Instructions for Sort Request Form:

Rename your completed form with the filename in the format:
"2026_mm_dd Instrument Firstname Lastname"
where mm_dd is the date you would like the sort to be run.
Instrument can be the following:

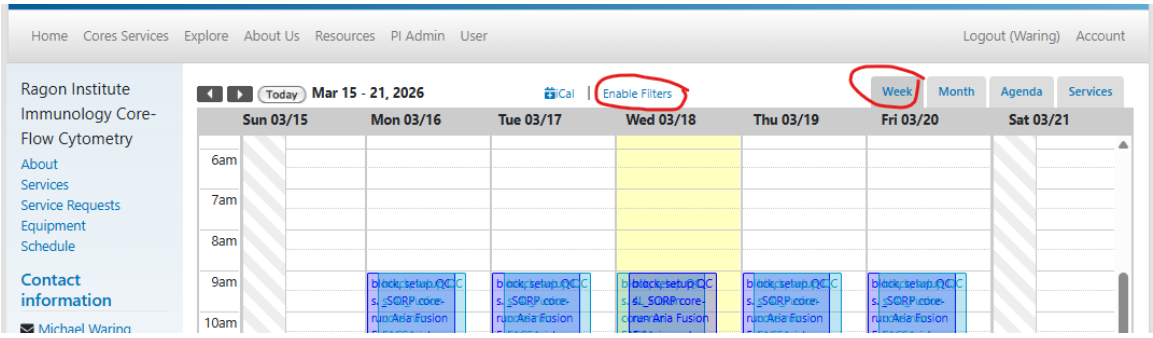
"SORP": 5 Laser SORP Fusion
"Fusion": 4 Laser standard Fusion
"BL2 SONY": SH800 in 334 for mammalian cells
"Yeast SONY": SH800 in 432C for yeast
"S8": FACSDiscover S8 imaging sorter

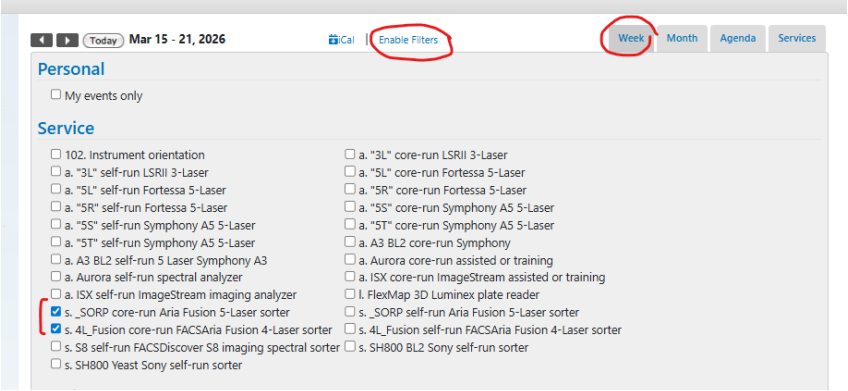
Use your full name on the form.

Email as an attachment to ragoncytometry@mgh.harvard.edu which will get sent to all core staff. Please include all user information—your full name, your email, a phone number in case we need to call you during the sort if there is a problem, department, PI on the grant that you will be using (FULL NAME, not just last name), and grant number (do NOT just say "Same as other person"—find out what the number is). Fund numbers are now GR followed by 7 digits (0 plus the old 6 digit fund number, in most cases).

MGB IBC number (formerly PIBC "Partners Institutional Biosafety Committee"): Please see the "sorting guidelines" document for full details. Only applies for MGB affiliated users, and is needed for unfixed human samples, infectious samples, or other experiments that are overseen by the IBC. If your sample is not pathogenic and not human (e.g. normal mouse), then just put "N/A". External users with hazardous or human samples will need to register their samples with the core using a different form that will be provided when you are onboarded.

Schedule can be viewed on researchcores.partners.org which requires an account to sign in. Go to "Schedule" and use the "Week" view which allows you to see all equipment and not just what you have booking access on (like "services" view). Use the "filters" to select for the core-run SORP and 4Laser Fusion:





Please provide a first and second choice for date of sort, in case the first choice is already booked. Include an earliest start time as mornings are usually more open than afternoons. First and second choices should be different days. Please provide any timing limitations (e.g. "must finish by 1:00 to drop off for sequencing"). Include how long the sort has run in the past if you've done it before, otherwise we will estimate based on the sample information you provide below.

If you save a copy of it to re-send for future sorts, make sure you update your information—the dates you are requesting, sample information, and the fund number if that has changed.

Sample information:

Species: (human, mouse, hamster, etc)

Cell type: indicate primary cell or cell line (identify the cell line, e.g. HEK, CHO, etc, and/or include tissue of origin.)

Biosafety Level: If you don't know, check with your safety officer BEFORE sorting! BL1 are samples that are totally non-infectious to humans and contain no human materials. BL2 are any noninfectious samples that are of Human origin, such as cell lines derived from human cells, or healthy patient samples. BL2+ are infectious samples such as HIV+ patient samples.

Hazards, Infectious agents: this includes any KNOWN diseases a patient sample may carry. Please also indicate any transfection agents used on the sample. If no known infectious agent is present, then please enter "uninfected cell line" or "Healthy Donor" or some other indication of sample status that makes it higher than BL1.

Number of samples to sort: how many different samples to be sorted (do not include single stained controls in this number, we expect to acquire single stained samples for the number of colors in your panel). If additional tubes are being acquired for data, please include here as well.

Cell number per sample: estimate how many cells are in each sample tube(s).

% of cells that fit sort criteria: what % of TOTAL EVENTS fit the parameters you want to sort by (if sample is 10% GFP+ and you want the top 10% of GFP, then 1% fit the sort criteria).

Total cell # you wish to collect: the number of cells where we can stop sorting, you don't want more than that. "Entire sample" is also acceptable to enter here.

Minimum # of cells you can use: what is the smallest number of cells that are useful to you. If we estimate that we will only get 10k and you can't do your experiment with less than 100k, then it doesn't make sense to run the sort—cells will have to be expanded, enriched, or more animals included next time.

Fluorochromes used and gating scheme: list the fluorochromes in your experiment and what they are labeling (including viability dyes!), and then identify the gates used to identify your target population.

For example:
FITC-Lin
PE-cKit
APC-Sca1
Live/Dead Violet
Sort Live FITC low, PE+, APC+

Please list the ACTUAL LABEL you are using—don't tell us you are using the PE-Texas Red channel, if your actual fluorescence is mCherry—just say mCherry!

Providing example plots of analyzed sample would be helpful for proper gating.
If there are not clearly defined + and – populations, please specify your gating preferences (above autofluorescence, top 10%, e.g. Treg cells are often identified as the top 30% of CD25 stain)

Instrument Info:

Nozzle Size: must be AT LEAST 3x the size of your cell. Smaller nozzle sizes can run faster, generate smaller volume, but can clog more and are more stressful to the cells. If a nozzle is too small, streams will "fan" and spray instead of targeting the tube. Fragile cells won't survive sorting with the 70um. Cell lines typically get best results with the 100. 130 is for very big cells. Larger nozzle sizes have a lower maximum event rate (100um around 20 million per hour, 70um around 60 million per hour).
Format: Type of sorting, either bulk (into tube) or plate (e.g. cloning into 96 well plate)
Purpose of sort: indicate whether you are going to collect RNA, 10x analysis, culture the sample, etc.
Special Instructions: include any special instructions here such as:

--for RNA extractions sorting into lysis buffer, "sample should be mixed every 10 minutes"