University of Colorado School of Medicine Metabolomics Core User Submission Guidelines

Updated 2026-01-05

SAMPLE AMOUNTS: For eukaryotic (and somatic) cell experiments, 1-2 million cells per sample is ideal; 100k is generally acceptable. For stem cells and rare cell populations, we will work with as many as you can reasonably obtain. For bacterial cells, 100 million is ideal. Please keep counts close (+/- 25%) within each cell type for best quality data. For tracing/flux experiments, better signal to noise and thus greater coverage is obtained with cells in the million range (minimum of 500k recommended if possible). For biofluids (e.g. media, plasma, RBCs), 50 uL.

Sample type	Ideal range	Maximum accepted	Lower limit for good coverage	Minimum
Eukaryotic cells (somatic)	1-2e6 cells	2e6 cells	75,000 cells	5000 cells
E coli	max 1e9 cells	1e9 cells	5e7 cells	
Biofluids	20-50 uL	100 uL	NA	1 uL
Tissue	2-20 mg	40 mg	NA	2 mg

*Tissue submissions must be accompanied by sample masses (to nearest 0.1 mg) on sample list.

*Tissues submitted for both metabolomics & proteomics must be powderized and weighed into 2 Eppendorf 1.5-2 mL clear safe-lock tubes (5-10 mg each). Tissues for only metabolomics/lipidomics can be submitted as 1 weighed chunk per sample in Eppendorf 1.5-2 mL clear safe-lock tubes.

EXPERIMENTAL DESIGN: For cell experiments, 3+ biological replicates required. For animal studies, 5+ biological replicates required. For human studies, 10+ biological replicates required. These n maximize our collective ability to generate publication-quality data. Technical replicates are not required.

**Data for all samples that are to be directly compared must be acquired at the same time/same batch.

SAMPLE PREPARATION: Cells – please count, wash 3x with cold PBS, and freeze pellets in 1.5-2 mL clear microcentrifuge tubes devoid of all supernatant. Tissue and biofluids – please freeze in pure/untreated form. Please write labels on tube lids with **basic 1 through n scheme** (no sticky labels, tape), and store tubes in a standard cardboard freezer box with divider in preparation for submission.

ALL samples must be free of salts (including PBS and other non-volatile buffer salts) and non-volatile solvents, for example, DMSO, DMF, and glycerol.

SAMPLE SUBMISSION:

FOR THOSE SUBMITTING IN PERSON:

1. Prepare sample list using 1 through n scheme for tube labels. Include cell counts and cell type if applicable.
2. Complete submission form via Qualtrics. Sample list is uploaded within form.
3. Provide samples frozen in 1.5-2 mL labeled microcentrifuge tubes (no screw caps, parafilm, or tape).
4. Samples must be in a standard size paper freezer box (organized w/ the cardboard divider) labeled with **submitter name, PI name, and date**. No labels or tape!!
5. Bring box of samples on dry ice to the Metabolomics Core (RC1-S, first floor, room 1303) on Tuesday 12-1:30 pm, Wednesday 12-1:30 pm. If you do not have RC1-S access, please call the core (303-724-3339) before leaving your lab so that we can meet you outside.

FOR THOSE SHIPPING SAMPLES:

1. Prepare sample list using 1 through n scheme for tube labels. Include cell counts and cell type if applicable.
2. Complete submission form via Qualtrics. Sample list is uploaded within form.
3. Provide samples frozen in 1.5-2 mL labeled microcentrifuge tubes (no screw caps, parafilm, or tape).
4. Samples must be in a **standard size paper freezer box** (organized w/ the cardboard divider) labeled with **submitter name, PI name, and date**. Please do not ship samples loosely in a ziploc bag or use labels/tape!!
5. Please package on **plenty** of dry ice and include a hard copy of the sample list that is labeled with submitter name and PI name.
6. Please email tracking information to julie.haines@cuanschutz.edu
7. Please ship overnight on Monday or Tuesday to the below address. If shipping from outside North America, please ship on Friday or Monday:

SOM Metabolomics Core
University of Colorado Anschutz
12801 E 17th Ave, Room 1303
Aurora, CO 80045 USA
phone 1-303-724-3339

ACKNOWLEDGEMENT/AUTHORSHIP: Co-authorship is warranted when core personnel make significant contributions to the research - defined as "the project would not have progressed, or progressed at a substantially slower pace, without the guidance of facility personnel." Such contribution is defined as a "*substantial input on the conception or design of the work; or the acquisition (i.e., development of analytical methods to acquire the data), analysis, or interpretation of data for the work*" – in compliance with the recommendations by the International Committee of Medical Journal Editors). In such cases, core personnel should have the opportunity to review/edit the appropriate sections of a manuscript before submission.

When conditions of co-authorship are not met, acknowledgement of facility contributions is expected. A sufficient acknowledgement is "The authors wish to thank the University of Colorado School of Medicine Metabolomics Core for their contributions to this manuscript."

For **cancer-related projects**, please acknowledge University of Colorado Cancer Center support as follows: "The Mass Spectrometry Shared Resource (RRID:SCR_021988) is supported in part by the University of Colorado Cancer Center Support Grant P30CA046934." Please deposit publications in PubMed Central.