# Bruker pXRF Handheld

## Initializing the device

1. Login to the computer using the login information on top of the computer keyboard.
2. First, turn on the instrument. To do this press the button on top of the device screen and hold it for a few seconds (Figure 1).


*Figure 1. Bruker pXRF Handheld instrument*

3. Click on **Bruker RemoteCtrl** in the computer screen (Figure 2). You will use this program to control the device from the computer while measuring your samples.

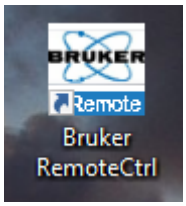


*Figure 2. Bruker Remote Ctrl program*

4. Go to **File** ➡ **Connect**. A window will appear that will show the device number Ex. 900G7838. Select it and click Ok (Figure 3).

### Manuals

User Manual, S1 TITAN, Tracer 5, CTX

Accessories Manual

pXRF Sample Cup Disassembler Guide

### Data

Bruker pXRF Upload Template

### Safety

Radiation Safety Manual

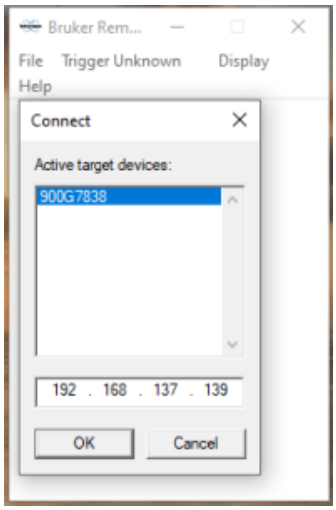


*Figure 3. Connecting the device to the computer.*

5. A login window will appear on the screen, login using the info on top of the computer keyboard (Figure 4).

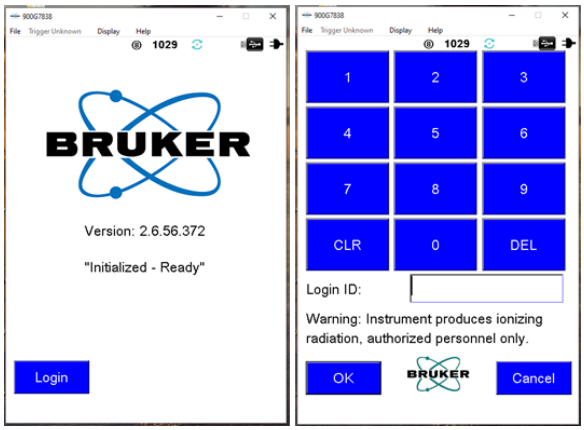


*Figure 4. Login screen in Bruker Remote Control*

6. A pop up message will appear after logging in that tells you the gun's configuration just click **O K** (Figure 5).


*Figure 5. Configuration window when initializing the device.*

7. When the device is connected, your screen should look like Figure 6. The device will say **Not Armed** when the x-ray is not active and the device will say **Ready to Test** when the x-ray is active.

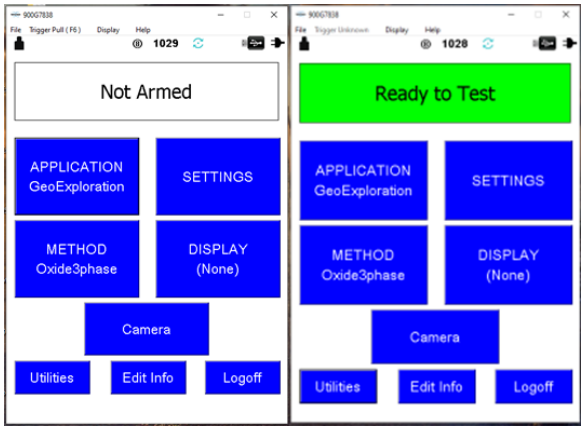


*Figure 6. pXRF initial screen. Left: X-ray is not active. Right: X-ray is active*

## Exporting Data

1. Click on 

in the bottom left of the main screen. After you click on **Utilities** the following window will appear on the screen (Figure 7).

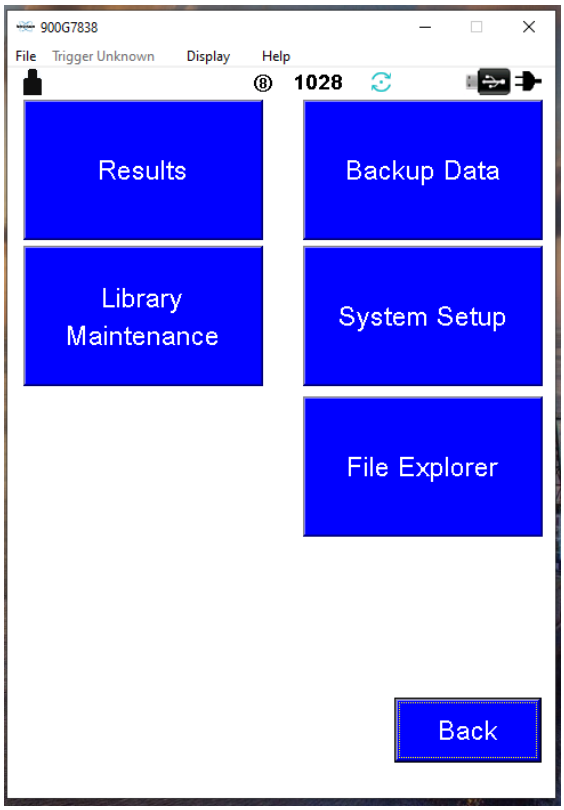


*Figure 7. Utilities Window.*

2. Click on **Backup Data.**

Then make sure **Copy** is selected.

**IMPORTANT: Never select Move as that will move the data from the internal memory into the computer, therefore deleting it from the device.**

3. Save to **Archive** instead of **USB** by changing the following (Figure 8).

4. Click the **blue down arrow** and change the selected file from **\USB** to **\ARCHIVE**

   Your Data File Destination Location should look like Figure 8.

   **Data File Destination Location: \ARCHIVE\Data\Backup-dd-mm-yyyy**

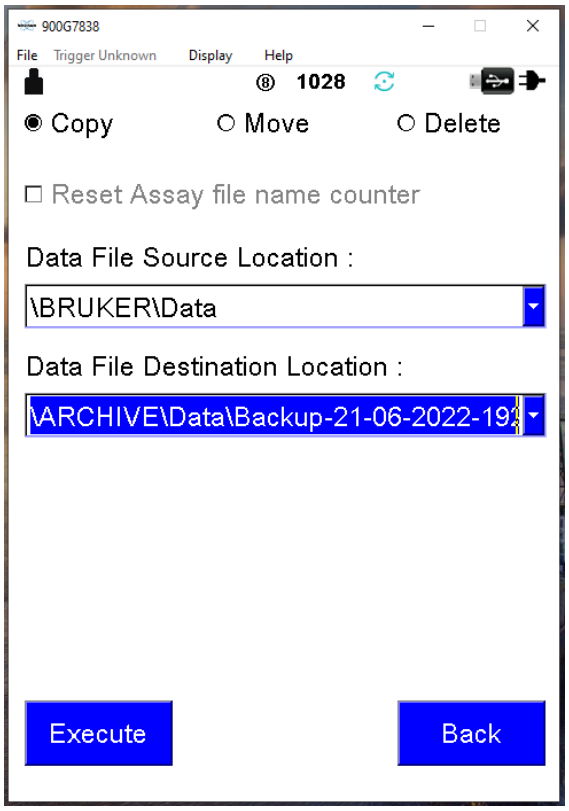


*Figure 8. Backup Data.*

5. After you have selected the file destination folder click on 


6. Close **Bruker RemoteCtrl**.

## Bruker Instrument Tools

After you backup the data go to **Bruker Instrument Tools** icon in the computer's initial window (Figure 9).

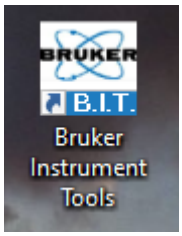


*Figure 9. Bruker Instrument Tools program*

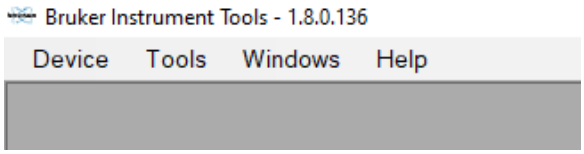


*Figure 10. Connect the device to Bruker Instrument Tools.*

1. Go to **Device** ➡ **Connect** ➡ Select **900G7838** ➡ and click **Connect** (Figure 10 & Figure 11).

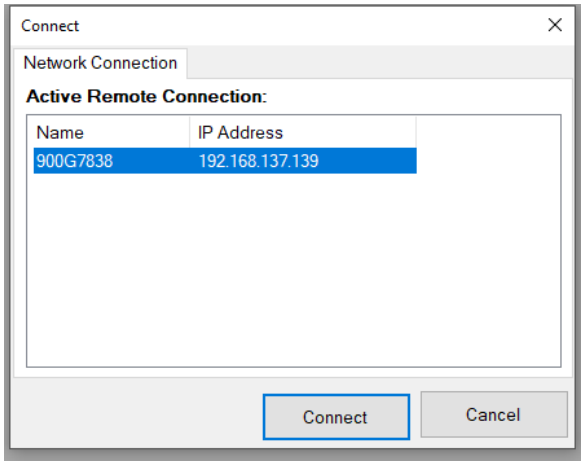


*Figure 11. Connect window.*

2. After you are connected in **Bruker instrument tools** on the left side of the screen you will see a folder that says **ARCHIVE**

3. Open the **ARCHIVE** folder and you will see a screen like figure 12.

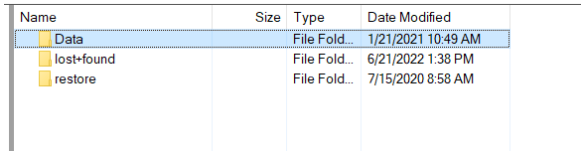


*Figure 12. Archive folder*

4. Go to **Data** ➡ **Open** the most recent backup (Figure 13).

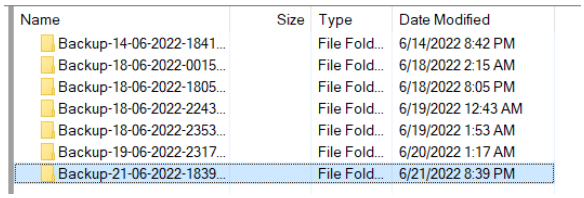


*Figure 13. Data folder*

5. Select the file called **GeoExploration.tsv** (Figure 14)

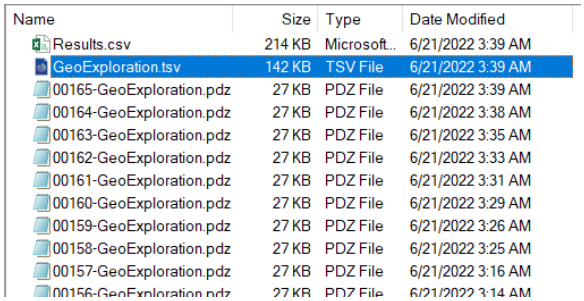


*Figure 14. GeoExploration file inside the backup folder.*

6. **Copy** the **GeoExploration.tsv** file by right-clicking the file name and selecting **copy** from the dropdown menu.

7. Without exiting the program find the folder you want to place the data in the bottom window (Figure 15).

**\\CLEAVELAND\VOL4\ ➡ scratch ➡ BCV**

8. After you find the folder right-click the selected folder and select **Paste** from the dropdown menu.

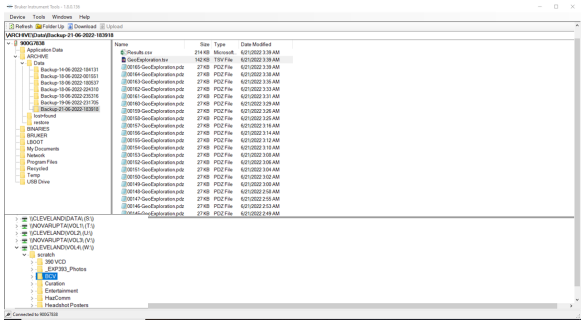

*Figure 15. Copy GeoExploration file and paste in to a folder in Windows(C:/)*

## Opening the file in Excel

1. Open Excel.
2. Open a new workbook and go to the **Data tab** and select 

(Figure 16).

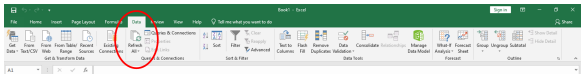

*Figure 16. Excel Data window Select From Text in the left.*

You will be prompted to your computer saved folders and you can select the folder where you saved the **GeoExploration.tsv** file.

3. Once you find the folder select **All Files** in the bottom right (Figure 17).

4. Then select the **GeoExploration.tsv** file and click **Import**. (Figure 17).

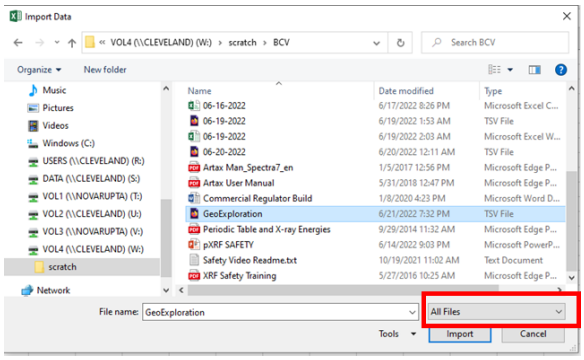


*Figure 17. Finding the GeoExploration file*

5. A window will open showing you a preview of the file and you have to click **Load.** (Figure 18)

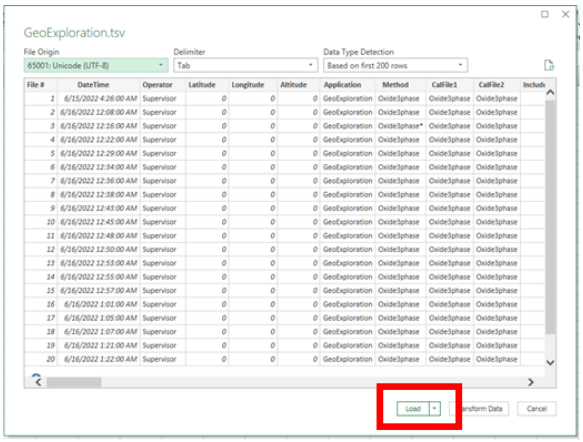


*Figure 18. Data Preview*

6. Click **load** and the data will be exported to excel and should look like Figure 19.

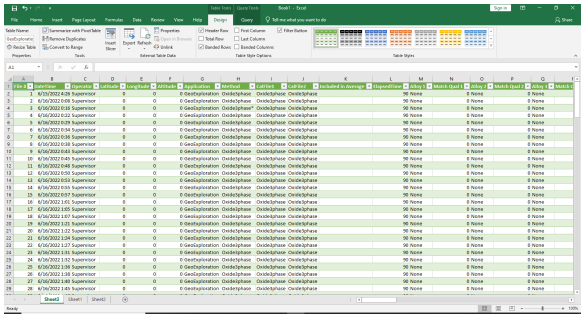

*Figure 19. Exported file from pXRF gun.*

7. Go to **Uservol** → **K_Inorganic_Geochemistry** → **pXRF 393** → **Raw Data** (Figure 20).

8. Open the most recent data and check the latest sample taken under **File #** EX. last file # was 209.

9. Go back to your new exported data file and delete all the samples before that last **File #** EX. total file number is from 1 to 309. Then delete 1 to 209. Only save sample 210 to 309.

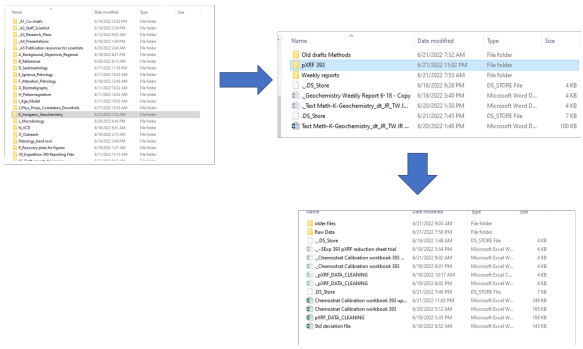

*Figure 20. Save the data to Uservol under the following folders.*

10. Save the data in the format **mm-dd-yyyy-hh-mm** (month-day-year-hour-minute) Was this a recommended file naming format? This format is hard to understand (Why is hour or minute needed? And why use month first?) or sorting the files by name. Perhaps PXRF YYYY-MM-DD?

11. Save the file to **Uservol** → **K_Inorganic_Geochemistry** → **pXRF 393** → **Raw Data** (Figure 20) for Exp 393.

# LIMS Component Table

| PLACEHOLDER until the new PXRF components and data structure is defined | | | |
|---|---|---|---|
| ANALYSIS | TABLE | NAME | ABOUT TEXT |
| PXRF | SAMPLE | Exp | Exp: expedition number |
| PXRF | SAMPLE | Site | Site: site number |
| PXRF | SAMPLE | Hole | Hole: hole number |
| PXRF | SAMPLE | Core | Core: core number |
| PXRF | SAMPLE | Type | Type: type indicates the coring tool used to recover the core (typical types are F, H, R, X). |
| PXRF | SAMPLE | Sect | Sect: section number |
| PXRF | SAMPLE | A/W | A/W: archive (A) or working (W) section half. |
| PXRF | SAMPLE | text_id | Text_ID: automatically generated database identifier for a sample, also carried on the printed labels. This identifier is guaranteed to be unique across all samples. |

| | | | |
|---|---|---|---|
| PXRF | SAMPLE | sample_number | Sample Number: automatically generated database identifier for a sample. This is the primary key of the SAMPLE table. |
| PXRF | SAMPLE | label_id | Label identifier: automatically generated, human readable name for a sample that is printed on labels. This name is not guaranteed unique across all samples. |
| PXRF | SAMPLE | sample_name | Sample name: short name that may be specified for a sample. You can use an advanced filter to narrow your search by this parameter. |
| PXRF | SAMPLE | x_sample_state | Sample state: Single-character identifier always set to "W" for samples; standards can vary. |
| PXRF | SAMPLE | x_project | Project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises |
| PXRF | SAMPLE | x_capt_loc | Captured location: "captured location," this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 |
| PXRF | SAMPLE | location | Location: location that sample was taken; this field is usually null and is unnecessary because any sample captured on the JR has a sample_number ending in 1, and GCR ending in 2 |
| PXRF | SAMPLE | x_sampling_tool | Sampling tool: sampling tool used to take the sample (e.g., syringe, spatula) |
| PXRF | SAMPLE | changed_by | Changed by: username of account used to make a change to a sample record |
| PXRF | SAMPLE | changed_on | Changed on: date/time stamp for change made to a sample record |
| PXRF | SAMPLE | sample_type | Sample type: type of sample from a predefined list (e.g., HOLE, CORE, LIQ) |
| PXRF | SAMPLE | x_offset | Offset (m): top offset of sample from top of parent sample, expressed in meters. |
| PXRF | SAMPLE | x_offset_cm | Offset (cm): top offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset, converted to cm) |
| PXRF | SAMPLE | x_bottom_offset_cm | Bottom offset (cm): bottom offset of sample from top of parent sample, expressed in centimeters. This is a calculated field (offset + length, converted to cm) |
| PXRF | SAMPLE | x_diameter | Diameter (cm): diameter of sample, usually applied only to CORE, SECT, SHLF, and WRND samples; however this field is null on both Exp. 390 and 393, so it is no longer populated by Sample Master |
| PXRF | SAMPLE | x_orig_len | Original length (m): field for the original length of a sample; not always (or reliably) populated |
| PXRF | SAMPLE | x_length | Length (m): field for the length of a sample [as entered upon creation] |
| PXRF | SAMPLE | x_length_cm | Length (cm): field for the length of a sample. This is a calculated field (length, converted to cm). |

| | | | |
|---|---|---|---|
| PXRF | SAMPLE | status | Status: single-character code for the current status of a sample (e.g., active, canceled) |
| PXRF | SAMPLE | old_status | Old status: single-character code for the previous status of a sample; used by the LIME program to restore a canceled sample |
| PXRF | SAMPLE | original_sample | Original sample: field tying a sample below the CORE level to its parent HOLE sample |
| PXRF | SAMPLE | parent_sample | Parent sample: the sample from which this sample was taken (e.g., for PWDR samples, this might be a SHLF or possibly another PWDR) |
| PXRF | SAMPLE | standard | Standard: T/F field to differentiate between samples (standard=F) and QAQC standards (standard=T) |
| PXRF | SAMPLE | login_by | Login by: username of account used to create the sample (can be the LIMS itself [e.g., SHLFs created when a SECT is created]) |
| PXRF | SAMPLE | login_date | Login date: creation date of the sample |
| PXRF | SAMPLE | legacy | Legacy flag: T/F indicator for when a sample is from a previous expedition and is locked /uneditable on this expedition |
| PXRF | TEST | test changed_on | TEST changed on: date/time stamp for a change to a test record. |
| PXRF | TEST | test status | TEST status: single-character code for the current status of a test (e.g., active, in process, canceled) |
| PXRF | TEST | test old_status | TEST old status: single-character code for the previous status of a test; used by the LIME program to restore a canceled test |
| PXRF | TEST | test test_number | TEST test number: automatically generated database identifier for a test record. This is the primary key of the TEST table. |
| PXRF | TEST | test date_received | TEST date received: date/time stamp for the creation of the test record. |
| PXRF | TEST | test instrument | TEST instrument [instrument group]: field that describes the instrument group (most often this applies to loggers with multiple sensors); often obscure (e.g., user_input) |
| PXRF | TEST | test analysis | TEST analysis: analysis code associated with this test (foreign key to the ANALYSIS table) |
| PXRF | TEST | test x_project | TEST project: similar in scope to the expedition number, the difference being that the project is the current cruise, whereas expedition could refer to material/results obtained on previous cruises |
| PXRF | TEST | test sample_number | TEST sample number: the sample_number of the sample to which this test record is attached; a foreign key to the SAMPLE table |
| PXRF | TEST | Top depth CSF-A (m) | Top depth CSF-A (m): position of observation expressed relative to the top of the hole. |
| PXRF | TEST | Bottom depth CSF-A (m) | Bottom depth CSF-A (m): position of observation expressed relative to the top of the hole. |
| PXRF | TEST | Top depth CSF-B (m) | Top depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user. |

| | | | |
|---|---|---|---|
| PXRF | TEST | Bottom depth CSF-B (m) | Bottom depth [other] (m): position of observation expressed relative to the top of the hole. The location is presented in a scale selected by the science party or the report user. |
| PXRF | RESULT | datetime | RESULT datetime: date/time stamp for each run |
| PXRF | RESULT | mode | RESULT mode: the calibration selected for the run (e.g., Geochem, Mudrock) |
| PXRF | RESULT | run_number | RESULT run number: serial number of the run (incremented by the instrument for each sample) |
| PXRF | SAMPLE | sample_name | SAMPLE sample name: repeated display of the sample label ID from the SAMPLE table |
| PXRF | RESULT | reading | RESULT reading number: human-input run number for each sample |
| PXRF | RESULT | run_spm_asman_id | RESULT spectrum file ASMAN_ID: serial number of the ASMAN link for the spectral raw data (.SPM) file |
| PXRF | RESULT | run_spm_filename | RESULT spectrum filename: file name for the spectral raw data (.SPM) file |
| PXRF | RESULT | run_main_asman_id | RESULT main report ASMAN_ID: serial number of the ASMAN link for the reduced data table (.CSV) file |
| PXRF | RESULT | run_main_filename | RESULT main report filename: file name for the reduced data table (.CSV) file |
| PXRF | RESULT | offset (cm) | RESULT offset (cm): position of the observation made, measured relative to the top of a section half. |
| PXRF | RESULT | result comments | RESULT comment: contents of a result parameter with name = "comment," usually shown on reports as "Result comments" |