



SAFETY Meeting Minutes
IBC Committee
Zoom

MEETING TIME RECORDS

Meeting start time: 10/8/2025
3:00 PM
Meeting end time: 3:55 PM

VOTING MEMBER ATTENDANCE

Name of Regular/Alternate Member	Status (Member or Alternate)	Present by Teleconference?
Karl McKinstry	Member	Yes
Gregory Danyluk	Member	Yes
Melina Kinsey	Member	Yes
Kyle Rohde	Chair - Member	Yes
Stanley Haimes	Member	Yes
Hubert Salvail	Member	Yes
Judith Hecker	Member	Yes
Lane Coffee	Vice-Chair - Member	Yes
Yulia Gerasimova	Member	Yes
Teresa Krisch	Member	Yes

QUORUM INFORMATION

Number of SAFETY members on the roster: 10
Number required for quorum: 5

All members present by teleconference received all pertinent material before the meeting and were able to actively and equally participate in all discussions.

ATTENDANCE STATUS AND VOTING KEY

ABSTAIN:	Present for the vote, but not voting "For" or "Against."
ABSENT:	Absent for discussion and voting for reasons other than a conflicting interest.
RECUSED:	Absent from the meeting during discussion and voting because of a conflicting interest.
SUBSTITUTION:	When regular members and their alternate(s) are listed in the ATTENDANCE table above and an alternate member substitutes for the

	regular member this identifies the name of the alternate to indicate which individual is serving as the voting member for this vote. May be deleted if there are no substitutions.
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GUEST NAMES

Sophia Vermeulen, Biosafety Specialist

Previous Meeting minutes approved: Yes

REVIEW OF SUBMISSIONS

De Novo Review

1. Review of SPROTO202500000019

Title:	De-identified Human Tissue Project - Fraser
Investigator:	Amoy Fraser
Submission ID	SPROTO202500000019
Funding:	• Name: College of Medicine , Grant Office ID: , Funding Source ID:
Documents Reviewed:	<ul style="list-style-type: none"> • MigrationPlaceholder • MigrationPlaceholder • Protocol_De-Identified Human Tissue Project_Fraser_Version 1.0_21June2022.pdf • 2022.06.21_IRB Letter.pdf • Institutions for Material Transfer Agreements.docx • Transporting-Infectious-Substances-Safely.pdf • MigrationPlaceholder
Agents:	<ul style="list-style-type: none"> • Saliva • Mucus Membrane Tissue • Cardiovascular Tissue • Digestive Tissue • Endocrine Tissue • Excretory Tissue • Immune Tissue • Integumentary • Lymphatic • Nervous Tissue

	<ul style="list-style-type: none"> • Reproductive Tissue • Respiratory Tissue • Skeletal Tissue • Blood • Brain
Agent Containment:	Biological Containment Levels: <ul style="list-style-type: none"> • Digestive Tissue: BSL-2 • Brain: BSL-2 • Blood: BSL-2 • Saliva: BSL-2 • Reproductive Tissue: BSL-2 • Respiratory Tissue: BSL-2 • Endocrine Tissue: BSL-2 • Skeletal Tissue: BSL-2 • Excretory Tissue: BSL-2 • Immune Tissue: BSL-2 • Integumentary: BSL-2 • Mucus Membrane Tissue: BSL-2 • Lymphatic: BSL-2 • Cardiovascular Tissue: BSL-2 • Nervous Tissue: BSL-2
Applicable NIH Guidelines:	None

- a. **Description:** The objective of this De-Identified Human Tissue Project is the receipt and banking of de-identified, discardable human tissue, blood and saliva from participants, medical, surgical, and clinical facilities. The human tissue can be fresh or paraffinized. The human biospecimens will be picked up by the Clinical & Aerospace Health Research Team and banked for up to 180 days. After transfer the PI will store biospecimens under their own IBC approvals. These separate protocols cannot be for genetic testing. The Project does not receive human tissue resulting from termination of pregnancy.

For the purposes of this Project, human tissue is defined as any bodily material collected from a human person, including brain tissue, bone marrow, skin, tumors, etc., through a clinical procedure.

The Clinical & Aerospace Health Research Team will receive the human biospecimens double bagged in saline in biohazard bags from the cooperating institution. The Clinical & Aerospace Health Research Team member will transfer the specimens to the COM/BSBS scientists for testing. The Clinical & Aerospace Health Research Team will not be involved with procedures. The Clinical & Aerospace Health Research Team will NOT do any lab testing. The human biospecimens will be saved in the -80C clinical research freezer for no longer than 180 days to accommodate transfer to the scientist. Thereafter, the human biospecimens will be disposed of as biological waste.

b. **Determination:** Modifications Required**Moved:** Stan Haimes**Second:** Lane Coffeec. **Required modifications:**

1. Exposure Assessment & Protective Equipment

- a. Add Amerisys contact information

d. **Votes:****For:** 10**Against:** 0**Recused:** 0**Absent:** 0**Abstained:** 0**Amendment/CR****2. Review of SAMENDCR202500000005**

Title:	Amendment/CR for SPROTO202200000021 - Santra
Investigator:	Swadeshmukul Santra
Submission ID	SAMENDCR202500000005
Funding:	None
Documents Reviewed:	<ul style="list-style-type: none"> • 526-24-345-34882_A-00421306_12-10-2024.pdf • MigrationPlaceholder • MigrationPlaceholder • SPROTO202200000021 BARA Amendments.docx • Safety and efficacy testing of novel antimicrobial formulations against various pathogens • SPROTO202200000021 BARA -02082023.docx • MTA In00000248_addgene.org_emta-addgene-public_886577_645_packet_FE.pdf • Updated funding sources • SPROTO202200000021 BARA Admendments 02062024

a. **Description:** Add personnel to protocol.b. **Determination:** Modifications Required**Moved:** Lane Coffee**Second:** Hubert Salvailc. **Required modifications:**

1. Primary Cells or Cell Lines

- a. HDF-CTD Cell line listed under summary of research not

included in the list of cell lines.

- b. Within “Summary of Research”, the rat Schwann cell line RSC96 is mentioned, but in this section, the cell line S16 is listed instead.
2. Bacteria, Yeasts, Fungi, and Parasites
 - a. Within Question 2, Pestalotiopsis microspora and Culvularia Lunata: ‘isolated from Melissa.’ Clarification needed that this was collected by Melissa, not isolated from them.
3. Recombinant or Synthetic Nucleic Acid Usage
 - a. Selected Section III-E-2-b-(2) indicating they are ‘using a complete genome’, but the protocol does not indicate they are using a complete genome.’ Under Question 1, they selected, “Section III-E-2-b-(2) Plants in which the introduced DNA represents the complete genome of a non-exotic infectious agent”. It seems unnecessary to include that, since there’s no mention of a “complete genome” being introduced, just “cis-acting replicational elements from the bean yellow dwarf virus”.
4. Recombinant or Synthetic Nucleic Acid Work Description
 - a. Question 6, Microbes
 - i. Please indicate if K-12, identify genus and species
5. Exposure Assessment and Protective Equipment
 - a. Question 1; Please specify the consequences of exposure or release of plant pathogens to plants in this area of Florida.

d. **Votes:**

For:	10
Against:	0
Recused:	0
Absent:	0
Abstained:	0

De Novo Review**3. Review of SPROTO202500000023**

Title:	KLF8 in diseases - Zhao
Investigator:	Jihe Zhao
Submission ID	SPROTO202500000023
Funding:	<ul style="list-style-type: none"> • Name: Florida Department of Health, Grant Office ID: , Funding Source ID: • Name: UCF/Burnett School of Biomedical Science, Grant Office ID: , Funding Source ID:
Documents Reviewed:	<ul style="list-style-type: none"> • 19-11_Zhao_190320.pdf • PROTO202000093_full printout 5.24.22.pdf • PROTO202000070_full printout 5.24.22.pdf • MigrationPlaceholder • MigrationPlaceholder
Agents:	<ul style="list-style-type: none"> • 293 • Lentivirus
Agent Containment:	Biological Containment Levels: <ul style="list-style-type: none"> • 293: BSL-2 • Lentivirus: BSL-2
Applicable NIH Guidelines:	<ul style="list-style-type: none"> • Section III-D-4 • Section III-D • Section III-D-3

- a. **Description:** KLF8 is a normal gene expressed in normal cells. However, its aberrant over expression has been associated with various diseases including cancer, heart failure and neurodegenerative disorders. Understanding roles of KLF8 in the regulation of these diseases could advance the understanding of the disease mechanisms and help design new diagnostic and therapeutic approaches. KLF8 could serve as a biomarker or target although it is not necessarily a bad, disease-causing gene.

The goals of the projects in my lab are to address the role of KLF8 in the disease progress and the mechanisms behind using tissue culture and mouse models where KLF8 expression is modified by approaches including ectopic overexpression, siRNA-mediated knockdown, CRSPR-CAS9-mediated knockout, or genetic engineering. Mouse cell lines are primary cells used in the lab. Human cancer cell lines are also used. however, none of the cells can survive or grow in human body due to immunorejection- our bodies do no accept anything foreign including these cell lines just like a transplanted kidney unless they are from an identical twin sibling or our immune system is significantly suppressed by prescribed immunosuppressant medications. The same is true even for mice. That's why in case of the cancer cell lines are to be tested in mice, immunodeficient mice- whose immune system has been artificially eliminated - have to be used. Lentiviruses are occasionally used to modify klf8 gene expression in the cells. However, we use the third and fourth generation of lentiviral production approach that has to combine three or four separate plasmid

vectors to produce the viruses. Other than lentiviruses, other recombinant DNA approaches are used in the projects which are even safer than lentiviral DNAs and almost have no chance to enter our bodies and do any harm. For example, standard plasmid DNAs may be prepared to produce gene of interest.

b. Determination: Modifications Required

Moved: Melina Kinsey

Second: Teri Krisch

c. Required modifications:

1. Primary Cells or Cell Lines

- a. Protocol mentions that human cell and mouse lines and/or cancer cell lines will be used, however none are listed

2. Animals

- a. Question 1. b. Animals should be listed in room 153 instead of 152 due to the hazard of tamoxifen being used
- b. Question 3, Need to include the use of tamoxifen in mice

d. Votes:

For: 10

Against: 0

Recused: 0

Absent: 0

Abstained: 0

Initial Protocol

4. Review of SPROTO202500000016

Title:	Bat Samples - Hoffman
Investigator:	Eric Hoffman
Submission ID	SPROTO202500000016
Funding:	None
Documents Reviewed:	<ul style="list-style-type: none"> • vlecek-et-al-2022-biosafety-practices-when-working-with-bats-a-guide-to-field-research-considerations.pdf • rocke-et-al-2025-transporting-common-vampire-bats-(desmodus-rotundus)-by-land-design-of-a-transport-container-and-care.pdf.pdf • gilman-duane-et-al-2025-field-safety-considerations-during-work-with-bats-returning-to-the-laboratory-environment.pdf.pdf
Agents:	• Non Human Derived Blood and Blood Types
Agent Characteristics:	Biological Agent Sources:

	• Field sampling, wildlife rehabilitation facilities, health departments
Agent Containment:	Biological Containment Levels: • Non Human Derived Blood and Blood Types: BSL-2
Applicable NIH Guidelines:	None

- a. **Description:** This research investigates the physiological, genetic, and ecological effects of microplastic exposure in insectivorous bats that utilize stormwater culverts and similar anthropogenic structures as roost sites in Florida. The focal species, *Tadarida brasiliensis* (Brazilian free-tailed bat), is abundant, non-listed, and commonly found in large colonies within stormwater systems, making it ideal for studying urban pollution impacts.

Bats will be captured at select rural and urban stormwater under approved FWC permits. Biological samples will be collected non-lethally when possible (e.g., guano, oral swabs, wing punches). A subset will be humanely euthanized for tissue sampling (gut, liver, kidney, lungs, reproductive organs) to quantify internal microplastic load, conduct prey DNA analysis, and assess physiological responses, including immune gene expression and stress biomarkers.

Additional genetic screening will be conducted on Major Histocompatibility Complex (MHC) Class I and II genes to assess adaptive immunity and potential links to viral susceptibility. Salvaged carcasses of other native insectivorous bat species (*Eptesicus fuscus*, *Myotis austroriparius*, *Lasiurus intermedius*, *Nycticeius humeralis*, and *Perimyotis subflavus*) will be used for molecular comparisons when available through permitted wildlife rehabilitators. No listed species will be captured or euthanized.

Standard biosafety protocols will be followed, including PPE use, zoonotic disease precautions (e.g., rabies vaccination), and waste disposal in accordance with institutional guidelines. PPE in the field will consist of long pants, long-sleeved shirt, leather gloves with latex gloves over the top, N95 mask, and safety goggles. Waders will be used in wet locations. PPE in the laboratory setting will consist of pants, a lab coat, latex-free gloves, N95 mask, and safety goggles. Necropsies will be conducted under a biosafety cabinet. All material and equipment to include any remaining carcasses, will be decontaminated through autoclaving. Carcasses will be double-bagged and properly labeled with the researcher's name, date, and kept in the freezer in a sealed 5-gallon bucket labeled with a biohazard sticker until enough volume for a biohazard waste pickup.

In light of these emerging threats, this study aims to address a critical gap in our understanding of how urban stormwater systems simultaneously function as both artificial refugia and vectors of pollutant exposure for bat populations.

- b. **Determination:** Tabled Modifications Required

Moved: Karl McKinstry

Second: Judy Hecker

c. Required modifications:

1. Exposure Assessment and Protective Equipment
 - a. Question 1, Rabies only mentioned in regard to vaccine requirements. It is not listed in the exposure assessment.
 - b. Question 3, Need clarification on how tissues handled, fixation, transport, and containment (centrifugation, etc.). How are tissues processed to look for microplastics? The concern is maintaining BSL2 containment until any possible pathogens fixed or sterilized? Also, clarification on where tissues handled (will they be removed from necropsy room and taken back to lab? Does lab have BSL2 appropriate BSC, biocontainment buckets for centrifuge, etc.).

d. Votes:

For: 10
Against: 0
Recused: 0
Absent: 0
Abstained: 0

Initial Protocol**5. Review of SPROTO202500000020**

Title:	Effectors of C. trachomatis 2025-2028 - TJewett
Investigator:	Travis Jewett
Submission ID	SPROTO202500000020
Funding:	• Name: National Institutes of Health (NIH), Grant Office ID: , Funding Source ID:
Agents:	<ul style="list-style-type: none"> • Chlamydia trachomatis • Escherichia coli K12 or derivative • HELA • Primary Cervical Epithelial Cells • McCoy Cells • L929 murine fibroblasts • HDFa cells
Agent Containment:	Biological Containment Levels: <ul style="list-style-type: none"> • Chlamydia trachomatis: BSL-2 • Escherichia coli K12 or derivative: BSL-1 • HDFa cells: BSL-2 • HELA: BSL-2 • L929 murine fibroblasts: BSL-2

	<ul style="list-style-type: none"> • McCoy Cells: BSL-2 • Primary Cervical Epithelial Cells: BSL-2
Applicable NIH Guidelines:	<ul style="list-style-type: none"> • Section III-D-1-a • Section III-D

- a. **Description:** We aim to employ our collection of wild type and mutant *C. trachomatis* (deletion mutants of early effectors and complement clones) to interrogate the role early effectors play in driving a successful infection. We are particularly interested in how the early signaling events (Hippo pathway) in the cell contribute to *C.t.* development. No animal work or toxins will be employed in our study. Recombinant-DNA in the form of a modified chlamydial plasmid is used for the complementation of modified effectors into the deletion mutants. For example we have recently cloned a version of the Tarp effector which is missing 27 tyrosines and is not phosphorylated by tyrosine kinases. We plan to introduce this mutant allele into *C. trachomatis* to study changes to hippo signaling.

We aim to determine the mechanism(s) by which the *Chlamydia trachomatis* (*C.t.*) secreted effector, Tarp, directs cellular changes through hijacking Hippo signaling. Our preliminary data has linked Tarp to disruption of the Hippo signaling pathway. Furthermore, Tarp-dependent disruption of the Hippo pathway was established in mammalian tissue culture infection model using wild-type, Δ tarp and Tarp complement *C.t.*, yet the molecular mechanism and cellular consequences of this dysregulation of host cell signaling remains unknown. We aim to determine the contribution of Hippo signaling to *C.t.* development and the role of Tarp in this process. The Hippo pathway is known to control critical host cell processes including cell proliferation, apoptosis, and stress responses. Perturbations in the Hippo pathway have been implicated in a number of different cancer types, suggesting that our work has the potential to establish new models for *C.t.*-mediated control of the Hippo pathway as a driver for these other disease processes. In sum, the Hippo pathway represents an unrecognized control point for the establishment of an intracellular environment favorable for *C.t.* development. Elucidation of the molecular mechanisms employed by *C. trachomatis* to initiate a successful infection may provide clues that can be applied to novel therapeutic interventions for this prolific pathogen. Other *Chlamydia* early effectors such as TmeA, TmeB and Tepp will also be examined for a potential role in Hippo signaling.

- b. **Determination:** Approved

Moved: Judy Hecker

Second: Hubert Salvail

- c. **Votes:**

For:	10
Against:	0
Recused:	0
Absent:	0
Abstained:	0

REVIEW OF OTHER AGENDA ITEMS