D, MCF7, ZR751, and MDA-MB-231) and comparison to controls showed that primary cell lines had approximately 30 percent higher shift in levels of mTK1 (p = .0001). The primary breast cell line MB 157 had the highest individual expression (98.0%, p = .0001), and MDA-MB-231 metastatic breast cancer cells showed the lowest levels of expression of mTK1 (47.2%; p = .01). Bioinformatic analysis of breast invasive carcinoma patients (n=1093) using the TIMER program developed by Li et al. investigated correlations between TK1 levels and various invasive proteins. There were several positive and negative correlations to invasive proteins (including MMPs, TIMPs, and transcription factors), including very strong positive correlations to MMP1, 8, 9, and

		12. To investigate the effect of TK1 on invasion *in vitro*, an invasion assay was performed on wild-type and TK1 knockdown cells for selected cell lines from metastatic and primary groups. Results showed that the metastatic cell line MDA-MB-231 TK1 knockdown had the highest invasion potential (p = .0001) when compared to wild-type MDA-MB-231. These findings point to a negative correlation *in vitro* between TK1 and invasion but will need to be investigated further.
70	Kiara Whitley	Helper T cells and T cell signaling
		Helper T cells are a vital component of the immune system responsible for regulating immune cell activation and function, such as directing other immune cells to eliminate mutated targets. Helper T cells serve an important role, yet the details about what produces an effective helper T cell response remain unclear. T cell activation requires a signal mediated by the T cell receptor (TCR) and co-receptors on the T cell membrane. The strength of TCR-mediated binding, called avidity, primarily determines the quality of T cell activation. To understand how avidity affects helper T cell activation, we will characterize a helper T cell system comprising of two helper T cells, called LLO118 and LLO56, by testing them against a panel of altered peptide ligands (APLs) which retain specificity but affect avidity. We will characterize the T cell response by measuring cytokine production, calcium signaling, and metabolic response. These three processes are critical primary functional measures of T cell activation and will provide valuable insight about T cell avidity in cancer and infection settings. Understanding how TCR signaling affects T cell function is crucial for improving cancer immunotherapies and vaccine design so T cells can more effectively target and kill cancer cells.
51	Braden Brundage, Joshua Michael Findley, Weston Larson	PCR analysis of widespread human fecal samples to identify common bacteriophage.
		Bacteriophages (Phages) are viruses that infect bacteria and are the most abundant and diverse biological entities on earth. Although they are diverse, there can be similarities between phages. Phages with genomes of 50% similarity or more constitute groups called phage “phamilies”. Due to their genome similarities, these phages tend to have similar hosts and functional proteins. Phages are found in great diversity in the human body (phageome) with only one known phage to be common between all humans (crAssphage–cross-assembly phage). We hypothesize that there are more phages which can be found in the majority of the human population. Because of the unique composition of DNA sequences within phamilies, we elected to identify a gene product highly conserved within each phamily that, if found, would suggest the presence of phages belonging to that phamily. We conducted Polymerase Chain Reaction (PCR) tests seeking to find and amplify these identifying gene products from human sewage samples collected from different locations. Herein, we present the findings of our PCR tests.
52	Emily Cluff, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O’Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	Host Range Analysis of Sinorhizobium Phages Reveals New Avenues for Studying Phage Receptor Binding

		Bacteriophages are viruses that infect bacteria by binding to host cell surface receptors. Different phages bind to different receptors, creating a range of host cells that the various phages are able to infect. Determining host range for a suite of phages is the basis of this study. We evaluated the host range of 9 newly-isolated phages and 9 previously-isolated phages by examining the infection of 36 strains of *Sinorhizobium meliloti,* the alpha-proteobacterium symbiont of legumes, such as *Medicago* sp. We employed spot assays to determine infectivity of each stain of *S. meliloti*. Infection varied widely, but no phage was able to infect all 36 strains. On average, the phages infected 70.61% of the bacterial strains tested. Clustering analysis of phage infectivity using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) demonstrated two distinct clusters of phages. Similar analysis of bacterial strains showed three clusters of bacterial strains infected by the phages in the study. This study increases our knowledge of binding specificity and suggests avenues for further research of *Sinorhizobium* phage biology.
53	Joshua D. Chamberlain, Kurt J. Ellis, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hailey Olsen, Hayden Phillips, Alexann Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Morgan Weatherred, Sam Weeks, Daniel Arens, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	Phages Infect, But Not All Phages Infect Absolutely. Or Something Like That.
		Even though phage infection is very specific for the host bacterium infected, not all phages infect every strain of host bacteria equally well. As has been already demonstrated for phages infecting *Sinorhizobium meliloti* strain 1021, phages employ RopA and LPS to infect bacteria. We used 6 *S. meliloti* phages to examine plaquing efficiency on 6 additional strains of *S. meliloti,* including a ropA and an lpsB mutant, to determine plaquing efficiency. Plaquing efficiency was calculated as the apparent phage titer on each bacterial strain divided by the phage titer on *S. meliloti* strain 1021. Our analysis demonstrates that some bacteria infect at rates less than, equal to, or higher than that of *S. meliloti* strain 1021. We attribute these differences in plaquing efficiency to naturally occurring variations in strains of *S. meliloti*. Our data suggest that mechanisms other than either LPS or RopA proteins may be involved in phage infection.
54	Hailey Olsen, Morgan Weatherred, Seth Abrams, Colby Allen, Bailey Calder, Owen Carter, Tom Clarke, Emily Cluff, Braeden Davies, Emily Doxey, David Eastley, Madeline C. Hendricks, Brian Merrill, Preston Miller, Chris O'Brien, Rachael Ochsner, Hayden Phillips, Alexann	The Genome of Squally, A Novel T4-like Sinorhizobium meliloti Phage.

	Riddle, Jared Routsong, Kevin Torgersen, Sam Wadsworth, Sam Weeks, Daniel Arens, Joshua D. Chamberlain, Kurt J. Ellis, Sandra Hope, Julianne H. Grose, and Donald P. Breakwell	
		Sinorhizobium meliloti is a nitrogen-fixing alphaproteobacterium that infects legumes such as *Medicago sp*. Phages that infect *S. meliloti* have been studied for many years. However, only about 15 *Sinorhizobium* bacteriophage genomes have been sequenced and reported in GenBank. This study adds the genome of *S. meliloti* phage Squally to that body of information. Bacteriophage Squally was isolated from soil using *S. meliloti* strain 1021. We have sequenced and annotated the genome of phage Squally and compared it to the genomes of other *Sinorhizobium phages*. We have determined that it is similar to N3 and M12. Squally has a genome of 205,781 bp with a GC content of 49.1%. It has 409 open reading frames, of which 24.6% have putative functions, 72.2% no known function, and 3.2% had no BLAST hit. This study illustrates that phage diversity is underestimated due to a paucity of sequenced and annotated bacteriophage genomes.
55	Karina Tovar Laura Uricoechea	Bacterial Killers: Infection of Unwanted Gut Bacteria
		In the United States, one in three adults suffers from obesity, and many with this disorder struggle to lose weight by means of diet and exercise. Recent studies have revealed a link between the human gut microbiota and obesity. One mechanism by which gut bacteria can promote obesity is if they release endotoxins such as lipopolysaccharide (LPS), which can trigger a systemic inflammatory response that interferes with insulin signaling and promotes obesity. Given this knowledge, a treatment that focuses on the destruction of harmful species of gut bacteria is a potential method of treating obesity. Bacteriophages are viruses that infect and can kill bacteria, and each phage has a range of bacterial hosts it can infect. Some phages have a broad host range, while others infect only a species or even strain of bacteria. In the development of phage-based treatments, a narrow host range is usually desirable in order to avoid off-target effects. In this study, 37 phages that target 8 different LPS-producing bacteria have been isolated. The goal of this work was to test each phage against all 8 bacteria to determine its host range. The host-range tests were performed by taking 5 ul of each phage lysate and dropping it within assigned segments on agar plates that were inoculated with the 8 potential host bacteria. If the droplet of phage cleared the bacteria in that zone, it was inferred that the phage infected and killed that specific bacterial host. We found some phages with multiple hosts, while others were highly specific. These results illustrate the importance of doing thorough host-range testing on phages that are intended for therapeutic purposes.
56		
57	Nicholas Carter	Discovery of Highly Conserved Protein Groups in Families of Bacteriophages
		Each year, 50,000 people die in Europe and the USA alone as the result of multidrug resistant bacterial infections. As a result of this reduced efficiency of antibiotics, alternatives for curing these infections are being researched with the frontrunner being the use of bacteriophages to lyse the bacteria. This study worked to discover and characterize new phage families and the proteins that differentiate them. In Dr. Julianne H. Grose's laboratory, bacteriophages to fight this antibiotic resistance epidemic were isolated, sequenced, annotated, and grouped into families based on similar morphology and common host bacteria. The families were compared based on protein function and interesting occurrences like the differences between *Serratia marcescens* phage families were investigated. Within the 78 phages isolated, there were 18 unique families. Inside each phage family, there were unique conserved proteins that allows that differentiate that family from the others. Before they can be used to cure antibiotic resistant bacterial strains in humans, bacteriophages must be fully understood and with this research, science is one step closer to saving lives through phage therapy.
58	Tanner Johns	Finding and assessing the lytic nature of phages that target Yokenella regensburgei
		Yokenella regensburgei is an opportunistic pathogen that is most often associated with infections in immunocompromised patients1,2. Phage therapy for *Y. regensburgei* infections would be a useful alternative to general antibiotic treatments3, because it would avoid adverse side effects like killing beneficial gut bacteria4. The purpose of this study was to determine if multiple lytic phages that target *Y. regensburgei* could be

		isolated from wastewater samples from distant locations. Untreated wastewater samples were collected from several cities. Phage isolation was accomplished by plating a mixture of untreated sewage with liquid *Y. regensburgei* culture. The isolated phage was purified by repeatedly picking a plaque from the plate, incubating it with *Y. regensburgei*, and plating it. After three rounds of purification, a high titer culture of purified phage was grown. In order to effectively kill their target bacteria, the phages in a therapeutic treatment must be lytic. Lytic activity assay of the isolated phages was therefore assessed by incubating 1 ml of 107 cfu/ml *Y. regensburgei* with 1 ml of 109 pfu/ml phage in 50 ml of LB broth. A sample was taken from the culture and plated by serial dilutions to track the concentration of bacteria in the mixture at hours 0, 3, 6, 9, 12, and 24 after addition of the phage. We successfully isolated lytic bacteriophages that target *Y. regensburgei* from six distant geographical locations. The lytic activity assay showed that each of the phages we isolated was initially lytic because the concentration of *Y. regensburgei* in the mixture dropped drastically within the first three hours. In every case, however, the bacterial culture recovered, suggesting either that the bacteria developed resistance, or that the phage entered the lysogenic cycle. This work has demonstrated that phages that target *Y. regensburgei* can be isolated from the environment and could potentially be used to develop a phage therapy for opportunistic *Y. regensburgei* infections. More research is required, however, to determine whether the recovery of *Y. regensburgei* after infection in the lytic activity assay was due to the evolution of resistance by bacteria or whether the phages entered the lysogenic cycle, allowing their bacterial hosts to recover. Either could impact the success of a phage therapy.
59	Trever Thurgood	First Bacteriophages Reported to Infect Pathogenic Bacillus anthracis
		Bacillus anthracis is a pathogenic member of the *Bacillus cereus* group, a small group of pathogenic and non-pathogenic *Bacillus* species. *B. anthracis* is a Gram-positive, spore-forming bacteria capable of causing serious infection in man and animal. *B. anthracis,* more commonly known as anthrax, has been studied for over a century by biologists and is commonly known for its potential use a bioweapon. While there have been no known bioterrorist attacks for almost two decades, the pathogen has been known to cause disease in humans and livestock from infected soil, its natural ecological niche. Once infected, unless intervention occurs quickly after onset of symptoms, anthrax has a high mortality rate for each of its three forms of infection: cutaneous, gastrointestinal and inhalation (20%, 50% and >80%, respectively). To date, only a dozen phages have been isolated against *B. anthracis*, none of which have been shown to infect any pathogenic strains of *B. anthracis.* In 2017, our lab isolated 23 bacteriophages on *B. anthracis* strain Sterne and sequenced all 23. While none of these phages were completely novel, preliminary results have shown that representative phages from 3 different phylogenetic groupings can infect a variety of pathogenic anthrax strains, the first bacteriophages ever reported to do so. Here, we explore the genomic content of these phages that allow for infection of their host bacteria and expanded host range. Furthermore, these phages will be the first published organisms that could serve as potential therapeutic treatments for anthrax infections.
60	Dillon Donaghy	Reduction of Plasmodium falciparum in Human Whole Blood Product Using Riboflavin and UV Light
		Many countries in Sub-Saharan Africa rely on the use of whole blood (WB) for emergency treatment for severe anemia secondary to blood loss or malaria. Many of the areas where this is done have very high prevalence of blood-borne pathogens such as malaria, and blood safety measures taken to prevent infection by these pathogens is insufficient. Pathogen reduction technology (PRT) applied to WB could improve the safety of blood products significantly. WB product from donors was infected with *Plasmodium falciparum in vitro*. This blood product was then treated with riboflavin and exposed to UV light in order to inactivate *P. falciparum* replication. Pre- and Post-treatment samples were taken from the infected blood product and were cultured for 21 and 12 days respectively. Pre-treatment samples showed parasite growth at 10^{-4} dilution and post-treatment samples showed no parasite growth. It was also found that this PRT did not significantly impact the cell quality of WB units, showing that the WB product would still be effective for clinical use when placed in cold storage for up to 21 days. The use of PRT to treat human WB product prevented the growth of *P. falciparum* in a significant manner, demonstrating its potential for use in controlling transfusion-transmissible disease in Sub-Saharan Africa where malaria is especially prevalent.
61	Dalton Karlinsey	Testing the effect of Viral Protein R (Vpr) on the progression of HIV-1 to AID
		The Viral Protein R (Vpr) of HIV may influence progression to AIDS, as well as play an important role in other aspects of HIV's virulence. The goal of our project is to better ascertain the role that Vpr plays in HIV's progression to AIDS. Previous studies have associated certain mutations in the Vpr gene of clinical HIV NL4-3 isolates with a significantly increased (R36W) or decreased (R77Q) rate of disease progression. [1]

		Using a Vpr-null as a control, we will recreate the results of this experiment, and also test the progression and replicability of R36W and R77Q mutants in the more common, JR-CSF strain. We expect that our positive controls, (Wild type, R36W) will replicate and kill cells at a normal or enhanced rate, our null mutants will have no replication in some cell types, but normal replication in others, and our experimental group (R77Q) will be able to replicate, but at a reduced rate. These data will also help us to plan and conduct similar experiments in an in vivo humanized mouse model sometime in the future. Through these experiments, we hope to establish a clear link between Vpr expression and progression of HIV to AIDS.
62	Rachel Palmer	Prospective Biomarkers in Endometrial Cancer
		As endometrial cancer becomes more prevalent, so does the need for discovery of diagnostic biomarkers associated with it. Because obesity has been identified as the most significant risk factor, many of the currently used biomarkers are related more to obesity than to cancer development. In order to identify malignant biomarkers for early detection based on cell proliferation, four genes were chosen for evaluation. In other cancer types, Jagged2 (JAG2), Aurora Kinase A (AURKA), Phosphoglycerate Kinase 1 (PGK1), and Hypoxanthine Guanine Phosphoribosyltransferase (HPRT1) have been identified as having diagnostic potential, but these genes have not het been analyzed in endometrial cancer. Using data obtained from The Cancer Genome Atlas (TCGA), we compared expression of the four selected genes in malignant versus normal tissue in 589 patients. AURKA, JAG2, HPRT1, and PGK1 all showed elevated levels of expression in the malignant tissue compared to the normal samples in each of the genes. AURKA demonstrated the highest elevation (p-value = 1.2×10^{-21}) while JAG2 showed the smallest increase (p-value = 4.6×10^{-3}). The differential expression between normal and malignant tissue suggests diagnostic biomarker potential due to the upregulation of these genes. Evaluation of protein expression by immunohistochemistry staining of normal and malignant tissue from a separate cohort showed higher levels of protein in the malignant tumor, confirming the analysis of the gene expression data. Additionally, HPRT1 and PGK demonstrated a stepwise elevation in protein expression relating significantly to cancer grade, indication potential as possible biomarkers for tumor aggressiveness. Overall patient survival was evaluated by comparing the highest 20% of biomarker expression with the lowest 20% of biomarker expression to determine if these genes had an impact on survival rats over 100 months. Despite their elevated gene expression, PGK1 (p-value = 0.589) and JAG2 (p-value = 0.46) showed insignificant differences between high and low biomarker expression. However, there was a statistically significant decrease in overall patient survival in the patients with the highest AURKA expression ($p < .0001$). Patients with high expressing HPRT1 showed similar results (p-value = .041), demonstrating the potential usefulness of these two genes as both diagnostic and prognostic biomarkers. Differential gene expression was observed in all four genes, indicating that these biomarkers show promise as diagnostic tools for the identification and classification of endometrial cancer.
63	Michael Tene	Testing a New Disinfection Tool
		Campus custodians purchased a new disinfection device, a Protexus Electrostatic Spraying System. We were asked to test the manufacturer's claims. The manufacturer claims that the chlorine solution (active ingredient sodium dichloro-s-triazinetrion) disinfects surfaces, and an electrostatic charge provides an "attractive force 15 times greater than gravity" allowing for "360 degree application" of the mist produced by the unit. The device itself is a gun-like apparatus that produces a mist of the solution that spreads over a surface, and applies the "electrostatic charge" to the mist. The hypotheses examined were in regard to the effectiveness of the chlorine disinfectant, as well as whether the electrostatic effect allows disinfection of inverted surfaces. We tested the device against *Staphylococcus aureus* and *Bacillus cereus* by applying 1.5 seconds of activation of the mist to approximately 6 x 102 cells in a 3.2cm square, and then sampled using RODAC plates. Against *S. aureus*, the manufacturer's recommended 528 ppm was 100% lethal but did not have a significant effect on endospore-forming *B. cereus*, there was no difference between treatments using the electrostatic effect and those not using the electrostatic effect. In addition, despite manufacturer's claims, there was no decrease to the cells on the underside of a surface treated by the mist. This has lead us to believe that while the chlorine solution itself is very effective, the electrostatic aspect does not appear to have any effect, bringing into question the cost effectiveness of the mister as opposed to spray bottles. Additional investigations will compare the effectiveness of this chlorine disinfectant with other disinfectants available to the custodial staff.
64	Michael Tene	Surface Sampling Methods
		The students in Microbiological Procedures are required to perform independent projects designed to test a hypothesis and apply statistical analysis. Over the years, many students have chosen to compare surface contamination using RODAC plates. In

		order to expand their experiences with surface testing, a lab exercise was designed to allow each student to compare results using RODAC plates, swabs, and 3M Post-it Durable Filing Tabs (tape). The main hypothesis being tested was that students would gain experience with different surface testing methods and be able to compare the methods in terms of ease of use, accuracy, precision, and appropriate application. Pre- and post-tests were used to evaluate students' knowledge of these enumeration methods, in addition to their statistical backgrounds. Dilutions of *Staphylococcus aureus* were spread onto 3.2 cm square areas on aluminum foil. Plastic and glass surfaces were tested, but aluminum foil worked well and is readily available. Comparisons made between the methods revealed that recoveries were highest with the RODAC plates, but even those were typically less than 20%. While RODAC plates were easiest to use, aseptic preparation of the plates could be a challenge. Using the tape was most awkward, largely due to handling the tape while sampling the surface and then inoculating agar plates, although students felt that using the tape to sample surfaces would become easier and more consistent with practice. While not as awkward as the tape, swabs required a consistency in handling (sterile swabs moistened in 3 mL saline, surface swabbed, swab vortexed in the saline for 15 seconds, spread plates inoculated from the saline) in order to reduce variance in the resultant colony counts. Overall, this exercise was deemed a success based on the pre- and post-test scores, lab reports, and use of swabs or tape for surface sampling in independent projects.
65	Josie Tueller	Flow Cytometry Education: A semester long course
		Flow cytometry is a versatile and high throughput technique for biological tests. It requires a high level of skill to operate machines and understand results. Most users learn the skills through trial and error, and many machines are underutilized. We report a course teaching flow cytometry skills to undergraduate and graduate students. This course is unique in being a full semester course, and its design to teach both technical and analytical skills related to flow cytometry. Students reported large increases in their confidence levels from the beginning to the end of the semester. This provides a resource for others who may want to implement a similar course.
66	Allen Weinert	Chemokine receptor CCBP2-V41A and its role in inflammation and Alzheimer's disease
		The leading cause of dementia in elderly patients is Alzheimer's disease (AD), a degenerating and fatal neurodegenerative condition. AD is a proteopathic disease caused by extensive accumulation of amyloid beta plaques and neurofibrillary tangles. A recent genome-wide association study analyzing 59 AD-associated cerebrospinal fluid (CSF) samples statistically associated chemokine receptor mutant CCBP2-V41A with increased CSF protein levels of the proinflammatory chemokine CCL2. CCBP2 is a known binding partner of CCL2. We hypothesize that CCBP2- V41A receptor alters CSF levels of CCL2 and that raised CCL2 levels alters immune cell function, resulting in amyloid beta deposition in the brain
67	Hailey Wilcox	Bacterial Effect of Fruit Fly Lifespan
		Drosophila melanogaster is a model for studying animal aging, and experiments in *Drosophila* have helped expand our understanding of lifespan-extension. For example, animals fed on a calorie- or methionine-restricted diet display increased longevity compared to full-fed controls. The basis for microbial influence on lifespan has also been a topic of recent interest, although the molecular mechanisms for these influences are not well established. To better understand how associated microorganisms are related to *D. melanogaster* lifespan we screened the lifespan influence of 41 strains of genome-sequenced bacteria and performed metagenome-wide association to identify bacterial genes that are predicted to influence fruit fly longevity. An analysis of the most significant genes identified cysteine and methionine metabolism as the sole significantly enriched pathway among the top significant hits. To confirm these predictions, we measured the influence on *Drosophila* lifespan of bacteria bearing mutations in methionine metabolism genes. The results supported that numerous bacterial methionine metabolism genes influence *D. melanogaster* longevity. To better understand how these genetic influences are related to nutrient cycling in the fly we measured the metabolomes of aging flies and their diets. In young flies the bacterial mutants influenced the levels of numerous metabolites, including those in glucose and methionine metabolism. In old flies a smaller set of metabolites were influenced, including methionine. We propose a model where bacteria that function as methionine sinks tend to promote lifespan; whereas if the bacteria are sources of methionine fly longevity is restricted. We are currently collecting additional metabolite data on aging flies reared with additional mutants to test this idea.
68	Stephen Funk	The yjbB gene controls phosphate import in E. coli
		Introduction: Phosphate homeostasis in *E. coli* is controlled by a complex interaction of enzymes, among which are *PitA* and *PitB*. These two membrane-bound symporters utilize the proton motive force to pump metal/phosphate complexes into and out of the cell, enabling the bacterium to live in low- or high-phosphate environments. Prior

		evidence had seemed to suggest that the *PitAB* system worked in tandem with another gene—*yjbB*—to regulate the amount of phosphate in the cell. However, it was uncertain whether the protein encoded by *yjbB* worked as a phosphate transporter or was involved in producing or utilizing polyphosphate (thereby associating the gene with genes *PpK* and *PpX*). *YjbB*'s role in regulating other phosphate-control genes was also uncertain. **Purpose**: The function of *yjbB* in phosphate homeostasis in *E. coli*, especially with relation to the *PitAB* system, was investigated. **Methods**: *E. coli* bacterial strain MG1655 was transduced to delete the *PitA* or *PitB* genes, or both. All 4 mutant strains and the wild-type were then transduced with Δ*yjbB::kan* to create 4 kanamycin-resistant *yjbB* mutants. Similar treatment was done to *PpK* and *PpX* mutants to create 6 *yjbB* mutants. All 14 strains were measured comparatively using growth curves and efficiency of plating assays. The experiments were repeated several times, both with and without constitutive SCAB transcription. **Results**: The *yjbB* deletion mutants consistently underperformed their non-deleted counterparts in fitness assays. This held true over several trials, using several different repeat transductants, in low-, medium-, and high-phosphate growth media. **Discussion**: The fact that *yjbB* was vital to the bacteria's health in any level of phosphate concentration suggests a duel importer/exporter role. As polyphosphate is only created to aid fitness in high levels of phosphate, it is unlikely that *yjbB* acts as a phosphate condensing enzyme or as a polyphosphatase. It is still uncertain to what extent *yjbB* helps regulate the PhoU regulon; further experiments with PhoU deletions could give more insights.
69	Rachel Erickson	Comparing Thymidine kinase 1 differences in human breast cell lines and its relationship to cellular invasion
		The purpose of this study is to investigate the role of thymidine kinase 1 (TK1) in invasion of breast cancer cells. TK1 is a salvage pathway enzyme that converts thymidine to thymidine monophosphate to be used in DNA synthesis and repair. TK1 is cell cycle dependent, and cytosolic levels of TK1 increase during the G1/S phase. It has also been observed that TK1 levels are elevated in the serum of patients with many different types of cancer. Studies have shown the use of TK1 as a biomarker to track cancer prognosis and patient response to treatment. Recently, it has been observed that TK1 also localizes to the cell membrane; although the mechanism, function, and timing of this process is not fully known. Due to TK1 involvement in cell proliferation, we hypothesize that membrane TK1 (mTK1) levels could be used as an indicator for invasion potential of breast cancer cells. When observing TK1 levels in various primary (n = 31) and metastatic (n = 39) cancer cell lines, RNA-seq shows that cytosolic levels of TK1 are elevated in the metastatic cells, although there was significant variability between samples and cancer types. To investigate a specific subset of cancer, we performed immunohistochemistry to stain ductal and lobular carcinoma tissue and compared to primary and normal tissue, the level of TK1 was elevated in the metastatic tissue ($p = .0001$). However, using flow cytometry, we tested various breast cancer cell lines (primary: HCC 1806, HCC 1937, JIMT-1 MB 157 and BT549; metastatic: T47D, MCF7, ZR751, and MDA-MB-231) and comparison to controls showed that primary cell lines had approximately 30 percent higher shift in levels of mTK1 ($p = .0001$). The primary breast cell line MB 157 had the highest individual expression (98.0%, $p = .0001$), and MDA-MB-231 metastatic breast cancer cells showed the lowest levels of expression of mTK1 (47.2%; $p = .01$). Bioinformatic analysis of breast invasive carcinoma patients (n=1093) using the TIMER program developed by Li et al. investigated correlations between TK1 levels and various invasive proteins. There were several positive and negative correlations to invasive proteins (including MMPs, TIMPs, and transcription factors), including very strong positive correlations to MMP1, 8, 9, and 12. To investigate the effect of TK1 on invasion *in vitro*, an invasion assay was performed on wild-type and TK1 knockdown cells for selected cell lines from metastatic and primary groups. Results showed that the metastatic cell line MDA-MB-231 TK1 knockdown had the highest invasion potential ($p = .0001$) when compared to wild-type MDA-MB-231. These findings point to a negative correlation *in vitro* between TK1 and invasion but will need to be investigated further.
70	Kiara Whitley	Helper T cells and T cell signaling
		Helper T cells are a vital component of the immune system responsible for regulating immune cell activation and function, such as directing other immune cells to eliminate mutated targets. Helper T cells serve an important role, yet the details about what produces an effective helper T cell response remain unclear. T cell activation requires a signal mediated by the T cell receptor (TCR) and co-receptors on the T cell membrane. The strength of TCR-mediated binding, called avidity, primarily determines the quality of T cell activation. To understand how avidity affects helper T cell activation, we will characterize a helper T cell system comprising of two helper T cells, called LLO118 and LLO56, by testing them against a panel of altered peptide ligands (APLs) which retain specificity but affect avidity. We will characterize the T cell response by measuring cytokine production, calcium signaling, and metabolic response. These three processes

		are critical primary functional measures of T cell activation and will provide valuable insight about T cell avidity in cancer and infection settings. Understanding how TCR signaling affects T cell function is crucial for improving cancer immunotherapies and vaccine design so T cells can more effectively target and kill cancer cells.