

User Bulletin

Sequencing Analysis Software v5.3

July 2007

SUBJECT: New Features in Version 5.3

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New Features in v5.3

This document describes the changes in Sequencing Analysis Software v5.3 which replaces Sequencing Analysis Software v5.2.X, v5.1.X, v5.0 and v3.7.

- Embedded KB Basecaller v1.4, replacing v1.2.
- Supports accurate printing electropherograms on HP® 6122 and HP® 6940 deskjet printers
- Support Windows Vista™

For more information about the KB™ Basecaller, see *FAQ, KB Basecaller v1.4* (PN 4362968).

Operating System Support

Sequencing Analysis Software v5.3 was tested on the following operating systems:

- Windows® 2000 SP3, SP4
- Windows XP SP1, SP2
- Windows Vista™

Safety

Complete Safety information is provided in the *DNA Sequencing Analysis Software Version 5.1 User Guide* (PN 4346366).

Instrument Support

Sequencing Analysis Software v5.3 replaces all previous versions of Sequencing Analysis Software. Sequencing Analysis Software v5.3 should be installed with the following versions of Data Collection Software for automated basecalling:

- 310 Data Collection Software v3.1
- 3730/3730xl Analyzer Data Collection Software v3.0
- 3130/3130xl Analyzer Data Collection Software v3.0

Manual Analysis Sequencing Analysis Software v5.3 can be used to re-analyze sample files generated with Data Collection Software versions prior to v3.0, from the following instruments:

- Applied Biosystems 3730/3730*xl* DNA Analyzers
- ABI PRISM[®] 310, 3100/3100-*Avant*, and Applied Biosystems 3130/3130*xl* Genetic Analyzers
- ABI PRISM[®] 3700 DNA Analyzer

Sample files generated from ABI PRISM[®] 377 DNA Sequencer:

- Can be displayed, edited, post-processed, printed and exported.
- Cannot be rebasecalled.

IMPORTANT! Due to differences in the basecaller algorithms between Sequencing Analysis Software v5.3 and earlier versions, reanalysis using Sequencing Analysis Software v5.3 may give slightly different results.

**Support for
Applied
Biosystems
Sequencing
Analysis Software
v5.3**

Sequencing Analysis Software v5.3 reads files created by the Applied Biosystems Genetic Analyzers Instrument that use Data Collection Software v3.0.

You can basecall sample files from these instruments using either of two basecallers.

- KB[™] Basecaller v1.4 – for calling pure or mixed bases, with quality values
- ABI Basecaller v1.6 – for calling pure bases only

KB Basecaller v1.4 has been updated to correctly call the bases generated by the 3130/3130x/ instruments. Appropriate mobility files are included with the software, as listed in Table 1.

Table 1 Mobility files for Sequencing Analysis Software v5.3 using the KB Basecaller

DNA Sequencing Chemistry	Capillary Array Length (cm)	DyeSet/Primer
ABI PRISM® BigDye® Terminator v1.X and v3.X	36	KB_3130_POP4_BDTv1.mob, KB_3130_POP4_BDTv3.mob
	50	
	80	
	36	KB_3130_POP6_BDTv1.mob, KB_3130_POP6_BDTv3.mob
	50	
	36	KB_3130_POP7_BDTv1.mob, KB_3130_POP7_BDTv3.mob
	50	
	80	
	50	

Features in v5.2 and later

The features in v5.2 and later that are not described in the User's Guide are:

- Support for Applied Biosystems DNA sequencing instruments has changed slightly
- Support for sample files generated by the Applied Biosystems 3130/3130xl Genetic Analyzers
- Electronic signature support
- New formats for exporting the analysis report
- The procedure for inactivating a user has changed slightly
- New Fill Down command for check boxes in the Sample Manager
- Additional run and analysis information in the Annotations tab in the Sample Manager
- Improved scaling options for raw data and electropherograms
- New basecalling status for the KB™ Basecaller
- An option to save only the clear range to the sequence file
- New basecalling options (for Ending Bases) for the KB Basecaller
- The ability to perform a BLAST search of the Celera Discovery System™ online platform databases, using your sequences

For more information about Sequencing Analysis Software, refer to the *Sequencing Analysis Software Version 5.3 Quick Reference Card* (PN 4359446) and the *DNA Sequencing Analysis Software Version 5.1 User Guide* (PN 4346366).

Electronic Signatures

Sequencing Analysis Software v5.3 allows you to electronically sign off when saving, printing and/or exporting an analysis report. You can also sign at any other time. A new tab in the Sample Manager has been added to display the electronic signatures.

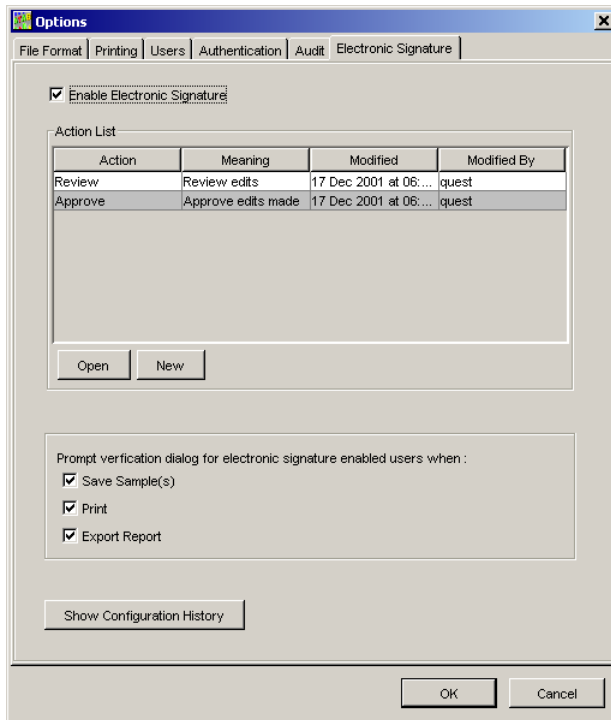
The electronic signatures feature is turned off by default. When it is enabled, an entry is made in the Electronic Signature tab of the Sample Manager, each time a user signs.

Enabling Electronic Signatures

To use the electronic signature feature, you must enable it for the application *and* for each user you want to have signature privileges.

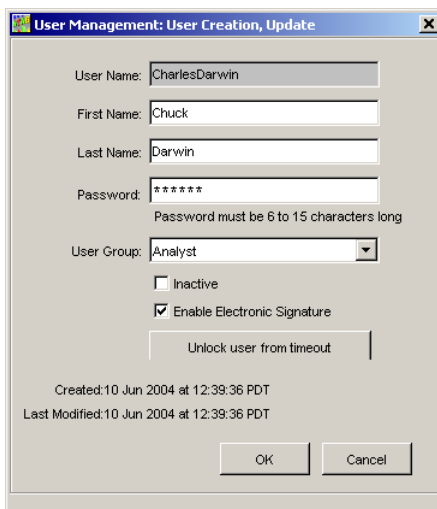
To set up your system for electronic signatures:

1. Log in as an Administrator.
2. Select **Tools > Options**.
3. Select the **Electronic Signatures** tab.



4. Select **Enable Electronic Signature**.
5. Select the actions for which you want to require electronic signatures. Select **Save Samples**, **Print** and/or **Export Result**.
Every time an electronic signature enabled user performs one of these actions, he or she is prompted to sign.
6. Select the **Users** tab.
7. Select a user, then click **Open**.

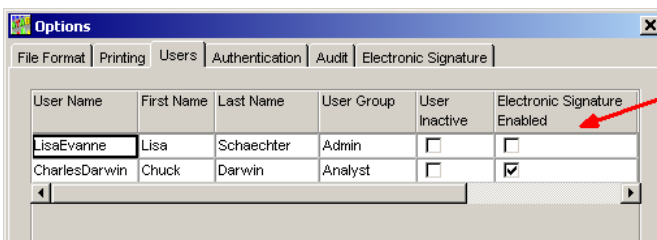
8. In the User Management dialog box, select **Enable Electronic Signature**, then click **OK**.



The dialog box titled "User Management: User Creation, Update" contains the following fields and options:

- User Name: CharlesDarwin
- First Name: Chuck
- Last Name: Darwin
- Password: ***** (Note: Password must be 6 to 15 characters long)
- User Group: Analyst
- Inactive
- Enable Electronic Signature
- Unlock user from timeout
- Created: 10 Jun 2004 at 12:39:36 PDT
- Last Modified: 10 Jun 2004 at 12:39:36 PDT
- Buttons: OK, Cancel

In the Users tab, Electronic Signature Enabled is selected for the specified user.



The "Options" dialog box, Users tab, displays a table of users with the following data:

User Name	First Name	Last Name	User Group	User Inactive	Electronic Signature Enabled
LisaEvanne	Lisa	Schaechter	Admin	<input type="checkbox"/>	<input type="checkbox"/>
CharlesDarwin	Chuck	Darwin	Analyst	<input type="checkbox"/>	<input checked="" type="checkbox"/>

A red arrow points to the "Electronic Signature Enabled" checkbox for CharlesDarwin.

9. Repeat for each user who should have electronic signature privileges.
10. Click **OK** to save.

Using Electronic Signatures

After electronic signatures are enabled, users can sign off as specified in the Electronic Signature tab.

To electronically sign your work:

1. Perform any of the actions chosen for electronic signatures.

or

Click a row header in the Sample Manager to select a sample then select **Tools > Electronic Signature > Sign**.

The Electronic Signature Verification dialog box opens.

Electronic Signature Verification

Action: Review

Created: 17 Dec 2001 at 06:30:47 PST Modified: 17 Dec 2001 at 06:30:47 PST
Created By: quest Modified By: quest

Meaning
Review edits

Challenge
Challenge Text

Comment
Looks good!

User ID: bearclaw
Password: *****

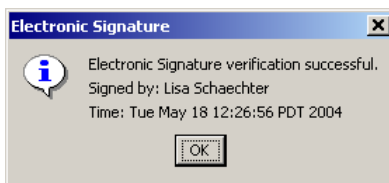
OK Cancel

2. In the Electronic Signature Verification dialog box, choose one of the actions from the drop-down list.
3. Enter your user ID and password and, optionally, any comments.

Note: If you do not have electronic signature privileges, another user with signature privileges may sign with his or her user ID and password.

4. Click **OK**.

If the signature is correct, the following message is displayed and the Electronic Signature tab in the Sample Manager is updated to display the signature.



If you do not have electronic signature privileges, a message indicates that you lack signature privileges.

5. Click **OK** to close the message box.
6. To view the electronic signatures for a sample, make sure **Show** is selected for the sample in the Sample Manager and then select the **Electronic Signature** tab.

Row	Show	Sample File Na...	Sample Name	BC	PP	P	BaseCaller	DyeSet/Primer	Matrix File	Spa...	Peak 1 Start	Stop
1	<input type="checkbox"/>	A1-2F_01	A1-2F_01	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	KB.bcp	KB_3100_POP...	None	15.33	316	316 11557
2	<input checked="" type="checkbox"/>	A1-2R_02	A1-2R_02	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Basecaller-310...	DT3100POP6(...	None	14.63	629	629 5918
3	<input checked="" type="checkbox"/>	A1-3F_01	A1-3F_01	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Basecaller-310...	DT3100POP6(...	None	14.22	566	566 5595
4	<input checked="" type="checkbox"/>	A1-3R_02	A1-3R_02	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Basecaller-310...	DT3100POP6(...	None	14.22	534	534 5543

A1-2R_02						
Action Name	User ID	User Name	Date Signed	Meaning	Comment	
Review	bearclaw	Lisa Schaechter	Mon May 17 16:22:18 PDT 2004	Review edits		
Disapprove	bearclaw	Lisa Schaechter	Tue May 18 12:26:55 PDT 2004	Sequence needs re-calling.		

To Verify a Sample

If you have electronically signed a sample, you can verify whether or not the sample has changed since the signature.

To determine if a sample has changed since the last signature:

1. Click the row number of the sample in the Sample Manager, then select **Tools > Electronic Signature > Verify**.

If the sample has not changed, the program displays:



If the sample has changed, the program displays:



Modifying the Actions for an Electronic Signature

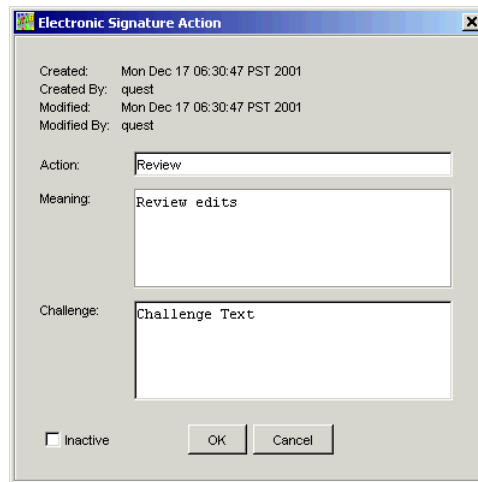
Each time you electronically sign, you must select an available action. The software comes with two built-in actions, Review and Approve. Administrators can modify them or add other actions.

To add or modify the actions for electronic signatures:

1. Log in as an Administrator.
2. Select **Tools > Options**.
3. Select the **Electronic Signatures** tab.

- To modify an action, select the action in the **Action** drop-down list and then click **Open**.

The Electronic Signature Action dialog box opens.



- Make changes to one or more of the fields:

The fields for an electronic signature action are:

- **Action** – The name of the action.
- **Meaning** – The meaning of the action.
- **Challenge** – Describes the legal implications of the action.

If you select **Inactive**, the selected action is grayed out (inactive) in the list of actions in the Electronic Signatures tab in the Options dialog box. In addition, it no longer appears in the list of actions for an electronic signature.

- Click **OK**.

Viewing the Configuration History

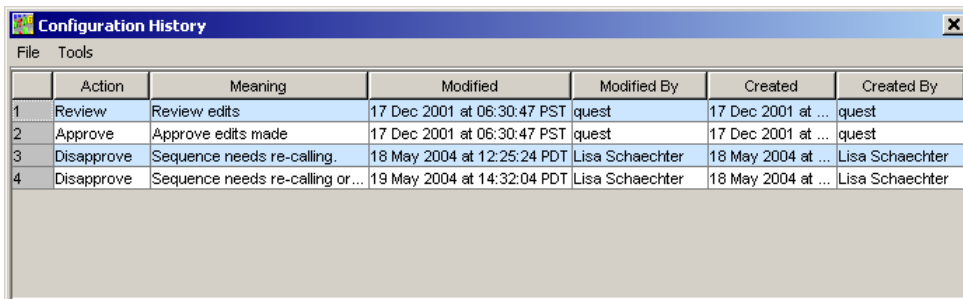
For each action, the program keeps a viewable history of the changes made to any action.

To view the history for any action:

1. Log in as Administrator, open the Options dialog box, then select the **Electronic Signatures** tab.
2. Click **Show Configuration History**.

In the Configuration History window, every action (active and inactive) is shown.

For those actions that have been modified, all versions of the action are shown, with the latest version at the bottom of the list.



The screenshot shows a window titled "Configuration History" with a menu bar containing "File" and "Tools". Below the menu bar is a table with the following data:

	Action	Meaning	Modified	Modified By	Created	Created By
1	Review	Review edits	17 Dec 2001 at 06:30:47 PST	quest	17 Dec 2001 at ...	quest
2	Approve	Approve edits made	17 Dec 2001 at 06:30:47 PST	quest	17 Dec 2001 at ...	quest
3	Disapprove	Sequence needs re-calling.	18 May 2004 at 12:25:24 PDT	Lisa Schaechter	18 May 2004 at ...	Lisa Schaechter
4	Disapprove	Sequence needs re-calling or...	19 May 2004 at 14:32:04 PDT	Lisa Schaechter	18 May 2004 at ...	Lisa Schaechter

3. In the Configuration History window you can also:
 - Select **File > Export** to save the history as a tab-delimited text file.
 - Select **Tools > Show Challenge Text** to display the Challenge text in the table.
 - Double-click an entry to view the description of the action in a dialog box.
4. Select **File > Close** to close the Configuration History window.

Other features in v5.2.X and later

Export Formats for the Analysis Report

You can export the analysis report in the following formats:

- Tab-delimited text
- HTML
- PDF
- XML

The default format is PDF. To change the format, select the format from the **Files of type** list in the Export Analysis Report dialog box.

For more information about exporting the analysis report, see page 7-14 in the *DNA Sequencing Analysis Software Version 5.1 User Guide*.

Changes to Inactivating Users

In previous versions of Sequencing Analysis Software, you could inactivate a user from the Users tab of the Options dialog box. Now you must make this change in the User Management dialog box.

To inactivate a user:

1. Log in as an Administrator.
2. Select **Tools > Options**.
3. Select the **User** tab, then double-click the user name of interest in the list to open the User Management dialog box.
4. Select **Inactive** to inactivate the user, then click **OK** to save the changes.
5. Click **OK** to close the Options dialog box.

The user's name now appears with a check mark in the Inactive column.

Fill Down Command in the Sample Manager

You can now quickly change the status of the Show check box and/or any of the Processing Parameter check boxes for all samples at once, using the Fill Down command.

To quickly change a check box for all or selected samples:

1. Click **Row** in the upper left corner of the Sample Manager pane to select all rows in the table.

or

Select a continuous range of rows using Shift-click or Shift-drag the sample row numbers.

or

Select a discontinuous range of rows using Ctrl-click.

2. Click the check box(es) of interest (**Show**, **BC**, **PP** and/ or **P**) for the first selected row to the state you want to set for the rest of them.
3. Press Ctrl-D or select **Edit > Fill Down**.

The check boxes for the selected samples are set to match the first row.

Sample Score Added to the Annotation View

The Sample Score has been added to the Annotation view of the Sample View pane in the Sample Manager. The Sample Score is only shown for those sequences for which post-processing is performed and a clear range sequence is present.

Scaling Options for Raw Data and Electrophero- grams

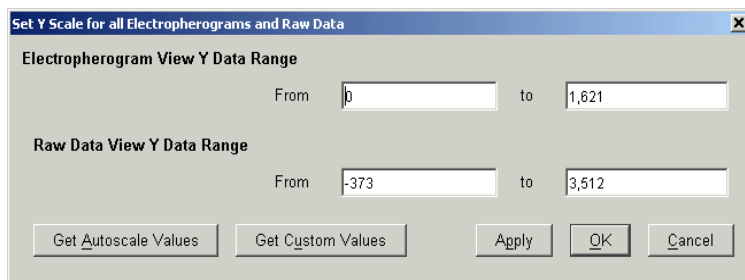
You can scale the Y axis for the raw data and/or electropherograms in the Sample Manager so that all plots use the same scale, making comparisons between samples easier.

For more information about the Raw view, see page 3-27 in the *DNA Sequencing Analysis Software Version 5.1 User Guide*. For more information about the Electropherogram view, see page 3-23.

To change the scaling for the Y axis:

1. Select **View > Y Axis Scale**, then select one of the following:
(The current setting appears with a check mark next to it.)
 - **Scale Individually** – For each plot, uses the range in the plot to set the Y axis range *for that plot*. This is the default.

- **Scale All to Max and Min Y** – For all currently displayed files, finds the overall minimum and maximum Y axis values, then sets the Y axis range *for every plot* to the *overall* minimum and maximum.
 - **Scale All to Custom Settings** – Scales every plot using the values set in the Display Settings dialog box (see below).
 - **Scale To** – Opens the Set Y Scale dialog box (see [step 2](#)).
2. If you select Scale To, the Set Y Scale dialog box opens, displaying the current settings for each type of plot in the From and to fields.



Perform one of the following actions:

- Edit the **From** and **to** values for either plot to define the range for the Y axis scale. The values must be at least 100 units apart.
 - Click **Get Autoscale Values** to update the dialog box with the minimum and maximum Y axis values for the electropherogram and the raw data for the files currently displayed in the Sample Manager (those files that have **Show** selected).
 - Click **Get Custom Values** to update the minimum and maximum Y axis values to those set in the Display Settings (see [page 16](#)).
3. Click **Apply** to rescale the plots using the new values and leave the dialog box open.

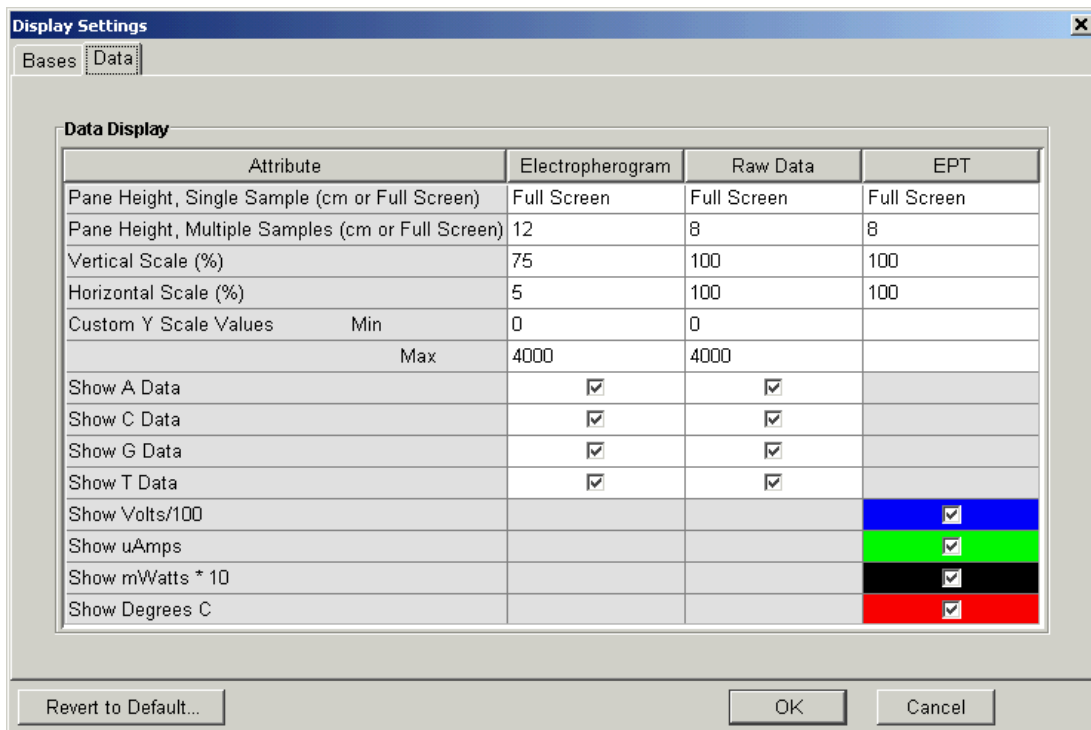
or

Click **OK** to rescale the plots using the new values and close the dialog box.

Note: If you show or hide files in the Sample Manager, the Y axis is not rescaled. Select **View > Y Axis Scale** again to rescale the plots.

To set the Y axis scaling in the Display Settings:

1. Select **Analysis > Display Settings**. In the Display Settings dialog box, select the **Data** tab.



2. For each plot, (Electropherogram and/or Raw Data), enter values for **Custom Y Scale Values Min** and **Max**. The values must be at least 100 units apart.
3. Click **OK** to make the changes.
4. Select **View > Y Axis Scale > Scale All to Custom Settings** to rescale the plots using the new values.




For more information about the Data tab in the Display Settings, see page 9-7 in the *DNA Sequencing Analysis Software Version 5.1 User Guide*.

New Basecaller Status

In Sequencing Analysis Software v5.2 and later, a fourth indicator of basecalling status has been added to the analysis report (Table 1). This indicator, a blue diamond, indicates successful basecalling but with some anomalies. In earlier versions of the software, only three indicators of basecalling status were available.

Also, the BC check box in the Sample Manager window now shows blue (when appropriate) in addition to green, yellow and red

Table 2 Basecalling Status Indicators

Symbol	Indication of Basecalling Status
	The basecaller analyzed the sample file correctly.
	The basecaller analyzed the sample file successfully, but detected some anomalies that may or may not be serious. Review the error message, the sample score, and the data.
	The basecaller analyzed the sample file successfully, but detected some anomalies that may or may not be serious. Review the error message, the sample score, and the data.
	This is a software failure. Check the software error messages.

For more information about check box colors in the Sample Manager window, see page 5-8 in the *DNA Sequencing Analysis Software Version 5.1 User Guide* and the following section. For more information about basecalling status, see page 7-5 in the *DNA Sequencing Analysis Software Version 5.1 User Guide* and the following section.

Basecalling Status Overview

Depending on the basecaller you use, either one of two or one of four of status indicators are displayed to indicate sequence quality.

- ABI Basecaller – Green and red indicators only
- KB™ Basecaller – Green, blue, yellow, or red

Typical samples that you run according to recommended protocols should be reported by the KB Basecaller with the green status. However, a sequence called by the ABI Basecaller with the green status is not necessarily of better quality than the same sequence called by the KB Basecaller but with the blue or yellow status.

Because the status that the KB Basecaller reports can be more precise than that reported by the ABI Basecaller, due to more signal-processing quality control, a green status assigned by the ABI Basecaller includes the criteria for the green, blue, and yellow statuses reported by the KB Basecaller. Therefore, a sample with green status as reported by the ABI Basecaller might receive only the yellow (for low-quality data) or blue status (for anomalies) if reported by the KB Basecaller. In addition, the KB Basecaller produces per-base quality values, but the ABI Basecaller does not. For these reasons, if you use the ABI Basecaller, you should carefully review all sequences against the processed electropherograms.

Blue Status

The KB™ Basecaller returns the blue status in cases where the sample data are sub-optimal or contain anomalous characteristics, but otherwise can still be called. Consult the analysis report for detailed diagnostic messages, and examine the processed electropherogram and basecalls to determine the severity of the problem. Note that samples in this category still contain long regions of high-quality calls, as indicated by the per base quality values.

Yellow Status

The KB Basecaller returns the yellow status when the sequencing experiment fails or is severely compromised in a way that prevents a successful analysis. In this case, the software saves the results to the sample file, but the called sequence is replaced with a placeholder sequence of five N's instead of basecalled data. A common reason for this status is a failed sample, where few or no DNA peaks are evident in the raw data. Note that if such a failed sample is basecalled using the ABI Basecaller, the green status is likely to be returned, but the data most often are unreliable.

Red Status

For both basecallers, the red status typically indicates a software configuration error or invalid input to the basecalling algorithm. No analysis results will be written to the sample file and the file remains in the unanalyzed state. Use the analysis report to diagnose the problem or contact Applied Biosystems Technical Support.

For more information about the KB™ Basecaller, see *FAQ, KB Basecaller v1.4* (PN 4362968).

Saving the Clear Range with the Sequence

When you save your samples you can save either all the sample data (as in previous software versions) or only the clear range.

To save the clear range only, in the General tab of the Sequence Analysis Protocol Editor, select **Write .Seq File** and **Write Clear Range in .Seq File**, then click **OK**.

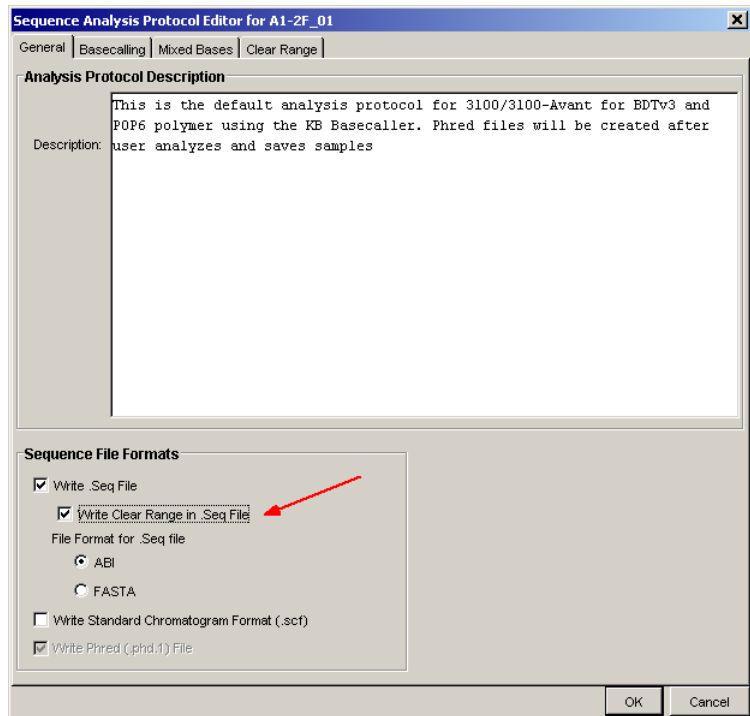


Figure 1 General tab in the Protocol Editor dialog box

When you save your samples, the sequence files will contain only the clear range.

This option, to save only the clear range, is also available in the Analysis Defaults dialog box.

For more information about the General tab in the Sequence Analysis Protocol Editor, see page 8-6 in the *DNA Sequencing Analysis Software Version 5.1 User Guide*.

New Basecalling Options for the KB Basecaller

All of the Ending Base options in the Basecalling tab of the Sequence Analysis Protocol Editor now apply to both the KB™ Basecaller and the ABI Basecaller. (Previously, the **After _Ns in _bases** and the **After _Ns** options were only applicable to the ABI Basecaller.)

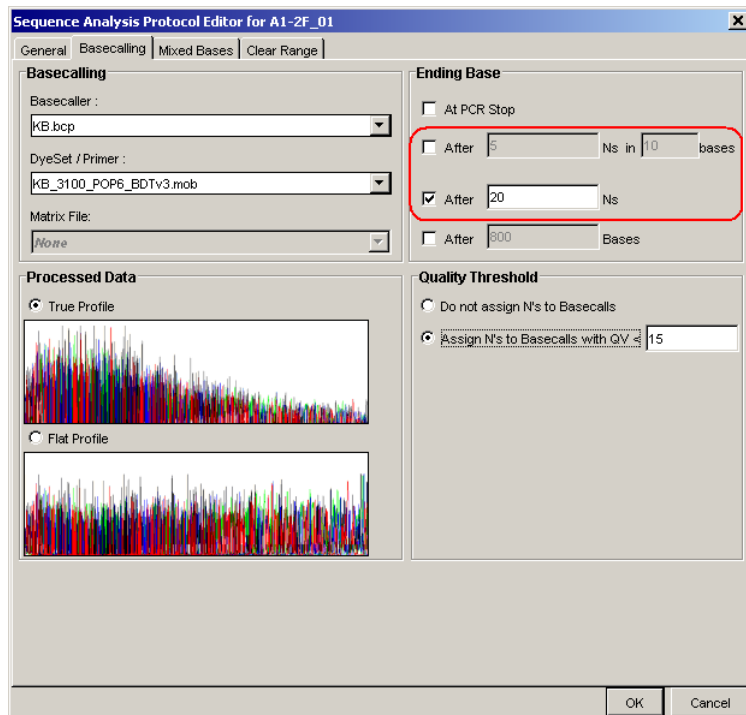


Figure 2 Basecalling tab in the Protocol Editor dialog box

Note: To use either **After _Ns in _bases** or **After _Ns**, you must also choose **Assign ‘N’ for bases with QV < 15** in the Quality Values section.

The behavior of the **After _ Ns in _ bases** option is slightly different for the two basecallers:

- ABI Basecaller: the window described by **in _ bases** begins at the first base.
- KB Basecaller: the window described by **in _ bases** begins at the 51st base.

The **After _ Ns** option is the same for each basecaller; the basecaller will start calling bases from the 5' end of the sequence and stop when the specified number of N's is reached.

For more information about the Basecalling tab in the Analysis Protocol, see page 8-7 in the *DNA Sequencing Analysis Software Version 5.1 User Guide*.

New BLAST Searching with the Celera Discovery System™ Online Platform

You can now easily connect to the Celera Discovery System Platform from Sequencing Analysis Software v5.3.

The Celera Discovery System (CDS) Platform provides comprehensive, regularly-updated mouse and human genome data from proprietary and public sources. The data are integrated, aggregated, validated, curated and classified, and are provided with analysis tools and super computer power. Sequencing Analysis Software v5.3 allows you to easily perform a BLAST search against the CDS Platform databases with your results.

To learn about the features of CDS Platform and how to purchase a subscription, go to:

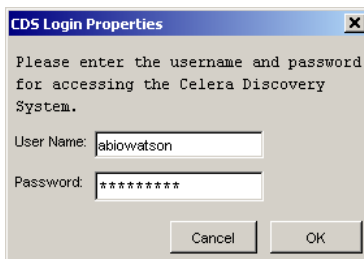
<http://www.celeradiscoverysystem.com/glance/home.cfm> or call your Applied Biosystems sales representative.

Note: You must have a subscription to use CDS Platform.

To run a BLAST search on CDS Platform:

1. Add data files and run your analysis as usual.
2. In the Sample Manager pane, click the row number of the sample for the sequence you want to use in a BLAST search, then select **DBSearch > CDS Nt BLAST Search**.

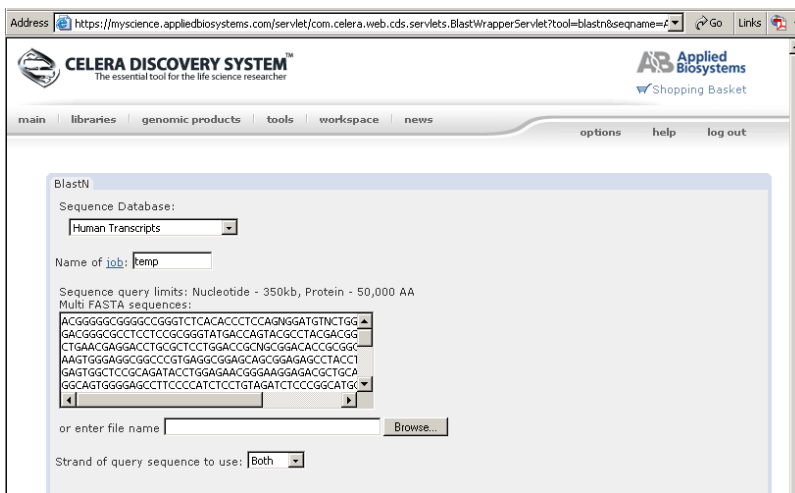
The CDS Platform Login Properties dialog box opens.



3. Enter your CDS Platform user name and password, then click **OK**.
4. The program opens a browser window and connects to CDS Platform.

Note: You may be prompted to synchronize your Applied Biosystems Store account with your myScienceSM Research Environment or Celera Discovery SystemTM Platform account. Synchronizing allows you to log in with just one User ID and password. If you want to synchronize your accounts, follow the instructions on the page. If not, click **Cancel**.

The BLASTN search form opens in the browser window, with the clear range of the sequence automatically entered in the form.



5. Modify the search parameters as desired and click **Submit** to begin the search.
(Click **help**, in the upper right of the web page, for information about the search parameters.)
6. CDS Platform will display the Queue tab, showing the searches you have in the queue, with the newest search at the top of the list.
7. To update the list with the current status, click **Reload** in your browser or the **processing** button on the web page.

The screenshot shows the Celera Discovery System web interface. The browser address bar displays the URL: <https://myscience.appliedbiosystems.com/servlet/com.celera.web.cds.servlets.PortalProxy?page=batchJobStatus>. The page header includes the Celera Discovery System logo and the Applied Biosystems logo. The main navigation bar contains links for main, libraries, genomic products, tools, workspace, and news. The current page is titled "workspace" and "KEEPING YOUR WORK TOGETHER". The "Queue" tab is selected, showing a "Queue Status: June 09, 2004" and "2 CPU seconds used." Below this, there is a table of search jobs:

Batch	Analysis	Job Name	Submitted (ET)	Status	# of hits (select to view completed results)
4.	-	BLASTN temp_job5	09-Jun-2004 18:49	processing	
3.	-	BLASTN temp_job4	09-Jun-2004 18:22	Complete	37 View Results
2.	-	BLASTN temp_job3	09-Jun-2004 18:10	Complete	47 View Results
1.	-	TRANSEQ temp_job2	29-Sep-2003 20:16	Complete	6 View Results

At the bottom of the page, there is a footer with links for Legal Notice, Terms of Use, Sales & License, and Privacy Policy, and a copyright notice for Applied Biosystems, 2004.

- When processing is complete, click the **View Results** link. The page containing the results is displayed.

The screenshot displays the Celera Discovery System web interface. At the top, the address bar shows the URL: <https://myscience.appliedbiosystems.com/servlet/com.celera.web.cds.servlets.PortalProxy?id+PERMABIOSCHAECHTER+e+BLAST>. The page header includes the Celera Discovery System logo and the Applied Biosystems logo. The main content area shows a BLAST search query: **BLASTN[BLASTN-JobName:temp_job5.blastn.1] (30 hits)**. Below the query, there is a sequence alignment visualization with a color key for alignment scores. The color key is as follows:

Score Range	Color
40-60	Blue
60-80	Green
80-200	Magenta
>=200	Red

Below the alignment visualization, there is a link to [View Raw Application Output](#). The search results are displayed in a table with the following columns: Query, 273 letters FastaSequence, ID, Gene Name, Gene Symbol, Score, E Value, Location (Scaffold), and Panther Best Hits.

<input type="checkbox"/>	ID	Gene Name	Gene Symbol	Score	E Value	Location (Scaffold)	Panther Best Hits
<input type="checkbox"/>	1. hCT2292573	major histocompatibility complex, class I, C	HLA-C	522	1e-147	GA_x5YUV32W6W6	MHC_CLASS I ANTIGEN
<input type="checkbox"/>	2. hCT2292574	major histocompatibility complex, class I, C	HLA-C	522	1e-147	GA_x5YUV32W6W6	MHC_CLASS I ANTIGEN
<input type="checkbox"/>	3. hCT2292576	major histocompatibility complex, class I, C	HLA-C	522	1e-147	GA_x5YUV32W6W6	MHC_CLASS I ANTIGEN
<input type="checkbox"/>	4. hCT2292570	major histocompatibility complex, class I, C	HLA-C	442	1e-123	GA_x5YUV32W6W6	MHC_CLASS I ANTIGEN

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