Standard Operating Procedure

Glitter

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| **Department:** | Earth and Environmental Sciences |
| **Date SOP was written/revised:** | 10/1/2020 |
| **Date SOP was approved by PI/lab supervisor:** | 3/5/2018 |
| **Principal Investigator:** | Guil Gualda |
| **Internal Lab Safety Coordinator/Lab Manager:** | Richard Bradshaw |
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| **Location(s) covered by this SOP:** | SC 5717 |
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**Type of SOP:** ☒ Process ☐Hazardous Chemical ☐ Hazardous Class

**Procedure:**

Rename files - \*\*\* This step is not strictly necessary, but makes setting up batches to run (next step below) easier\*\*\*

1. Open Spyder
2. Run the script named “GlitterRename” (should open with Spyder) by clicking the green play button
	1. An open folder dialog box will open (it might be hidden behind the main Spyder window)
	2. Navigate to the folder that contains the data you want to process and click “Select Folder”
3. This script renames all the files to the following format: “001\_AnalysisName.csv”, “002…”
4. You can close Spyder

File setup options

1. Can process all the data at once, in which case you don’t need to do anything with the files
2. Can process in smaller batches, which would reduce any changes due to drift of the instrument
	1. In your data folder create subfolders for each batch
	2. Copy and paste the files into each folder
		1. Make sure you bracket the unknowns with calibration standards (generally NIST-610)
		2. You will have duplicates of the calibration standards to be able to bracket your unknowns

Glitter

Setup

1. Open Glitter “Glitter-Shortcut” on desktop
2. Select “Element concentrations” to process trace element data, or “Isotope ratios” to process U/Pb geochronology data
3. Select first dropdown at the bottom and select “Qtegra”
4. Load your data in File → Load Data
	1. Navigate to your sample folder (or the batch folders within this folder) with your data and select OK
5. This opens the Standards window
	1. Select your internal standard (generally Si 28)
	2. We always use one isotope as internal standard
	3. Set the dwell times
		1. This was set in your LabBook on the ICP-MS
		2. Generally, we use equal dwell times of 10 ms, but you may have changed some for certain elements
	4. Input the internal standard values in the first column of the table
		1. For the standards:
			1. Select the standard in the “Reference Material” dropdown (always use the standard with the most recent date)
				1. Start with the secondary standards, do the calibration standard last
			2. Click on the standard name in the table, this will put in the correct internal standard value
			3. The rows that you click on will have an asterisk next to the name, this means that Glitter will treat those rows as the calibration standard, which may not be what you want.
				1. For the secondary standards, click on the name again to remove the asterisk
			4. Add the internal standard value for all the standards, leaving the asterisk next to your calibration standard
		2. For your unknowns
			1. Manually type in the internal standard value for each spot analysis
				1. This value should come from your SEM data
		3. Select “Accept” when you are done inputting internal standard values
6. The active window shows the calculated concentrations
	1. Can switch between concentration, 1 sigma error, and detection limits at the bottom
7. Check signal selection
	1. Select the “Review Signal Selection” in the “Window” dropdown
	2. Can select different isotopes to view in the dropdown at the bottom
	3. Can select to view either “counts/sec” or “Counts/s, ratio to IS” in the dropdown at the bottom
		1. In the “counts/s, ratio to IS” view, the ablation intervals should be relatively flat
	4. The vertical green lines show the intervals for the background and the ablation interval selections
		1. Move these by clicking and dragging the lines to the left or right to select the desired intervals
	5. Click next to move to the next spot
	6. When you finish checking/changing the intervals, click save
		1. This saves all the settings (internal standards, ablation interval)
8. Can change the fit to the standards
	1. In the Glitter! Window, select Window → Options
		1. Dropdown under “Select Std Yield Ration Interpolation”
			1. Select either “Linear fit to ratios” or “Average all standards”
	2. Click “Close OPTIONS window”
9. Export the data
	1. In the Glitter! Window select File → Export
		1. Select what you want to export
		2. Select OK

**Documentation of Training** (signature of all users is required)

* Prior to conducting any work, the PI or LM must provide training to his/her laboratory personnel specific to the hazards involved in working with this equipment, work area, and emergency procedures.
* The Principal Investigator must provide his/her laboratory personnel with a copy of this SOP.
* The Principal Investigator must ensure that their laboratory personnel have attended appropriate laboratory safety training and are current with any refresher training required.

**I have read and understand the content of this SOP, and have completed the accompanying safety checklist:**

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| **Name** | **Signature** | **Date** |
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