

Zero-contact sample drop-off: Protocol and Form.

Zero-contact sample drop-off for the Proteomics Resource Center (PRC) was set in place as of July 17, 2020 and interacting between users and the PRC team is restricted to Zoom, phone and/or email. To allow the PRC team to 1) prepare sample submissions and 2) have preliminary information regarding the samples to be analyzed, we ask that the questions below are answered. Not answering the questions can cause delays. We understand that some questions can be difficult to answer or are not relevant. Please reach out to the PRC regarding any doubts.

1. This completed form must be shared with the PRC ahead of sample drop-off. Sharing the PTAE0# will ease processing.
2. Based on the provided information the PRC will generate a submission entry which include sample identification labels. Labels will be made available for pick-up at the PRC door or as .pdf.
3. The user and PRC team member must agree on a sample drop-off time at the entrance to the PRC (RRB 101 corridor). Please use the doorbell to summon the PRC. Important: Do not leave the samples unattended.
4. The PRC team will share results per email and if needed via Drop Box or similar. The User is very much encouraged to contact the PRC team by electronic means and the PRC team will set up a time to discuss experiments in a virtual setting.

...Sample related questions continued

<p>Names, Address & Affiliation <u>Rockefeller University user only.</u> RUNet Username: <u>PTAEO#</u> <i>example: 1234567-01-CEN6402716-64110-123456</i> <u>NON-Rockefeller University users.</u> If you have submitted in the past, we only need email and your names.</p> <p>Last Name: First Name: Email: Telephone: Affiliation: Department: Building: Street number/street: Room number: City: State: Zip: Country:</p> <p>Name, Lab Head: Email, Lab Head: Telephone, Lab Head:</p> <p>Name, Admin: Email, Admin: Telephone, Admin:</p>	<p>Primary Taxonomy/ Sample Origin:</p> <p>Possible other Taxonomies:</p> <p>Sample matrix:</p> <p>Exp. type:</p> <p>Sample prep.:</p> <p>Describe sample/buffer composition:</p> <p>Type of mass spec experiment envisioned:</p> <p>Number of samples:</p> <p>Sample names listed in <u>appropriate order</u>. Separate by semicolon:</p>
<p>Sample related questions Request type. Proteomics: Small molecules: Metabolomics/Lipidomics: Met./Lip. Sample Submission Form.</p>	<p>Notes:</p>

To be continued...