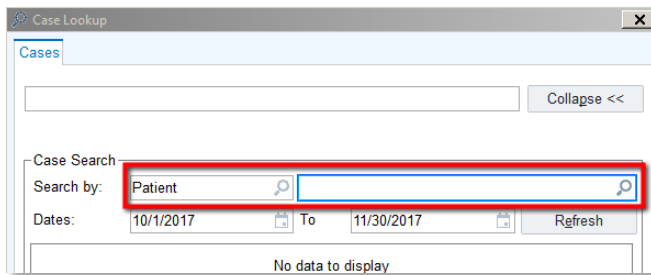


Grossing-Surg Path Beaker AP Guide:

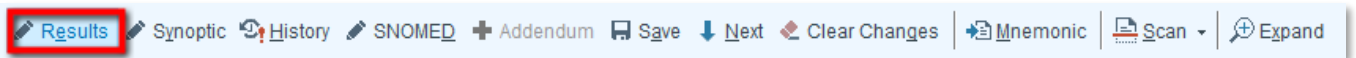
Entering Clinical History in Case Results:

Case Results:

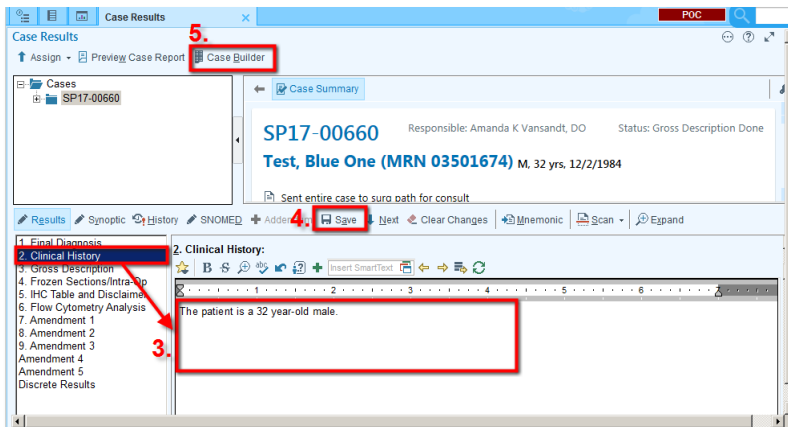
1. The first step when working on a case is entering the clinical history for the case before you start the gross. There are several ways to open a case in **Case Results**.
 - a. The most efficient way to enter **Case Results** is to scan the specimen's barcode while you are viewing the **Outstanding List**.
 - b. If you have the Case ID# and do not have a barcode, you can click on the **Case Results** link on your dashboard and type Case ID# in first field.
 - i. Alternately, you can search by Patient name in this window by clicking the **Expand** button. Search for the patient's name (Format: Lastname, Firstname).



2. When **Case Results** opens, click on the **Results** button in the middle of the screen.



3. On the left side of the screen, make sure **2. Clinical History** is selected, and enter text for the Clinical History. Alternatively, say Dragon command: "Clinical History"
 - a. Input patient's clinical history by stating age, sex, etc. Alternatively, say Dragon command: "Patient Info"
4. Click on the **Save** button.



5. After you save the Clinical History, you can start the gross by going directly into **Case Builder** via the **Case Builder** button. Alternatively, say Dragon command: "Start case"

Entering the Gross in Case Builder:

Assigning Roles and Reviewing Case Comments:

1. If you did not enter **Case Builder** directly from **Case Results**, there are variety of ways to start **Case Builder**.
 - a. You can click on the **Case Builder** button at the top of your screen and scan your barcode label directly or enter the Case ID # manually.
 - b. You can select the case in the Outstanding List, and click the Case Builder button that is located right above the list of specimens. Alternatively, say Dragon command: "Start case"
2. Once you are in **Case Builder**, check to make sure that you assign the case to yourself as the grosser. If Resident Pathologist has not been assigned, put their name in the User Assigned field and choose Resident Pathologist in the Role field so that it pops on their list the next morning.
3. You need to assign yourself as the "Grosser." Click in the next empty row.
 - a. In the **User Assigned** field, type part of your first or last name and it will try to autofill the full name.
 - b. In the **Role** field, choose "Grosser".

Case Builder

✓ Accept Accept & Stay Clear Changes Intra-op Grossing Case Results Holds Labels & Docs

Case type:

Case number:

Users Assigned	Role
JACKMAN, ANGELICA	Grosser
BEAKER, HERBERT V	Staff Pathologist

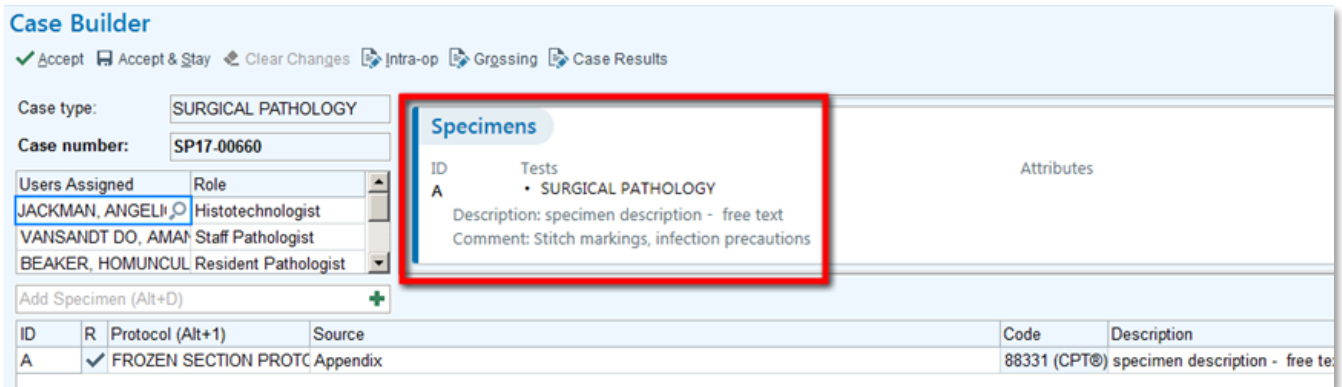
Add Specimen (Alt+D)

ID	R	Protocol (Alt+1)	Source	Code
A	✓	FROZEN SECTION PROTC	Appendix	88331 (CPT®)

Case Summary

Procedure: APPENDECTOMY
Surgeon: Daniel O Herzig, MD (Primary)
Pre-op Diagnosis: sick
Comment: Clinical indications

- Using the Case Summary section of **Case Builder** (right side), scroll down until you find the **Specimens** section. Make sure to read the **Description** and **Comments** in this section. If during accessioning the Description and Comments fields were not used, then nothing will show below the Specimen ID and Tests.

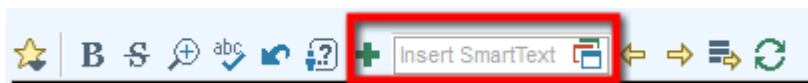


Grossing in Quick Results:

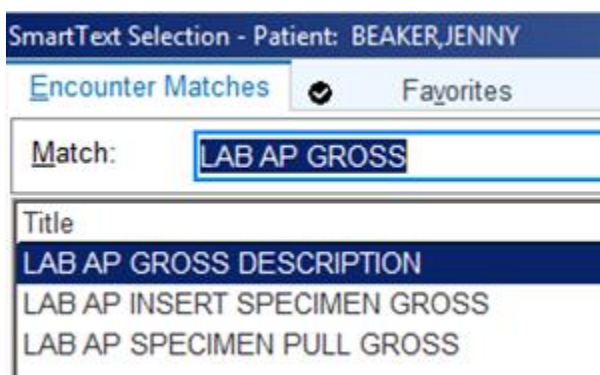
- Click on the **Grossing** button to start the gross. Alternatively, say Dragon command: "Start gross"
- This will bring up the **Quick Results** window. Make sure the **2. Gross Description** tab is selected at the top of the window.



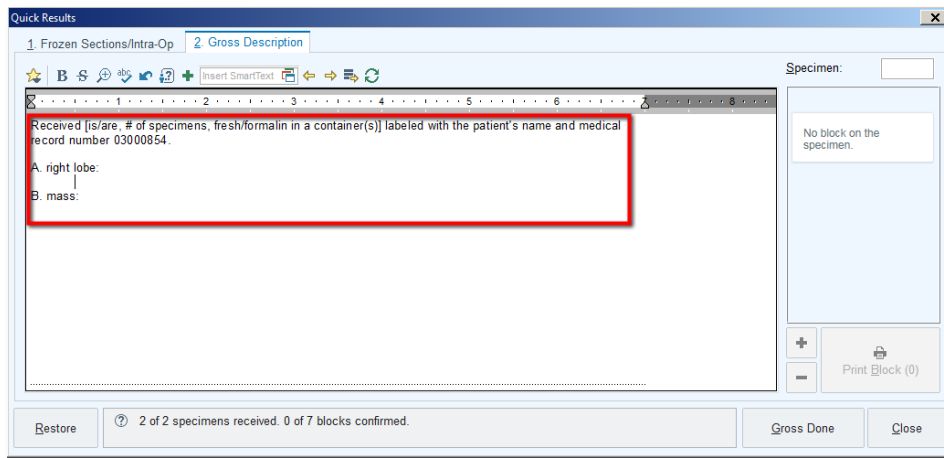
- To pull in all the headers and initial statement in the gross, click in the **Insert SmartText** field and type "LAB AP GROSS". Speak Dragon Command: "Case Header"



- In the SmartText Selection window, choose the "LAB AP GROSS DESCRIPTION" and click the Accept button.

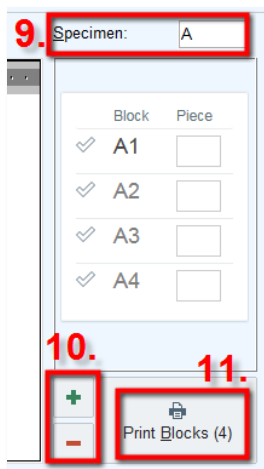


8. Use Dragon keywords or edit the text manually to fill out the editable sections of the SmartText.



Adding/Deleting and Printing Cassettes:

9. To view cassettes for a specimen, click on the **Specimen** field on the right side of the Quick Results window. Type "A" and type Enter. You can also type in "B", "C", etc. Alternatively, say Dragon command: "Specimen A", "Specimen B", etc.



10. This will show all the cassettes for this specimen. Click the "+" or "-" buttons to add or remove cassettes as needed. Alternatively, say Dragon command: "Add Block" or "Delete Block"

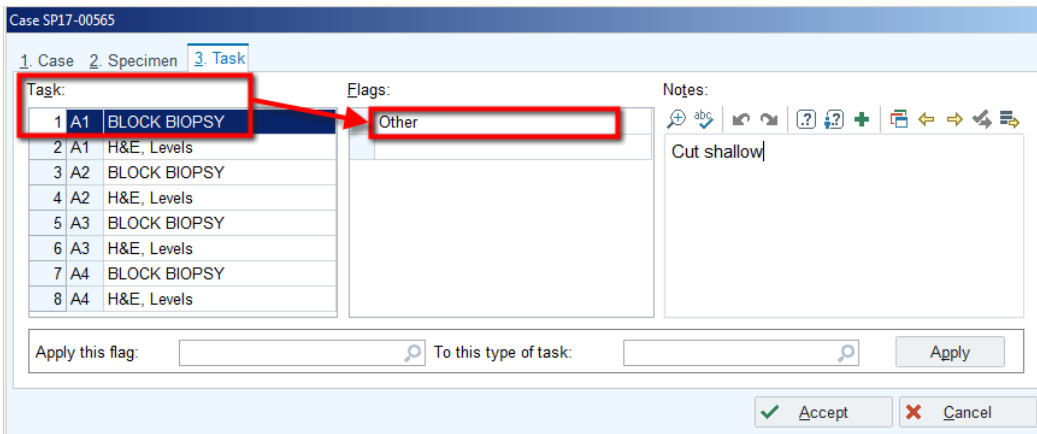
11. Once you have the correct number of cassettes listed, then click the **Print Blocks** button. Alternatively, say Dragon command: "Print Blocks"

12. In the **Pieces** fields next to each Block listed, if the sample is a biopsy then you can enter the actual number of pieces. This field only allows for numeric values so if there are multiples for each block, type in "123". If it is not a biopsy, leave the **Pieces** fields empty.

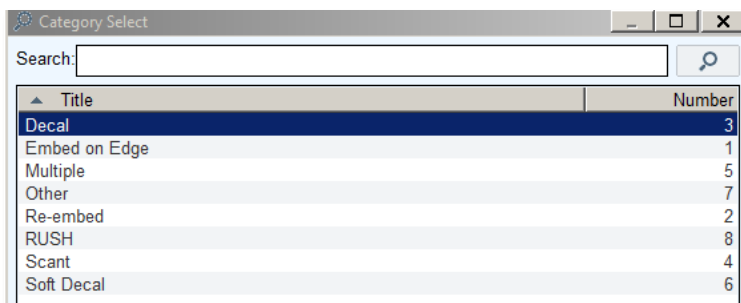
- a. You can also just scan a specimen block multiple times and it will automatically increase the piece out by one.

Adding Cassette Flags and Notes:

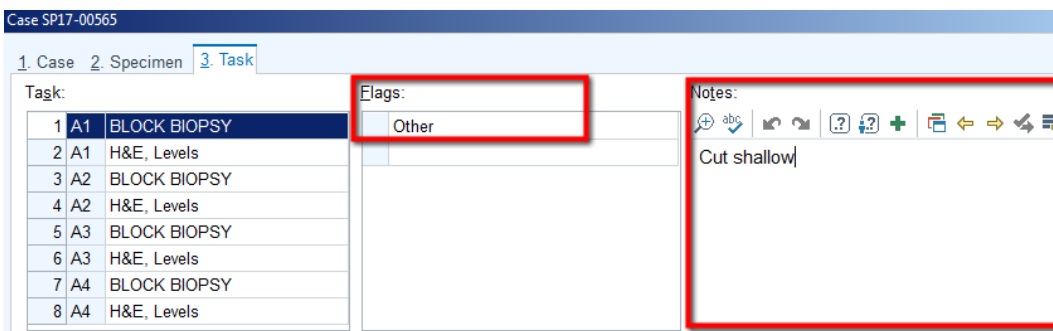
13. To add **Flags** or customizable free text **Notes** to each cassette, click on the Block ID (A1, A2, etc.). That will bring up a Flag and Notes window for that particular case.



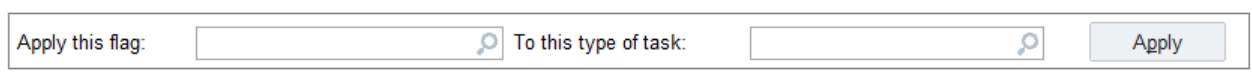
14. The cassette you picked should already be highlighted, but confirm that the selection is correct. In the **Flags** column, click on an empty row and then click on the magnifying glass icon. This will allow you to pick off a list of preset **Flag** options. Choose one and click the **Accept** button.



15. If you want to type in a text note, you can choose the **Flag** category of "Other". This will allow you to type a longer free text message in the Notes field.



16. If you want to apply a certain Flag to multiple tasks at once, you can use the **Apply this flag** field on the bottom of the window to choose a flag, and then use the **To this type of task** field to choose a type of task (Ex. All Block Biopsy). Click the **Apply** button to confirm your multiple flag choices.

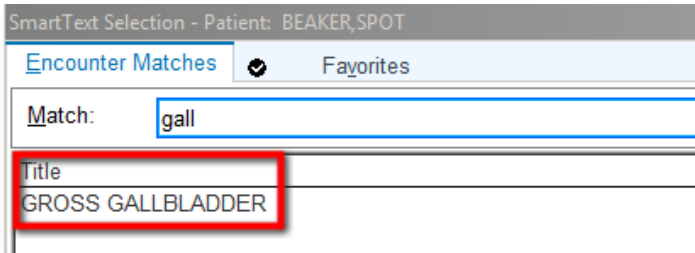


Adding Templates:

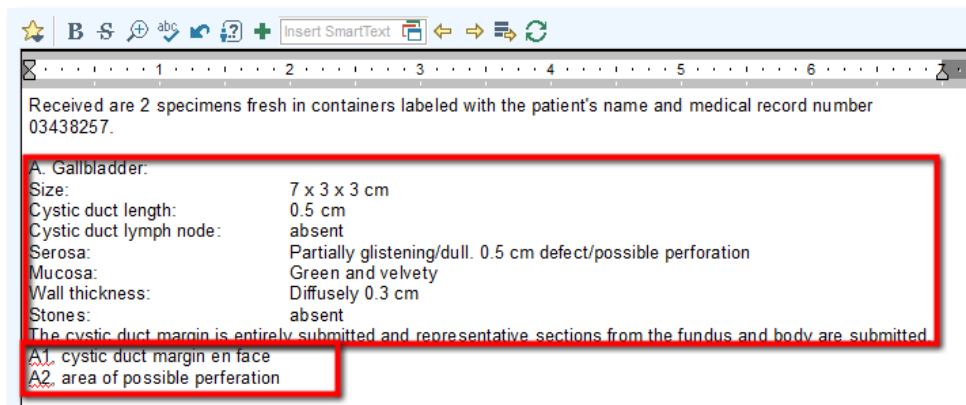
1. Make sure your cursor is under the header text we inserted in the Gross Description window. Use the Insert SmartText field to type part of the name for the gross Smarttext you want to enter.



2. Select the SmartText/template you want to insert, and click the **Accept** button.



3. Edit the text with Dragon or type text manually. Type the cassette index directly under the gross template text.




4. When you are done entering information into the templates, verify your information is correct. Below the text for the last cassette index, type your initials in parenthesis: Ex. (AMJ).

Alternatively, say Dragon command: "Insert my initials"

B1, margins en face
B2-5, lesion
B6, normal

(AMJ)

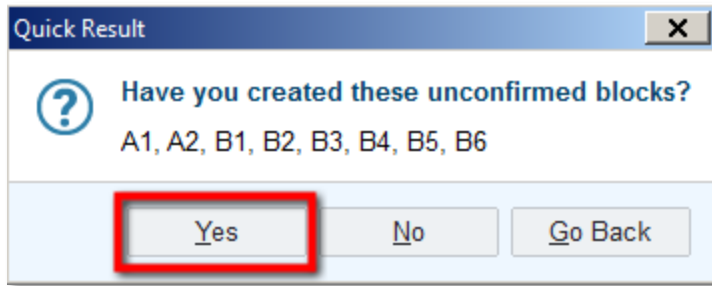


If you need to leave the Quick Results window to look up information in other activities, use the Close button and NOT the Gross Done button! To come back to the Gross Description, return to Case Builder and click the  **Grossing** button again.

5. When you are completely done with the gross, press the **Gross Done** button.

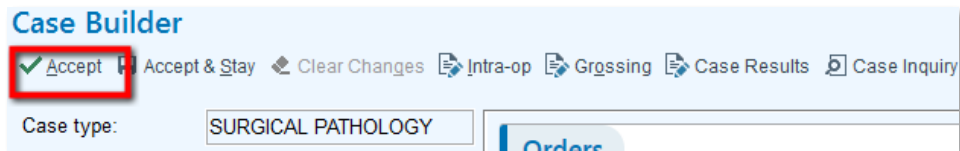
Alternatively, say Dragon command: "End Gross"

- A message will come up: Have you created these unconfirmed blocks? Click on the **Yes** button.



NOTE: This step will also advance the **Case Status** from **Accessioned** to **Gross Description Done**.

- You will return to the **Case Builder** window. Click the **Accept** button to close the **Case Builder** window. Alternatively, say Dragon command: "Accept Gross"



- If the **Case Result** window is still open, close the window by pressing the blue X in the top right below the search box.

Alternatively to execute steps 5-7, say Dragon Command: "End Case".



NOTE: Dragon commands "End Gross" and "End Case" only works the first time when confirming "Gross Done".

Tracking:

1. To track which cassettes are filled, open the **Tracking** activity by clicking on **Tracking** link on the Beaker AP Lab Dashboard.

The screenshot shows the 'Tracking - Specimen Tracking - 1 of 1 selected' window. At the top, there is a toolbar with 'Refresh', 'Views', 'Remove', 'Lookup', 'Inquiry', and 'Results' buttons. Below the toolbar are input fields for 'Case:', 'Specimen:', and 'Batch/Packing List:'. A table below these fields shows a single entry: 'SP17-00553 C2 | Indian, Ocean | BLOCK, H&E | Pathologist... | 10/10/2017 10:35'. To the right of the table is a detailed view for 'SP17-00553' with patient information: 'Indian, Ocean (MRN 03440069)', 'F, 60 yrs, 6/17/1957', 'Location: UHS 14A GENERAL SURG, 16, 01', and 'Responsible: Rita M Braziel, MD'. Below this is a table of tracking events for 'SP17-00553 C2'. The 'Reason' field is set to 'Filled'. A 'Track' button is at the bottom right.

Container	Patient	Task	Status	Order Date/Time
SP17-00553 C2	Indian, Ocean	BLOCK, H&E	Pathologist...	10/10/2017 10:35

SP17-00553 Status: Pathologist Review Complete
Indian, Ocean (MRN 03440069)
F, 60 yrs, 6/17/1957
Location: UHS 14A GENERAL SURG, 16, 01
Responsible: Rita M Braziel, MD

Reason: Filled

Date	Tracked	User	Location
01/03/2018			
1112	Tracked	Herbert West Beaker	LAB SURG HWSA5079
			Filled
1111	Tracked	Herbert West Beaker	LAB SURG HWSA5079
			Filled
11/30/2017			
1551	Tracked	Angelica Jackman	LAB SURG GENERICWORKSTATION
			Filled
1548	Tracked	Angelica Jackman	LAB SURG GENERICWORKSTATION
			Filled
1543	Tracked	Angelica Jackman	LAB SURG GENERICWORKSTATION
			Filled
			decal

2. Click the magnifying glass next to the Reason field. Choose **Filled**.
3. Click the **Lookup** button on the toolbar. The **Case**, **Specimen** and **Batch/Packing List** fields will appear.
4. Click in the **Case** field.
5. Scan the cassettes with a barcode scanner. Click the **Track** Button.

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