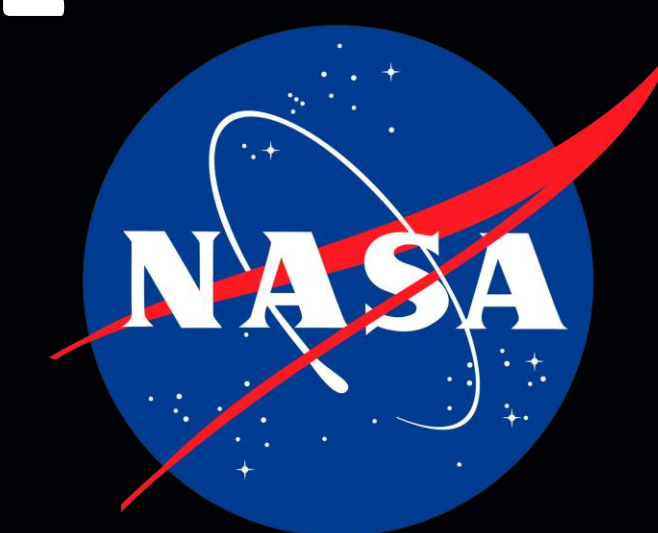# METADATA ENTRY OPTIMIZATION FOR NASA's BIOLOGICAL INSTITUTIONAL SCIENTIFIC COLLECTION (NBISC)
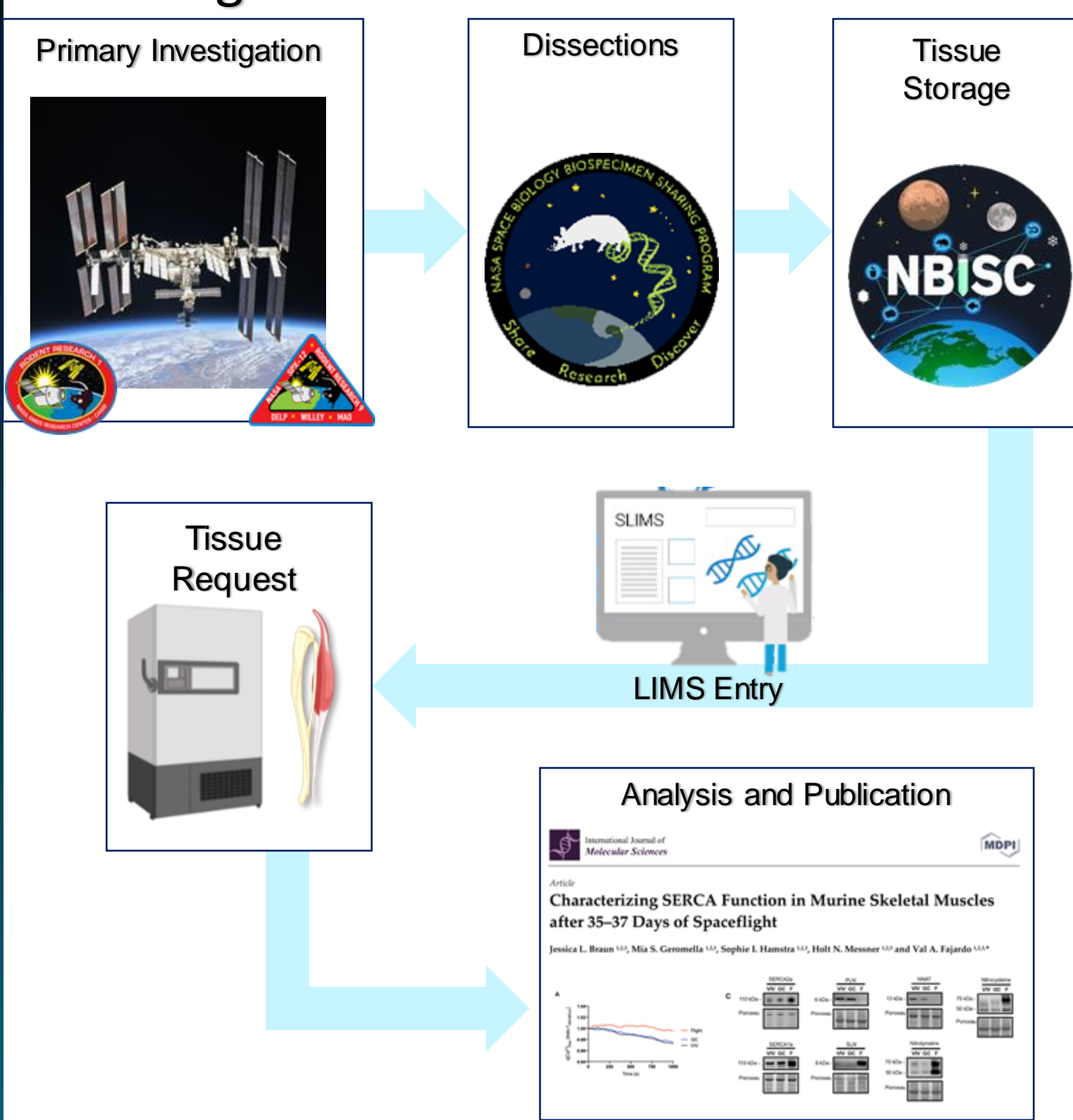
Vishnu Prasad[1], Harlan Phillips[1], Lael-River Williams[1], Catherine Omeh[1], Joseph Varelas[2], Samrawit Gebre[3], Sigrid Reinsch[3]

[1]OSTEM Intern, NASA Ames Research Center, [2]KBR Wyle, [3]Space Biosciences Division, NASA Ames Research Center, Moffett Field, CA
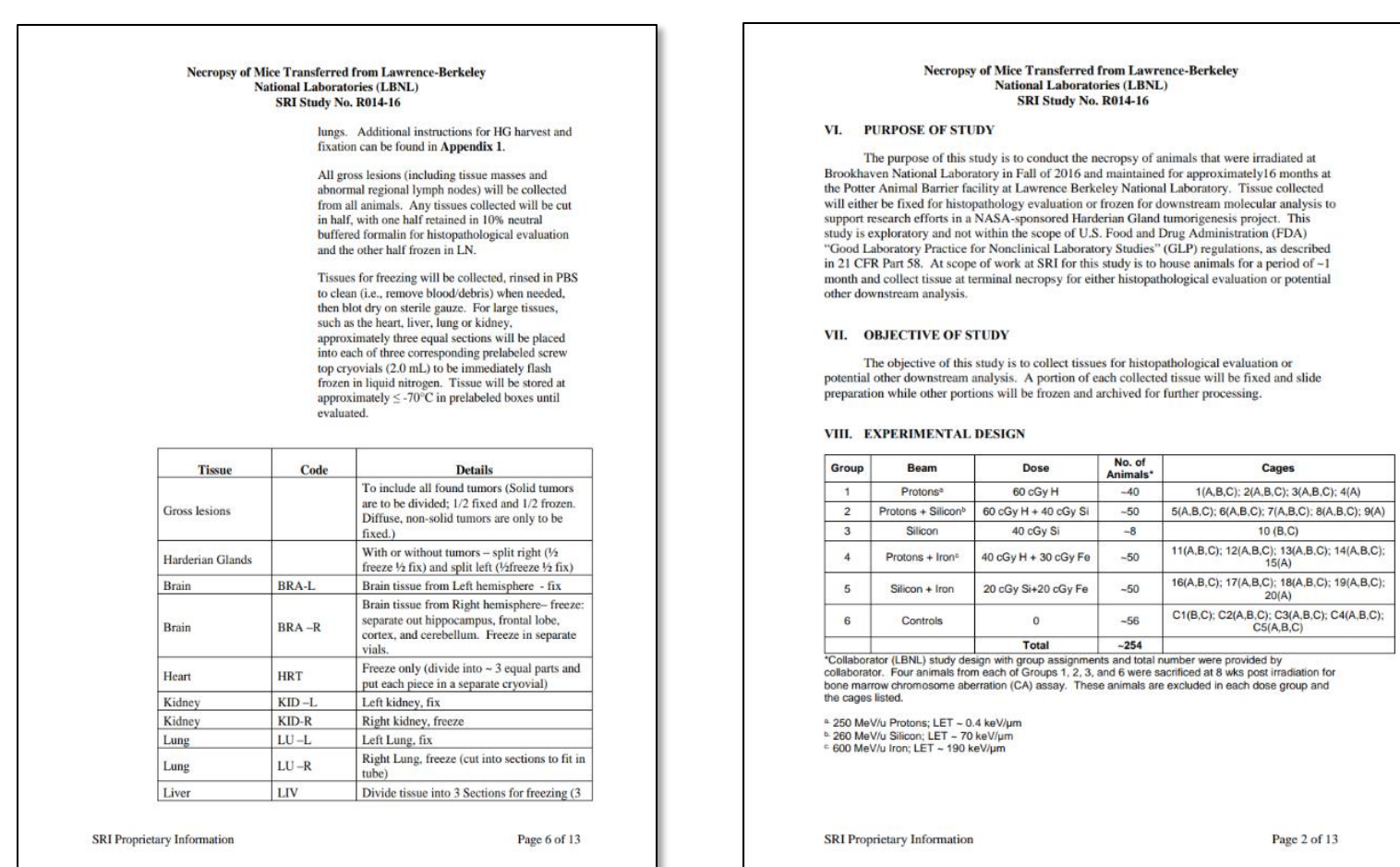
NBISC

NASA Biological Institutional Scientific Collection

- Biorepository of non-human samples from spaceflight missions and correlative ground studies
- Samples are mostly from rats and mice with some microbes as well
- Purpose is to receive, document, preserve, and make samples available to the scientific community
- Any researcher can request access to samples by filling out an online request form
- Promote international access and collaboration
- Samples housed at Ames Research Center are from Dr. Blakely and Dr. Chang

Research Questions

1. How do we best streamline the process from receiving, processing, and updating the repository?

2. How should we proceed now, to set ourselves up for the fall, in order to finish the influx of all 50,000 samples?

Methodology

1. Metadata is inputted into an excel listing the animal ID and the type of tissue.
2. The data is transferred and formatted into a template for SLIMS (Laboratory Information Management System) using an in-house script.
3. The SLIMS data is then exported into another developed script to grab established data from the animal's barcode and assign values like the type, organ system, and preservation method and temperature.
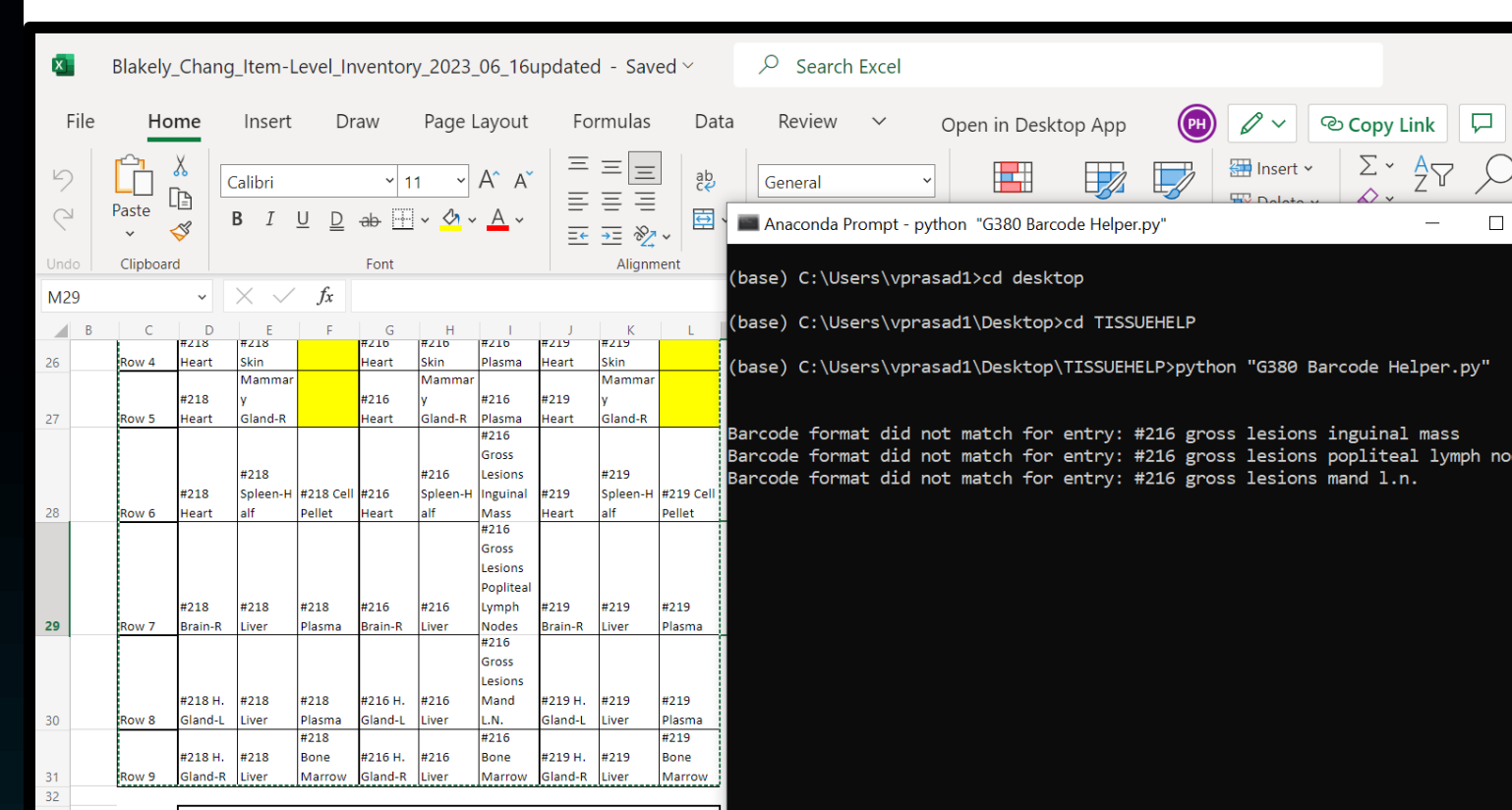4. The updated file is then imported back into SLIMS ready for requests.

Required # of Days to Ingest 50,000 samples
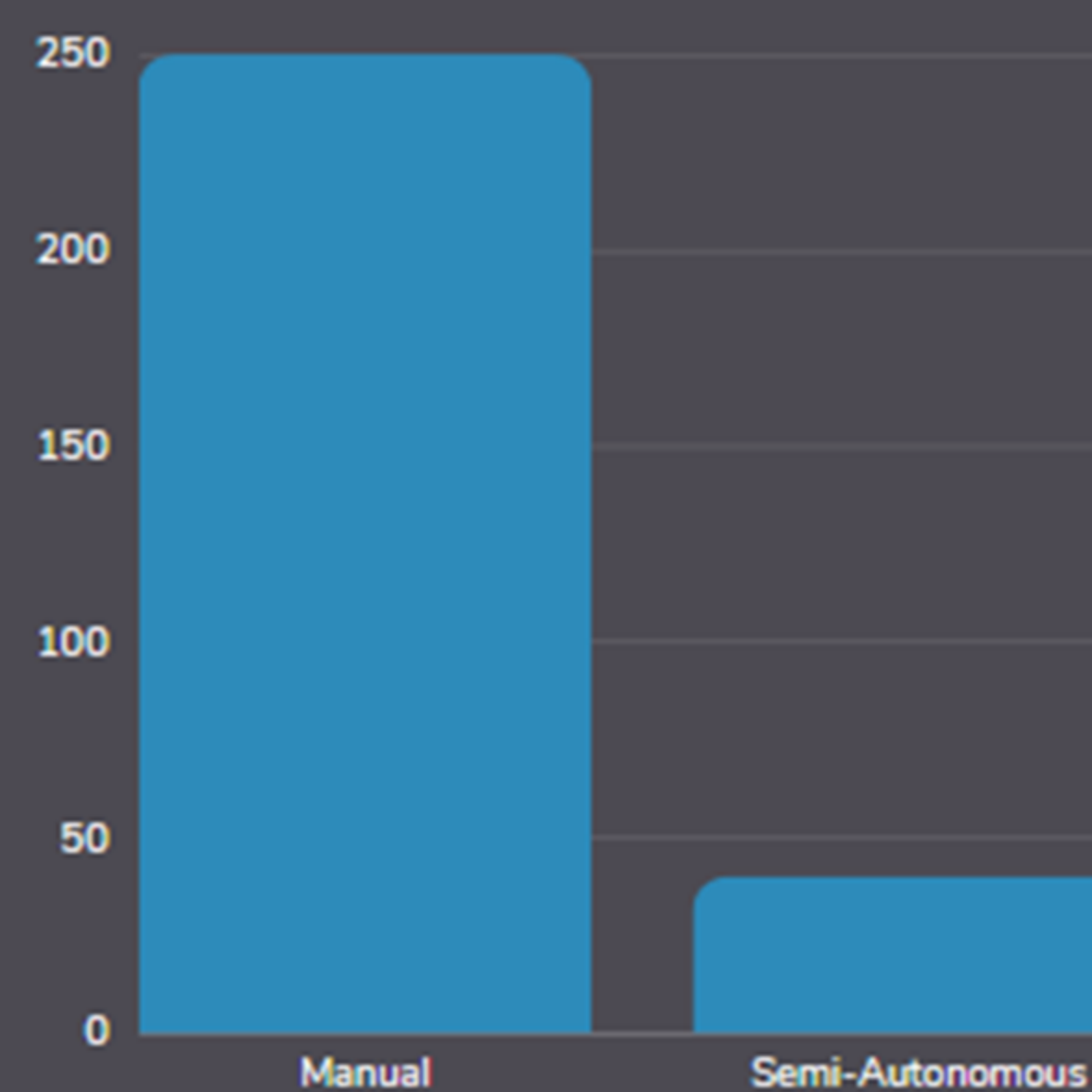
Challenges and Improvements

Old Method Challenges:

- Fully Manual
- Non-standardized protocols
- Prone to human error
- Inefficient error handling: time consuming debugging and fixing process

New Method Improvements:

- Created an organized system in the freezers to make data ingestion smoother
- Implemented error checks in the Anaconda terminal
- Created different dictionaries for each experiment
- Created a Verification and Validation Document

Implications

- Automation is important for NBISC because it leaves time for advertising for the reuse of samples
- The Biospecimen Sharing Program benefits from this because their dissection data can be ingested easier
- This project's feasibility helps other projects like HRP and Genelab focus on sample research rather than ingestion
- Samples will be wasted if not made available to the scientific community
- Fall 2023: transfer sample data into public facing repositories like NLSP and OSDR
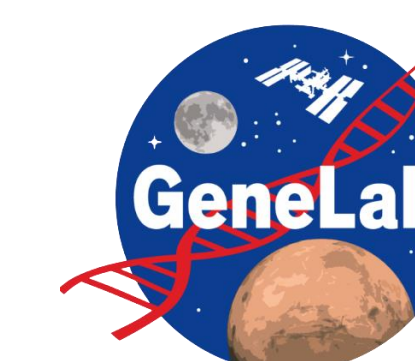
Why this is important: NBISC's digitized mouse sample collection significantly advances global scientific capabilities, benefiting space biology research and astronaut health insights while offering potential implications for radiobiology and cancer treatment advancements

Acknowledgements