



Smithsonian  
*National Museum of Natural History*  
*Collections Program*

**NMNH Biorepository Workflow for Legacy Collections**  
**Updated February 2014**

**1. Legacy Collections for Biorepository Integration Identified**

- a. Biorepository Staff
  - i. Use prioritized list to contact Department Staff.
- b. Biorepository Staff and Department Staff
  - i. Agree the collection is appropriate for inclusion in Biorepository.

**2. Evaluate and Inventory Collections**

- a. Biorepository Staff and Department Staff
  - i. Assess collection and decide if samples require rehousing and labeling. Identify any reasons for rejecting samples (e.g., no voucher, lack of documentation, or condition of material).
- b. Biorepository Staff
  - i. Inventory all samples in the collection and map locations.
    1. If the unit provides a list, verify sample presence and location.
- c. Department Staff
  - i. Assess and decide if the sample requires data completion, or data cleaning.

**Scenario A:** If no rehousing is required and a catalog record for the genetic sample already exists in EMu, then proceed from **step four**.

**Scenario B:** If rehousing is required and a catalog record for the genetic sample already exists in EMu, then proceed from **step three**.

**Scenario C:** If rehousing is required and no catalog record for the genetic sample exists in EMu, then proceed from **step three** or **step seven** (if “readily-importable” to EMu).

**Scenario D:** If no rehousing is required and no parent catalog record exists in EMu, then proceed from **step four**.

### **3. Cleanup Data and Rehouse Collections**

- a. Biorepository Staff
  - i. Work with the Department Staff to clean data.
  - ii. Collaborate with Department Staff on resolving any other issues, if necessary.
  - iii. Rehouse as necessary from step two above. Apply Biorepository numbers while rehousing tubes. Follow step seven to produce labels. Produce a final map and complete inventory of the rehoused/re-boxed/consolidated samples and document this in a spreadsheet (if necessary).
  - iv. Upload sample location information into FreezerPro. Export inventory file from FreezerPro. Inventory file includes assigned Biorepository IDs and original vial label data.
  - v. Pass exported inventory to Department Staff.
- b. Department Staff
  - i. Clean data as necessary from step 3ai above.
  - ii. Sleuth problematic data by checking catalog records, field notebooks, checking with researchers, etc.
  - iii. Insert and/or update EMu records based on Biorepository inventory using bulk data import or manual entry.
  - iv. Evaluate and check off publish/embargo flags.

### **4. Hand Off Completed Inventory**

- a. Biorepository Staff
  - i. Hand off to Department/Division.

### **5. Create Sample Records**

- a. Department Staff
  - i. Create genetic sample records in EMu and new FreezerPro records through EMu (if necessary).
  - ii. Inform Biorepository Staff.

### **6. Data is pushed from EMu to FreezerPro automatically**

### **7. Print and apply labels to sample containers**

- a. Biorepository Staff
  - i. Supply Department Staff with inventory spreadsheet from step four above.
  - ii. Once EMu data is pushed to FreezerPro, data is exported for label printing. Data must be sorted to match inventory order.
  - iii. Create labeling work list. Need name of original box, rack, information written or printed on tubes (should match inventory list). Identify destination box.
  - iv. Create labels in LabelMark 5. Bag printed labels with work list.
  - v. Affix labels to tubes. Verify ProjectUnit\_ID numbers/Field ID number, origin box locations etc.

- vi. Return new box of legacy tubes to original rack for holding until FreezerPro is updated with location information.
  - b. Department Staff
    - i. Use inventory to create/add to EMu record for genetic resources listed on inventory sheet. Collections staff compares Biorepository supplied inventory to EMu records and makes edits when necessary. Adds EMu IRN to Biorepository inventory list.
    - ii. Inform Biorepository Staff.
- 8. Update FreezerPro with location information**
- a. Biorepository Staff
    - i. Create an “Update CSV” (OR use “Scan & Move” feature in FreezerPro; file for FreezerPro import/move. Must match FreezerPro’s template.
    - ii. Spot-check sample tubes in the update CSV vs. box contents. Verify first, last, and moved tubes, and three or four random interior samples.
    - iii. Identify destination box in the Freezers and Boxes section of left pane. Double click to open box view.
    - iv. In Box view window, locate the Actions drop down menu. Click Update Samples. FreezerPro will move samples (update locations) from staging area to destination box. OR Use “Scan & Move” feature to scan Biorepository numbered tubes into destination box.
    - v. Update FreezerPro records with tube size, elution buffer, etc.
- 9. Move samples to final freezer location**
- a. Biorepository Staff
    - i. Move the actual box to its permanent storage location.
- 10. Location information is automatically passed from FreezerPro to EMu.**

**Milestone 1: Data and samples fully integrated**

**Milestone 2: Data ready for upload to GGBN**