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MAESTRO
CARE

QUICK START GUIDE

BEAKER
CLINICAL PATHOLOGY

DukeMedicine

For more information, visit **maestro.duke.edu**

Table of Contents

Online Resources

Online resources for Maestro Care include documents referenced in this class, **Quick Tip** sheets, and other supplemental training materials. You can view these resources from any computer via the Maestro Care website:

https://maestro.duke.edu

Accessing the Maestro Care Playground

You can use the playground to practice using the Maestro Care application. To access the playground, follow the steps below.

To Access from a PIN Workstation

- Login to the Pin Workstation as you normally do.
- In the lower left corner, click **Start.**
- On the menu that opens, select **Training** then select **Maestro Care** and then select **Playground.**
- When the Maestro Care login screen displays, login with the IDs from the log ins provided that you received in class.

Note: Be aware that other class attendees may use the same logins for Playground.

For issues with Playground on a PIN Station or on the AWI website, **DHTS Service Desk @ 919-684-2243**

Clinical Pathology – Playground Logins

Lab Tech:

IDs: trn93610 – trn93639
(log in as any user in this range of IDs)
Password: Train2

Lab Supervisor:

IDs: trn13730 – trn13749
(log in as any user in this range of IDs)
Password: Train2

Admin Assistant:

IDs: trn74200 – trn74219
(log in as any user in this range of IDs)
Password: Train2

Phlebotomist:

IDs: trn73970 – trn74009
(log in as any user in this range of IDs)
Password: Train2

Micro Tech:

IDs: trn74320 – trn74349
(log in as any user in this range of IDs)
Password: Train2

Blood Bank Tech:

IDs: trn74080 – trn74099
(log in as any user in this range of IDs)
Password: Train2

Additional Log-ins:

IP Nurse: trn090
Outpatient Provider: trn061
Inpatient Provider: trn081

Clinical Pathology Patients:

Inpatients: Irene and Latoya

Outpatients:
Alicia/Beatrix/Brooklyn/Carlotta/
Charles/Doris/Gabriel/Hannah/
Juanita/Madison/Oliver/Sally/Victor

Getting Started

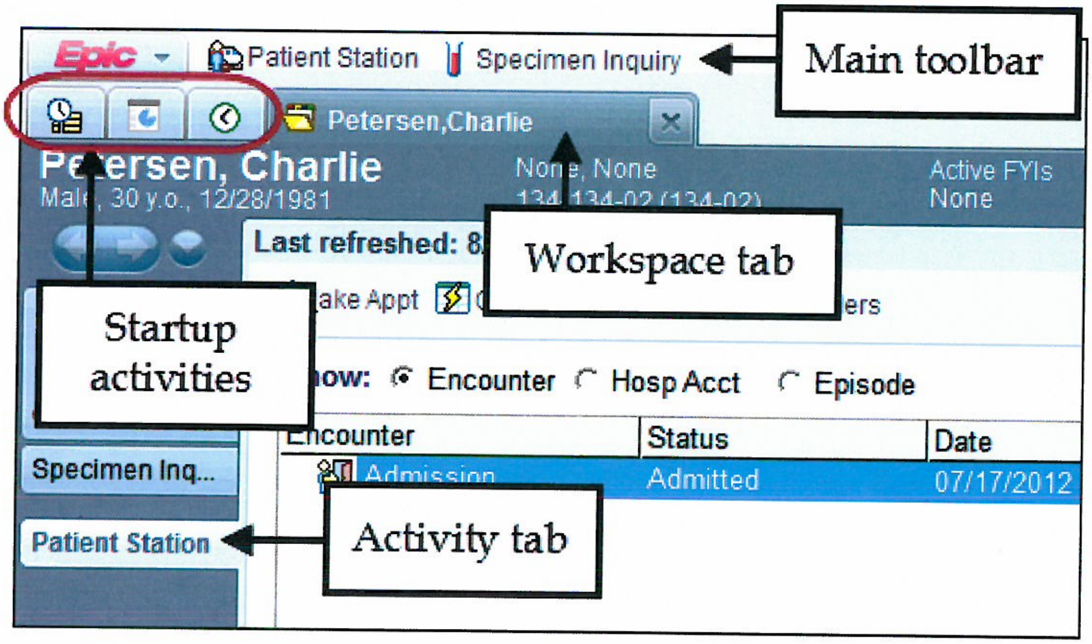
Welcome to Beaker Clinical Pathology, Epic's laboratory information system. This guide walks you through a lab tech's most common tasks in Epic.

Each organization configures Epic differently, so what you see in this guide might differ from what you see in your system.

Understand Epic terms

Throughout this guide, you'll see terms like activity and workspace used to refer to different parts of the screen. The image below shows examples of what these terms refer to, and the terms are defined on the following page.

Watch the *Overview of Hyperspace for Clinical Applications* e-learning lesson to learn more about how to navigate in the system.



Main toolbar

The main toolbar is the set of buttons that appear at the top of the screen. Using the buttons in the main toolbar, you can quickly open other activities, like Specimen Update or Patient Station.

Workspace

The tabs across the top of the screen represent different workspaces, such as your home page, a patient chart, and a patient visit. To view a workspace, select the corresponding tab.

You can have more than one workspace open at the same time, but you can view only one at a time.

Activity

An activity is a feature in Epic that supports a specific task, such as collecting specimens or entering test results. Activities are similar to tabs on a paper chart. An activity toolbar appears toward the top of most activities and includes buttons for the different actions you might need to take.

You can access activities from the tabs on the left side of a workspace, as shown below. Some of your frequently-used activities are also available from the main toolbar.

Startup activity

Startup activities automatically appear as workspace tabs when you log in to the system. Each startup activity appears in a separate home workspace. Your startup activities are meant to help you complete common tasks throughout your day.

As a lab tech, your startup activities are:

- Outstanding Specimen List ()
- Laboratory User Dashboard ()
- Receiving ()

Dashboard

A dashboard is a hub where you can view important information at a glance, like an outstanding specimen summary, and access commonly used reports and activities with a single click.

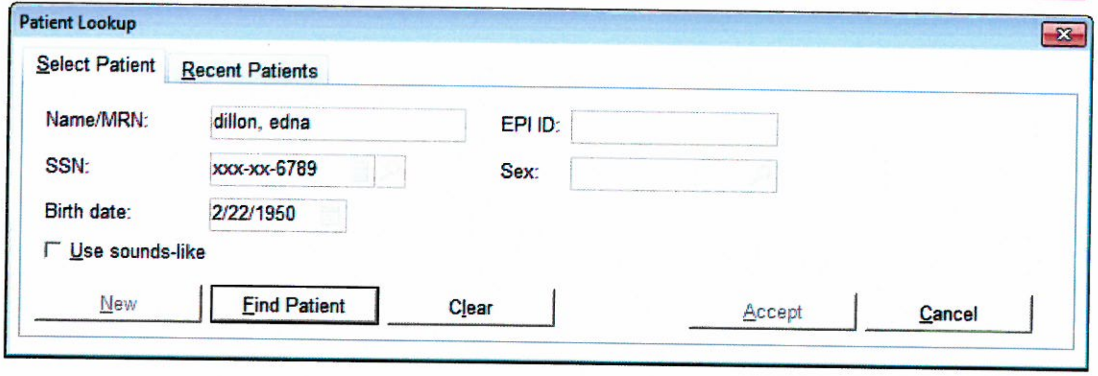
Look up a patient

1. On the Patient Lookup window, enter as much of the patient's information as possible.

> Search for a patient by entering her medical record number (MRN), or by entering her full name and Social Security number or birth date.
>
> If the patient doesn't want to provide her complete Social Security number, you can use the last four digits by entering * before the digits in the **SSN** field.

2. Press **ENTER**. If more than one patient matches the search criteria, the Patient Select window appears. Otherwise, the patient-specific activity opens.

> Review the Patient Select window carefully to be sure you choose the correct patient.



Name/MRN: dillon, edna
EPI ID:
SSN: xxx-xx-6789
Sex:
Birth date: 2/22/1950
☐ Use sounds-like

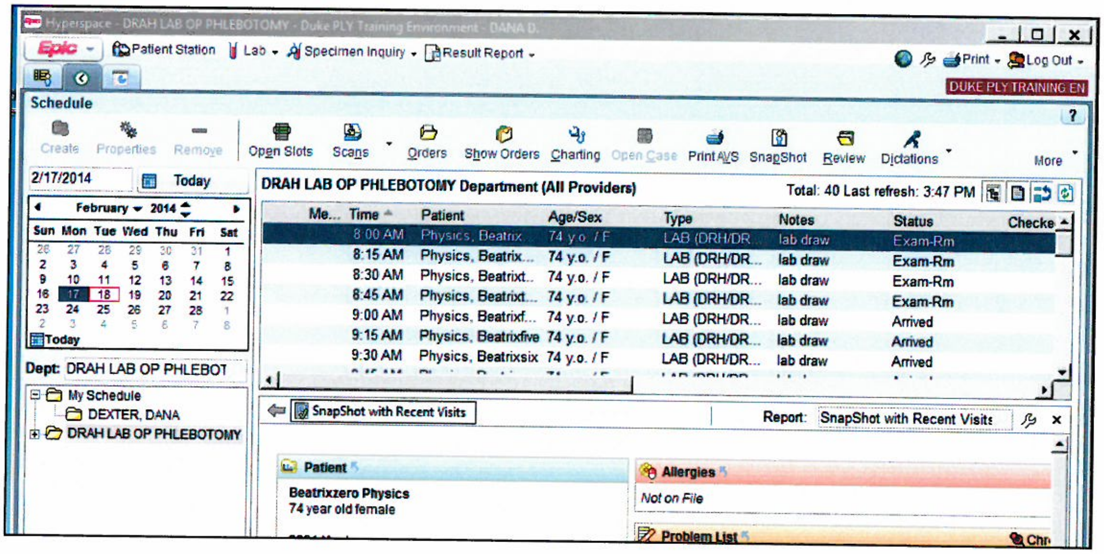
Collect Specimens

Collect an Outpatient Specimen

Identify which specimens to collect for a patient

When an outpatient arrives in the lab, use the Order Inquiry activity to view all of her orders.

1. If you're not already on the schedule, select the 🗓 tab.
2. Double-click the patient's name on the schedule. Order Inquiry opens.



DRAH LAB OP PHLEBOTOMY Department (All Providers)

Total: 40 Last refresh: 3:47 PM

Me...	Time	Patient	Age/Sex	Type	Notes	Status	Checke
	8:00 AM	Physics, Beatrix	74 y.o. / F	LAB (DRH/DR...	lab draw	Exam-Rm	
	8:15 AM	Physics, Beatrix...	74 y.o. / F	LAB (DRH/DR...	lab draw	Exam-Rm	
	8:30 AM	Physics, Beatrixt..	74 y.o. / F	LAB (DRH/DR...	lab draw	Exam-Rm	
	8:45 AM	Physics, Beatrixt...	74 y.o. / F	LAB (DRH/DR...	lab draw	Exam-Rm	
	9:00 AM	Physics, Beatrixf...	74 y.o. / F	LAB (DRH/DR...	lab draw	Arrived	
	9:15 AM	Physics, Beatrixfive	74 y.o. / F	LAB (DRH/DR...	lab draw	Arrived	
	9:30 AM	Physics, Beatrixsix	74 y.o. / F	LAB (DRH/DR...	lab draw	Arrived	

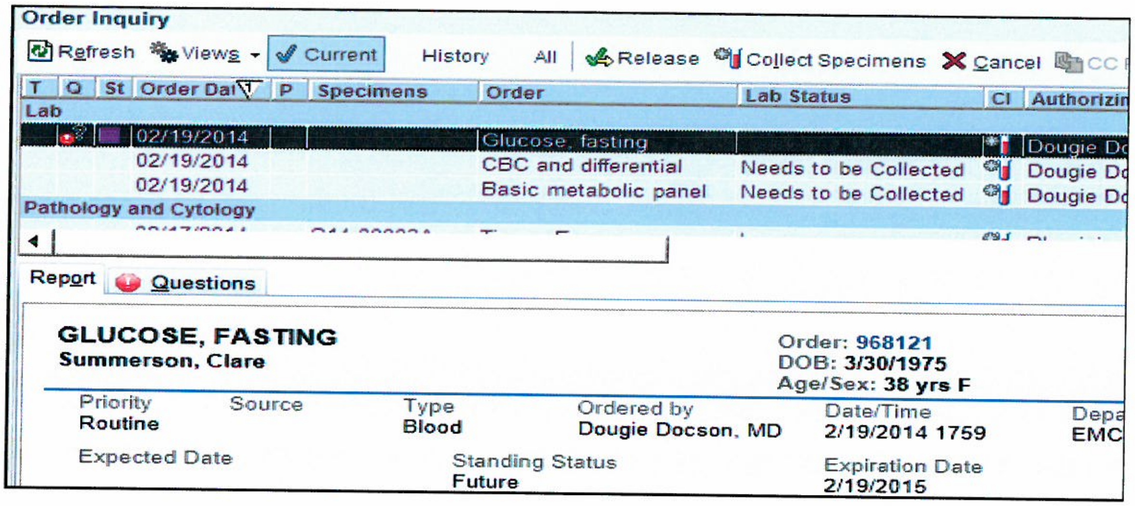
Beatrixzero Physics
74 year old female

Not on File

In Order Inquiry, you see a list of all of the patient's orders, including future and standing orders. Orders placed in different encounters and from different providers appear.

You can easily identify which orders still need to be collected by looking for the 🧪 icon in the Cl column.

If an order has a question associated with it, you see a ? icon in the Q column, and a Questions tab appears in the bottom section of the activity, where you can answer the related questions. If the question is required, a ❗ icon also appears in the report and on the Questions tab. When the required questions are answered, the ❗ icon disappears.



T	Q	St	Order Dat	P	Specimens	Order	Lab Status	Cl	Authorizin
Lab									
			02/19/2014			Glucose, fasting			Dougie D
			02/19/2014			CBC and differential	Needs to be Collected		Dougie D
			02/19/2014			Basic metabolic panel	Needs to be Collected		Dougie D
Pathology and Cytology									

GLUCOSE, FASTING
Summerson, Clare

Order: 968121
DOB: 3/30/1975
Age/Sex: 38 yrs F

Priority	Source	Type	Ordered by	Date/Time	Depa
Routine		Blood	Dougie Docson, MD	2/19/2014 1759	EMC

Expected Date	Standing Status	Expiration Date
	Future	2/19/2015

Collect a specimen

You can jump to Collect Specimens activity from Order Inquiry, and can collect one or more outpatient specimens at the same time. The activity includes a summary on the right side that indicates the number and types of tubes you need to collect and the order in which you should collect them.

1. In Order Inquiry, select an order.

- To select all of the orders at the same time, click anywhere in the list of orders and press **CTRL+A**.
- To select multiple orders that are not next to each other in the list, use **CTRL+CLICK**.
- To remove any selected orders, hold **CTRL** while clicking the orders you need to remove.

2. If there is a Questions tab in the bottom half of the screen for a particular test, select it and fill out the questionnaire.
3. Click **Collect Specimens**. The Collect Specimens activity opens.

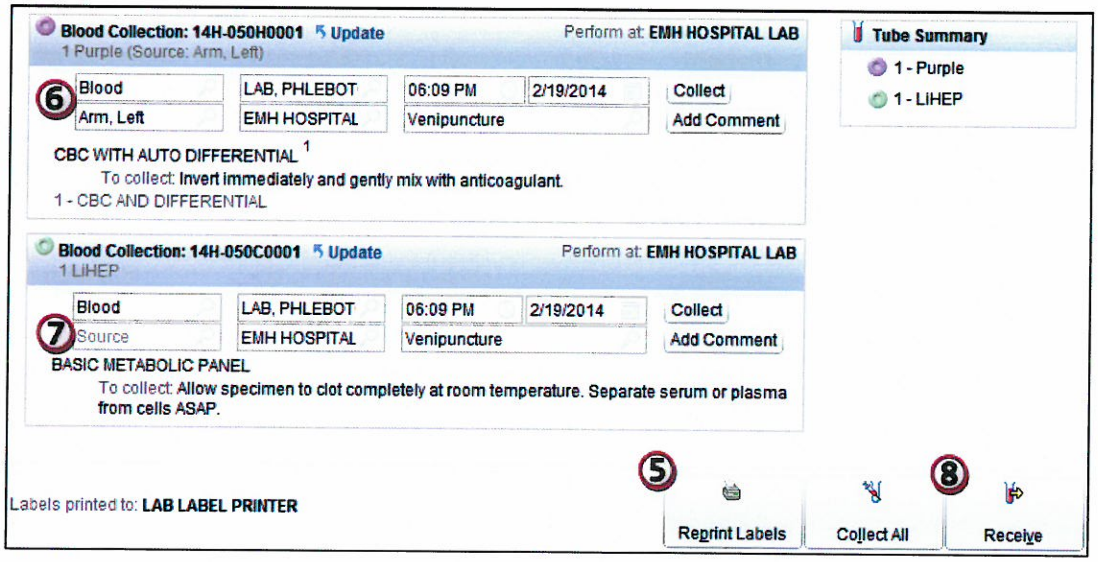
4. Review the collection information for each test and make sure it is correct. In particular, make sure the correct tests are listed and that the performing lab is correct.

   - If you selected any tests by mistake, remove them by clicking ✕ for those tests.
   - If you need to update the performing lab for a test, click on the blue hyperlink to open the **Update Performing Lab** window. You may also update the perfoming lab through the **Actions** drop down. In the Update Performing Lab section that appears, select the correct lab, select the check boxes next to the tests that should be updated, and then click **Update**.

5. Click **Print Labels**. The specimen ID is created, labels print, and collection fields appear for each of the tests. Note: The button name changes to **Reprint Labels**.
6. Enter collection information for each specimen.

   - Scan each specimen's barcode to add some of the collection information automatically.
   - If you are unable to scan a specimen, click **Collect** for that specimen instead.
   - Complete any fields that aren't automatically completed, like **Source** and **Draw type**.

7. Click **Receive**. The specimens are received into the lab and appear on the Outstanding List.



Blood Collection: 14H-050H0001 Update Perform at: EMH HOSPITAL LAB
1 Purple (Source: Arm, Left)
Blood | LAB, PHLEBOT | 06:09 PM | 2/19/2014
Arm, Left | EMH HOSPITAL | Venipuncture
CBC WITH AUTO DIFFERENTIAL [1]
To collect: Invert immediately and gently mix with anticoagulant.
1 - CBC AND DIFFERENTIAL

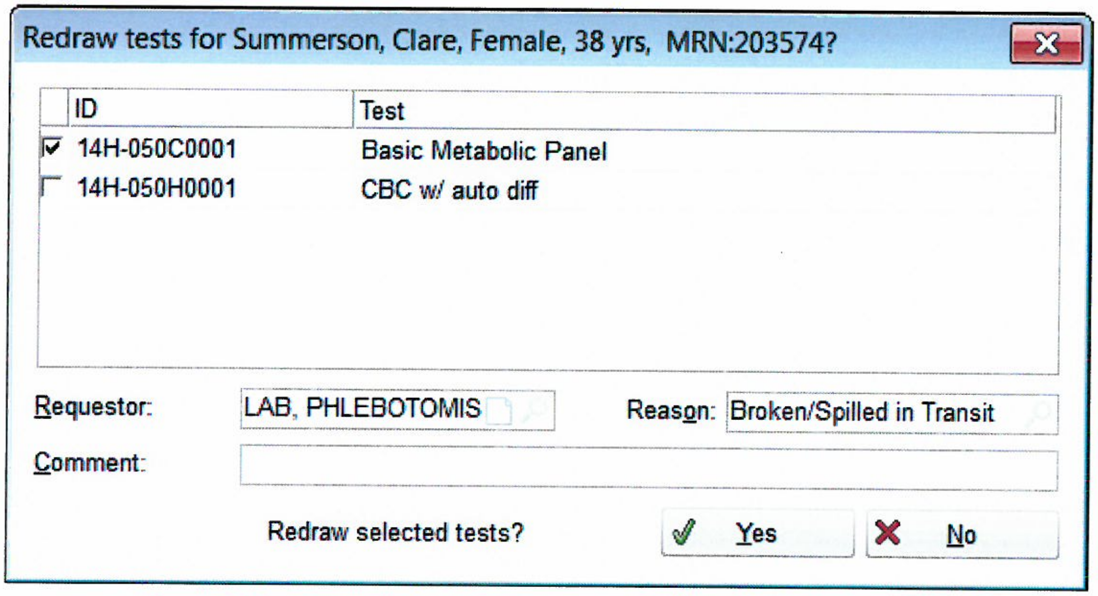
Blood Collection: 14H-050C0001 Update Perform at: EMH HOSPITAL LAB
1 LIHEP
Blood | LAB, PHLEBOT | 06:09 PM | 2/19/2014
Source | EMH HOSPITAL | Venipuncture
BASIC METABOLIC PANEL
To collect: Allow specimen to clot completely at room temperature. Separate serum or plasma from cells ASAP.

Tube Summary
1 - Purple
1 - LIHEP

Labels printed to: LAB LABEL PRINTER

Document a redraw

1. If you need to redraw a specimen and you're in the Collection activity, click Actions and select Redraw.
2. In the window that appears, select the tests you need to redraw for and enter a reason for the redraw.
3. Click ✓ Yes.
4. Collect the redraw specimen.



Redraw tests for Summerson, Clare, Female, 38 yrs, MRN:203574?

	ID	Test
☑	14H-050C0001	Basic Metabolic Panel
☐	14H-050H0001	CBC w/ auto diff

Requestor: LAB, PHLEBOTOMIS
Reason: Broken/Spilled in Transit
Comment:

Redraw selected tests?

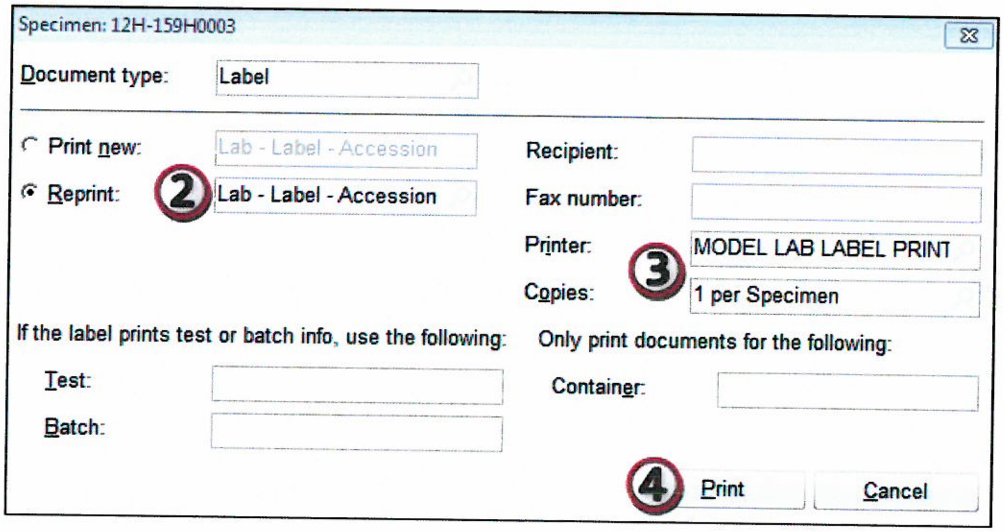
Reprint specimen labels

You can quickly print new specimen labels from the Collect Specimens activity. You might need to do this if the labels didn't print correctly the first time.

1. In the Collect Specimens activity, click **Reprint Labels.**
2. In the window that opens, select the printer you want to use. The printer you originally used is selected by default. To use a new printer, select the **Override label printer** check box and select the printer you want to use.
3. Click **Print.**

If you've already left the Collect Specimens activity, you can reprint from the Labels and Docs activity.

1. Go to **Epic button > Tools > Laboratory Tools > Labels and Docs.**
2. On the window that appears, select the **Reprint** option and select the type of label you want to print.
3. Select a printer and the number of copies you need.
4. Click **Print.**



Specimen: 12H-159H0003

Document type: Label

○ Print new: Lab - Label - Accession

● Reprint: Lab - Label - Accession

Recipient:

Fax number:

Printer: MODEL LAB LABEL PRINT

Copies: 1 per Specimen

If the label prints test or batch info, use the following:

Test:

Batch:

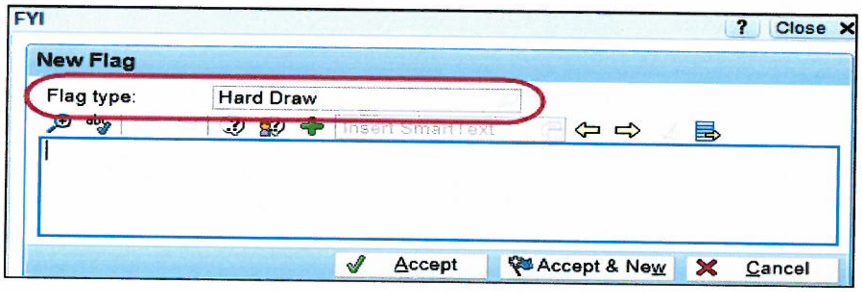
Only print documents for the following:

Container:

Notify others that the patient is a hard draw

If the patient is a hard draw, you can let others know by adding a patient flag. Patient flags are a notification tool that let other users know important information about the patient. You add patient flags from within the patient's chart.

1. Open the Order Inquiry activity for the patient.
2. In the bottom-left corner, click **More Activities** and select ⚑ **FYI** from the menu. The Patient FYI activity opens.
3. Click ⚑ **New Flag**.
4. In the **Flag type** field, completion match on Hard Draw.
5. Add a comment in the text box to provide additional information, if necessary.
6. Click ✓ **Accept**. The new flag appears in the list.
7. Click **Close** to exit the Patient FYI activity.



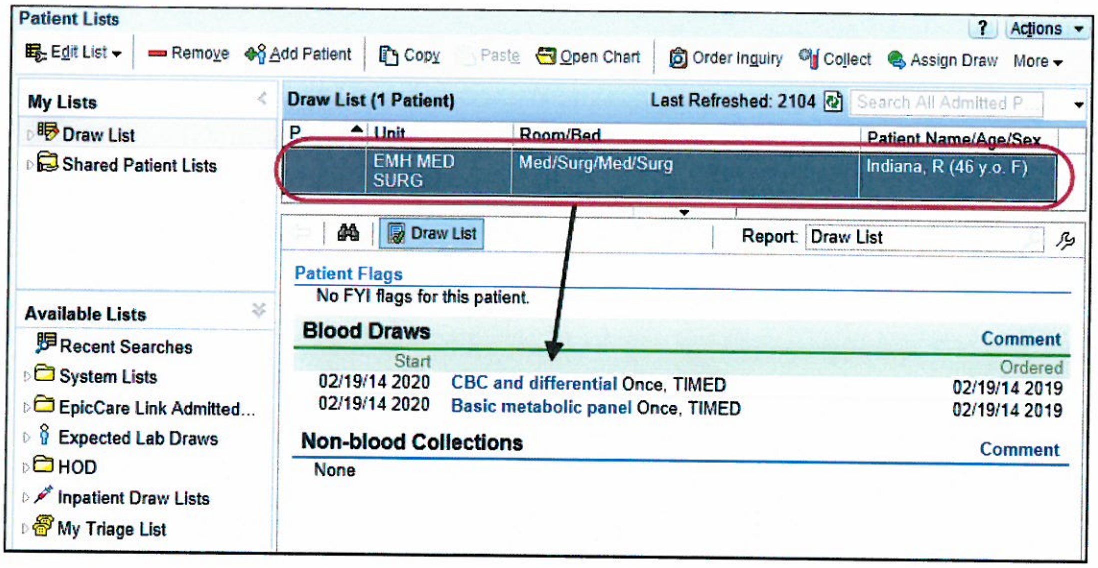
Flag type: Hard Draw

Collect an Inpatient Specimen

Find patients needing draws

1. Go to Patient Lists. If you're not already there, select the workspace tab. The draw list is open by default.

2. Select a patient in the list to review the specimens that must be collected and determine the patient's location.



EMH MED SURG | Med/Surg/Med/Surg | Indiana, R (46 y.o. F)

No FYI flags for this patient.

02/19/14 2020 CBC and differential Once, TIMED 02/19/14 2019
02/19/14 2020 Basic metabolic panel Once, TIMED 02/19/14 2019

None

Print labels and collect the specimen

When you are in the patient's room, print the barcode labels and collect the specimen.

1. Scan the patient's ID band to open Order Inquiry in the patient's chart.
2. Select the specimens that need to be collected.

- To select all of the orders at the same time, click anywhere in the list of orders and press **CTRL+A**.
- To select multiple orders that are not next to each other in the list, use **CTRL**+click.
- To remove any selected orders, hold **CTRL** while clicking the orders you need to remove.

3. If there is a **Questions** tab in the bottom half of the screen for a particular test, select it and fill out the questionnaire.
4. Click **Collect Specimens**. The Collection activity opens.

Receive Specimens

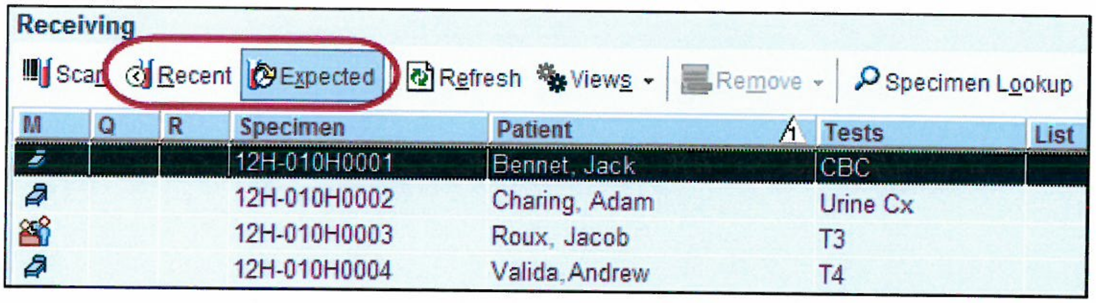
Record that a specimen has arrived at the lab

1. Select the workspace tab to open the Receiving activity.
2. Scan the label for each specimen you are receiving into the lab.
   - The collection information entered by the nurse or phlebotomist appears, and the specimen is automatically received into the lab.
   - The tests for the specimens you received now appear on the Outstanding List.

See expected and recently received specimens

You can see a list of all the specimens that are destined for your lab from the Expected view of the Receiving activity. To see a list of specimens that were recently received into the lab, use the Recent view.

1. In the Receiving activity, click the button for the view you want to open: **Expected** or **Recent**.
2. Click the Patient column header to sort the specimens by patient.



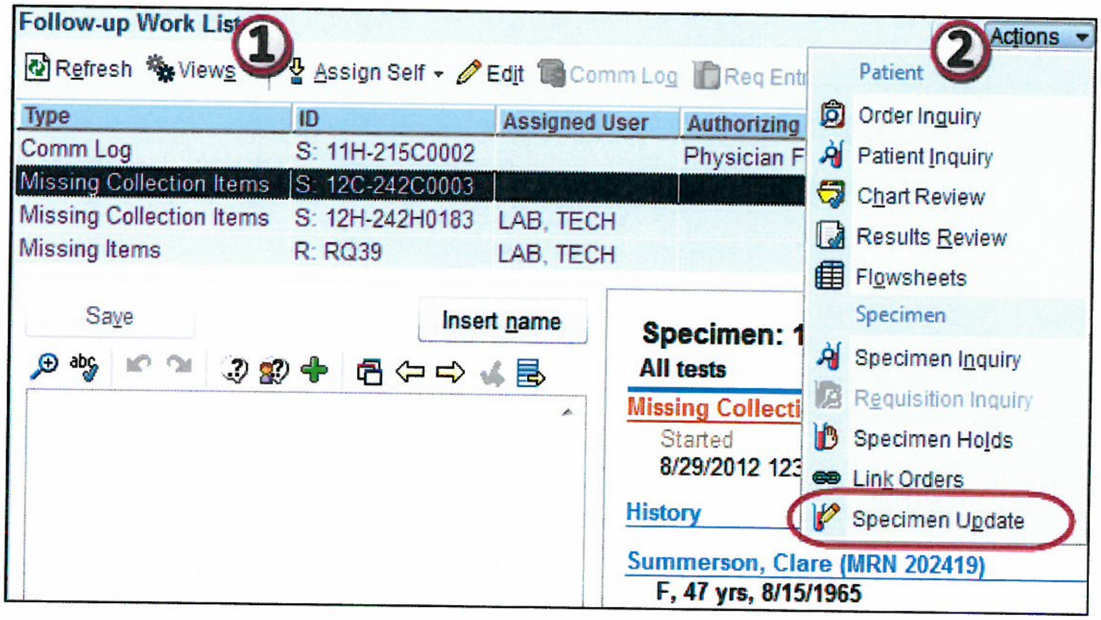
M	Q	R	Specimen	Patient	Tests	List
			12H-010H0001	Bennet, Jack	CBC	
			12H-010H0002	Charing, Adam	Urine Cx	
			12H-010H0003	Roux, Jacob	T3	
			12H-010H0004	Valida, Andrew	T4	

Enter missing collection information for a specimen

If required collection information is missing when you scan a specimen in the Receiving activity, a follow-up task is created automatically so that the necessary information can be updated. Any specimens that are flagged for follow-up appear on the Follow-up Work List. From the work list, you can assign tasks to yourself or others, and complete the necessary follow-ups.

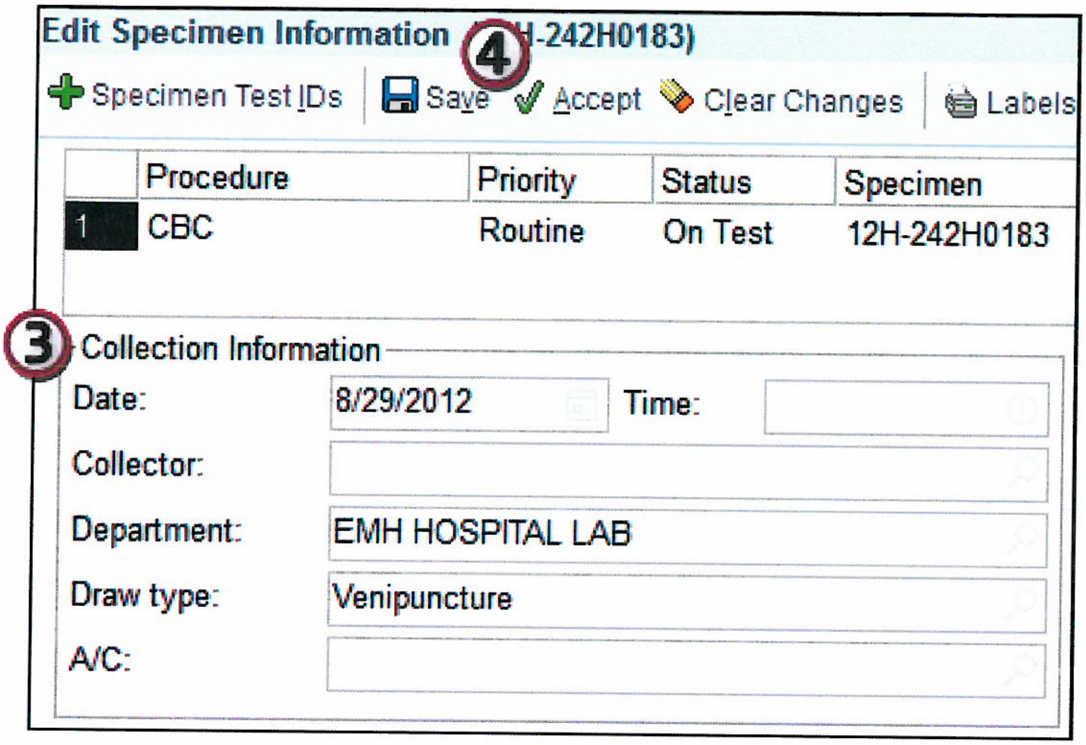
Specimens that are missing collection information have a follow-up type of Missing Collection Items. To enter the missing information:

1. Assign the task to yourself. Select the specimen and click **Assign Self** on the activity toolbar.
2. Click **Actions** in the top-right corner and select **Specimen Update**. The Specimen Update activity opens.



Type	ID	Assigned User	Authorizing
Comm Log	S: 11H-215C0002		Physician F
Missing Collection Items	S: 12C-242C0003		
Missing Collection Items	S: 12H-242H0183	LAB, TECH	
Missing Items	R: RQ39	LAB, TECH	

3. In the Collection Information fields, enter any required information that's missing.
4. Click **Accept**. You return to the Follow-up Work List.



	Procedure	Priority	Status	Specimen
1	CBC	Routine	On Test	12H-242H0183

Collection Information

Date: 8/29/2012 Time:

Collector:

Department: EMH HOSPITAL LAB

Draw type: Venipuncture

A/C:

5. Click ✓ **Complete** on the activity toolbar to indicate that the task is done.
6. Enter a comment in the window that appears and click ✓ **Accept**. The completed task disappears from the work list.

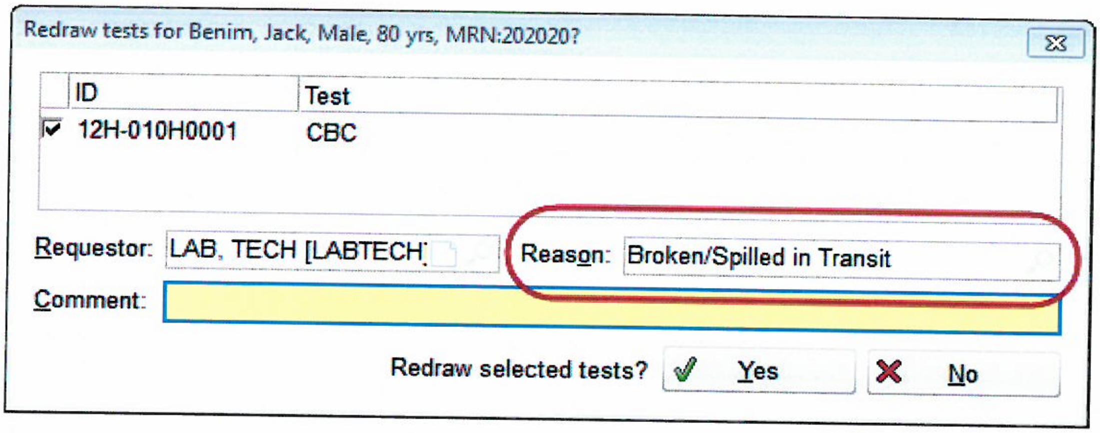
Cancel or redraw a specimen

If you can't use a specimen, you can either cancel the test or redraw the specimen. It is important to understand the difference between when you would cancel and when you redraw:

- *Cancel* a test if it is no longer needed or was entered in error (for example, if the wrong order was released in Order Inquiry).
- *Redraw* a specimen if the original is unusable (for example, if it was contaminated or spilled in transit).

The steps for canceling and redrawing are very similar. To cancel a test or redraw the specimen:

1. In the Receiving activity, select the specimen.
2. Click ✗ **Cancel** or **Redraw**, as appropriate.
3. On the window that appears, enter a reason.
4. Click ✓ **Yes**.



Redraw tests for Benim, Jack, Male, 80 yrs, MRN:202020?

	ID	Test
☑	12H-010H0001	CBC

Requestor: LAB, TECH [LABTECH]

Reason: Broken/Spilled in Transit

Comment:

Add tests to an existing specimen

If you can use an existing specimen for more than one test, you can add a test to the specimen from the Specimen Update activity.

1. From the Outstanding List, select the specimen and click **Specimen Update** on the activity toolbar.

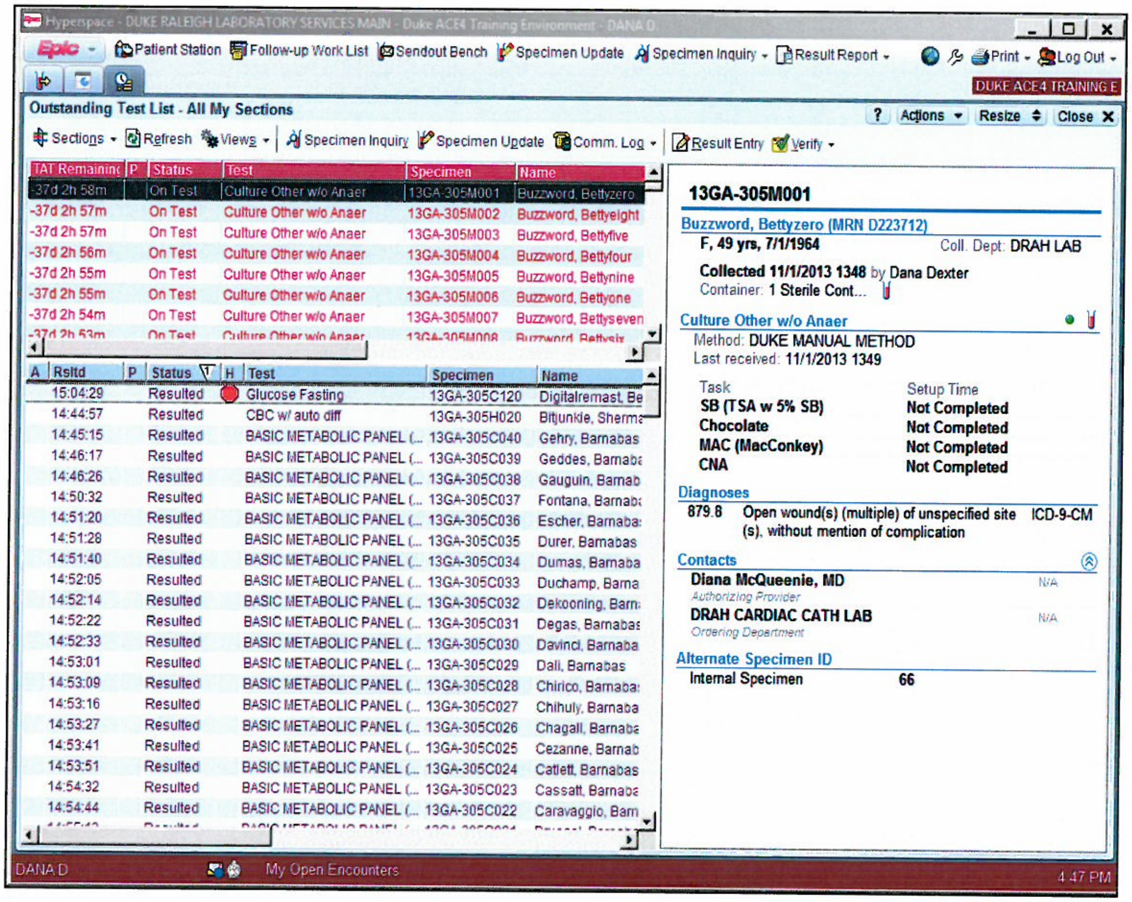
If the specimen is not on the Outstanding List, go to **Epic button > Lab > Specimen Update**, then scan the specimen label to open the Specimen Update activity.

2. Click **Add-ons** and select **New Orders**.
   - For non-requisition specimens, Order Entry opens.
   - For requisition specimens, Requisition Entry opens.
3. Enter the orders.
4. If you are in Order Entry, sign the orders.
5. Click **Accept** on the Specimen Update activity toolbar.

You can also add existing orders to a specimen. In Specimen Update, go to **Add-ons > Available Orders.** On the Add-ons window, select the order you want to add and click ✚ **Add Orders.** Click **Yes** at the prompt, then click ✓ **Accept** on the activity toolbar.

In Basket Add-Ons

When an physician for an admitted patient, enters a new order with a frequency of Add-on, a message is sent to your In Basket Orders folder. The Orders folder will be visable from your red tickler bar at the bottom of your screen, no matter what activity you are working in.



Outstanding Test List - All My Sections

TAT Remaining	P	Status	Test	Specimen	Name
-37d 2h 58m		On Test	Culture Other w/o Anaer	13GA-305M001	Buzzword, Bettyzero
-37d 2h 57m		On Test	Culture Other w/o Anaer	13GA-305M002	Buzzword, Bettyeight
-37d 2h 57m		On Test	Culture Other w/o Anaer	13GA-305M003	Buzzword, Bettyfive
-37d 2h 56m		On Test	Culture Other w/o Anaer	13GA-305M004	Buzzword, Bettyfour
-37d 2h 55m		On Test	Culture Other w/o Anaer	13GA-305M005	Buzzword, Bettynine
-37d 2h 55m		On Test	Culture Other w/o Anaer	13GA-305M006	Buzzword, Bettyone
-37d 2h 54m		On Test	Culture Other w/o Anaer	13GA-305M007	Buzzword, Bettyseven
-37d 2h 53m		On Test	Culture Other w/o Anaer	13GA-305M008	Buzzword, Bettysix

A	Rsltd	P	Status	H	Test	Specimen	Name
	15:04:29		Resulted	●	Glucose Fasting	13GA-305C120	Digitalremast, Be
	14:44:57		Resulted		CBC w/ auto diff	13GA-305H020	Bitjunkie, Sherma
	14:45:15		Resulted		BASIC METABOLIC PANEL (...	13GA-305C040	Gehry, Barnabas
	14:46:17		Resulted		BASIC METABOLIC PANEL (...	13GA-305C039	Geddes, Barnaba
	14:46:26		Resulted		BASIC METABOLIC PANEL (...	13GA-305C038	Gauguin, Barnab
	14:50:32		Resulted		BASIC METABOLIC PANEL (...	13GA-305C037	Fontana, Barnab
	14:51:20		Resulted		BASIC METABOLIC PANEL (...	13GA-305C036	Escher, Barnaba
	14:51:28		Resulted		BASIC METABOLIC PANEL (...	13GA-305C035	Durer, Barnabas
	14:51:40		Resulted		BASIC METABOLIC PANEL (...	13GA-305C034	Dumas, Barnaba
	14:52:05		Resulted		BASIC METABOLIC PANEL (...	13GA-305C033	Duchamp, Barna
	14:52:14		Resulted		BASIC METABOLIC PANEL (...	13GA-305C032	Dekooning, Barn
	14:52:22		Resulted		BASIC METABOLIC PANEL (...	13GA-305C031	Degas, Barnabas
	14:52:33		Resulted		BASIC METABOLIC PANEL (...	13GA-305C030	Davinci, Barnaba
	14:53:01		Resulted		BASIC METABOLIC PANEL (...	13GA-305C029	Dali, Barnabas
	14:53:09		Resulted		BASIC METABOLIC PANEL (...	13GA-305C028	Chirico, Barnaba
	14:53:16		Resulted		BASIC METABOLIC PANEL (...	13GA-305C027	Chihuly, Barnaba
	14:53:27		Resulted		BASIC METABOLIC PANEL (...	13GA-305C026	Chagall, Barnaba
	14:53:41		Resulted		BASIC METABOLIC PANEL (...	13GA-305C025	Cezanne, Barnab
	14:53:51		Resulted		BASIC METABOLIC PANEL (...	13GA-305C024	Catlett, Barnabas
	14:54:32		Resulted		BASIC METABOLIC PANEL (...	13GA-305C023	Cassatt, Barnaba
	14:54:44		Resulted		BASIC METABOLIC PANEL (...	13GA-305C022	Caravaggio, Barn

13GA-305M001

Buzzword, Bettyzero (MRN D223712)
F, 49 yrs, 7/1/1964 Coll. Dept: DRAH LAB
Collected 11/1/2013 1348 by Dana Dexter
Container: 1 Sterile Cont...

Culture Other w/o Anaer
Method: DUKE MANUAL METHOD
Last received: 11/1/2013 1349

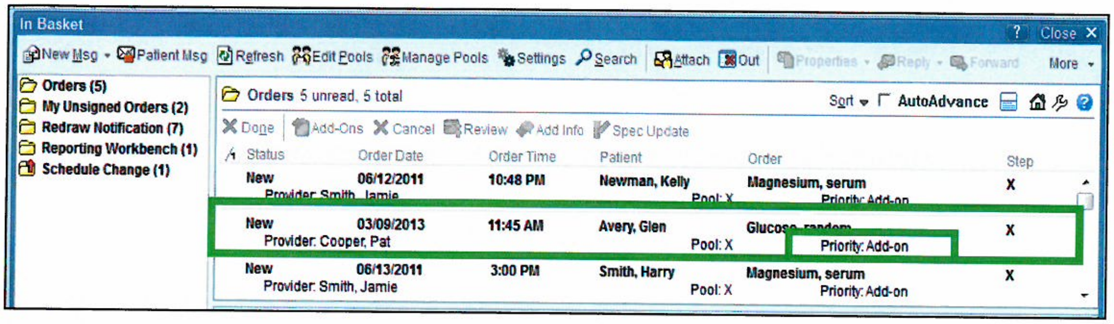
Task	Setup Time
SB (TSA w 5% SB)	Not Completed
Chocolate	Not Completed
MAC (MacConkey)	Not Completed
CNA	Not Completed

Diagnoses
879.8 Open wound(s) (multiple) of unspecified site (s), without mention of complication ICD-9-CM

Contacts
Diana McQueenie, MD N/A
Authorizing Provider
DRAH CARDIAC CATH LAB N/A
Ordering Department

Alternate Specimen ID
Internal Specimen 66

1. Select the **Orders** icon from the tickler bar. (The In Basket Orders folder opens.)



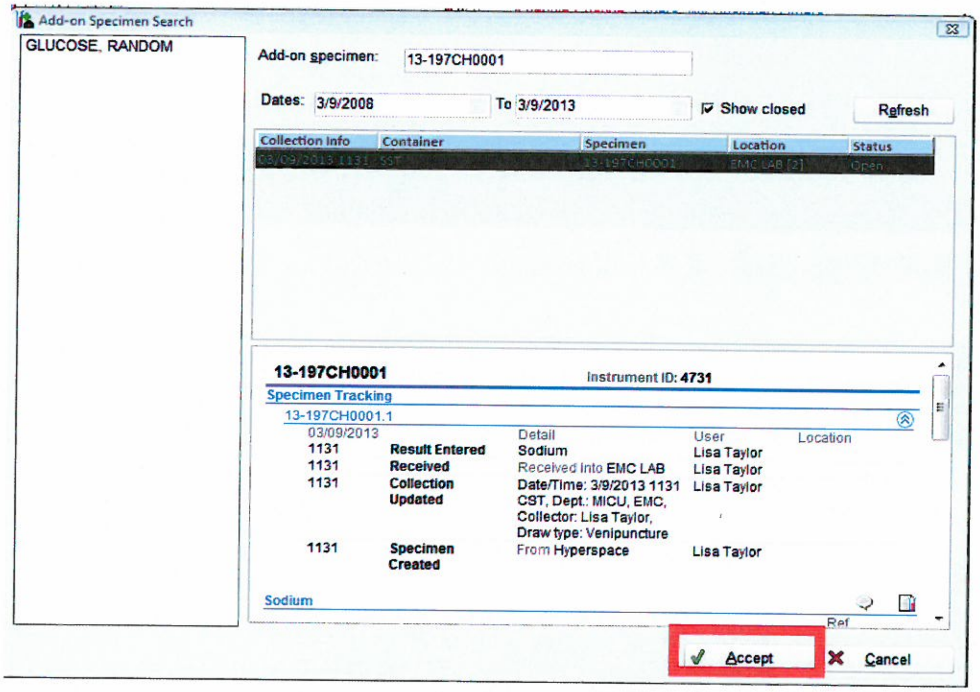
Status	Order Date	Order Time	Patient	Order	Step
New Provider: Smith, Jamie	06/12/2011	10:48 PM	Newman, Kelly Pool: X	Magnesium, serum Priority: Add-on	X
New Provider: Cooper, Pat	03/09/2013	11:45 AM	Avery, Glen Pool: X	Glucose, random Priority: Add-on	X
New Provider: Smith, Jamie	06/13/2011	3:00 PM	Smith, Harry Pool: X	Magnesium, serum Priority: Add-on	X

2. Highlight the new message.
3. Clicks **Add-ons** to add this new order to an existing specimen.

Status	Order Date	Order Time	Patient	Order	Step
New Provider: Smith, Jamie	06/12/2011	10:48 PM	Newman, Kelly Pool: X	Magnesium, serum Priority: Add-on	X
Read Provider: Cooper, Pat	03/09/2013	11:45 AM	Avery, Glen Pool: X	Glucose, random Priority: Add-on	X
New Provider: Smith, Jamie	06/13/2011	3:00 PM	Smith, Harry Pool: X	Magnesium, serum Priority: Add-on	X

The Add-on Specimen Search window opens. Available orders will appear in this window.

4. Select an appropriate existing specimen.
5. Click **Accept**.



GLUCOSE, RANDOM

Add-on specimen: 13-197CH0001

Dates: 3/9/2008 To 3/9/2013 ☑ Show closed

Collection Info	Container	Specimen	Location	Status
03/09/2013 1131	SST	13-197CH0001	EMC LAB [2]	Open

13-197CH0001 Instrument ID: 4731

Specimen Tracking

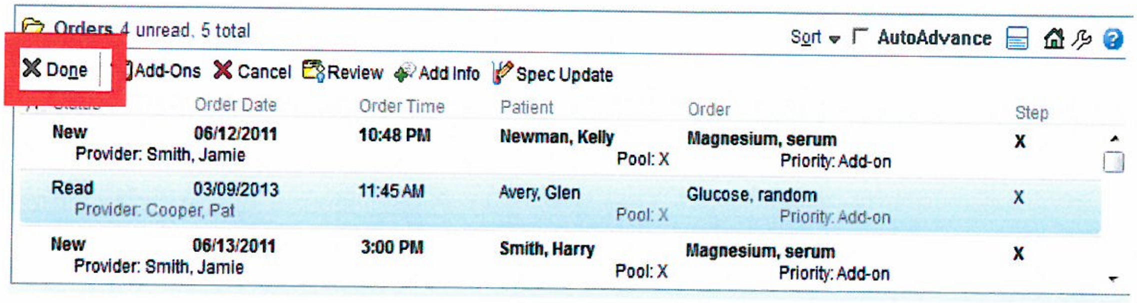
13-197CH0001.1

03/09/2013		Detail	User	Location
1131	Result Entered	Sodium	Lisa Taylor	
1131	Received	Received into EMC LAB	Lisa Taylor	
1131	Collection Updated	Date/Time: 3/9/2013 1131 CST, Dept.: MICU, EMC, Collector: Lisa Taylor, Draw type: Venipuncture	Lisa Taylor	
1131	Specimen Created	From Hyperspace	Lisa Taylor	

Sodium

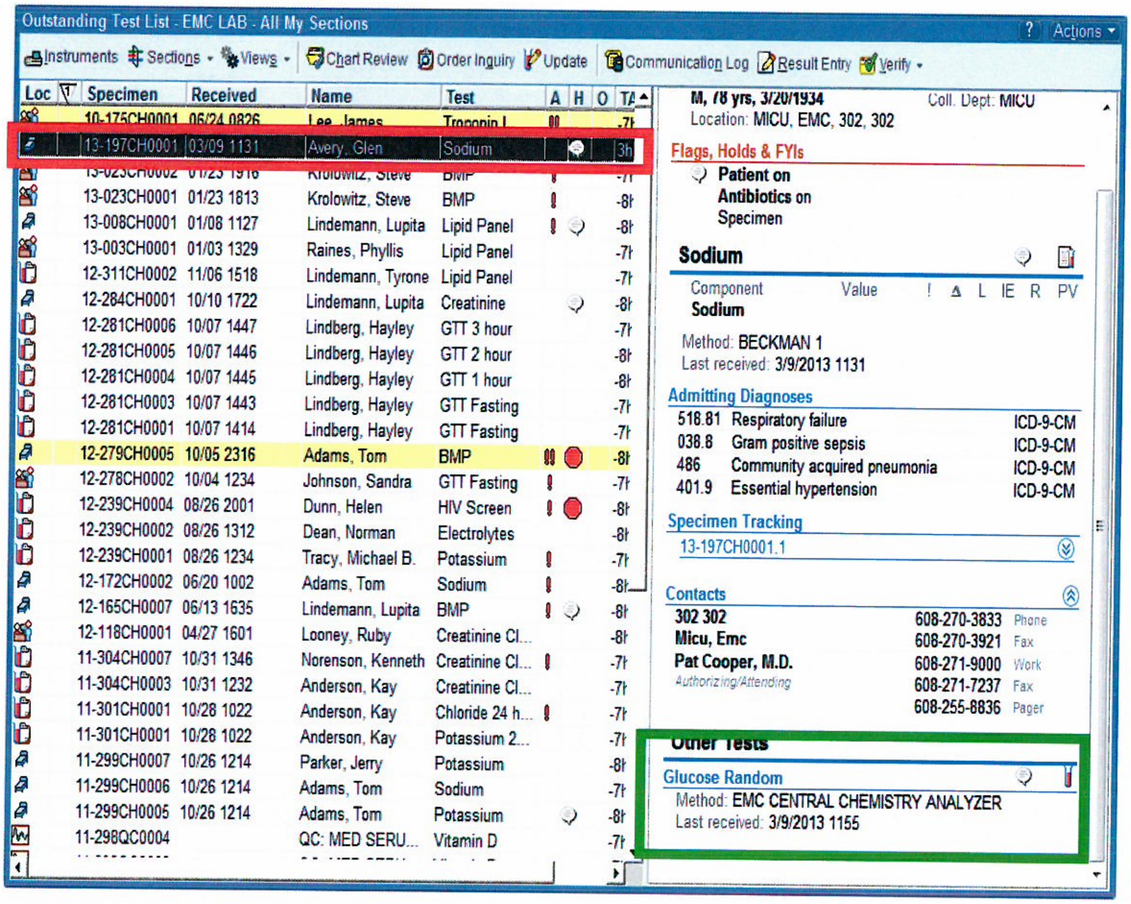
Ref

6. With the specimen still highlited, click **Done** to complete the add-on.



	Order Date	Order Time	Patient		Order		Step
New	06/12/2011	10:48 PM	Newman, Kelly		Magnesium, serum		X
Provider: Smith, Jamie				Pool: X		Priority: Add-on	
Read	03/09/2013	11:45 AM	Avery, Glen		Glucose, random		X
Provider: Cooper, Pat				Pool: X		Priority: Add-on	
New	06/13/2011	3:00 PM	Smith, Harry		Magnesium, serum		X
Provider: Smith, Jamie				Pool: X		Priority: Add-on	

**Both tests are now on the same specimen and can be resulted normally.



Loc	Specimen	Received	Name	Test	A	H	O	TA
	10-175CH0001	06/24 0826	Lee, James	Troponin I	!!			-7h
	13-197CH0001	03/09 1131	Avery, Glen	Sodium				3h
	13-023CH0002	01/23 1916	Krolowitz, Steve	BMP	!			-7h
	13-023CH0001	01/23 1813	Krolowitz, Steve	BMP	!			-8h
	13-008CH0001	01/08 1127	Lindemann, Lupita	Lipid Panel	!			-8h
	13-003CH0001	01/03 1329	Raines, Phyllis	Lipid Panel				-7h
	12-311CH0002	11/06 1518	Lindemann, Tyrone	Lipid Panel				-7h
	12-284CH0001	10/10 1722	Lindemann, Lupita	Creatinine				-8h
	12-281CH0006	10/07 1447	Lindberg, Hayley	GTT 3 hour				-7h
	12-281CH0005	10/07 1446	Lindberg, Hayley	GTT 2 hour				-8h
	12-281CH0004	10/07 1445	Lindberg, Hayley	GTT 1 hour				-8h
	12-281CH0003	10/07 1443	Lindberg, Hayley	GTT Fasting				-7h
	12-281CH0001	10/07 1414	Lindberg, Hayley	GTT Fasting				-7h
	12-279CH0005	10/05 2316	Adams, Tom	BMP	!!	●		-8h
	12-278CH0002	10/04 1234	Johnson, Sandra	GTT Fasting	!			-7h
	12-239CH0004	08/26 2001	Dunn, Helen	HIV Screen	!	●		-8h
	12-239CH0002	08/26 1312	Dean, Norman	Electrolytes				-8h
	12-239CH0001	08/26 1234	Tracy, Michael B.	Potassium	!			-7h
	12-172CH0002	06/20 1002	Adams, Tom	Sodium	!			-8h
	12-165CH0007	06/13 1635	Lindemann, Lupita	BMP	!			-8h
	12-118CH0001	04/27 1601	Looney, Ruby	Creatinine Cl...				-8h
	11-304CH0007	10/31 1346	Norenson, Kenneth	Creatinine Cl...	!			-7h
	11-304CH0003	10/31 1232	Anderson, Kay	Creatinine Cl...				-7h
	11-301CH0001	10/28 1022	Anderson, Kay	Chloride 24 h...	!			-7h
	11-301CH0001	10/28 1022	Anderson, Kay	Potassium 2...				-7h
	11-299CH0007	10/26 1214	Parker, Jerry	Potassium				-8h
	11-299CH0006	10/26 1214	Adams, Tom	Sodium				-7h
	11-299CH0005	10/26 1214	Adams, Tom	Potassium				-8h
	11-298QC0004		QC: MED SERU...	Vitamin D				-7h

M, 78 yrs, 3/20/1934 Coll. Dept: MICU
Location: MICU, EMC, 302, 302

Flags, Holds & FYIs
Patient on Antibiotics on Specimen

Sodium

Component	Value	!	Δ	L	IE	R	PV
Sodium							

Method: BECKMAN 1
Last received: 3/9/2013 1131

Admitting Diagnoses

518.81	Respiratory failure	ICD-9-CM
038.8	Gram positive sepsis	ICD-9-CM
486	Community acquired pneumonia	ICD-9-CM
401.9	Essential hypertension	ICD-9-CM

Specimen Tracking
13-197CH0001.1

Contacts

302 302	608-270-3833	Phone
Micu, Emc	608-270-3921	Fax
Pat Cooper, M.D.	608-271-9000	Work
Authorizing/Attending	608-271-7237	Fax
	608-255-8836	Pager

Other Tests
Glucose Random
Method: EMC CENTRAL CHEMISTRY ANALYZER
Last received: 3/9/2013 1155

Complete a Requisition

Receive specimens collected by a submitter

When you receive specimens for testing from another organization, a paper requisition arrives with each specimen. Enter the specimen details into the system using the Requisition Entry activity.

1. Go to **Epic button > Lab > Requisition Entry**. A blank requisition form opens.
2. In the **Submitter** field, completion match on the organization submitting the specimens. The system assigns a requisition number.
3. In the **Patient** field, enter the patient's name. The patient's demographics appear.
4. In the **Code** field of the Diagnoses table, enter the diagnosis code from the form, if appropriate.

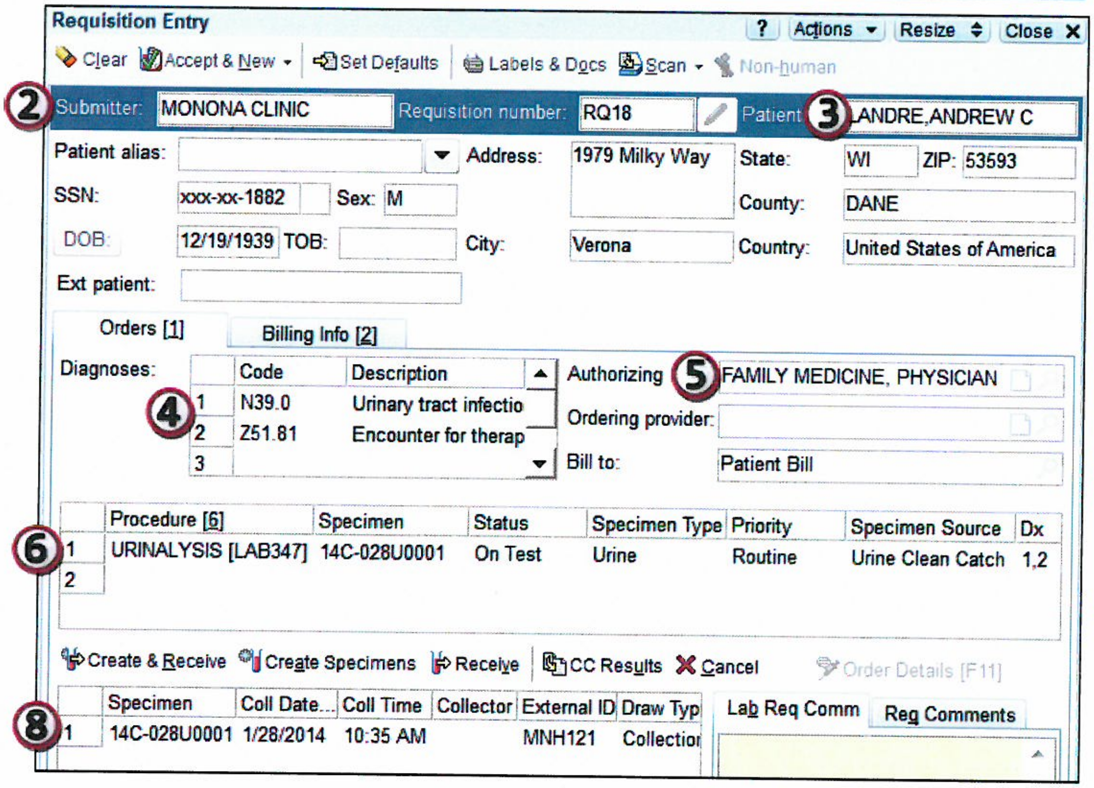
> If the requisition is from a toxicology submitter, complete the **Reason for test** fields instead of entering a diagnosis.

5. Enter the authorizing provider.
6. In the Procedure table:
   - Enter the test being performed in the **Procedure** field.
   - Enter the associated specimen source in the **Specimen Source** field.
   - If you entered diagnoses, verify that the associated diagnoses in the **Dx** field are correct. Update them if necessary. Remember, the numbers here correspond to lines in the Diagnoses table.
7. When the form is filled out, click **Create & Receive (ALT+R)** to create and receive the specimen. The

specimen ID appears in the bottom left of the form and the collection information fields are enabled.

8. Complete the collection information, including date, time, ID, and draw type.
9. To save your work and close Requisition Entry, click **Accept & New** (ALT+N) and select ✓ **Accept** (ALT+A).

> If you have several requisitions to enter from the same submitter that share similar information, you can set default values so you don't have to enter that information manually for every form.
>
> After you fill out the first requisition, click **Set Defaults** then click the fields you want to carry over. The selected fields turn green and bold. When you're done, click **Set Defaults Complete**, and then click **Accept and New** to save the current requisition and apply your defaults to the new requisition.



Submitter: MONONA CLINIC
Requisition number: RQ18
Patient: LANDRE,ANDREW C
Patient alias:
Address: 1979 Milky Way
State: WI
ZIP: 53593
SSN: xxx-xx-1882
Sex: M
County: DANE
DOB: 12/19/1939
TOB:
City: Verona
Country: United States of America
Ext patient:

Diagnoses:

	Code	Description
1	N39.0	Urinary tract infectio
2	Z51.81	Encounter for therap
3		

Authorizing: FAMILY MEDICINE, PHYSICIAN
Ordering provider:
Bill to: Patient Bill

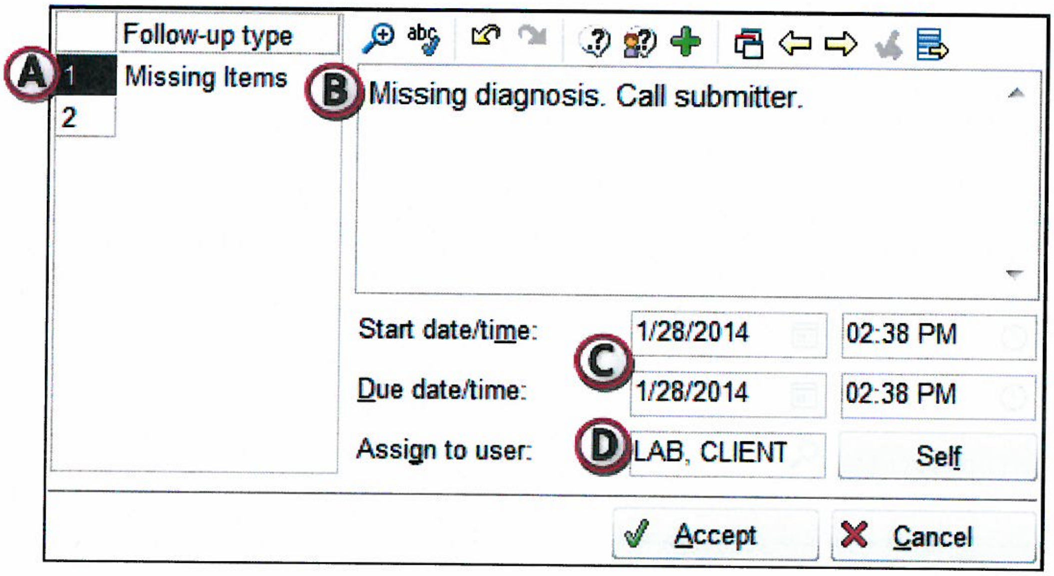
	Procedure [6]	Specimen	Status	Specimen Type	Priority	Specimen Source	Dx
1	URINALYSIS [LAB347]	14C-028U0001	On Test	Urine	Routine	Urine Clean Catch	1,2
2							

	Specimen	Coll Date...	Coll Time	Collector	External ID	Draw Typ
1	14C-028U0001	1/28/2014	10:35 AM		MNH121	Collectior

Create a follow-up task for the requisition

If the requisition is missing information, you can create a follow-up task so that you or another staff member can find the necessary information later.

1. In Requisition Entry, click **Actions > Add Follow-up Task.**
2. On the window that appears, enter the following:
    a. Follow-up type
    b. Comments explaining the follow-up needed
    c. Start and due date/times
    d. User assigned to the task (Click **Self** to assign the task to yourself.)
3. Click ✓ **Accept.**



1 Missing Items
2

Missing diagnosis. Call submitter.

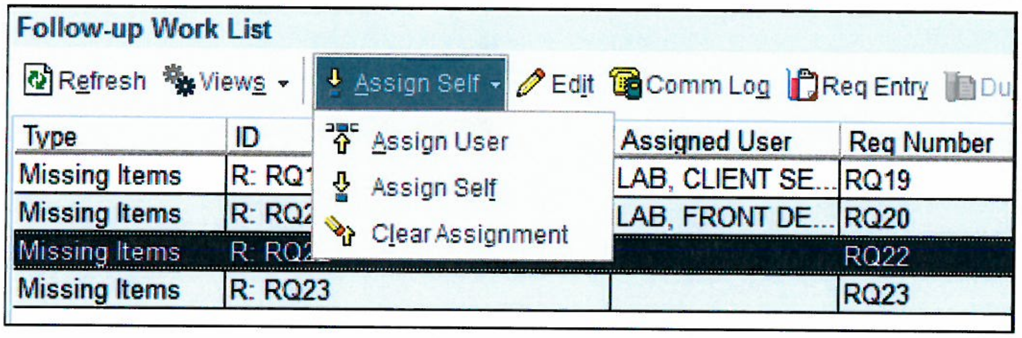
Start date/time: 1/28/2014 02:38 PM
Due date/time: 1/28/2014 02:38 PM
Assign to user: LAB, CLIENT

Assign a requisition to others or yourself for follow up

1. Go to **Epic button > Follow-up Work List.**
2. Select a requisition to assign.

Use **CTRL+CLICK** to select multiple requisitions.

3. Assign the requisition to yourself or to another person.
    - To assign the requisition to yourself, click **Assign Self** on the activity toolbar.
    - To assign the requisition to another user, click the arrow next to **Assign Self** and select **Assign User**. Enter the person's name in the User Select window.



Type	ID	Assigned User	Req Number
Missing Items	R: RQ1	LAB, CLIENT SE...	RQ19
Missing Items	R: RQ2	LAB, FRONT DE...	RQ20
Missing Items	R: RQ2		RQ22
Missing Items	R: RQ23		RQ23

Complete missing requisition information

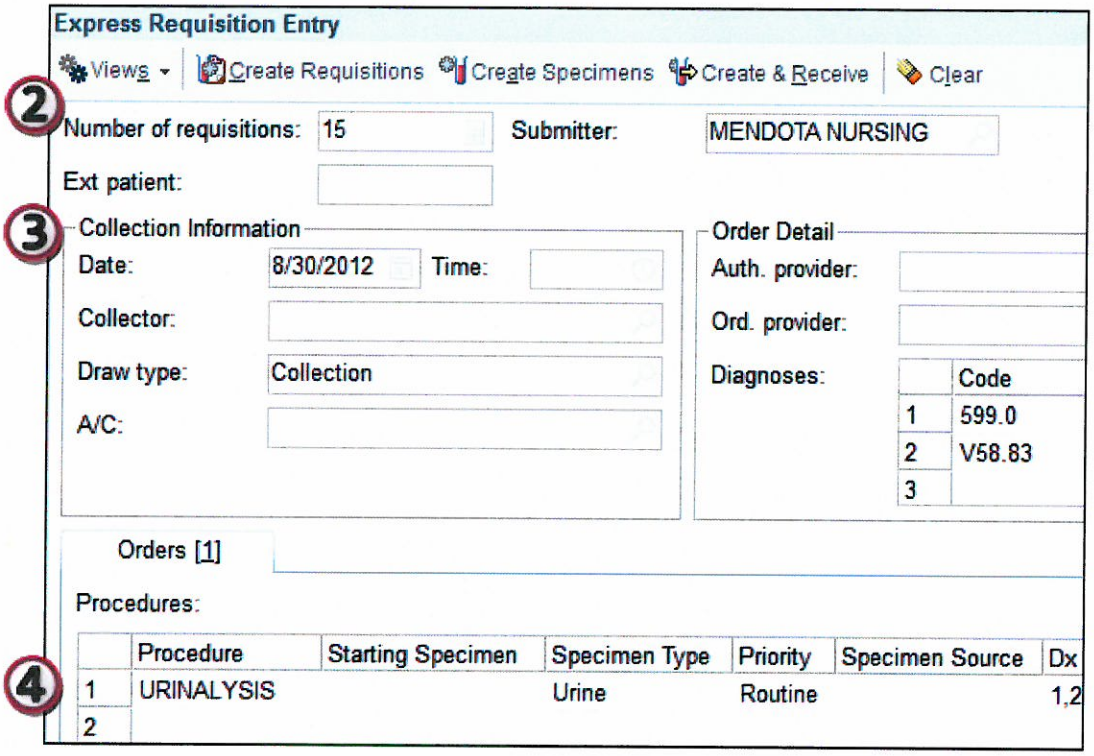
If you began a requisition in Requisition Entry, but were unable to complete the information at that time, you can complete the missing information later from the Follow-up Work List.

1. Go to **Lab > Follow-up Work List**.
2. Filter on "Missing Items" from the list.
3. Find your patient's requisition number under "ID"
4. Click **Requisition Entry** on the activity toolbar.
5. Complete the missing information.
6. Click ✓ **Accept**.

Create a requisition batch

Use Express Requisition Entry to create a number of specimens with common information at once. You can print labels and begin testing before entering any requisition information. You might do this, for example, if you are preparing for a health fair.

1. Go to **Epic button > Express Requisition Entry**.
2. Enter the number of requisitions you want to create and the submitter.
3. Complete the Collection Information and Order Detail sections, as appropriate.
4. Enter the test being performed in the **Procedure** field.
5. Press **ALT+A** to create the specimens.
    - The labels for your specimens print.
    - A batch is created. Note the batch ID at the bottom of the screen. You will need this information when you are ready to enter patient information after the specimens are collected.



Number of requisitions: 15
Submitter: MENDOTA NURSING
Ext patient:

Collection Information
Date: 8/30/2012
Time:
Collector:
Draw type: Collection
A/C:

Order Detail
Auth. provider:
Ord. provider:
Diagnoses:

	Code
1	599.0
2	V58.83
3	

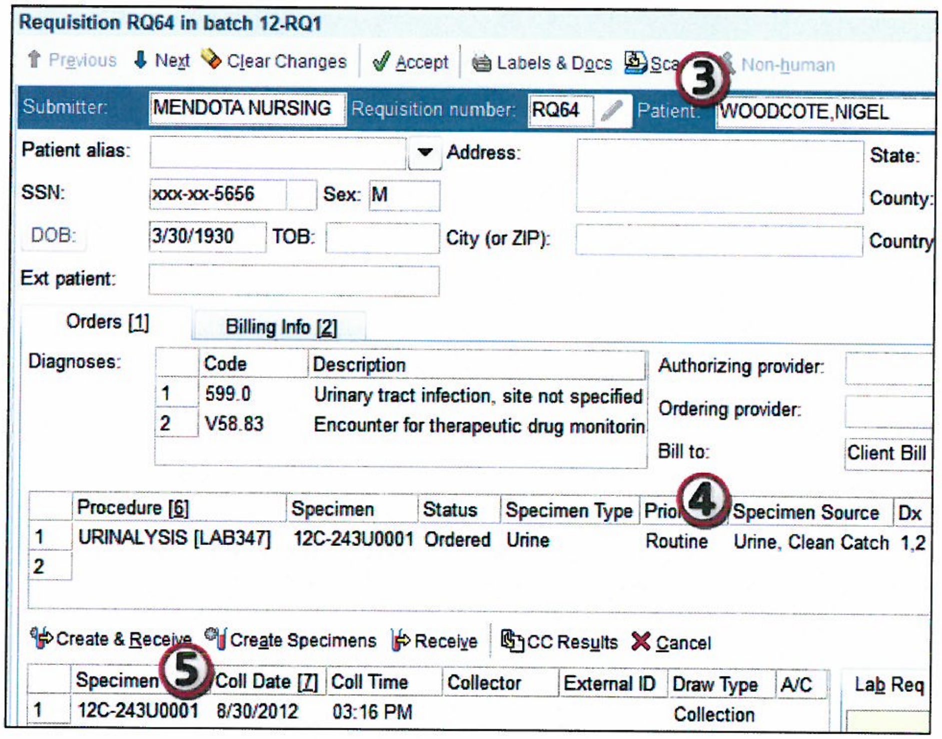
Orders [1]

Procedures:

	Procedure	Starting Specimen	Specimen Type	Priority	Specimen Source	Dx
1	URINALYSIS		Urine	Routine		1,2
2						

Enter patient information in a requisition batch

1. Go to **Epic button > Lab > Requisition Entry Work List**.
2. Select the batch for which you need to enter patient information and click **Requisition Entry**. Requisition Entry opens for the first requisition in the batch, and any information that was entered when the batch was created is already filled out.
3. In the **Patient** field, enter the name of the first patient.
4. Complete the **Specimen Source** field.
5. In the **Coll Time** field, enter the time the specimen was collected.
6. Press **ALT+X** to open the next requisition in the batch.
7. Repeat steps 3-6 to enter information for all of the remaining patients.
8. When you are done entering patient information, press **ALT+A** to accept the requisitions. You return to the Requisition Entry Work List.
9. When you are ready to receive the specimens into the lab, press **ALT+V**.



Requisition RQ64 in batch 12-RQ1

Submitter: MENDOTA NURSING
Requisition number: RQ64
Patient: WOODCOTE,NIGEL
Patient alias:
Address:
State:
SSN: xxx-xx-5656
Sex: M
County:
DOB: 3/30/1930
TOB:
City (or ZIP):
Country
Ext patient:
Authorizing provider:
Ordering provider:
Bill to: Client Bill

Diagnoses:

	Code	Description
1	599.0	Urinary tract infection, site not specified
2	V58.83	Encounter for therapeutic drug monitorin

	Procedure [6]	Specimen	Status	Specimen Type	Prio	Specimen Source	Dx
1	URINALYSIS [LAB347]	12C-243U0001	Ordered	Urine	Routine	Urine, Clean Catch	1,2
2							

	Specimen	Coll Date [7]	Coll Time	Collector	External ID	Draw Type	A/C	Lab Req
1	12C-243U0001	8/30/2012	03:16 PM			Collection		

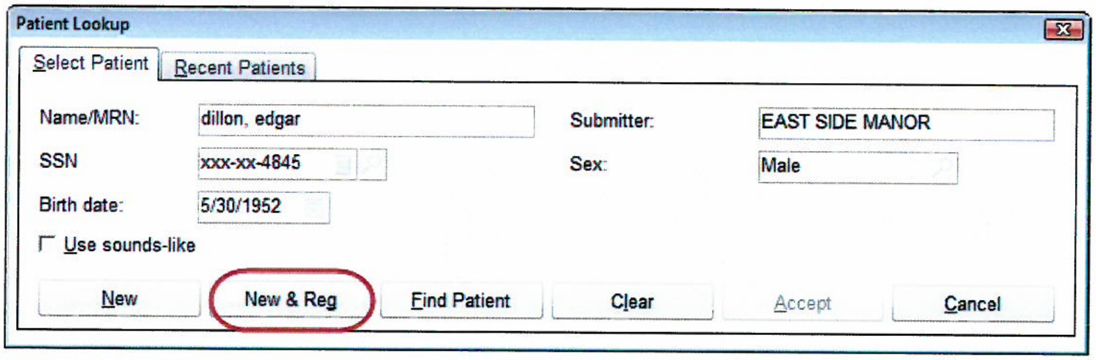
Create a requisition for an unregistered patient

If you receive a specimen from a submitter for a patient who hasn't been entered in your system, you must create the patient record and enter registration information for the patient before entering the requisition information.

1. In Requisition Entry, enter the submitter.
2. In the **Patient** field, enter the patient's name. If the patient doesn't have a record in the system, no matching patient will be found.
3. On the Patient Lookup window, complete all fields of patient information (name, Social Security number (SSN), sex, date of birth).
4. Click **New & Reg** to create the patient record and open the Registration activity.
5. Complete the patient's registration information, including demographics, guarantor accounts, and coverages, and then click ✓ **Finish**. You return to Requisition Entry and the patient's name appears in the **Patient** field.

> Refer to your Cadence quick start guide for more information on creating patient records and completing registration information.

6. Enter the requisition information and collection information, and create the specimen as usual.



Name/MRN: dillon, edgar
SSN xxx-xx-4845
Birth date: 5/30/1952
Submitter: EAST SIDE MANOR
Sex: Male
☐ Use sounds-like

Sending Out Specimens

Create a packing list

A packing list is simply a list of the specimens that will be sent to another lab. This list is sent along with the specimen containers.

1. Go to **Epic button > Packing List Editor**.
2. On the Packing List Lookup window, select the **Create** option.
3. In the **List Type** field, select the type of packing list you're creating (for example, a refrigerated list). The system generates an ID for the list.
4. Click ✓ **Accept**. The Packing List Editor opens.
5. Scan the specimen barcodes to add the specimens to the list.
6. If you want to see if there are other specimens that could be added to the list, click **Sendout Bench** to find and add them.

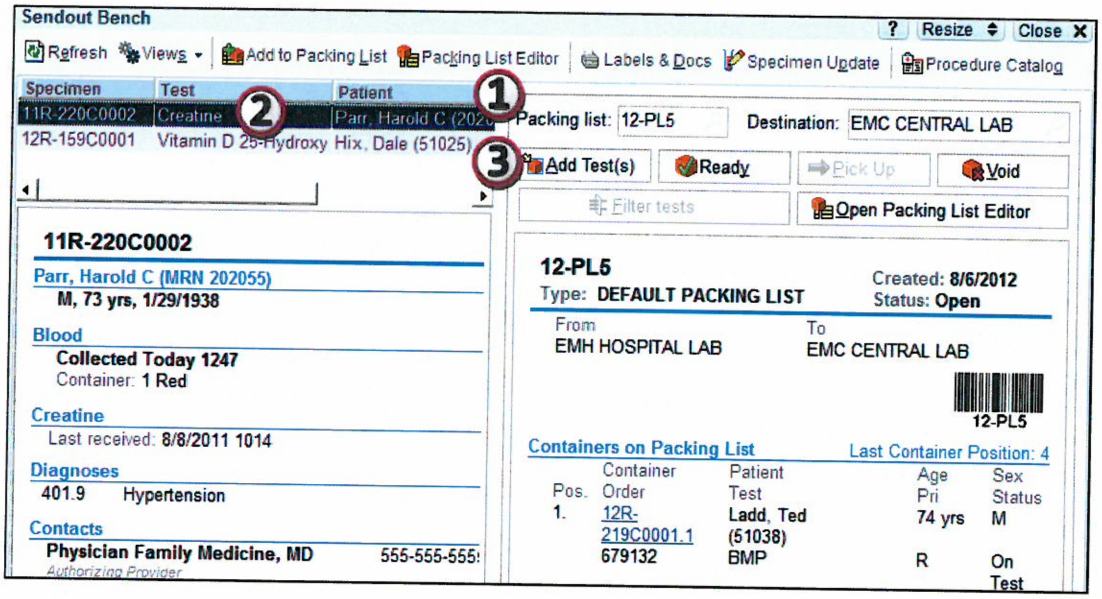
Add specimens to a packing list

If a packing list was already created, you can use the Sendout Bench activity to add specimens to the list for shipping. Tests that match the criteria of the selected packing list and the current report settings appear in the upper left. The report on the right lists the containers that are already on the selected packing list.

1. Open the Sendout Bench activity and open the packing list you want to use.
    - If you have the packing list open in the Packing List Editor, click **Sendout Bench** on the activity toolbar. The Sendout Bench opens with the packing list selected and open.

- Otherwise, go to **Epic button > Lab > Sendout Bench**. Then enter the packing list ID in the **Packing list** field and verify the lab that appears in the **Destination** field.

2. Select the tests you want to add to the packing list. Use **CTRL+CLICK** to select multiple containers.
3. Click **Add Test(s)**. The tests you selected disappear from the list on the left and are added to the report on the right.



Specimen	Test	Patient
11R-220C0002	Creatine	Parr, Harold C (202
12R-159C0001	Vitamin D 25-Hydroxy	Hix, Dale (51025)

11R-220C0002

Parr, Harold C (MRN 202055)
M, 73 yrs, 1/29/1938

Blood
Collected Today 1247
Container: 1 Red

Creatine
Last received: 8/8/2011 1014

Diagnoses
401.9 Hypertension

Contacts
Physician Family Medicine, MD 555-555-555
Authorizing Provider

Packing list: 12-PL5
Destination: EMC CENTRAL LAB

12-PL5
Type: DEFAULT PACKING LIST
Created: 8/6/2012
Status: Open

From
EMH HOSPITAL LAB
To
EMC CENTRAL LAB

12-PL5

Containers on Packing List
Last Container Position: 4

Pos.	Container Order	Patient Test	Age Pri	Sex Status
1.	12R-219C0001.1 679132	Ladd, Ted (51038) BMP	74 yrs R	M On Test

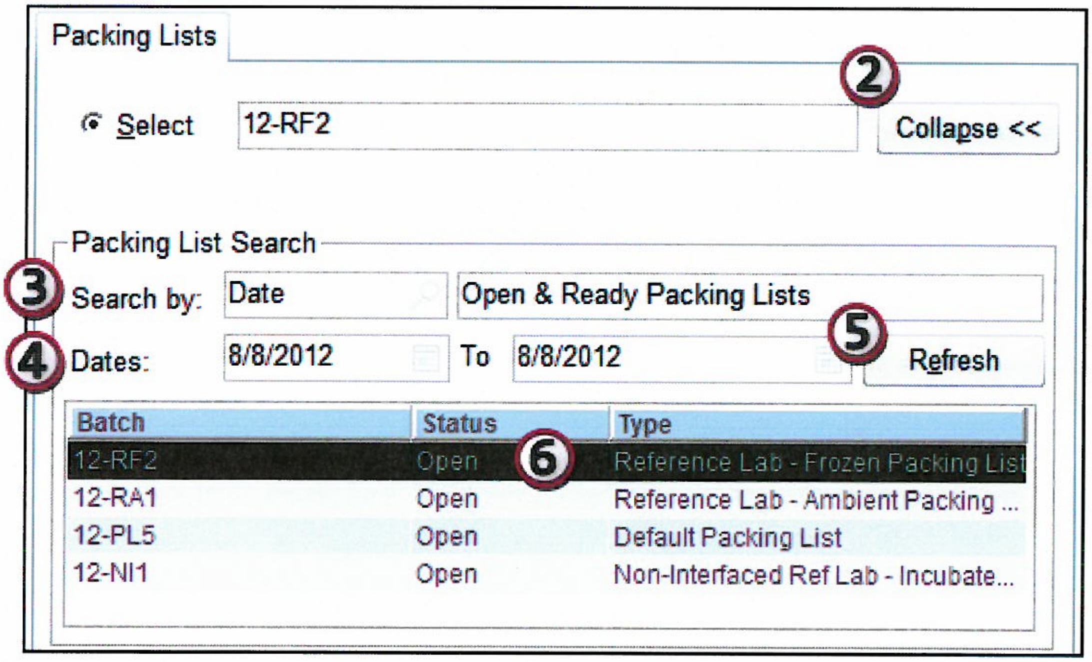
If the Report Settings window appears when you open the Sendout Bench activity, select the criteria for the tests you want to see, or select the appropriate report on the left. Then click **Run**.

You can change the tests that are included at any time by returning to the Report Settings window. To do so, click **Views** and select **Settings**.

Locate a packing list that's going to a specific lab

If you receive specimens and know you'll be sending them out to another lab, you can check to see if there are any open packing lists destined for that lab before you create a new one.

1. Go to **Epic button > Lab > Packing List Editor**. The Packing List Lookup window appears.
2. Click **Expand>>** to view all of the search fields.
3. To search for all packing lists with a status of Open or Ready, enter "date" in the **Search by** field.
4. Set the search date range. It is set to today by default.
5. Click **Refresh**. A list of open and ready packing lists within the date range appears below the search fields.
6. Double-click a packing list to open it, and then look in the **Destination** field for the lab it is being sent to.



● Select 12-RF2

Search by: Date Open & Ready Packing Lists

Dates: 8/8/2012 To 8/8/2012

Batch	Status	Type
12-RF2	Open	Reference Lab - Frozen Packing List
12-RA1	Open	Reference Lab - Ambient Packing ...
12-PL5	Open	Default Packing List
12-NI1	Open	Non-Interfaced Ref Lab - Incubate...

You can also look up a packing list by specimen. You might want to do this if you want to see what packing list a specimen is on and find out the status of that list.

1. On the Packing List Lookup window, enter "specimen" in the **Search by** field.
2. Scan the specimen's barcode or manually enter the ID.
3. Click **Refresh**.
4. Click ✓ **Accept** to open the packing list you located.

Send a packing list to another lab

After adding all the appropriate containers to a packing list, you need to indicate that the list is complete and that the associated containers are ready for pickup.

To do this, click ✓ **Ready**. When you mark a packing list as Ready, a few things happen:

- The packing list is locked in the system, meaning no more containers can be added. This ensures that no extra containers get added to the list accidentally.
- The packing list's status changes to Ready for pickup.
- The packing list prints.

> ⓘ Clicking ✓ **Ready** locks the packing list, meaning no more containers can be added. If you need to add more tests, you can unlock the packing list again by clicking ✓ **Unready**.

When the package is picked up, click ⇨ **Picked Up**. The packing list is closed and can no longer be unlocked for editing.

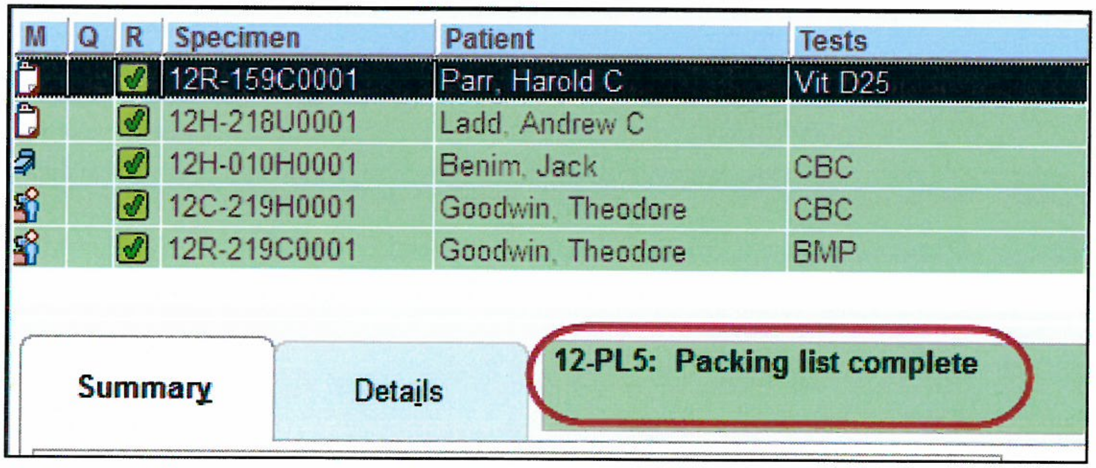
Receive specimens from labs within your organization

If specimens were collected at another lab within your organization and were then sent to your lab to have the tests performed, you need to indicate when those containers arrive in your lab.

1. Open the Receiving activity.
2. Scan the barcode of each specimen being received. If necessary, you can enter the IDs manually.

> **!** It is important to scan the specimens individually to make sure that you have physically received all the specimens from the packing list.

3. After the specimens are all scanned, scan the packing list barcode to ensure that all containers from the list have been accounted for.
4. If you missed any of the specimens on the list and you have the physical specimens, receive them now.
5. If all of the specimens on the list have been received, you are alerted that the packing list is complete. Close the Receiving activity.



M	Q	R	Specimen	Patient	Tests
		☑	12R-159C0001	Parr, Harold C	Vit D25
		☑	12H-218U0001	Ladd, Andrew C	
		☑	12H-010H0001	Benim, Jack	CBC
		☑	12C-219H0001	Goodwin, Theodore	CBC
		☑	12R-219C0001	Goodwin, Theodore	BMP

12-PL5: Packing list complete

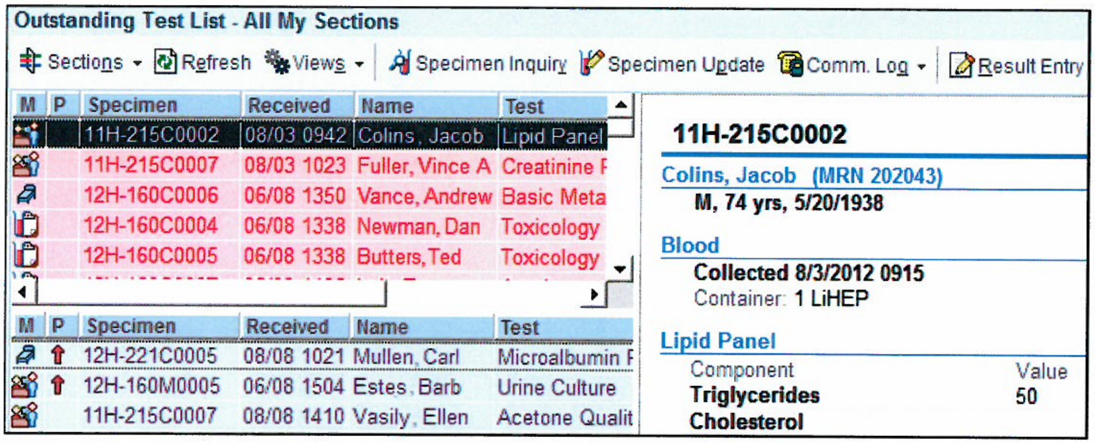
Result Entry – General

Find tests awaiting results

Select the workspace tab to open the Outstanding List. Here, you can view the outstanding and overdue tests in your laboratory and monitor result entry and verification. All specimens received in your lab appear here.

The Outstanding List is composed of three sections:

- The Overdue List in the top left. If a test nears or exceeds its turnaround time, it appears here.
- The Outstanding List in the bottom left. This is the main section of the activity, and shows all outstanding tests.
- The report preview on the right side. This preview shows information about the test you have selected on the left.



Outstanding Test List - All My Sections

M	P	Specimen	Received	Name	Test
		11H-215C0002	08/03 0942	Colins, Jacob	Lipid Panel
		11H-215C0007	08/03 1023	Fuller, Vince A	Creatinine F
		12H-160C0006	06/08 1350	Vance, Andrew	Basic Meta
		12H-160C0004	06/08 1338	Newman, Dan	Toxicology
		12H-160C0005	06/08 1338	Butters, Ted	Toxicology

M	P	Specimen	Received	Name	Test
	↑	12H-221C0005	08/08 1021	Mullen, Carl	Microalbumin F
	↑	12H-160M0005	06/08 1504	Estes, Barb	Urine Culture
		11H-215C0007	08/08 1410	Vasily, Ellen	Acetone Qualit

11H-215C0002

Colins, Jacob (MRN 202043)
M, 74 yrs, 5/20/1938

Blood
Collected 8/3/2012 0915
Container: 1 LiHEP

Lipid Panel

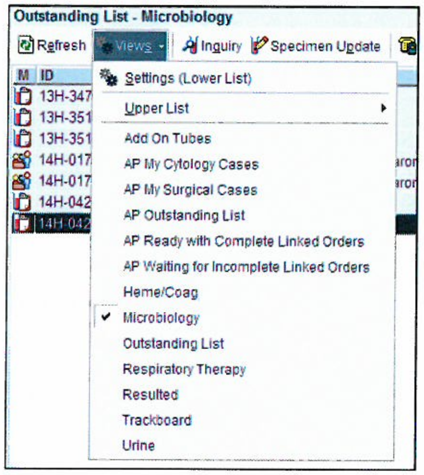
Component	Value
Triglycerides	50
Cholesterol	

Filter or sort the Outstanding List

The Outstanding List can contain a large number of specimens for an entire laboratory. To help you see the tests that are most relevant to you, you can select different views of the list, or filter it by laboratory section. Because a filtered list has fewer specimens, it's easier to see which tests you need to perform and when they must be completed.

To view the tests that are most relevant to you:

1. Click **Views.**
2. Select the group of tests you want to see.



Review results from an interfaced analyzer

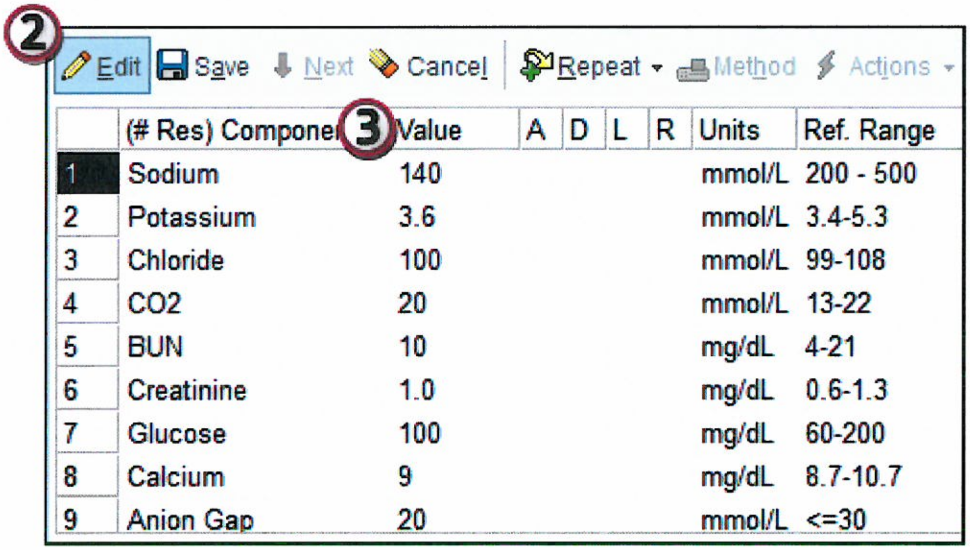
1. On the Outstanding List, select the test whose results you want to view. If the test results were interfaced from the analyzer, the results appear in the report pane at the right.
2. If no further action is needed, click **Verify** on the activity toolbar to final verify the results.

Enter Manual and Paper Results

Enter test results manually

There might be times when you have to enter results manually, such as when your analyzer is not interfaced with the system. In the Result Entry activity, you can enter the results of a single specimen or a group of specimens.

1. On the Outstanding List, scan the specimen you need to enter results for. Result Entry opens.
2. Click ✎ **Edit** on the toolbar in the middle of the activity to access the Result Editor.
3. Enter the values for the test. The values are saved automatically.
4. If necessary, update the method.
5. When you are done, verify the results.



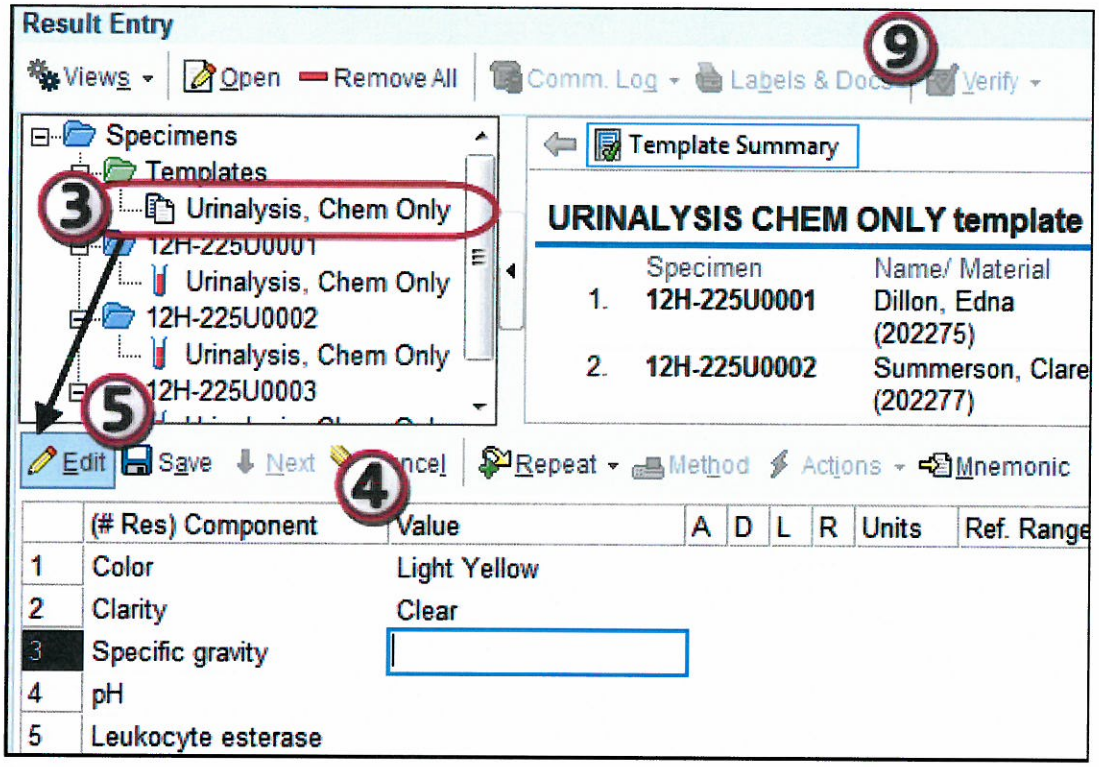
	(# Res) Compone	Value	A	D	L	R	Units	Ref. Range
1	Sodium	140					mmol/L	200 - 500
2	Potassium	3.6					mmol/L	3.4-5.3
3	Chloride	100					mmol/L	99-108
4	CO2	20					mmol/L	13-22
5	BUN	10					mg/dL	4-21
6	Creatinine	1.0					mg/dL	0.6-1.3
7	Glucose	100					mg/dL	60-200
8	Calcium	9					mg/dL	8.7-10.7
9	Anion Gap	20					mmol/L	<=30

Enter results for similar tests together

Quickly enter common results for a group of specimens that underwent similar testing by scanning those specimens in the Result Entry activity, and then using the Result Entry template that appears to enter and apply the same result for multiple specimens at once.

For example, if you scan several urinalysis specimens in Result Entry, a Urinalysis template appears. If most of the specimens have the same results, you can use that template to apply the results to all of the specimens at the same time, and then simply update the values for the few specimens with different results.

1. On the Outstanding List, select a specimen, and click **Result Entry** on the activity toolbar.
2. In Result Entry, scan the other specimens that you need to enter results for. If any of the tests' results can be entered together, a template appears in the top-left pane.
3. Select the template and click **Edit**.
4. In the Value column, enter the results that you want to apply to all or most of the specimens.
5. Click **Save**. The Apply Results window opens.
6. Click **Select All** to apply the results from the template to all of the specimens in the batch. Clear the check boxes next to any specimens you don't want to apply the results to.
7. Click ✓ **Accept**. The results are applied to the selected specimens.
8. Add results for any specimens you did not apply the template to.
9. Select the Specimens folder in the upper-left and click **Verify** to final verify all of the results at once.
10. Ensure that you have selected the appropriate tests and click **Verify Selected Results**.



URINALYSIS CHEM ONLY template

	Specimen	Name/ Material
1.	12H-225U0001	Dillon, Edna (202275)
2.	12H-225U0002	Summerson, Clare (202277)

	(# Res) Component	Value	A	D	L	R	Units	Ref. Range
1	Color	Light Yellow						
2	Clarity	Clear						
3	Specific gravity							
4	pH							
5	Leukocyte esterase							

Enter results from an external non-interfaced lab

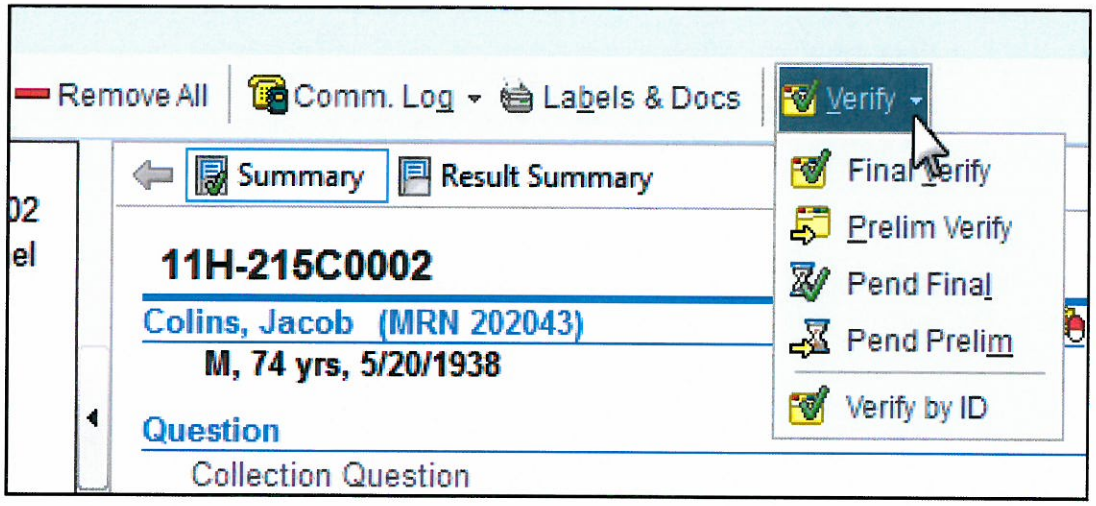
1. Go to **Epic button > Sendout Bench**.
2. On the Report Settings window, double-click the Sent Out Specimens report in the list on the left. The Sendout Bench activity opens.
3. Select the specimen and click **Result Entry** on the activity toolbar. You might have to click **More** to see this option.
4. Scan the paper results into the system.
5. Verify the results.

Verify results

After you finish entering and saving results, you need to verify the results. You can verify results from either the Outstanding List or Result Entry. Verifying results releases the results to the patient's chart and sends the results to the provider.

Click the arrow next to ✓ **Verify** and select one of the following options:

Final Verify	Releases results to the patient's chart and sends the results to the patient's primary care provider.
Prelim Verify	Sends results to the patient's chart with a preliminary status.
Pend Final	Indicates to a supervisor that final results are ready to be reviewed.
Pend Prelim	Indicates to a supervisor that preliminary results are ready to be reviewed.



11H-215C0002

Colins, Jacob (MRN 202043)

M, 74 yrs, 5/20/1938

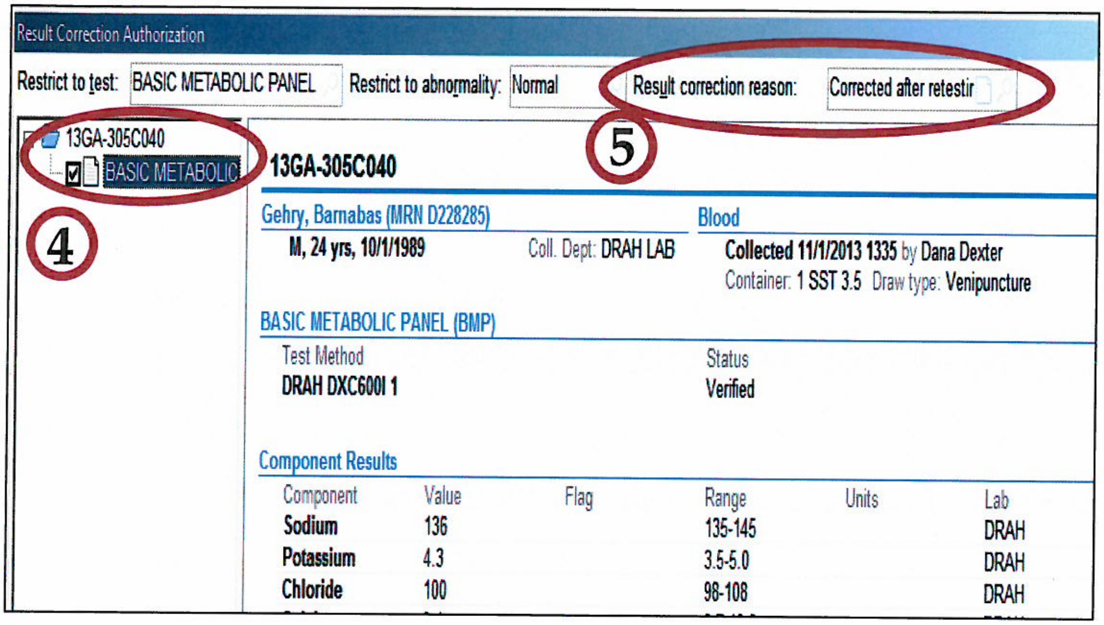
Collection Question

Correct a Verified Result

Sometimes lab techs make errors and incorrect results are verified. If results are mistakenly verified as final results and you need to correct them, use Result Entry to correct the results. If you have the proper security, you can authorize verified results to be corrected.

To correct the results of a verified test, follow these general steps:

1. Log in a Supervisor or tech with Result correction ability.
2. Follow the path **Epic > Tools > Lab Tools > Result Correction Authorization.**
3. Enter the **specimen ID** for the patient results that need to be corrected,in the Select field and click **Accept**. (Barcode scanning in reality)
4. In the left pane of the Result Correction Authorization window, select the test or tests that you need to edit.
5. Choose a reason in the Result correction reason field.
6. **Click Accept** on the Result Correction Authorization window.
7. The specimen appears on the **Outstanding List** again.
8. Take your specimen into **Result Entry.**
9. The Edit button is now enabled in the Result Editor.
10. **Click Edit** and change the result.
11. A correction comment becomes part of the results. It appears in the patient's chart in Chart Review, Results Review, and Specimen Inquiry.
12. **Verify** the result.



Restrict to test: BASIC METABOLIC PANEL

Restrict to abnormality: Normal

Result correction reason: Corrected after retestir

13GA-305C040

☑ BASIC METABOLIC

13GA-305C040

Gehry, Barnabas (MRN D228285)

M, 24 yrs, 10/1/1989

Coll. Dept: DRAH LAB

Blood

Collected 11/1/2013 1335 by Dana Dexter

Container: 1 SST 3.5 Draw type: Venipuncture

BASIC METABOLIC PANEL (BMP)

Test Method	Status
DRAH DXC600I 1	Verified

Component Results

Component	Value	Flag	Range	Units	Lab
Sodium	136		135-145		DRAH
Potassium	4.3		3.5-5.0		DRAH
Chloride	100		98-108		DRAH

Enter results for a test sent to an external non-interfaced lab

Go to Epic button > Lab > Sendout Bench.

On the Report Settings window, double-click the Sent Out Specimens report in the list on the left. The Sendout Bench activity opens.

In the Packing list field, scan the packing list barcode.

Select the specimen and click ✎ Result Entry on the activity toolbar. You might have to click More to see this option.

Enter the test's results manually, if needed.

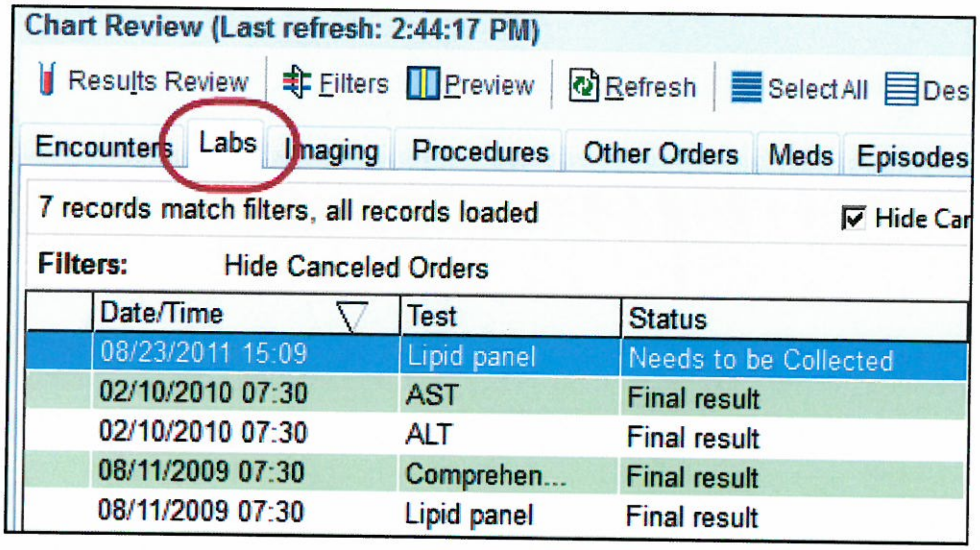
Or Scan the paper results into the system using OnBase.

Verify the results.

Review patient results

Chart Review offers easy access to a wide range of information in a patient's chart, including past lab results. Chart Review is divided into many tabs, each for a specific kind of information. For example, to see only the patient's lab results, select the **Labs** tab.

1. Open Patient Station for the patient.
2. Select the **Chart Review** activity tab.
3. Select the **Labs** tab. You see a list of the patient's past lab tests.
4. To view details about a specific test, select the test and review the information that appears in the bottom pane.



7 records match filters, all records loaded

Filters: Hide Canceled Orders

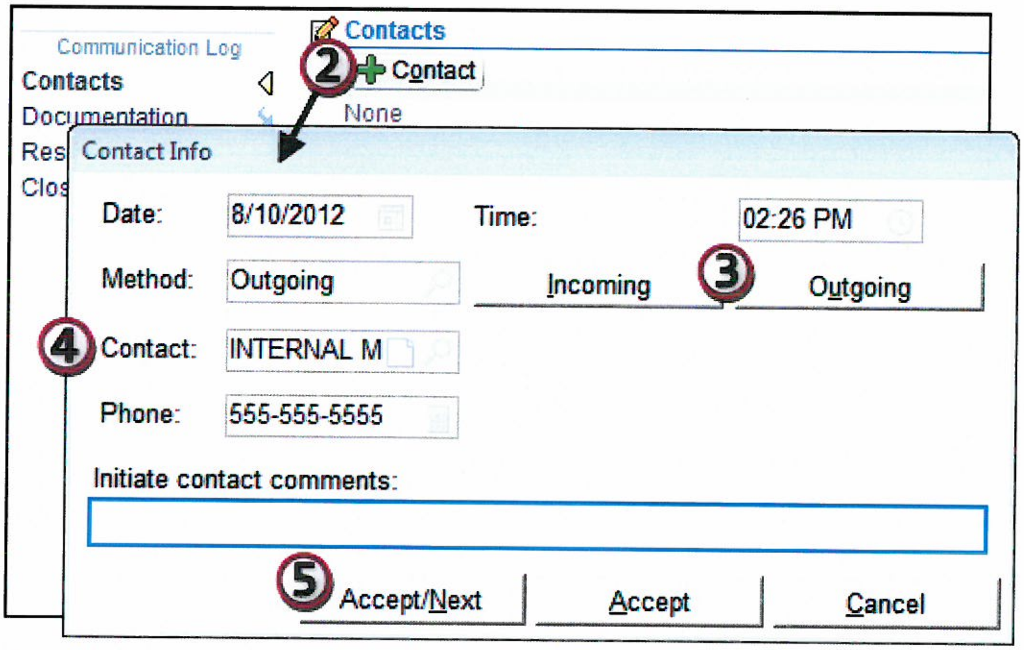
Date/Time	Test	Status
08/23/2011 15:09	Lipid panel	Needs to be Collected
02/10/2010 07:30	AST	Final result
02/10/2010 07:30	ALT	Final result
08/11/2009 07:30	Comprehen...	Final result
08/11/2009 07:30	Lipid panel	Final result

Communicate Critical Results

Document communication of critical results

When results are critical, the provider needs to be notified as soon as possible. Use the Communication Log Navigator to enter and track your communication with the provider.

1. In Result Entry, click **Comm. Log** and select **Communication Log**.
2. Click **Contact**. Today's date and time appear.
3. Click **Outgoing** to indicate that you're calling the provider.
4. In the **Contact** field, enter the person you are contacting. If the contact's phone number is in the system, the number appears in the **Phone** field.
5. Click **Accept/Next** to go directly to the Documentation navigator section.
6. Enter any comments about the communication.
7. When the provider is successfully notified and no more contacts need to be made, open the Close Log section and click the appropriate **Close log** link.



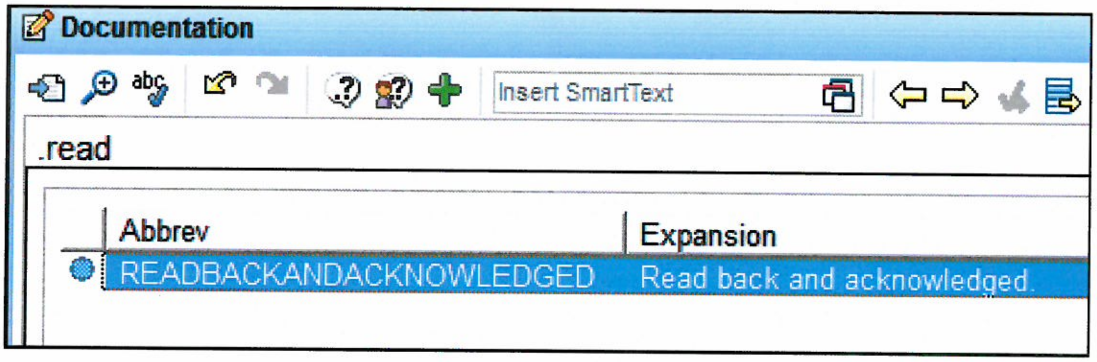
Date: 8/10/2012
Time: 02:26 PM
Method: Outgoing
Contact: INTERNAL M
Phone: 555-555-5555

ⓘ You can also access the Communication Log from the Follow-up Work List.

Use a SmartPhrase

Use SmartPhrases to insert a long phrase or paragraph by typing only a few characters in your text. For example, typing ".read" expands to "Read back and acknowledged."

1. In a SmartTool-enabled field, such as the Documentation navigator section, enter a period (.) followed by the SmartPhrase's name. As you type, a list of matching SmartPhrases and SmartLinks appears.
2. Use the arrow keys to select the SmartPhrase you want to use in your note and press **SPACEBAR** to insert it.
3. Complete any SmartLists or wildcards (***) in the SmartPhrase.



.read

Abbrev	Expansion
READBACKANDACKNOWLEDGED	Read back and acknowledged.

ⓘ You can use SmartTools in many places throughout Epic, including when documenting communication with clinicians. If you see these buttons, the field is SmartTool-enabled:

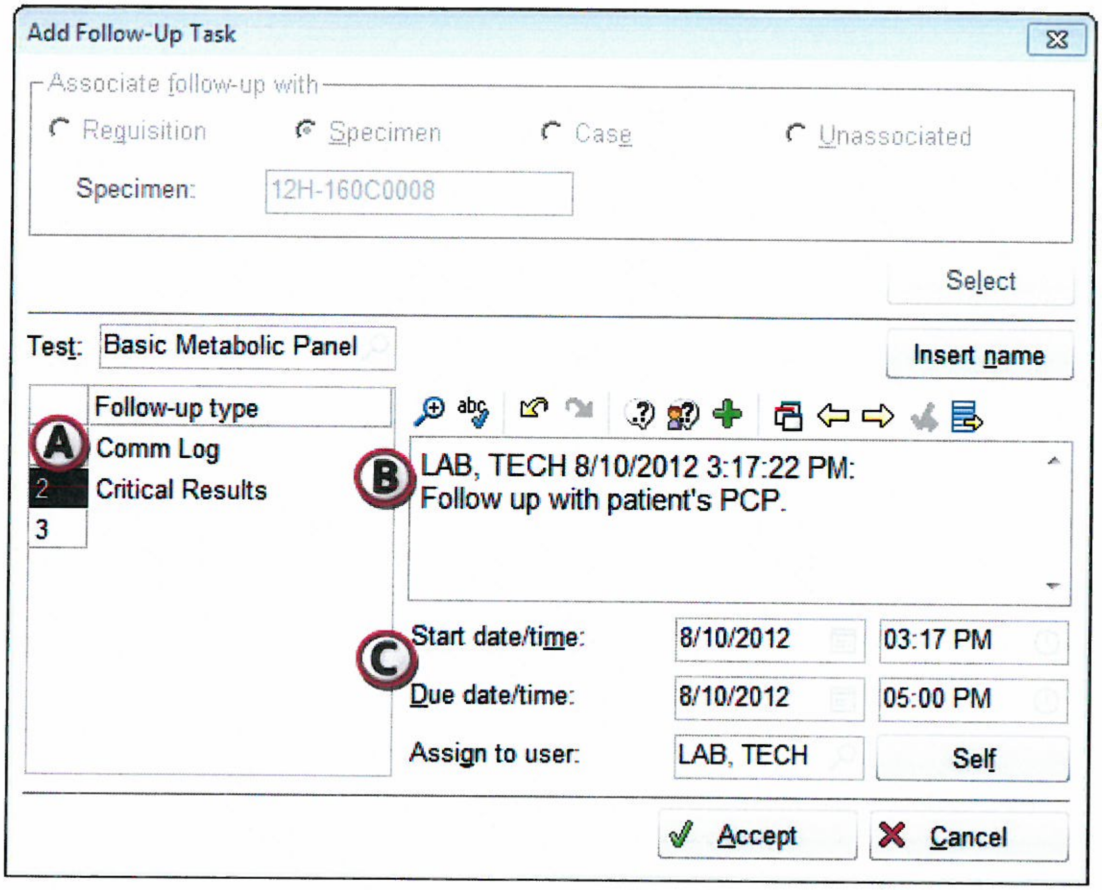
Create your own SmartPhrase

If you often type the same phrases and sentences when documenting a call or follow-up task, turn it into your own SmartPhrase and quickly pull in the text in the future.

1. In a SmartTool-enabled field, enter the text you want to save as a SmartPhrase. Don't include any patient-specific information, so you can use it for other patients.
2. Select the text and click ✚. The SmartPhrase Editor opens with your text on the Content tab.
3. Make any necessary edits.
4. Enter a short, intuitive name for your SmartPhrase in the **Name** field. This is the abbreviation you'll use to look up the phrase.
5. Enter a summary of your SmartPhrase in the **Short Description** field. This description appears when you look up your phrase.
6. Click **Accept**. The SmartPhrase is now available for use.

Add a test with critical results to the Follow-up Work List

1. On the Outstanding List, open Result Entry for a test.
2. Click **Comm Log** and select **Add Follow-up Task**.
3. In the Add Follow-up Task window, enter the following information:
   a. Follow-up type
   b. Comments to explain the follow-up that is needed
   c. Start and due times
4. Click **Self** to assign the task to yourself. You can also assign the task to another user by entering that person's name in the **Assign to user** field.
5. Click **Accept**. The task appears on the Follow-up Work List.



○ Requisition ● Specimen ○ Case ○ Unassociated

Specimen: 12H-160C0008

Test: Basic Metabolic Panel

	Follow-up type
	Comm Log
2	Critical Results
3	

LAB, TECH 8/10/2012 3:17:22 PM:
Follow up with patient's PCP.

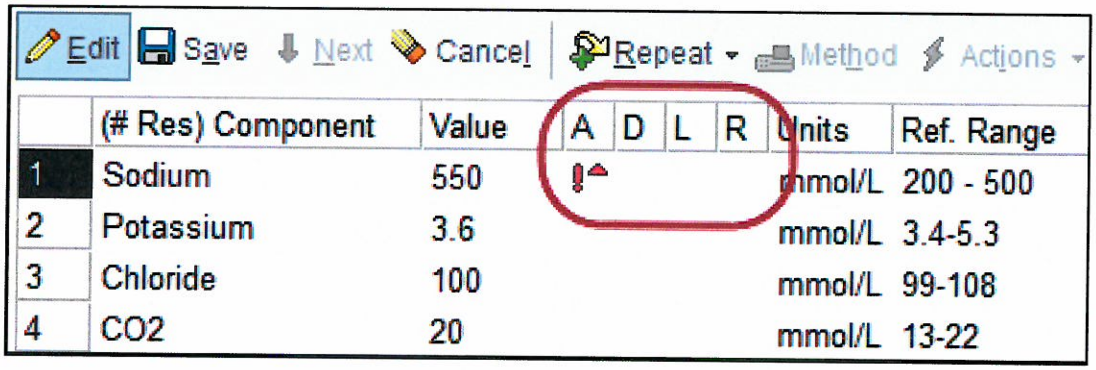
Start date/time: 8/10/2012 03:17 PM
Due date/time: 8/10/2012 05:00 PM
Assign to user: LAB, TECH

Repeats

Identify results that might need to be retested

When various icons appear in the Abnormality (**A**) and Delta checking (**D**) columns in the Result Editor, tests or components might need to be re-run. Different abnormal icons appear, based on the level of abnormality identified. If there are large changes in a value since the previous result, they are indicated in the **D** column. An icon can also appear in the Linearity (**L**) column to indicate that the result is outside the reportable range of the analyzer, and in the Reportable (**R**) column to indicate that the result will be reported to a state health agency.

The chart below explains what the icons in each column mean.



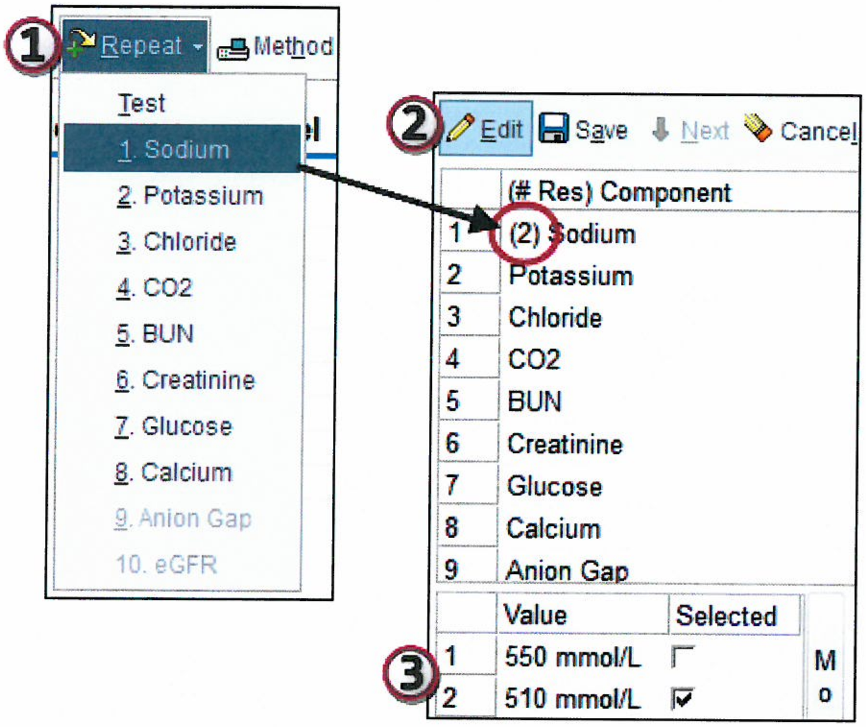
	(# Res) Component	Value	A	D	L	R	Units	Ref. Range
1	Sodium	550	!▲				mmol/L	200 - 500
2	Potassium	3.6					mmol/L	3.4-5.3
3	Chloride	100					mmol/L	99-108
4	CO2	20					mmol/L	13-22

Icon	Type	Column	Significance
!	Abnormal	A	The result is outside the reference range, but isn't severely abnormal. A ▲ indicates the result is above the range; a ▼ indicates the result is below the range.
!!	Abnormal-Critical	A	The result is significantly outside the reference range. The physician should be notified immediately. A ▲ indicates the result is above the range; a ▼ indicates the result is below the range.
⚠	Delta	D	There was a significant change between the previous and current result.
📈	Linearity	L	The result is outside the reportable range of the analyzer.
📋	Reportable	R	The result must be reported to an external health agency.

Repeat a component for a test

At times it might be necessary to repeat an entire test containing multiple components, but in other situations, it might only be necessary to repeat one component. You can accomplish both of these workflows using the Repeat menu in Result Entry.

1. In the Result Editor, click **Repeat** and select the whole test or a single component. The repeated component is prefaced with a number in parentheses denoting the number of times it is resulted.
2. Click ✏ **Edit** and enter the result of the repeat test.
3. In the bottom-left section of the Result Editor, select the check box to the right of the value you want to report for the repeated component.
4. Click 💾 **Save.**



	(# Res) Component
1	(2) Sodium
2	Potassium
3	Chloride
4	CO2
5	BUN
6	Creatinine
7	Glucose
8	Calcium
9	Anion Gap

	Value	Selected
1	550 mmol/L	☐
2	510 mmol/L	☑

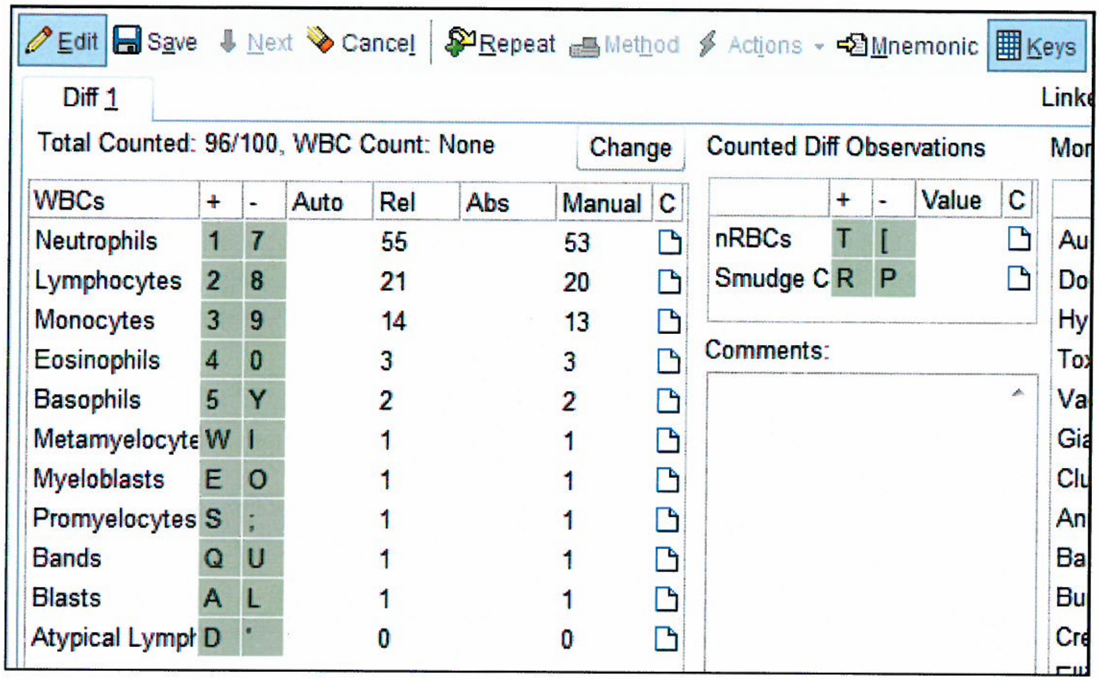
Hematology: Manual Differentials

Add a manual differential

1. On the Outstanding List, double-click the related hematology test for which you need a manual differential added. The Result Entry activity opens.
2. On the Result Editor toolbar in the middle of the activity, click ⚡ **Actions** and select **Add a Slide Review**. A manual differential is added to the specimen and the Result Editor opens. Keyboard listening is turned on by default.

> If the manual differential has already been added, it appears on the Outstanding List. In this case, you don't need to open the associated hematology test and add a manual differential.
>
> Instead, just double-click the manual differential on the Outstanding List, and then click ✏ **Edit** in Result Entry to begin entering results.

3. Using the appropriate keys, enter results for the manual differential. The system beeps and displays a message when the required number of cells has been recorded.
4. Click **Yes** to stop counting.
5. If you do not want to report the manual differential, click **Modify**, select the differential you want to report on the Reporting options window, and then click ✓ **Accept**.
6. Click 💾 **Save**.
7. Select the manual differential in the top-left pane of Result Entry and click ☑ **Verify**.



Total Counted: 96/100, WBC Count: None

WBCs	+	-	Auto	Rel	Abs	Manual	C
Neutrophils	1	7		55		53	🗋
Lymphocytes	2	8		21		20	🗋
Monocytes	3	9		14		13	🗋
Eosinophils	4	0		3		3	🗋
Basophils	5	Y		2		2	🗋
Metamyelocyte	W	I		1		1	🗋
Myeloblasts	E	O		1		1	🗋
Promyelocytes	S	;		1		1	🗋
Bands	Q	U		1		1	🗋
Blasts	A	L		1		1	🗋
Atypical Lymph	D	'		0		0	🗋

Counted Diff Observations

	+	-	Value	C
nRBCs	T	[		🗋
Smudge C	R	P		🗋

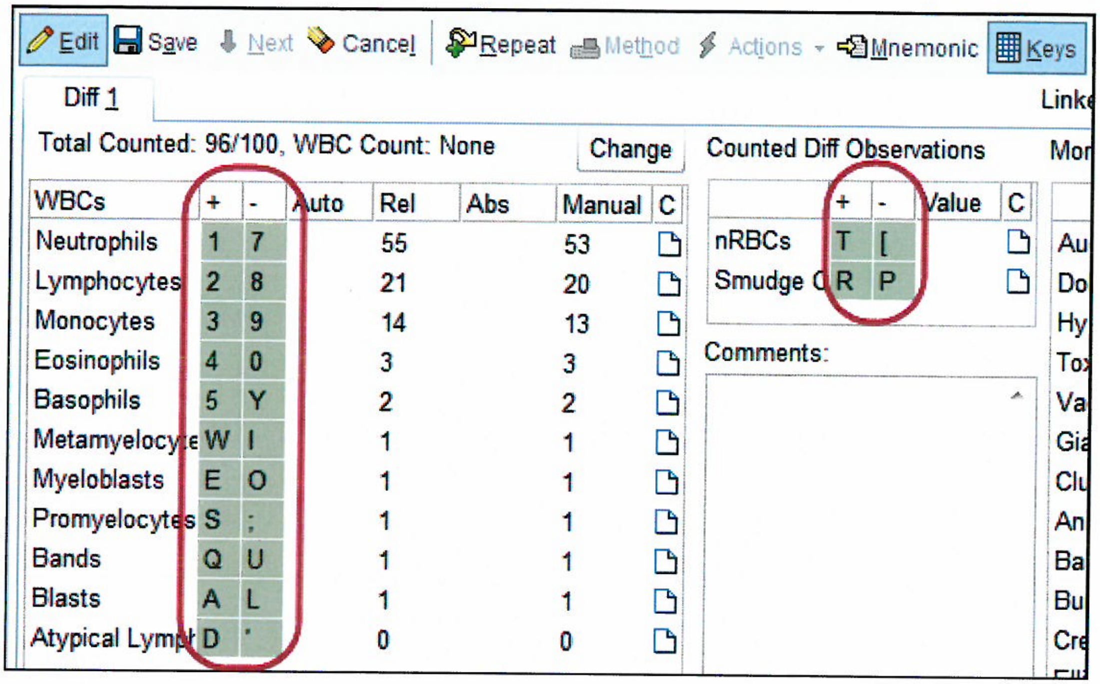
Repeat a manual differential

1. Click **Repeat** on the Result Editor toolbar.
2. Enter the results for the repeat differential on the new tab.
3. Click **Modify**, select which results to report in the **Slide review/Diff to report** field, and click ✓ **Accept**.
4. Click **Save**.

Identify which keyboard keys represent each cell type

When you enter results for a manual differential, keyboard listening is turned on automatically. When keyboard listening is on, you see green columns in the Result Editor that have numbers and letters in them. These + and - columns indicate which keys to press for each cell type to increase or decrease that cell type's total count.

For example, for neutrophils in the image below, you press 1 to increase the count and press 7 to decrease the count.



Total Counted: 96/100, WBC Count: None

WBCs	+	-	Auto	Rel	Abs	Manual	C
Neutrophils	1	7		55		53	🗋
Lymphocytes	2	8		21		20	🗋
Monocytes	3	9		14		13	🗋
Eosinophils	4	0		3		3	🗋
Basophils	5	Y		2		2	🗋
Metamyelocyte	W	I		1		1	🗋
Myeloblasts	E	O		1		1	🗋
Promyelocytes	S	;		1		1	🗋
Bands	Q	U		1		1	🗋
Blasts	A	L		1		1	🗋
Atypical Lymp	D	'		0		0	🗋

Counted Diff Observations

	+	-	Value	C
nRBCs	T	[		🗋
Smudge C	R	P		🗋

Comments:

Microbiology

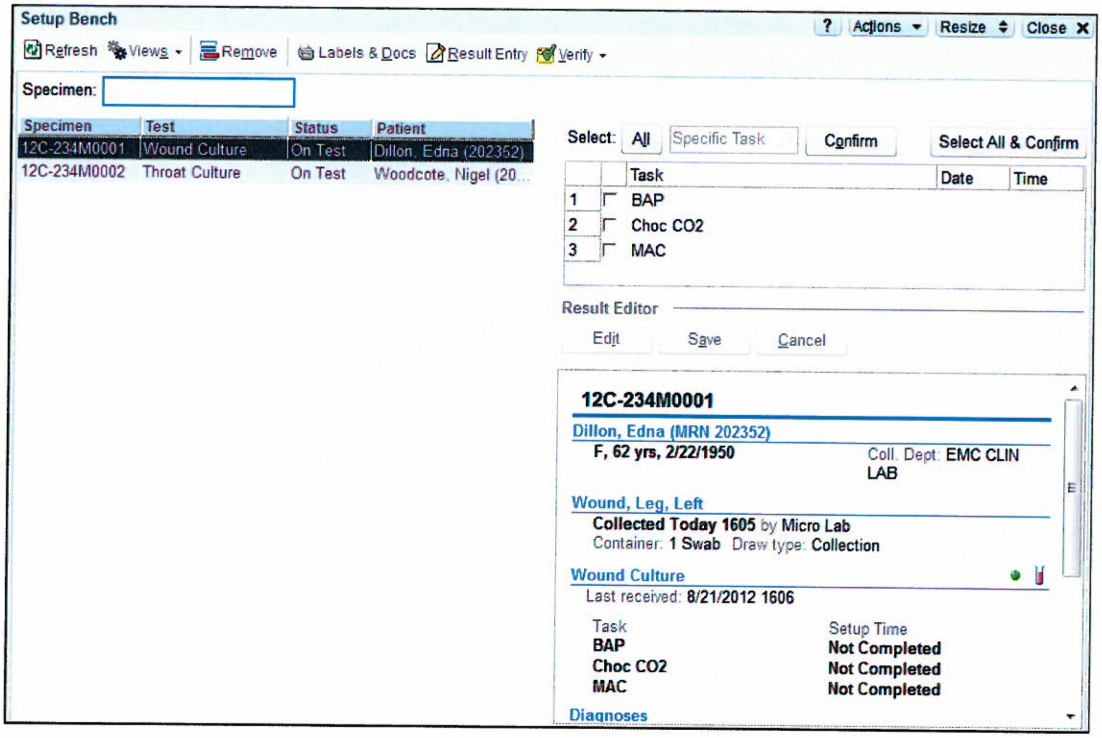
Setup Tasks

View setup tasks for microbiology tests

Pre-testing tasks, such as preparing a slide or plating a specimen, can be viewed and confirmed in the Setup Bench activity. Depending on the setup of the test, you might also enter results from this activity.

To access the Setup Bench, select the **Laboratory Work Lists** workspace tab. If you don't have that tab or don't see the Setup Bench there, you can access it from **Epic button > Setup Bench**.

In the Setup Bench, a list of tests appears on the left. The pre-testing tasks for the selected test appear in the upper-right pane, and details about the selected task appear in the lower-right pane.



Specimen:

Specimen	Test	Status	Patient
12C-234M0001	Wound Culture	On Test	Dillon, Edna (202352)
12C-234M0002	Throat Culture	On Test	Woodcote, Nigel (20...

		Task	Date	Time
1	☐	BAP		
2	☐	Choc CO2		
3	☐	MAC		

12C-234M0001

Dillon, Edna (MRN 202352)

F, 62 yrs, 2/22/1950

Coll. Dept: EMC CLIN LAB

Wound, Leg, Left

Collected Today 1605 by Micro Lab

Container: 1 Swab Draw type: Collection

Wound Culture

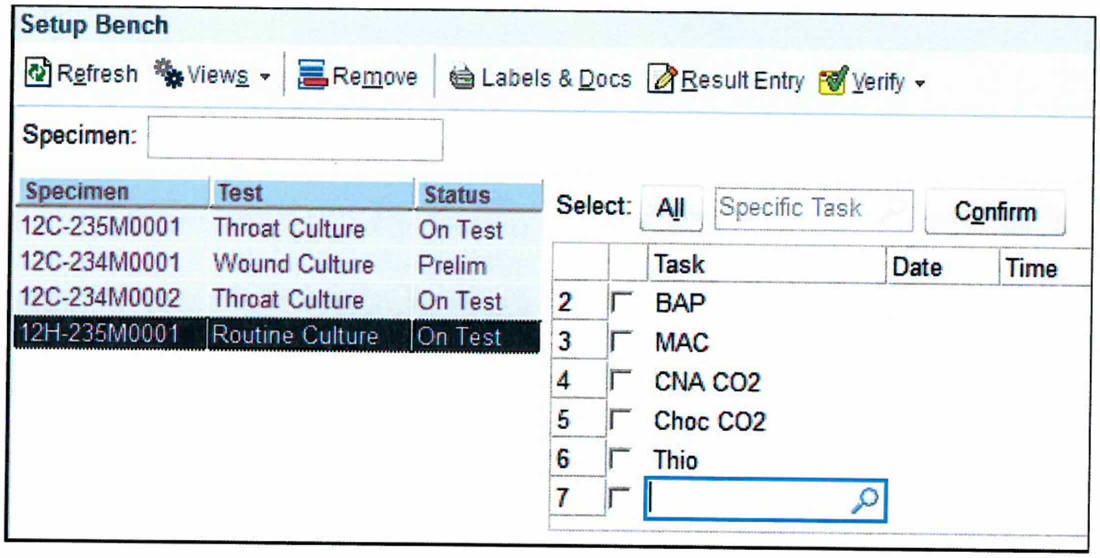
Last received: 8/21/2012 1606

Task	Setup Time
BAP	Not Completed
Choc CO2	Not Completed
MAC	Not Completed

Diagnoses

Add a setup task to the list

You can add a setup task if an empty line appears at the bottom of the list of tasks. Click 🔍 to view your options.



Specimen	Test	Status
12C-235M0001	Throat Culture	On Test
12C-234M0001	Wound Culture	Prelim
12C-234M0002	Throat Culture	On Test
12H-235M0001	Routine Culture	On Test

		Task	Date	Time
2	☐	BAP		
3	☐	MAC		
4	☐	CNA CO2		
5	☐	Choc CO2		
6	☐	Thio		
7	☐			

Document your plating tasks

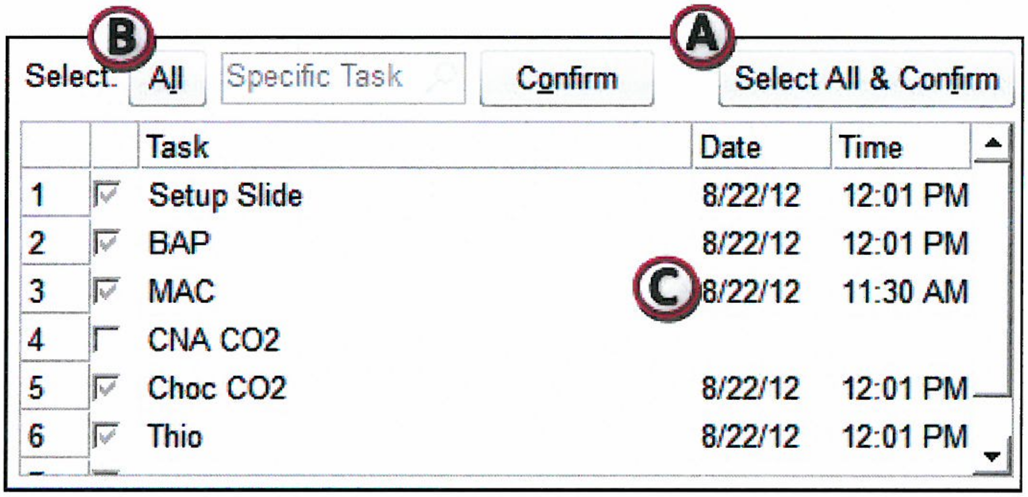
When all of your setup tasks are done, you need to confirm them in the system. The growth timer starts when you enter your confirmation that all setup tasks are complete.

!	After you click **Confirm**, you cannot undo it.

1. While in the Setup Bench, be sure that you have completed all of the tasks listed in the top-right pane. Add any additional tasks to the list, if necessary.
2. Select the tests you completed and confirm them.
    a. If you completed all of the tasks, click **Select All & Confirm**. Today's date and the current time are applied to the tasks automatically.
    b. If you did not complete a default task and do not plan to, click **All** instead, clear the check boxes next to the tasks you didn't complete, and then click

Confirm. Today's date and the current time are applied to the tasks you confirmed.

c. If you need to edit the date and time for a task, click **All** to select all of the tests, edit the dates and times as necessary, and then click **Confirm**. Today's date and the current time are applied to the tasks you confirmed.



		Task	Date	Time
1	☑	Setup Slide	8/22/12	12:01 PM
2	☑	BAP	8/22/12	12:01 PM
3	☑	MAC	8/22/12	11:30 AM
4	☐	CNA CO2		
5	☑	Choc CO2	8/22/12	12:01 PM
6	☑	Thio	8/22/12	12:01 PM

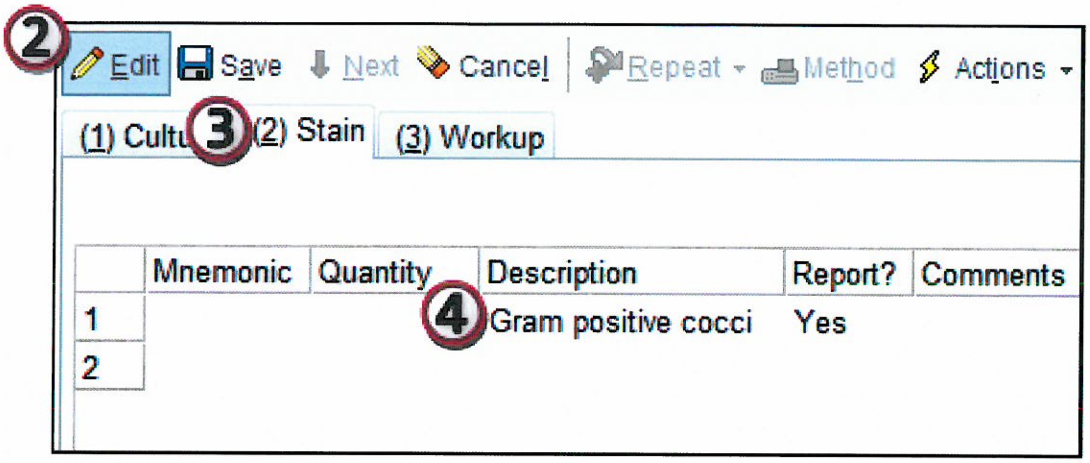
Report the results of a Gram stain

1. In the Setup Bench, double-click the specimen on which you are performing the Gram stain. The Result Entry activity opens.
2. Click **Edit** to open the Result Editor pane.
3. Select the Stain tab.
4. In the **Description** field, enter the results of the Gram stain.
5. Click **Save**.
6. Preliminarily verify the result.

   a. Right-click the test in the tree and select **Prelim Verify**.

   b. Click **Accept** in the Verification Wizard window.

7. Close Result Entry to return to the Setup Bench.



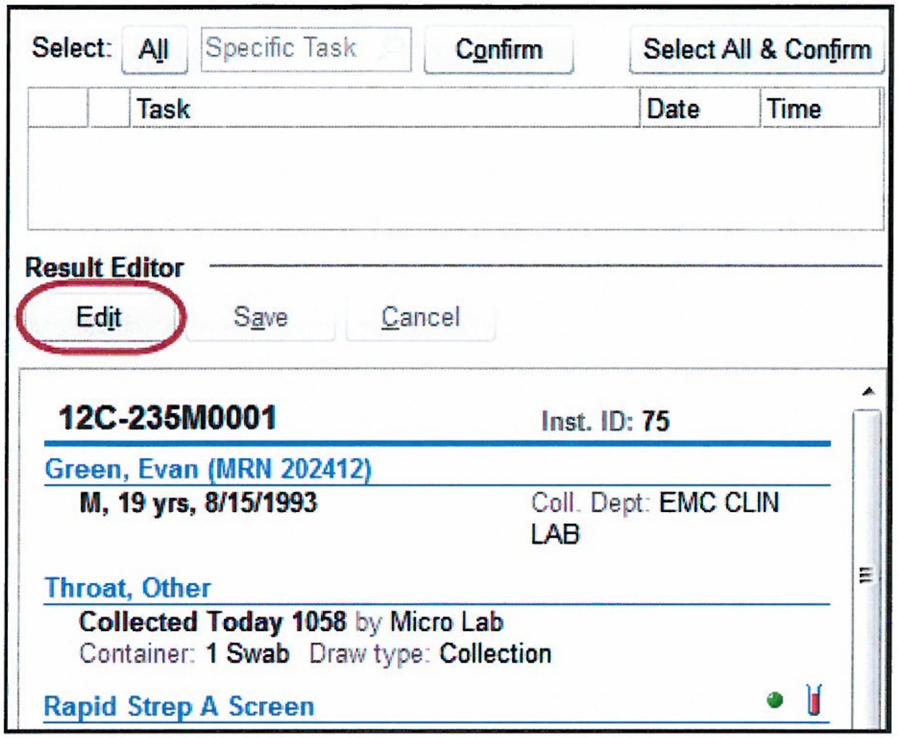
	Mnemonic	Quantity	Description	Report?	Comments
1			Gram positive cocci	Yes	
2					

Documenting Culture Growth

Enter results directly from the Setup Bench

You can enter certain test results, such as rapid strep test results, directly from the Setup Bench. For tests you can result directly from the Setup Bench, the **Edit** button is enabled.

1. Select a test and click **Edit**.
2. Enter the results in the **Value** field.
3. Click **Save**, and then click ☑ **Verify** on the activity toolbar.
4. Click ☑ **Final Verify** in the Verification Wizard. The provider is notified of the results, and the results are sent to the patient's chart.



12C-235M0001 Inst. ID: 75

Green, Evan (MRN 202412)

M, 19 yrs, 8/15/1993 Coll. Dept: EMC CLIN LAB

Throat, Other

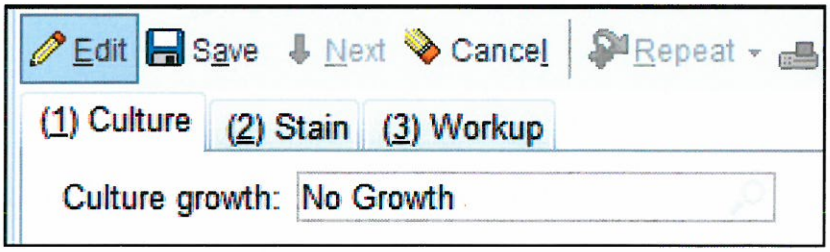
Collected Today 1058 by Micro Lab

Container: 1 Swab Draw type: Collection

Rapid Strep A Screen

Report that no growth has appeared

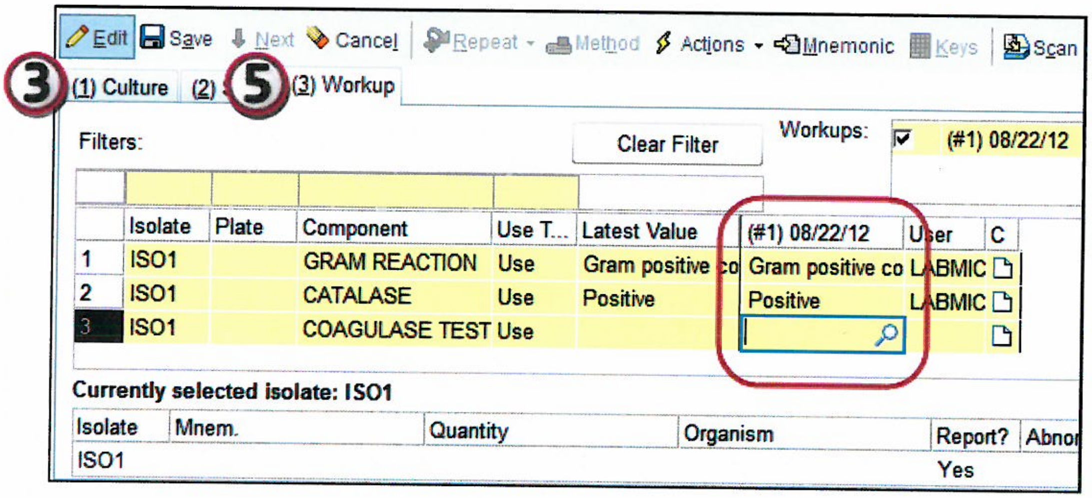
1. On the Outstanding List, double-click the test to open Result Entry.
2. Click ✎ **Edit**.
3. In the **Culture growth** field, enter "no" to completion match on No Growth at 18-24 hrs and press **ENTER**.
4. Preliminarily verify the result.
   a. Right-click the test in the tree and select **Prelim Verify**.
   b. Click **Prelim Verify** in the Verification Wizard.
5. Close Result Entry.



Culture growth: No Growth

Record organism identification tasks

1. On the Outstanding List, double-click the test.
2. Click ✎ **Edit**.
3. In the **Culture growth** field, completion match on See table below.
4. Click **Add Isolate**.
5. Select the **Workup** tab and enter the result of the first component for ISO1 in the **#1** column. The next component is automatically added to the organism identification workup.
6. Enter the results for the next component by entering a value in the **#1** column.
7. Enter the results for all subsequent components until the organism is identified. A message appears.
8. Click **OK** to remove the message.
9. Preliminarily verify the results if appropriate.



☑ (#1) 08/22/12

	Isolate	Plate	Component	Use T...	Latest Value	(#1) 08/22/12	User	C
1	ISO1		GRAM REACTION	Use	Gram positive co	Gram positive co	LABMIC	
2	ISO1		CATALASE	Use	Positive	Positive	LABMIC	
3	ISO1		COAGULASE TEST	Use				

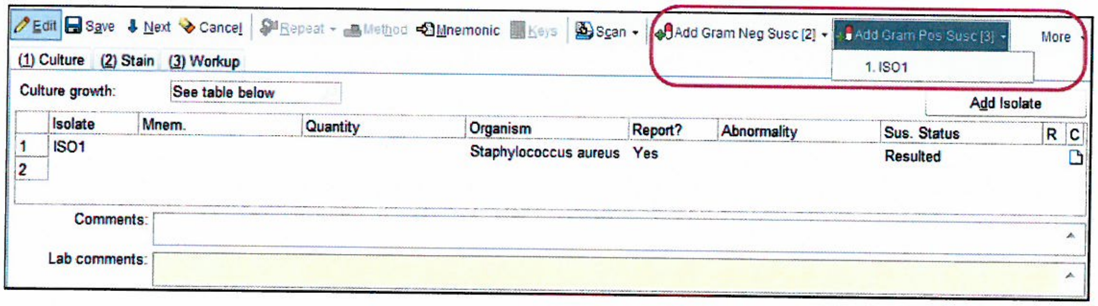
Currently selected isolate: ISO1

Isolate	Mnem.	Quantity	Organism	Report?	Abnor
ISO1				Yes	

Enter results for a susceptibility test

1. Open the Result Editor pane in Result Entry.
2. Select the **Culture** tab and confirm that the correct organism ID appears there.

3. On the Result Editor toolbar, click the appropriate **Add** button and select the isolate. You might need to click **More** to see the button you need.



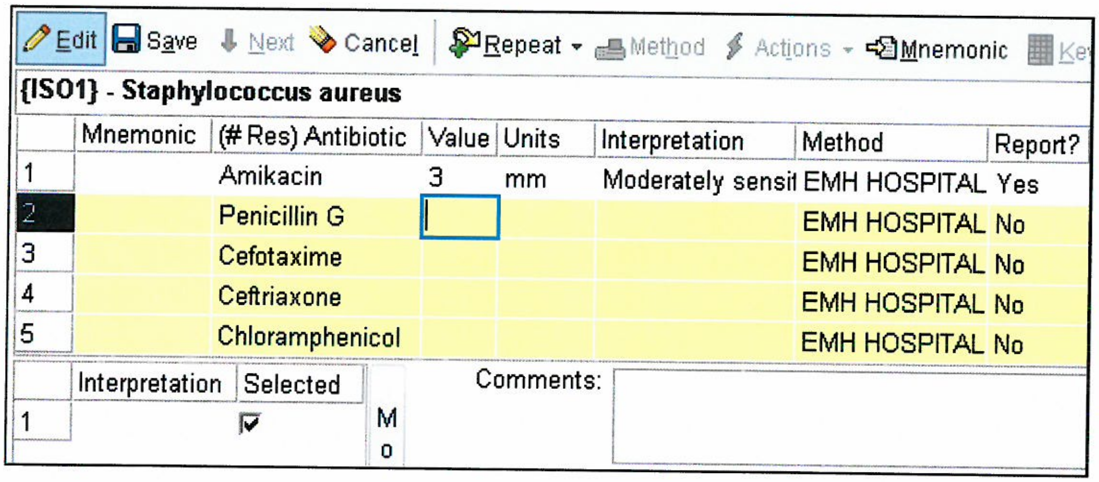
Culture growth: See table below

	Isolate	Mnem.	Quantity	Organism	Report?	Abnormality	Sus. Status	R	C
1	ISO1			Staphylococcus aureus	Yes		Resulted		
2									

Comments:

Lab comments:

1. Document the susceptibility of the organism to various antibiotics. Add appropriate units.
2. In the **Interpretation** column, document the sensitivity of the organism to the antibiotics.
3. If an organism is sensitive to an antibiotic that is set to No in the **Report?** column, change the value to Yes if you want to report it.
4. Verify the culture identification and susceptibility results together. Right-click the specimen in the tree, select **Final Verify**, and then click **Final Verify** in the Verification Wizard.



{ISO1} - Staphylococcus aureus

	Mnemonic	(# Res) Antibiotic	Value	Units	Interpretation	Method	Report?
1		Amikacin	3	mm	Moderately sensit	EMH HOSPITAL	Yes
2		Penicillin G				EMH HOSPITAL	No
3		Cefotaxime				EMH HOSPITAL	No
4		Ceftriaxone				EMH HOSPITAL	No
5		Chloramphenicol				EMH HOSPITAL	No

	Interpretation	Selected
1		☑

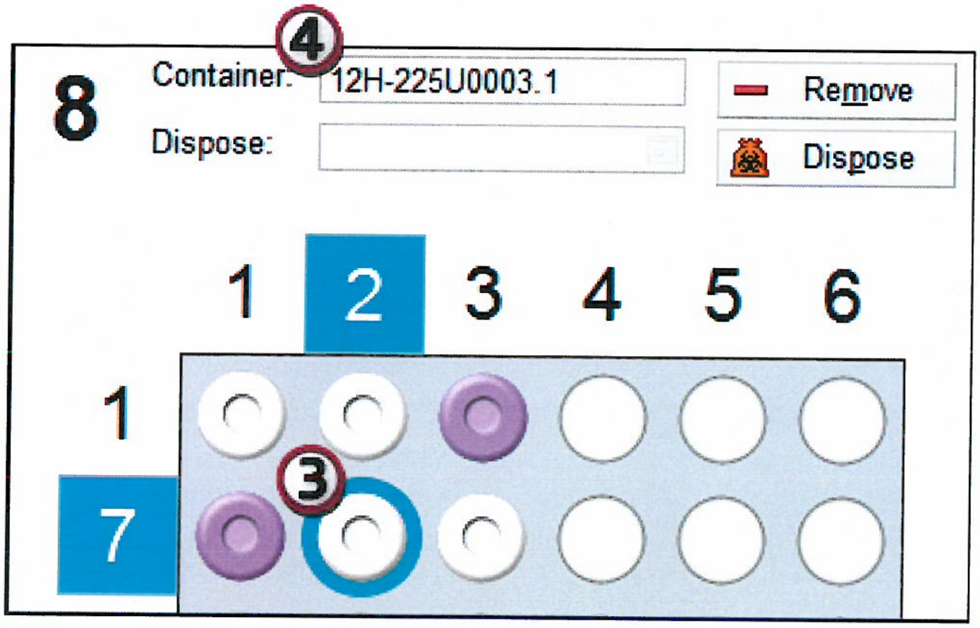
Comments:

Specimen Storage

In the system, you use an activity called Container Storage to document where specimens are being kept and when they were put in storage. When you open a rack in Container Storage, a grid on the right provides a visual representation of the actual storage rack. The grid includes color-coded tube types and container slot numbers that correspond with what is in the physical rack to make it easier to find where each specimen is located.

Add specimens to a storage rack

1. Go to **Epic button > Container Storage**.
2. On the Storage Container Lookup window, select a storage rack and click ✓ **Accept**. Container Storage opens.
3. In the grid on the right, click the slot where you have placed the given specimen. Notice that a cursor appears in the **Container** field.
4. Scan the barcode of your first specimen or manually enter the specimen ID. The specimen appears in the corresponding line in the list on the left.
5. Repeat steps 3-4 for all remaining specimens.

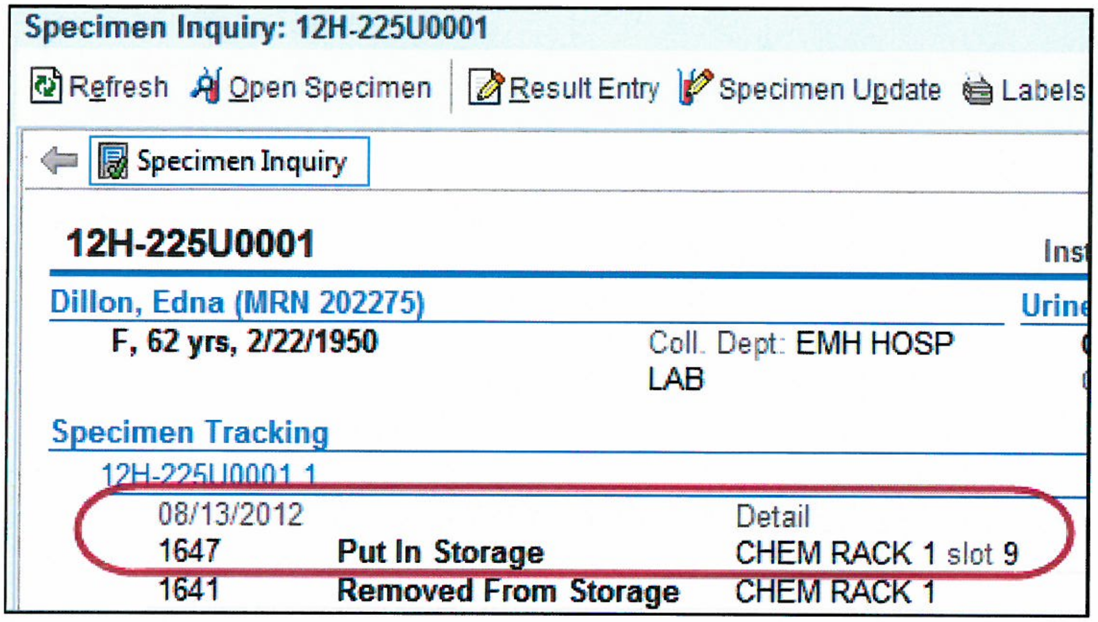


Container: 12H-225U0003.1

Dispose:

Locate a stored specimen

1. Click **Specimen Inquiry** on the main toolbar. The Specimen Lookup window opens.
2. In the **Search by** field, enter "pat" to completion match on Patient and press **TAB**.
3. Enter the pat name and select the patient.
4. Enter the date range you want to search. Then click **Refresh**.
5. Double-click the specimen you want to view.
6. Go to the Specimen Tracking Information section of the report.
7. In the **Logged Action** column, find the most recent Put In Storage status. On this line, under the **Detail** column, you see the name of the storage rack and the slot.



Specimen Inquiry: 12H-225U0001

12H-225U0001

Dillon, Edna (MRN 202275)
F, 62 yrs, 2/22/1950
Coll. Dept: EMH HOSP LAB

Specimen Tracking
12H-225U0001 1
08/13/2012 Detail
1647 Put In Storage CHEM RACK 1 slot 9
1641 Removed From Storage CHEM RACK 1

Remove a stored specimen from a rack

If a specimen needs to be removed from storage for further testing, document the removal in Container Storage. When you are ready to return the specimen to storage, you simply add it back onto the rack.

1. Go to **Epic button > Container Storage**.
2. Select the shelf, rack, or refrigerator whose specimens you want to remove from storage and click **Accept**.
3. Select the specimen you need and click − **Remove**. The specimen disappears from the rack, and the Specimen Tracking section of Specimen Inquiry is updated with an action of Removed from Storage.

Dispose of stored specimens

When specimens have been permanently disposed of, you can mark one or more specimens as disposed in the system. Disposing of a specimen is different from removing a specimen from the rack. When you remove a specimen, you can add it back to the rack later. When you dispose of a specimen, it can't be added back.

1. Go to **Epic button > Container Storage**.
2. Select the shelf, rack, or refrigerator whose specimens you want to dispose of and click **Accept**.
3. To dispose of a single specimen, select it and click **Dispose**.
4. To dispose of all the specimens, click **Dispose All** in the bottom-left corner.
5. Click **Dispose** in the warning window to dispose of all the specimens within that storage container.

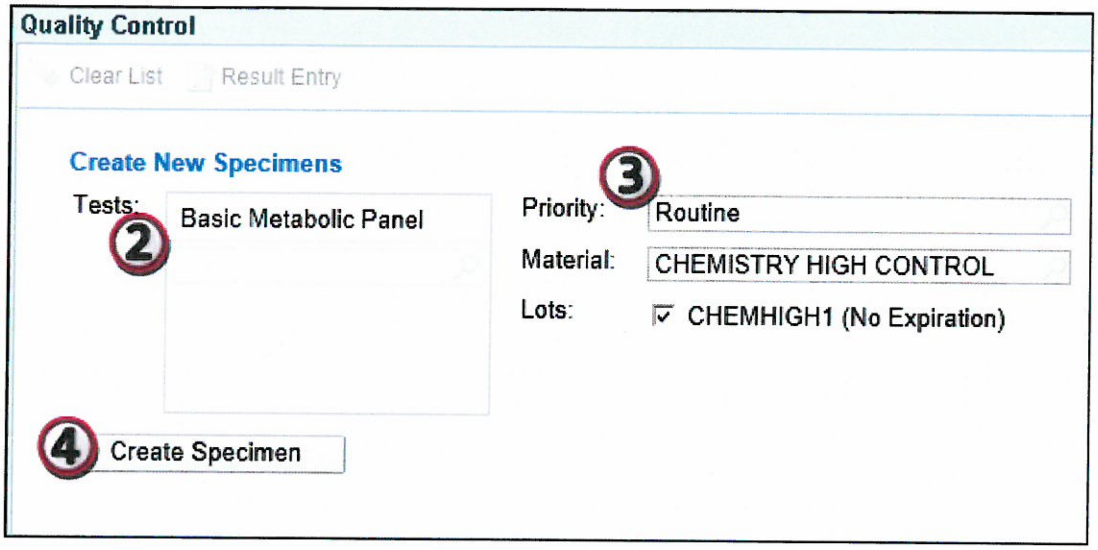
General QC

Create QC specimens manually

Usually in the lab, the system automatically creates QC specimens to be tested at a certain time of day, after a certain amount of time has passed, or after a certain number of specimens have been processed. The QC specimens and their results appear on the Outstanding List.

If your testing process changes and you need to add QC specimens, you can do so manually by following these steps:

1. Go to **Epic button > Tools > Laboratory Tools > Quality Control**. The Quality Control activity opens.
2. In the **Tests** field, completion match or use a synonym to find each test for which you are creating specimens. For example, enter "BPM" for Basic Metabolic Panel and press **ENTER**.
3. Complete the **Priority** and **Material** fields, and if applicable, select the appropriate Lots check boxes.
4. Click **Create Specimen**. The specimens are created in the system, and the **Material** field and Lots check boxes are cleared so you can create new specimens if needed.
5. Continue to create new specimens as needed. If you are creating specimens for the same test, you only need to enter the material and lot information. If you are creating specimens for a different test, update the test as well.
6. When you are done, close the Quality Control activity.



Create New Specimens

Tests: Basic Metabolic Panel

Priority: Routine

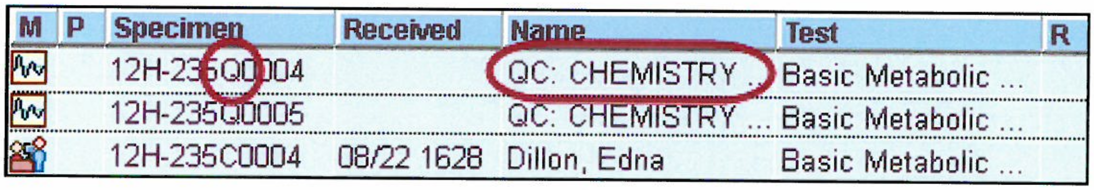
Material: CHEMISTRY HIGH CONTROL

Lots: ☑ CHEMHIGH1 (No Expiration)

Distinguish patient specimens from QC specimens

QC specimens appear on the Outstanding List, just like patient specimens. However, the QC specimens look different because:

- They have no associated patient.
- The section code of their specimen IDs is Q.



M	P	Specimen	Received	Name	Test	R
		12H-235Q0004		QC: CHEMISTRY ...	Basic Metabolic ...	
		12H-235Q0005		QC: CHEMISTRY ...	Basic Metabolic ...	
		12H-235C0004	08/22 1628	Dillon, Edna	Basic Metabolic ...	

View a QC graph

1. Go to **Epic button > Tools > QC Reports**.
2. In the QC Report Lookup window, select an existing report or create a new one, and then click **Accept**. The report settings window opens.
3. Adjust the report's criteria settings as needed and click Accept. The QC Report activity opens.

Result QC

Enter QC results

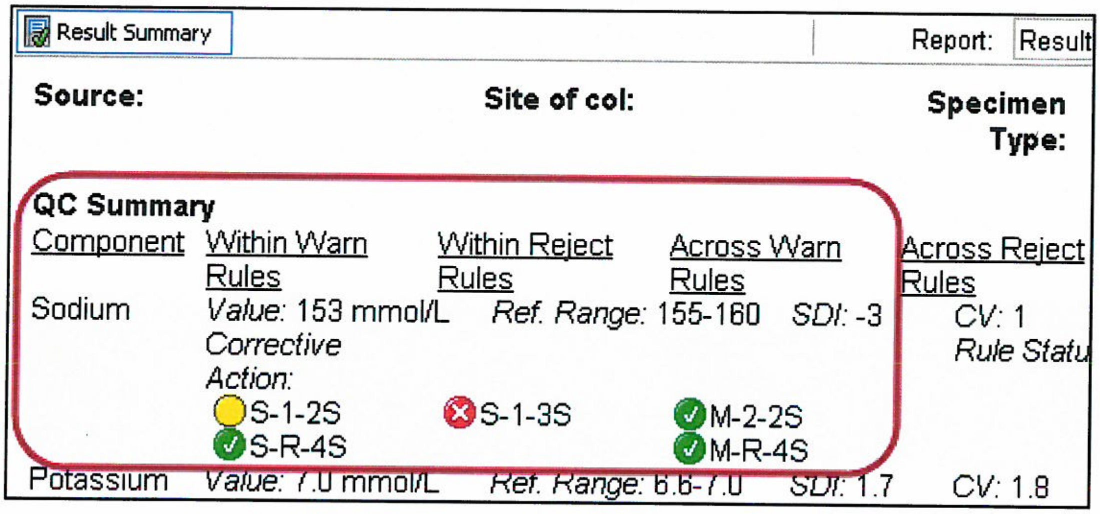
1. On the Outstanding List, locate the QC specimen and double-click it. Result Entry opens.
2. Click **Edit** and enter the test results.
3. Click **Save**.

Verify that QC results are in range

The system evaluates rules for each component to determine if the QC is in control. The icons you see in the Result Summary report indicate which rules passed, failed, or caused warnings.

1. After you result a QC specimen in Result Entry, click **Save**.
2. Select the test in the tree in the top-left pane.
3. In the preview pane, select the Result Summary report.
4. Scroll through the Result Summary report that appears, and find the components that caused warnings. Icons appear for the component-specific QC rules in the report.

   - ✓ - the result is within the rules.
   - ● - the result is outside of the Warn rule.
   - ✗ - the result is outside the Reject value.



Result Summary

Report: Result

Source: **Site of col:** **Specimen Type:**

QC Summary

Component | Within Warn Rules | Within Reject Rules | Across Warn Rules | Across Reject Rules

Sodium *Value:* 153 mmol/L *Ref. Range:* 155-160 *SDI:* -3 *CV:* 1 *Corrective Action:* *Rule Statu*

● S-1-2S ✗ S-1-3S ✓ M-2-2S

✓ S-R-4S ✓ M-R-4S

Potassium *Value:* 7.0 mmol/L *Ref. Range:* 6.6-7.0 *SDI:* 1.7 *CV:* 1.8

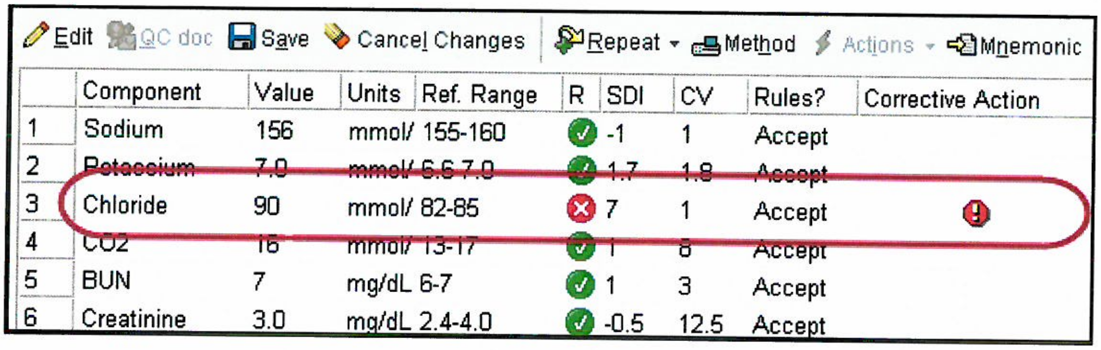
Accept or reject QC values

QC specimens are processed and resulted just like regular specimens. When the results are out of the control range, however, the **QC doc** button appears with a stop sign (🛑). This indicates that there is required documentation that you must complete for the corrective action before you can verify the QC specimen results.

1. In Result Entry, click 🛑 **QC Doc**.
2. In the **Stats?** field, enter an appropriate value if it doesn't appear.

   - **Accept** - The system will use this value when evaluating QC rules for this component.
   - **Exclude** - The system will exclude this value and use values obtained prior to this value and after the last rejected value when evaluating QC rules for this component.
   - **Reject** - The system will not use this value or any prior values obtained for this component when evaluating QC rules. This option should not be used often.

3. For any components with a ✗ in the R column, indicate your follow-up action in the **Corrective Action** field.
4. Complete the corrective action.
5. Click **Save** and, if appropriate, verify the results.

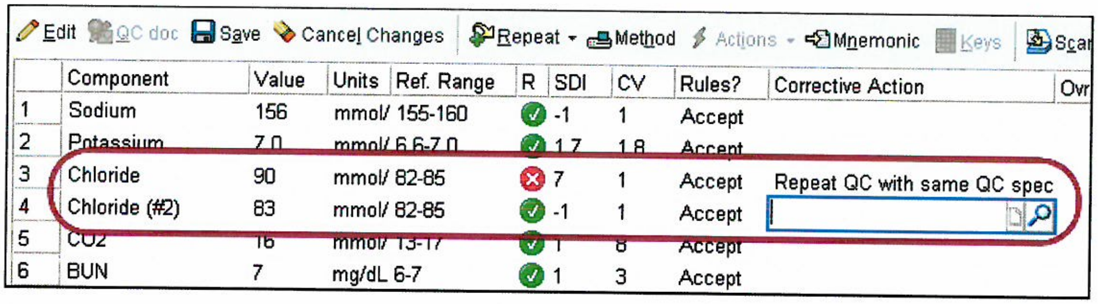


	Component	Value	Units	Ref. Range	R	SDI	CV	Rules?	Corrective Action
1	Sodium	156	mmol/	155-160	✓	-1	1	Accept	
2	Potassium	7.0	mmol/	6.6-7.0	✓	1.7	1.8	Accept	
3	Chloride	90	mmol/	82-85	✗	7	1	Accept	!
4	CO2	16	mmol/	13-17	✓	1	8	Accept	
5	BUN	7	mg/dL	6-7	✓	1	3	Accept	
6	Creatinine	3.0	mg/dL	2.4-4.0	✓	-0.5	12.5	Accept	

Repeat a component for a QC specimen

You can retest the components of a QC specimen or repeat the entire test.

1. In the Result Editor, click **Repeat** to repeat the entire test or click the arrow next to **Repeat** to select an individual component to repeat. Repeating a component adds a row to the documentation form.
2. Click **Edit**, add the new results, and click **Save**.
3. If this was part of a corrective action, click **QC Doc**.
4. Enter the appropriate value in the **Corrective Action** field.
5. Click **Save** and, if appropriate, verify the results.



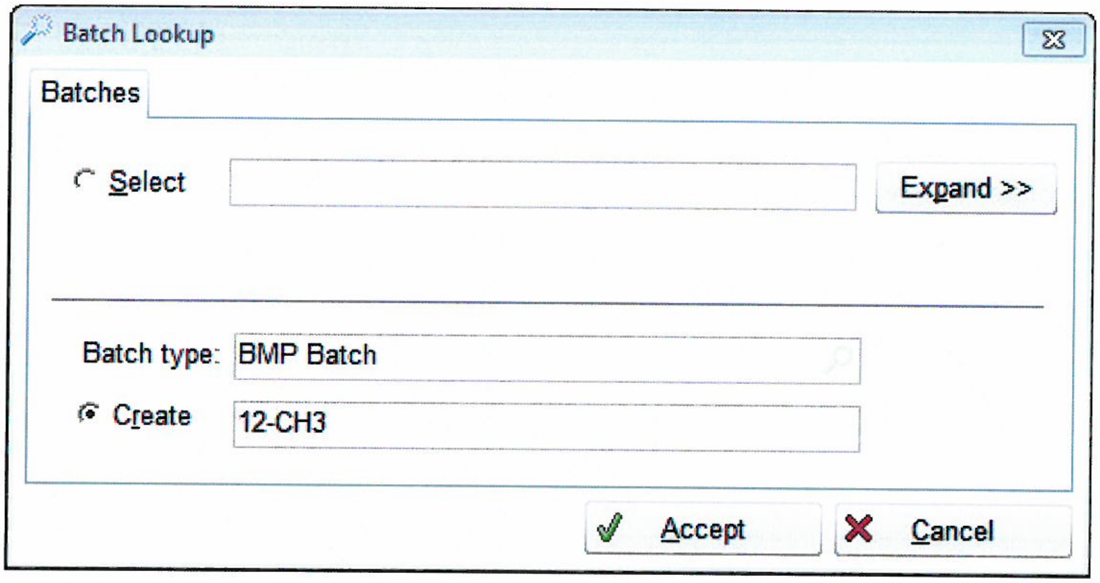
	Component	Value	Units	Ref. Range	R	SDI	CV	Rules?	Corrective Action	Ovr
1	Sodium	156	mmol/	155-160	✓	-1	1	Accept		
2	Potassium	7.0	mmol/	6.6-7.0	✓	1.7	1.8	Accept		
3	Chloride	90	mmol/	82-85	✗	7	1	Accept	Repeat QC with same QC spec	
4	Chloride (#2)	83	mmol/	82-85	✓	-1	1	Accept		
5	CO2	16	mmol/	13-17	✓	1	8	Accept		
6	BUN	7	mg/dL	6-7	✓	1	3	Accept		

Batches

Use batches to process a group of specimens or containers that have similar testing requirements. Using a batch, the system tracks the specimens throughout testing, result entry, and verification.

Create or open a batch

1. Go to **Epic button > Lab > Batch Editor**.
2. On the window that appears, select the **Create** option.
3. Select a batch type. The system assigns an ID to the batch.
4. Click **Accept** to finish creating the new batch. The Batch Editor opens.



Batch type: BMP Batch

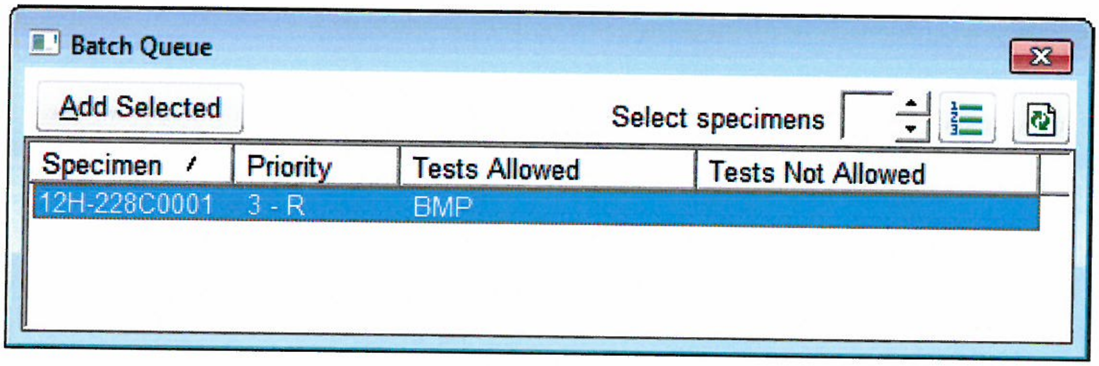
● Create 12-CH3

Edit a batch

1. In an open batch, click **Queue** to see a list of all specimens that can potentially be added to the batch.

A specimen's section code must match the batch type for that specimen to appear in the Batch Queue window.

2. Add specimens to the batch by dragging and dropping them from the Batch Queue window into specific positions in the Batch Editor. You can also use **CTRL+CLICK** to select multiple specimens, and then click **Add Selected**.
3. Close both the Batch Queue window and the Batch Editor.



Specimen	Priority	Tests Allowed	Tests Not Allowed
12H-228C0001	3 - R	BMP	

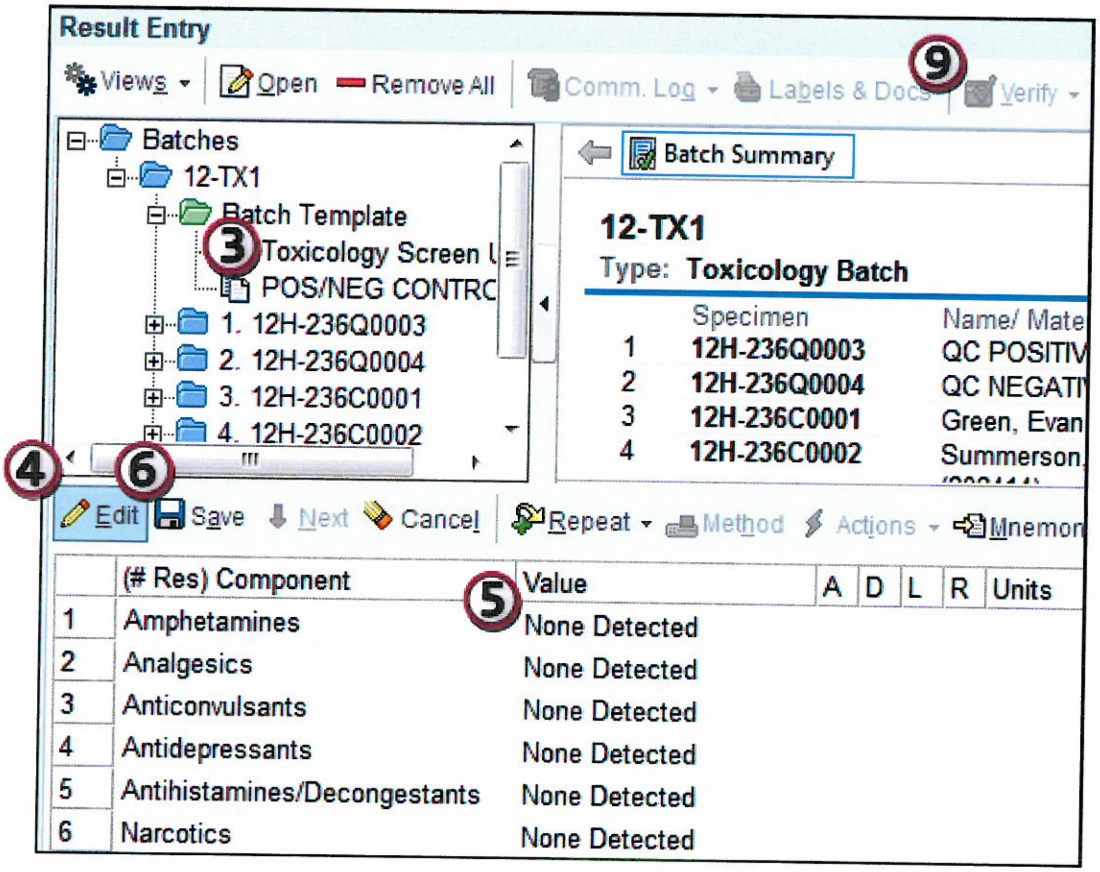
Create QC specimens in a batch

1. In the Batch Editor, place the cursor in an open position and click **Quality Control** on the activity toolbar. The Create QC Specimens window appears.
2. Complete the **Tests**, **Priority**, and **Material** fields.
3. If applicable, select the appropriate **Lots** check box.
4. Click **Create Specimen**.

Result a batch

1. Click the **Epic button > Batch List**.
2. Select the batch that you want to result and click **Result Entry**.
3. To enter results for an entire batch, select the Result Template in the tree for the batch you want to result.
4. Click **Edit** in the Result Editor.

5. In the Value column, enter the results that will be applied to all or most of the batch's specimens.
6. Click **Save**. The Apply Results window appears.
7. Click **Select All** to apply the results from the template to all specimens on the batch. Clear the check boxes next to specimens to which these results don't apply and enter those results separately.
8. Click **Accept** in the Apply Results window.
9. Select the batch ID in the tree and click **Verify**.
10. In the Verification Wizard, click **Accept**.



12-TX1

Type: **Toxicology Batch**

	Specimen	Name/ Mate
1	**12H-236Q0003**	QC POSITIV
2	**12H-236Q0004**	QC NEGATI
3	**12H-236C0001**	Green, Evan
4	**12H-236C0002**	Summerson,

	(# Res) Component	Value	A	D	L	R	Units
1	Amphetamines	None Detected					
2	Analgesics	None Detected					
3	Anticonvulsants	None Detected					
4	Antidepressants	None Detected					
5	Antihistamines/Decongestants	None Detected					
6	Narcotics	None Detected					

Important Telephone Numbers

Write your Help Desk or other support numbers here.

Signature Manifest

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Title: Maestro Care Quick Start Guide Beaker Clinical Pathology JA4

All dates and times are in Eastern Time.

STCL-SOP-058 JA4 Maestro Care Quick Start Guide Beaker Clinical Pathology JA4

Author

Name/Signature	Title	Date	Meaning/Reason
Barbara Waters-Pick (WATE02)		27 Mar 2015, 10:52:23 AM	Approved

Manager

Name/Signature	Title	Date	Meaning/Reason
Barbara Waters-Pick (WATE02)		27 Mar 2015, 10:52:35 AM	Approved

Medical Director

Name/Signature	Title	Date	Meaning/Reason
Joanne Kurtzberg (KURTZ001)		30 Mar 2015, 09:35:11 AM	Approved

Quality

Name/Signature	Title	Date	Meaning/Reason
John Carpenter (JPC27)		30 Mar 2015, 11:58:05 AM	Approved

Document Release

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Sandy Mulligan (MULLI026)		02 Apr 2015, 04:38:15 PM	Approved

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System Administrator (SYSADMIN)		13 Apr 2015, 09:13:31 AM	Approved