Bone/Tooth Extraction Batch Setup

1. In Justice-Trax:
    a. Itemize cutting of bone/tooth in LIMS. If no bone powder is being retained, this item can be sent over to STACS (ex. #1-1 sent over to STACS). If bone powder is being retained, itemize again. (ex. #1-1-1 sent over to STACS, #1-1 retained in LIMS).
    b. Make the request for the item sent over to STACS as **DNA-STACS-Sero.** This is used for samples requiring examination.
2. Associate the appropriate item to the request. Item should be in your possession if testing is starting the same day as itemization. If not, transfer the item to an appropriate storage location in LIMS until testing begins.
3. Import the samples into STACS:
    a. In the **Processing** module, open **Sample Setup** → select the **Import** button
    b. Select the appropriate date range and click **Connect**
    c. Select the samples to import into STACS. Select **Import**
4. In the **Processing** module, open **Sample Setup.** Under the **Sample Status** dropdown, choose **New**.
5. Select the newly imported case exhibit(s) and click **Assign**. Select yourself as the Analyst. The Reporting Analyst can be selected at this time but is not required.
6. In the **Processing** module, open **Serology Worklist.** Select the item imported from LIMS for bone/tooth extraction. Click **Open Exams.** This will open the **Serology Worksheet.**
    a. In the serology worksheet, click **Cut for DNA.** The 'Cut for DNA' screen will open.
    b. Select how many 'cuttings' (powder tubes) are being extracted in the **drop down box**.
    c. Click **Save**. The **Sample Details** window for the first powder tube will open.
    d. Adjust information as needed.
    e. Click **Save**. The barcode will print and then STACS will prompt you to scan it. After barcode is scanned, the **Sample Details** window will automatically move to the next powder tube. Repeat above steps until all powder tubes have a barcode printed. A pop-up box will appear when all the tubes are done.
7. If not already done, take custody of the sample tube(s) to be processed. In **Storage Subsystem**, select the **Retrieve** tab, scan the item bar code(s) to be put into your custody. Select **Save.**
8. In **Sample Setup**, highlight the sample(s) and click **Start Processing**.
9. Create a batch worksheet: Open **Processing → DNA Processing → Batch Setup.** Click **Create.**

10. Select the appropriate extraction under **Batch Type** (Bone and Tooth Extraction) the corresponding **Evidence Classification** (Question), and the **Fill Order** (Horizontal).
11. Click **Create**. A unique barcode associated with the extraction will be generated and printed. Moving forward, this barcode may be used to transfer the samples as a whole set.
12. Scan the extraction barcode to begin sample allocation.
13. Select samples to be extracted from the available samples window on the left. Click **Allocate** to add selected samples to the extraction worksheet.
14. To add a reagent blank to the extraction worksheet, click **Create Blank** to launch the preparation module. Do not modify the default settings. Click **Save**. A barcode will print for this reagent blank. In the allocation screen, highlight the well where the reagent blank will be assigned. Scan the barcode. Repeat these steps for all the reagent blanks that are needed, leaving one reagent blank without a barcode.
15. Click **Complete** in the **Batch Setup** window.
16. By completing the batch, a **Blank** sample will automatically be generated. In the pop-up window, click **Save**. The barcode will automatically print. There is no need to enter a lot number. This will be the barcode for the last reagent blank.
17. If the barcode does not print, proceed to **extraction** (see step 1 below). Select the batch and click **Content** on the right side of the screen. In the content window, highlight the RB without a barcode. Click **Print Selected Barcode** at the bottom. Close window.

Extraction/Isolation

Extraction refers to sample EDTA nutation, dH2O rinse, and extraction buffer incubation steps. Isolation encompasses PCIA clean-up and microcon purification.

1. Open **Processing → DNA Processing → Extraction.**
2. Select the batch to be processed from the worklist and click **Select Scenario**. Bone and tooth extraction consumables are split into 3 groups.
3. Scan the consumable barcode for EDTA. The Consumable window will display the reagent volumes required for the lysis.
4. Click **Start Process**.
5. Complete the tube check by scanning the tube labels.
6. When the samples are ready to come off the nutator (typically overnight), scan the consumable barcode for dH2O. Click **Continue**.
7. When the samples are finished with rinsing, scan the consumable barcodes for extraction buffer, prepared Proteinase K, and DTT Bones/Teeth. Click **Continue**.
8. When the samples are finished with extraction (6 hours up to overnight), click **Complete Process** and record the results using the Complete Batch Activity screen.

- **Process Successful**: the batch advances to the next processing step.
- **Process Aborted:** the batch remains on the Extraction Batches worklist. A **Batch Comment** is required with this option.
- **Process Failed:** the batch is abandoned and all samples return to Batch Setup. A batch comment is required with this option

9. Click **Save**.
10. Create an Isolation (purification)worksheet: Open **Processing → DNA Processing → Isolation.**
11. Click **Create Batch.**
12. Click the **Create** button under the New Batches worklist.
13. Select a **Batch Type (Bone and Teeth Microcon)** and click **Create** to create the unique barcode associated with the isolation.
14. Scan the newly created barcode into the **Destination Batch** section.
15. Scan the extraction barcode into the **Source Batch** section. Click **Allocate** to add the lysed samples to the isolation worksheet.
16. Once finished, click **Complete**.
17. In the Batches Worklist window, click **Select Scenario.**
18. Scan the consumable barcodes for PCIA, microcons, and dH2O.
19. Click **Start Process**.
20. Complete the tube check by scanning the tube labels.
21. Once the isolation is complete, click **Complete Process** and select the appropriate option. Adjust the elution volumes if needed.
    - **Process Successful:** the batch advances to the next processing step.
    - **Process Aborted**: the batch remains on the Isolation worklist. A **Batch Comment** is required with this option.
    - **Process Failed:** the batch is assigned a **Status** of '**Abandoned**' and its samples are returned to Isolation Batch Create to be allocated to a new batch. A **Batch Comment** is required with this option.
22. Proceed to SOP for **Combine** and **Concentrate**.