

*Approved by Director: Dr. Guy Vallaro***Knowns Examination**

1. In JusticeTrax (i.e., LIMS): In lieu of the typical DNA knowns request, create a **DNA-STACS-Sero** request. The Sero request is for any item that must be examined like knowns. Associate the **parent** item #X to the request. See STACS SOP-2 for details involving Justice Trax (LIMS).
2. Transfer the #X parent item to yourself in LIMS.
3. Open the submission packaging.
4. Itemize the contents in JusticeTrax.
  - a. **Note:** When processing in STACS, the (\*) designations will no longer be used.
  - b. **Itemize only the #X-1 subitem** in Justice Trax. Further cuttings will be completed in STACS.
5. Associate the newly created sub-item #X-1 to the existing **DNA-STACS-Sero request**.
6. Import the request to STACS: both the parent #X (for examination documentation) and sub-item #X-1 (sample from packaging) are imported.
  - a. In the **Processing** module, open **Sample Setup** → select the **Import** button.

The screenshot shows the 'Sample Setup' window in the STACS application. The left sidebar is titled 'Processing' and lists various modules, with 'Sample Setup' highlighted. The main window has a 'Case Management' tab and a 'Sample Setup' sub-tab. It contains several input fields and buttons. The 'Sample Status' is set to 'New'. The 'Start Date' is '03/26/2025' and the 'End Date' is '06/26/2025'. There are buttons for 'Refresh', 'Show Temp Bar Codes', and 'My Samples'. Below these are fields for 'Priority', 'Supplement', 'Evidence Classification', 'Sample Nature', and 'Extraction Type'. An 'Exhibit Worklist' table is displayed with 3 rows, each containing 'Serology' data. At the bottom, a toolbar contains buttons for 'New', 'Edit', 'Cancel', 'Assign', 'Files', 'Import' (highlighted with a red circle), 'Retain', 'Print', 'Sample Label', and 'Sample Import'.

- b. In the popup window, select the appropriate date and click **Connect**. Note that the Sample Create Date, shown below, refers to the date the STACS request was created in JusticeTrax.

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Select	Result	Assignment Type	Lab Case Number	Exhibit Number	Exhibit Description	Case Created Date	Submitting Organization	Agency Case Number	Offense	Victim	Suspect	Other	Incident Date
<input type="checkbox"/>	LIMS Identifier Already Exists	DNA - STACS - Sero	DSS-25-062725	001	Env with 'one FTA buccal card and swab - Maeson Hagen	06/27/2025	New Haven Police Department	062725AMA	Assault	Maeson Hagen			04/14/2025
<input type="checkbox"/>	LIMS Identifier Already Exists	DNA - STACS - Sero	DSS-25-062725	001-001	One known FTA buccal card- Maeson Hagen	06/27/2025	New Haven Police Department	062725AMA	Assault	Maeson Hagen			04/14/2025



c. Select the evidence sub-item to import into STACS and click **Import**.

Note: If duplicates of the sample are listed, pick the sample with the primary agency's name and agency case number that the sample was submitted under. Ensure only 1 line for each sample or packaging is imported into STACS.

d. Once imported, the '**Results**' column will change to '**Saved**'. Already imported items will say '**LIMS Identifier Already Exists**'.

Selected	Result	Assignment Type	Lab Case Number	Exhibit Number
<input checked="" type="checkbox"/>	Saved	DNA - STACS - Sero	MGR-24-080924	12-1
<input checked="" type="checkbox"/>	Saved	DNA - STACS - Sero	MGR-24-080924	012

e. Select **Close**.

7. Open **Sample Setup (Processing → Receipt → Sample Setup)**. Under the **Sample Status** dropdown, choose '**New**'.

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Sample Bar Code	Input Type	Processing Analyst	Report Analyst	Cus
	Serology			
	Serology			
	Serology			
	Serology			
	DNA			
	DNA			
	DNA			
	DNA			
	DNA			
	Serology			

8. The samples just imported will be here with **Serology Input Type**. If not, select refresh at the top and ensure the dates are correct.
9. Select the newly imported case exhibit(s) (**#X and #X-1**) and click **Assign** at the bottom of the screen. Select yourself as the Analyst. The Reporting Analyst does not need to be selected at this time.
10. In **Justice Trax**, ensure the parent item **#X** of the known is transferred into your custody for examination. The sub-item **#X-1** will also stay in your custody at this point.
11. To define what the item designations are in relation to STACS; see below:
  - **#X-1** for an FTA: is the FTA card in a foil envelope. Imported from LIMS
  - **#X-1-1** for an FTA: is the punch on the BSD. Made in STACS (made by the processor)
  - **#X-1** for a buccal swab is the entire swab. Imported from LIMS. COC in LIMS to Freezer Storage.

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- **#X-1-1** for a buccal swab: is the ½ of cut swab to be tested. Made in STACS (made by the processor)

### 12. Document the packaging examination of #X:

- Double-click the parent item **#X** or highlight the exhibit and click **Edit** to open the **Sample Details** window. Ensure the yellow highlighted areas are filled out appropriately.
  - **Supplement** will typically be '0'. Subsequent numbering will be used for supplemental testing on the same exhibit number.
  - **Priority** should be 'Low', unless the case is an expedite
- Fill out all applicable examination notes in the **Packaging Information** section of the **Sample Details** window. This may be done using the **Autofill** options (Right click; Auto-fill; Knowns Packaging options). Free text is also an option. See image below.
- If the submission contains additional evidence that will not be examined and containerized into the packaging, document these contents in the **Comments** section to the left of the window.
- Additional auto-fill options (Knowns NEATT) are available for these statements.

Sample Details (SampleSetupForm)

Sample Details

Lab Case Number: DSS-25-063705 Supplement: 0 Container: Exhibit Number: 001 STACS Bar Code: Priority: Low

Exhibit Description: Env with "one FTA buccal card and swab - Maeson Hagen"

Sample Status: New

Agency: New Haven Police Department Offense: Assault

Incident Date: 04/14/2025 Agency Case Number: 062725AMA Agency Item Number: Other(s):

Victim(s): Maeson Hagen Suspect(s):

Elimination(s): Case Created Date: 06/27/2025 Sample Create Date: 6/27/2025 10:40:26 AM Case Released Date:

TAT (days): Case Due Date: LIMS Bar Code: Sexual Assault Kit Bar Code: Release Form Received:

Input Type: Serology Evidence Classification: Sample Nature: Extraction Type:

Processing Analyst: Alicia Amatruda PA Assigned Date: 06/27/2025 Report Analyst: RA Assigned Date:

Not Examined Mark Complete

Comments: Packaging Information: Large manila envelope Red evidence tape

Create Blank Where Am I Sample Label Itemize Reprocess Apply Save & New Files Report Results Link Exhibit Cut For DNA Save Close

- Once all notes are added, click **Save**. It will disappear and move to **Processing**.
- Now the **#X** can be closed out.

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Division of Scientific Services

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- g. In the Sample Setup module, select '**Processing**'. It is easier to select 'My Samples' to select the new items.

The screenshot shows the 'Sample Setup' window with the 'Amplification Setup' tab active. The 'Sample Status' dropdown is set to 'Processing'. The 'Start Date' is 04/13/2025 and the 'End Date' is 07/13/2025. A 'Refresh' button is present. To the right, there are two checkboxes: 'Show Temp Bar Codes' (unchecked) and 'My Samples' (checked). The 'My Samples' checkbox is circled in red.

- h. Double-click on the #X exhibit or highlight and click Edit to open the Sample Details window.
- i. If all the information is complete, and no further action is needed for the #X, click **Mark Complete** (arrow above). The #X will be removed from the Processing list, however, there is one more step to finishing the completion of the packaging exam.
- Select **Close**.
    - In **Sample Setup** select '**Pending Conclusion**' from drop down and select the **sample #X** (parent/packaging) that was just completed.
    - At the bottom of the screen, click **Complete** for #X.

The screenshot shows the 'Sample Details' window. The 'Input Type' is 'Serology' and the 'Evidence Classification' is 'Processing Analyst'. There are checkboxes for 'Stain Consumed' and 'Rehydration Required'. Below these are buttons for 'Not Examined' and 'Mark Complete'. The 'Mark Complete' button is circled in red. A 'Comments' section with a text area is at the bottom.

- c. The sample will stay in the '**Pending Conclusion**' status if it is not also 'completed' on this screen. See below.

The screenshot shows the 'Sample Setup' window with the 'Amplification Setup' tab active. The 'Sample Status' dropdown is set to 'Pending Conclusion'. The 'Start Date' is 04/13/2025 and the 'End Date' is 07/13/2025. A 'Refresh' button is present. To the right, there are two checkboxes: 'Show Temp Bar Codes' (unchecked) and 'My Samples' (checked). Below this is an 'Exhibit Worklist : 1' table with columns: Sample Bar Code, Input Type, Lab Case Number, Exhibit Number, Processing Analyst, Report Analyst, and Custodian/LC. The table contains one row with data: Serology, DSS-25-001541, 003, Cheryl Carreiro, Cheryl Carreiro. At the bottom, there is a row of buttons: New, Edit, Itemize, Assign, Results, Files, Import, Print, Complete, Assign Conclusions, Sample Label, Sample Import, and Close. The 'Complete' button is circled in red.

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13. Document the evidence examination (Subitem #X-1):

- a. Go to '**Sample Setup**' → '**New**'; the subitem (serology input) will be listed here after import.
- b. Double click the exhibit #X-1 or highlight the evidence item and click **Edit** to open the **Sample Details** window. Ensure the yellow highlighted areas are filled out appropriately.
  - Supplement will typically be '0'. Subsequent numbering will be used for supplemental testing on the same exhibit number.
  - Priority should be 'Low', unless the case is an expedite.
- c. **Fill out all applicable examination notes** in the Sample Details window. This may be done using the autofill options (Right click; Auto-fill; Knowns/Staining options).
- d. Click **Save**. The #X-1 item will disappear from '**New**' and move to the '**Processing**' dropdown as a Sero input. A DNA input will be made at later steps.
- e. After an FTA card is examined, the FTA card can be moved in **LIMS** to '**Knowns to Be Tested**'. *The FTA card in the envelope is a Sero request and cannot be transferred in STACS.*
- f. Make sure #X is completed. FTA card is done until punching by the processor.
- g. **For Swabs continue below.**



- h. Examination of buccal known submissions containing **swabs or filter paper** that will **not** go through punching, will proceed to the next step below.

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- i. In the Sample Details window for the #X-1, click '**Cut for DNA**' to create the testable portion of the sample (#X-1-1). Fill out the **Stain Designator** (typically 1). **Do not** check off **Stain Consumed**.

New cuttings

How many cuttings? 1

Stain Designator	Stain Consumed	Reference	Comment
1	<input type="checkbox"/>	<input type="checkbox"/>	Comment

Comment

Processing Analyst: Cheryl Carneiro (CLC)

Apply Apply All

Consumables : 1

Optional	Consumable Name	Format	Bar Code	Lot Number	Expiry Date	QA/QC Expiry Date
<input checked="" type="checkbox"/>	dH2O (FB sample collection/dropper bottles)	WT#####				

- j. A comment may be added to indicate the amount of sample cut (e.g., ½ cut; ½ retained). After making a comment click **Apply** and the comment will go to the top comment bar.
- i. Click **Save**. A new **Sample Details** window will populate related to the Swab Cutting. It will be titled #X-1-1.
- ii. In the new **Sample Details** window of #X-1-1, ensure the Supplement = 0 and select the **Known** option in the **Evidence Classification** in the drop-down.

Evidence Classification: Known

Sample Nature: Cutting

Extraction Type: Non Differential

PA Assigned Date: 07/07/2025

Report Analyst

RA Assigned Date

Packaging Information

- iii. Click **Save**. A unique STACS barcode will be generated for the cutting sample.
- iv. Scan the barcode in the '**Barcode Verification**' window and affix to the sample. Scan the sample barcodes in the window that pops up.
- v. See below that once '**Cut for DNA**' is selected the input field is now DNA. This signifies that this sample is the testing portion of the sample.
- vi. The cutting #X-1-1 is moved automatically to **Sample Setup → 'Received'**.



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vii. Click **Save**.

Lab Case Number	Supplement	Container	Exhibit Number
DSS-25-001541	0		003-002-1

Exhibit Description  
cutting of buccal swab

- k. Once **#X-1-1 (cutting of swab)** is created, the examination on the item **#X-1 (swab)** is complete.
- l. In the **'Sample Details'** window for **#X-1** click **'Mark Complete'**. An additional **'Mark Complete'** is needed in **Sample Setup** dropdown **'Pending Conclusions'** similar to closing out **#X**.
14. Going back to Justice Trax (that will have the COC for **#X-1**) move **#X-1** to **freezer storage**. If the other ½ of the swab needs to be tested in the future, it can be imported into STACS and "cut for DNA" with the consumption button selected.
15. To summarize:
  - d. **Parent Item** = Transfer in LIMS to the **'Knowns Completed'** storage to be returned. COC is completely tracked in JusticeTrax.
  - e. **Subitem (#X-1)** = After cutting made, transfer the rest in LIMS to **Freezer Storage**; Examination COC is completely tracked in LIMS.
    1. If the other ½ of the swab needs to be tested, it can be imported into STACS and "cut for DNA" with the consumption button selected.
  - f. **Subitem Cutting (#X-1-1)** = In STACS transfer the cutting to **'Knowns To Be Tested'** (**KNN00001**). The cutting does **not exist** in LIMS/JusticeTrax. All applicable COC for the cutting is tracked in STACS.
    - a. Open **Utilities → Storage → Storage Subsystem**.
      1. Under the **Store** tab, scan the storage location bar code and the item bar code to be put into **'Knowns to be Tested'**. Select **Save**. Storage Location below is "Knowns To Be Tested" in STACS.

Storage Unit Bar Code	Item Bar Code
KNN00001	CC031

Store Items : 1

Storage Location Bar Code	Item Bar Code	Lab Case Number
KNN00001	CC031	MGR-24-080924

14. If Database or Staff search samples need to be added to a knowns processing batch, see step below.
  - a. **Staff search/other samples:**



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- b. Samples are not being imported through JusticeTrax, so they must be manually entered into STACS.
- c. In **Sample Setup**, click **New**. Enter the mandatory information into the yellow highlighted boxes.
- d. It is critical to select **Non-Evidence** for the Evidence Classification. The Offense is put as **Other**. See below.
- e. For the **Lab Case Number** field:
  - i. **Database Cards:** DB cards will be the **DB-XXXXX** (DB identifier).
  - ii. **Staff/Visitor:** For these samples the format is **Other-[Name of the Person]**.
- f. For the **Exhibit** and **Offense** Fields:
  - i. For Exhibit: Enter number 1.
  - ii. For Offense: Other
  - iii. For Agency: z- My Test Agency

- g. Transfer the non-evidence samples to '**Knowns to be Testied**' in STACS.

### **Known – Pre Processing**

15. First, make sure the Processor has taken custody of the sample(s) to be processed.
  - a. **FTA blood/buccal cards**, will be transferred into their custody in JusticeTrax by normal procedures (DNA SOP-12). FTA cards are in the LIMS storage location '**Knowns To Be Tested**'. The LIMS barcode is keeping the COC for this sample.
    - i. The **FTA Sero Input** will still be in '**Processing**' as seen below, but without a custody/location or barcode. See highlights below.

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Exhibit Worksheet : 15											
Sample Bar Code	Input Type	Processing Analyst	Report Analyst	Custodian/Location	Input Action	Sample Nature	Extraction Type	Lab Case Number	Supplement	Exhibit Number	Exhibit Description
CC022	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Differential	CLC-250522-1417	0	12	Differential
CC023	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Differential	CLC-250522-1417	0	13	test
CC027	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1434	0	200	Non Differential
CC028	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1624	0	1	Non Differential
CC029	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1624	0	2	swab
CC030	DNA	Cheryl Carreiro	Cheryl Carreiro	RCK00001 - Pending Non-SA Rack	Normal	Cutting	Non Differential	MGR-24-080924	0	005-002	swab of shirt test cl
CC033	DNA	Cheryl Carreiro		Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250711-2332	0	1-1-1	Known Buccal
CC040	DNA	Cheryl Carreiro		Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250712-1026	0	105	FTA
CC044	DNA	Cheryl Carreiro		Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250712-2256	0	12-1-1	BSD Punch
	Serology	Cheryl Carreiro			Normal			CLC-250712-2313	0	8-1	FTA
	Serology	Cheryl Carreiro			Normal			CLC-250712-2333	0	30	Package FTA
	Serology	Cheryl Carreiro			Normal			CLC-250712-2333	0	30-1	FTA
CC048	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	DSS-25-001541	0	002-002-1	Buccal Swab
CC049	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	DSS-25-001541	0	002-001-1	FTA CARD
	Serology	Cheryl Carreiro	Cheryl Carreiro		Normal			DSS-25-001541	0	003-001	FTA Card of known

- b. Double click the **#X-1 FTA** sample to open the **Sample Details**.
- c. In the **Sample Details** window for item **#X-1 (FTA card)**, click **'Cut for DNA'**. This will generate the "punch" **#X-1-1** for further testing.

New cuttings

How many cuttings?

Stain Designator	Stain Consumed	Reference	Comment
1	<input type="checkbox"/>	<input type="checkbox"/>	FTA Punch

Comment  
FTA Punch

Apply Apply All Process

- d. Click **Save**. A new **Sample Details** window will populate related to the cutting.
  - e. In the new **Sample Details** window, ensure the Supplement = 0 and select the **Known** option in the **Evidence Classification** in the drop-down.
  - f. Click **Save**. A unique STACS barcode will be generated for the cutting. Scan the barcode in the **'Barcode Verification'** window.
  - g. The barcode can be affixed to a sheet of paper since "the punch" is tracked with the LIMS BSD barcode.
  - h. At this point while having the **#X-1 Sample Details** open, mark the sample **'Complete'**. Also mark the sample **#X-1** complete in the **'Pending Conclusion'** dropdown.
  - i. The **#X-1-1 FTA Punch** will be in **Sample Setup → Received** as a DNA Input.
  - j. Click **Start Processing** at the bottom for this sample.
16. The **#X-1-1 Swabs in Storage → Subsystem → 'Knowns to Be Tested'** in STACS have a barcode already affixed on the item from the examination step. The physical swab sample is in a rack **'Knowns to Be Tested'**.
- a. Open **Utilities → Storage → Storage Subsystem**.

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- b. For swabs or non-evidence samples, under the **Retrieve** tab, scan the **item bar code(s)** that are to be tested in 'Knowns to be Tested' to be put into your custody.

Item Bar Code	Custodian/Location	Lab Case Number
CC050	KNN00001	DSS-25-001541
CC051	KNN00001	Other-FirstLastName

- c. Select **Save**.
- d. The samples will move to '**Received**'.

Input Action	Sample Nature	Extraction Type	Lab Case Number	Supplement	Exhibit Number	Exhibit Description	Sample Create Date
Normal	Cutting	Non Differential	MGR-25-00529A	0	001	A test item	05/29/2025
Normal	Cutting	Non Differential	DSS-25-00test	0	003-001-1	FTA blood card	07/07/2025
Normal	Cutting	Non Differential	CLC-250712-1026	0	105-1	FTA to be punched	07/12/2025
Normal	Cutting	Non Differential	CLC-250712-2313	0	8-1-1	FTA	07/12/2025
Normal	Cutting	Non Differential	CLC-250712-2336	0	50-1-1	FTA punch	07/13/2025
Normal	Cutting	Non Differential	CLC-250713-0008	0	80-1-1	FTA	07/13/2025
Normal	Cutting	Non Differential	DSS-25-001541	0	003-002-1	cutting of buccal swab	07/13/2025
Normal	Cutting	Non Differential	Other-FirstLastName	0	1	Visitor	07/13/2025

- e. Swab cuttings will be found in the '**Received**' dropdown.
- f. For swabs, select the sample and at the bottom click '**Start Processing**'.

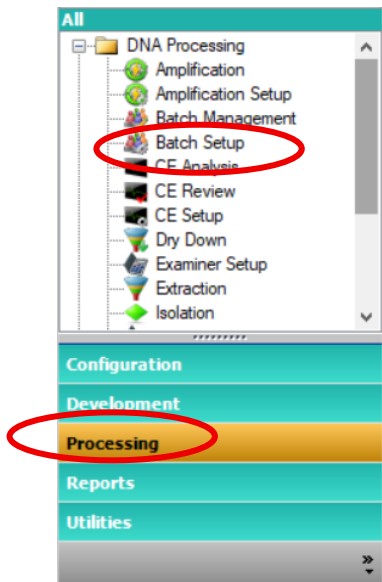
Note: A swab cut from FB will come in as a 'DNA input'. These will only need to be received by the processor (STACS Knowns Storage) and put into '**Start Processing**'.

Sample Bar Code	Input Type	Processing Analyst	Report Analyst	Custodian/Location	Input Action	Sample Nature	Extraction Type	Lab Case Number	Supplement	Exhibit Number	Exhibit Description	Sample Create Date	Agency	Cutting S
CC022	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Differential	CLC-250022-1417	0	12	Differential	05/22/2025	Brookfield Police Department	
CC023	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Differential	CLC-250022-1417	0	13	test	05/22/2025	Brookfield Police Department	
CC027	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1434	0	200	Non Differential	04/20/2025	Ansonia Police Department	
CC028	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1624	0	1	Non Differential	04/20/2025	Ansonia Police Department	
CC029	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	CLC-250620-1624	0	2	swab	04/20/2025	Ansonia Police Department	
CC030	DNA	Cheryl Carreiro	Cheryl Carreiro	RICK0001 - Pending Non-SA Rack	Normal	Cutting	Non Differential	MGR-24-080924	0	005-002	swab of shirt test dc	07/08/2025	z - My Test Agency	
CC031	DNA	Cheryl Carreiro	Cheryl Carreiro	Cheryl Carreiro	Normal	Cutting	Non Differential	MGR-24-080924	0	12-1-1	1 FTA Card J.B dc	07/11/2025	z - My Test Agency	

## Knowns – Processing Continued

### Direct Amplification – Batch Setup

1. Use the **Batch Setup** module to create an Extraction Batch and assign samples and controls to it. You select the Batch Type here as well.
2. Open **Processing → DNA Processing → Batch Setup**.

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3. Click **Create**.

Batches Worklist : 7					
Create Date	Bar Code	Batch Type	Evidence Classification	Custodian/Location	Created By
06/20/2025	E2L-250620-13	EZ2 Lysis	Question	Cheryl Carreiro	Cheryl Carreiro
03/12/2025	BTE-250312-61	Bone and Tooth Extraction	Question	In Lab	Angela Przech
03/13/2025	E2L-250313-33	EZ2 Lysis	Question	In Lab	Kristen Madel
04/14/2025	E2L-250414-06	EZ2 Lysis	Question	In Lab	Cheryl Carreiro
05/23/2025	E2L-250523-03	EZ2 Lysis	Question	Cheryl Carreiro	Cheryl Carreiro
05/23/2025	E2L-250523-04	EZ2 Lysis	Question	Cheryl Carreiro	Cheryl Carreiro
06/20/2025	E2L-250620-02	EZ2 Lysis	Question	Cheryl Carreiro	Cheryl Carreiro
<div> <div>Create</div> <div>Content</div> <div>Comment</div> <div>Rework</div> <div>Refresh</div> </div>			Auto Fill Well (DEV) <div>1</div> <div>Auto Fill Well</div>		

4. Select the appropriate extraction under Batch Type, the corresponding Evidence Classification, and the Fill Order.

- Select the Batch Type as appropriate:
- Direct Amp Punch** (partial or full)
- Direct Amplification Swabs (requires Prep and Go Buffer)**
- Direct Amplification Swabs – No BIS**; Use when combining GFE Swabs with FTA Punch samples on a single amplification set.
- \*\*It is important to note here that Punches and Swabs will be combined at the Amplification step.
  - For example, a batch of **Direct Amp Punch (partial or full)** will be made for the FTA cards and a **Direct Amplification Swabs-No BIS** for Swabs will be made.

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- After the batches are made, it is at the **Amplification** step the two batches will be merged. Details are below further down in this SOP.
- f) Evidence Classification **Known**, unless non-evidence (i.e. staff) samples are to be tested.
- g) Fill Order = **Vertical**. See Below.

Create Batch (CreateBatchForm)

Batch Type: Direct Amp Punch (partial plate) | Evidence Classification: Known | Kit: Not Defined | Fill Order: Vertical | Create

	1	2	3	4	5	6	7	8	9	10	11	12
A	Direct Amp Punch	DNA	DNA	DNA	DNA	DNA	Direct Amp Punch	DNA	DNA	DNA	DNA	DNA
B	Direct Amp Punch	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
C	Blank	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
D	Direct Amp Punch	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
E	BIS	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
F	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
G	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
H	DNA	DNA	DNA	DNA	DNA	Direct Amp Punch	DNA	DNA	DNA	DNA	DNA	Direct Amp Punch

Show/Hide Grid | Close

5. Click **Create**. A unique barcode associated with the extraction will be generated and printed.
6. Moving forward, this barcode may be used to transfer the samples as a whole set.
7. To begin sample allocation, scan the extraction barcode into the blue-highlight or double-click the batch in the upper Batches Worklist window.
8. Allocate the sample(s). Highlight the sample(s), select a destination well labeled “DNA” and click “**Allocate**”.

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Bar Code	Lab Case Number	Exhibit Number	Lot Number	Sample/Control
AA068	DSS-25-000004	001-001-01-1c	Cut	
AA069	DSS-25-062725	002-001-1c	Cut	
AA070	DSS-25-062725	001-001-1c	Cut	

	1	2	3	4	5	6	7	8	9	10
A	●	DNA	DNA	DNA	DNA	DNA	●	DNA	DNA	DNA
B	●	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
C	Blank	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
D	●	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
E	BIS	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
F	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
G	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
H	DNA	DNA	DNA	DNA	DNA	●	DNA	DNA	DNA	DNA

Buttons: Multi-Tube, Discontinue, Create Blank, Allocate, Clear Wells, Print Bar Code, Clear Form, Import, Show/Hide Grid, Complete

9. To add the BIS (positive controls) to the worksheet, select the designated BIS well and scan the barcode for the control.
10. When all samples and controls are added, click **Complete** in the **Batch Setup** window.
11. By completing the batch, the **Blank** sample(s) will automatically be generated. In the pop-up window, click **Save**.
  - a) The barcode will automatically print. Initials/date may be entered as a lot number, although not necessary.

Blank Control Lot Number

STACS Barcode: 250094

Lot Number:

Well: C01

☐ Apply All

Save

- b) If for some reason a bar code does not automatically print; see below:

Buttons: Multi-Tube, Discontinue, Create Blank, Allocate, Clear Wells, Print Bar Code, Clear Form, Import, Show/Hide Grid

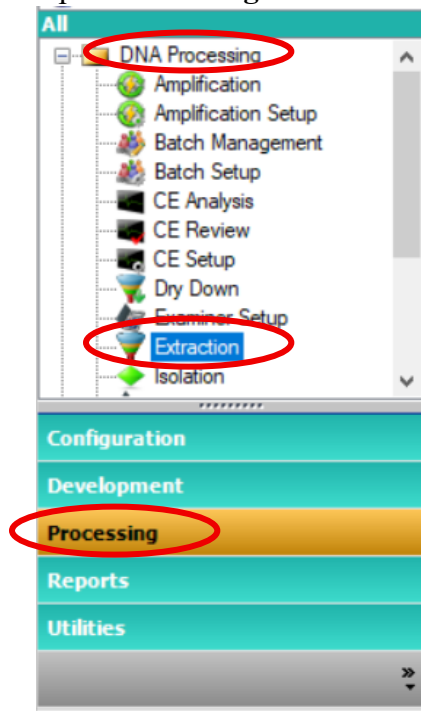


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12. The BSD Punchbot file will open to be saved on the Udrive: U:\STACS share\BSD. This file can be uploaded to the instrument for punching of the cards.

### Direct Amplification – Extraction Step

1. Open **Processing** → **DNA Processing** → **Extraction**.



2. Select the batch to be processed from the worklist and click **Select Scenario**. Select the appropriate corresponding scenario:
- **Direct Amp Punch**
  - Note: This scenario for **Direct Amp Punch** will skip the isolation step and lead straight into **Amplification Setup**.

Batches Worklist : 4						
	Selected	Create Date	Bar Code	Batch Type	Kit	Custodian/Location
	<input type="checkbox"/>	04/11/2025	BTE-250411-01	Bone and Tooth Extraction	Not Defined	In Lab
	<input type="checkbox"/>	02/25/2025	E2L-250225-01	E22 Lysis	Not Defined	In Lab
	<input type="checkbox"/>	05/01/2025	E2L-250501-01	E22 Lysis	Not Defined	Adrianne Schoefer
	<input checked="" type="checkbox"/>	06/29/2025	PPP-250629-01	Direct Amp Punch (partial plate)	Not Defined	Alicia Amatruda



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Required Batches		
Batch Type	Custodian/Location	Bar Code

Additional Instruments

Refresh

Select Scenario

Load Scenario

Print Scenario

Select Scenario (ScenarioSelectorForm)
×

Available Scenarios : 2

Scenario	Model	Default Directory	Comments
Copy of Direct Amp Punch			
Direct Amp Punch			

Select

Close

3. Scan the required barcodes highlighted blue. This will include the batch barcode, BSD barcode and/or Prep and Go Buffer (for swabs) barcode, as applicable.
4. Click **Start Process**.

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Optional	Instrument Name 1	Model 1	Bar Code 1
<input checked="" type="checkbox"/>	BSD Automated Puncher	BSD Duet Punch	BSD6005

Consumable List

Robot Bar Code  
Manual

Start Process

Complete Process

Close

5. Complete the tube check by scanning the sample barcodes.
6. A window will pop up to save the BSD file. Save in the folder BSD in the STACS Share folder on the U:drive. It should automatically open up at that folder.
7. When done, 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.

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Additional Instruments			
Optional	Instrument Name 1	Model 1	Bar Code 1

Consumable List

Robot Bar Code

Continue

**Complete Process**

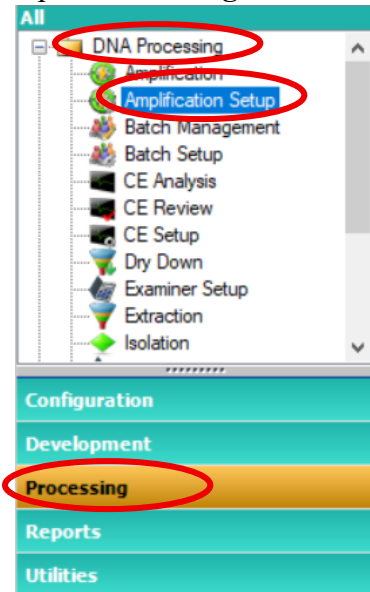
Close

☒ Process Successful
☐ Process Aborted
☐ Process Failed

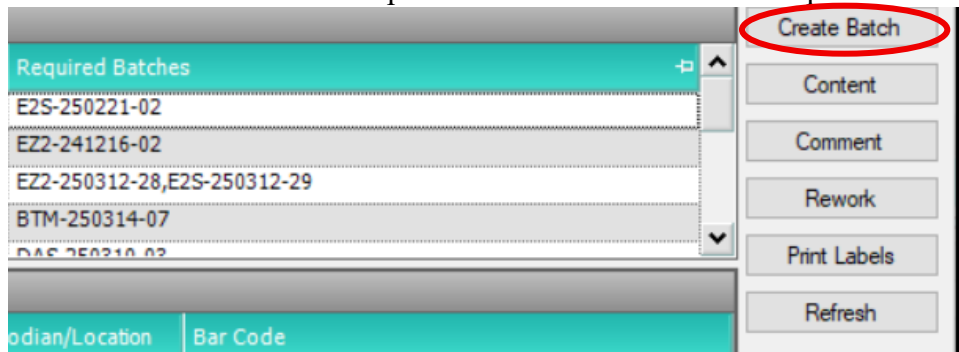
Batches : 1				
Bar Code	Process	Status	New Status	Batch C
PPP-250629-01	Success	Extraction Batch Create	Complete	

*Approved by Director: Dr. Guy Vallaro***Direct Amplification – GFE**

1. Open **Processing** → **DNA Processing** → **Amplification Setup**.



2. Click **Create Batch**. The Amplification Batch Create screen opens.



3. In the **New Batches** window, click **Create**.
4. Select a Batch Type (typically GFE) and click **Create**.
5. **Note: If no swabs are part of the set, only punches, select the 'no TE' which means no TE will be needed for the addition to the NEG.**

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Create Batch (CreateBatchForm)

Batch Type	Kit	Fill Order	Batch Bar Code
Globalfiler Express	Globalfiler Express	Vertical	Create

	1	2	3	4	5	6	7	8	9	10	11	12
A	L	DNA	DNA	DNA	DNA	DNA	L	DNA	DNA	DNA	DNA	DNA

6. Scan the newly created batch barcode into the **Destination Batch** field.
7. Scan the **Extraction Batch** barcode(s) in the **Source Batch** field.
8. Select Samples and Allocate onto the **Destination Batch**.
9. Select **Close**. If completed, please see **Step 16**.
10. Below will be a section of directions for when **Multiple Extraction Batches** can be merged together at this step.

11. Below is where Swabs can be merged with Punches.

- a. Batch Type '**Direct Amplification Swabs-No BIS**' should be for the **Swab Batch Type** to merge with punches as described in the beginning of the SOP.
- b. The "**Direct Amplification-Swabs**" could also be merged if picked accidentally, but an extra BIS will be included.
- c. Select **Create Batch**.

Selected	Create Date	Bar Code	Batch Type	Kit	Custodian/Location	Created By	Required Batches
<input type="checkbox"/>	02/21/2025	YFP-250221-05	Yfiler Plus	Yfiler Plus	In Lab	Frances Rue	E2S-250221-02
<input type="checkbox"/>	01/24/2025	GFA-250124-02	Globalfiler	Globalfiler	In Lab	Alicia Amatrua	E2Z-241216-02
<input type="checkbox"/>	03/12/2025	GFA-250312-59	Globalfiler	Globalfiler	In Lab	Angela Przech	E2Z-250312-28,E2S-250312-29
<input type="checkbox"/>	03/14/2025	GFA-250314-27	Globalfiler	Globalfiler	In Lab	Adrienne Schoefer	BTM-250314-07
<input type="checkbox"/>	03/10/2025	GFE-250310-04	Globalfiler Express	Globalfiler Express	In Lab	Sevasti Papakanakis	DAS-250310-03
<input type="checkbox"/>	03/12/2025	GFE-250312-65	Globalfiler Express	Globalfiler Express	In Lab	Angela Przech	PPP-250312-64
<input type="checkbox"/>	03/12/2025	GFE-250312-66	Globalfiler Express	Globalfiler Express	In Lab	Michael Morganti	PPP-250312-63
<input type="checkbox"/>	03/12/2025	GFE-250312-67	Globalfiler Express	Globalfiler Express	In Lab	Stephanie Lopez	PPP-250312-62
<input checked="" type="checkbox"/>	07/11/2025	GFE-250711-08	Globalfiler Express	Globalfiler Express	Cheryl Carreiro	Cheryl Carreiro	DNB-250711-07
<input type="checkbox"/>	03/12/2025	YFP-250312-60	Yfiler Plus	Yfiler Plus	In Lab	Angela Przech	E2Z-250312-12

- d. On the next screen, **Amplification Batch Create** – Select **Create**. This is where you will select the batch type.
- e. If you are merging punches and swabs together; Select GlobalFiler Express. Click **Create** on the right.

*Approved by Director: Dr. Guy Vallaro*

Create Batch (CreateBatchForm)

Batch Type: Globalfiler Express Kit: Globalfiler Express Fill Order: Vertical Batch Bar Code: Create

	1	2	3	4	5	6	7	8	9	10	11	12
A	L	DNA	DNA	DNA	DNA	DNA	L	DNA	DNA	DNA	DNA	DNA
B	CNEG	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
C	Pos	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
D	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
E	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
F	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
G	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA
H	DNA	DNA	DNA	DNA	DNA	L	DNA	DNA	DNA	DNA	DNA	L

Show/Hide Grid Close

- f. A new batch barcode will print and scan the barcode into the **Destination Batch** field on the top right.
- g. Scan the Source Batch barcodes of the samples that are to be merged will be added one batch at a time.
  - i. **Scan 1<sup>st</sup> Source Batch.**
  - ii. Select Samples and click **Allocate**.
  - iii. Then **Scan 2<sup>nd</sup> Source Batch.**
  - iv. Select Samples and click **Allocate**.
  - v. Continue this process until all Batches are on the Amp Plate.

*Approved by Director: Dr. Guy Vallaro*

Source Batch		
PPP-250711-10		
Available Batches : 6		
Bar Code	Batch Type	Kit
DNB-250711-06	Direct Amplification Swabs - No BIS	Not Defined
E2S-250312-14	EZ2 Trace - Sperm	Not Defined
EZ2-250312-28	EZ1/2 Purification	Not Defined
EZ2-250312-48	EZ1/2 Purification	Not Defined
EZS-250312-49	EZ1 Trace - Sperm	Not Defined
PPP-250711-10	Direct Amp Punch (partial plate)	Not Defined

12. In the image below the first source batch (PPP-250711-10) above has been added and the second source batch (DNB-250711-06) is ready to be allocated to that same plate.



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Sample Bar Code: [Redacted]

Samples For Batch 'DNB-250711-06' : 2

Action	Well	Bar Code	Lab Case Number	Exhibit Number	Lot Number	Index	Create Date	Custodian/Location	Rework
Globalfiler Express	C01	250105			BUCCAL		07/11/2025	Cheryl Carreiro	
Globalfiler Express	E01	CC033	CLC-250711-2332	1-1-1			07/11/2025	Cheryl Carreiro	

Destination Batch 2

Destination Batch

[Redacted]

1 2 3 4 5

A L DNA DNA DNA DNA

B NE DNA DNA DNA DNA

C Pos DNA DNA DNA DNA

D Blank DNA DNA DNA DNA

E BIS DNA DNA DNA DNA

F DNA DNA DNA DNA DNA

G DNA DNA DNA DNA DNA

H DNA DNA DNA DNA DNA

Allocate

13. After samples are allocated in STACS extra ladders can be removed by right clicking the green **L** and select “**clear well**”. This also can be done with plates that are not merged together.
14. When finished; **Save** the batch and click **Complete** at the top. The below image is a plate with a punch sample and a swab sample. Remember to click **Complete**.

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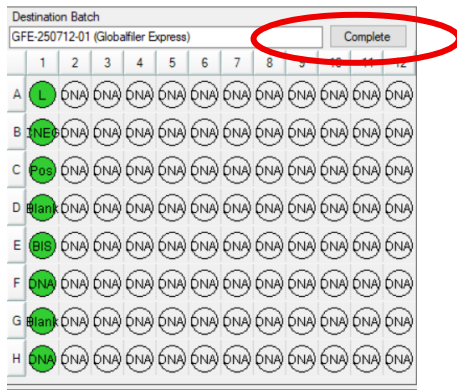
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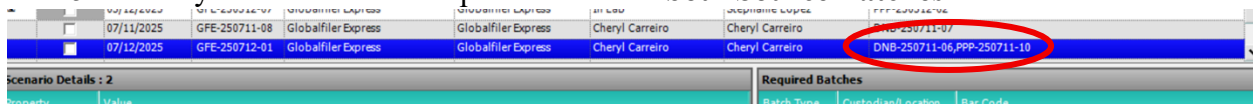
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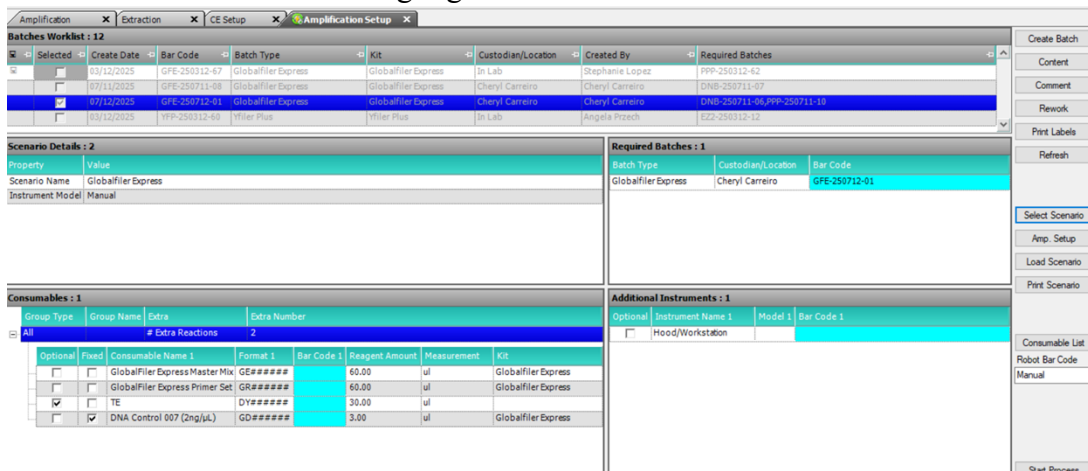


15. Below you will see that the plate above has **both Source Batches** listed.



16. Whether it is a merged plate, a punch plate or swab plate, the next steps are as follows:


- In **Amplification Setup**;
- Select the newly made batch.
- Select **Scenario**. It will pre-populate the scenario with the GFE process.
- Scan all blue highlighted fields as shown below:



- Select **Start Process**.
  - When finished with Amplification select **Complete Process**.
17. The remaining steps of Amplification and CE can proceed as described in the DNA Unknown Processing sections (e.g., STACS SOP-6 and SOP-7).

*Approved by Director: Dr. Guy Vallaro***Knowns – EZ2**

1. **Except as noted below**, Known EZ2 processing is identical to the DNA Unknown Processing sections (STACS SOP-3, -5).
2. **Batch Setup:** Select **EZ2 Lysis** as the Batch type. Select **Known** for Evidence Classification.


 Create Batch (CreateBatchForm)

Batch Type	Evidence Classification	Kit
EZ2 Lysis	Known	Not Defined

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
A	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA	DNA

3. **Extraction:** When selecting a scenario, select **Knowns Non-whole Blood (i.e., buccals)** or **Knowns Whole Blood (i.e., blood)**.

 Select Scenario (ScenarioSelectorForm)

**Available Scenarios : 4**

Scenario	Model	Default Directory
EZ1/2 Hair Lysis		
EZ1/2 Lysis Knowns (non-whole blood)		
EZ1/2 Lysis Knowns (Whole Blood)		
EZ1/2 Lysis Unknowns (non-diff)		

4. **Quantitation Setup:** In the ‘create batch’ window, select all the known samples and click **Send to ES (Examiner Setup)** to bypass quantitation.

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New Batches : 4			
Bar Code	Batch Type	Kit	Custodian/Location
QTR-250313-44	Quant Trio	Quant TR10	In Lab
QTR-250414-04	Quant Trio	Quant TR10	In Lab
QTR-250414-05	Quant Trio	Quant TR10	In Lab
QTR-250613-01	Quant Trio	Quant TR10	Cheryl Carreiro

< >

Create Content Comment Rework

Source Batch

Available Batches : 1

Bar Code	Batch Type	Kit	Custodian/Location
EZ2-250224-02	EZ1/2 Purification	Not Defined	In Lab

< >

Content Sample List Comment Rework

Dilute Discontinue

Send to ES