

User Guide to



DNASTAR

GenVision Pro

DNASTAR, Inc. 2020

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Welcome to GenVision Pro

GenVision Pro supports visualization and analysis of multiple samples from a single genome. In RNA-seq, ChIP-seq and copy number variation (CNV) studies, where coverage and peak plots are compared and used to interpret gene expression and regulation, the ability to display and compare genome-wide data sets for multiple samples makes GenVision Pro an essential tool

With GenVision Pro, you can visually navigate between single-segment chromosomes and/or contigs of a genome, then export publication-quality images.

The following video shows how easy it is to use GenVision Pro:

These support pages contain written help and tutorials, as well as video tutorials.

- For help **INSTALLING** Lasergene, see our separate [Installation Guide](#).
- For written **TUTORIALS** with free data, see [GenVision Pro Tutorials](#).
- [Click here](#) for a list of all topics that include **VIDEOS**.
- To **PRINT** the current page of the User Guide, click the printer icon in the top right corner ().
- To download a **PDF** of the entire User Guide, scroll to the bottom of the table of contents on the left, and press **Download as PDF**.

GenVision Pro Tutorials

GenVision Pro tutorials are listed below. Any data needed can be downloaded for free using the link provided in the tutorial.

- [Analyze an E. coli assembly](#) – Links to the first of four parts.
- [Analyze Copy Number Variation \(CNV\) results](#) – This tutorial is located in the SeqMan NGen User Guide. The workflow begins with assembly in SeqMan NGen and uses ArrayStar and GenVision Pro for downstream analysis.


Try It! – Analyze an E. coli assembly

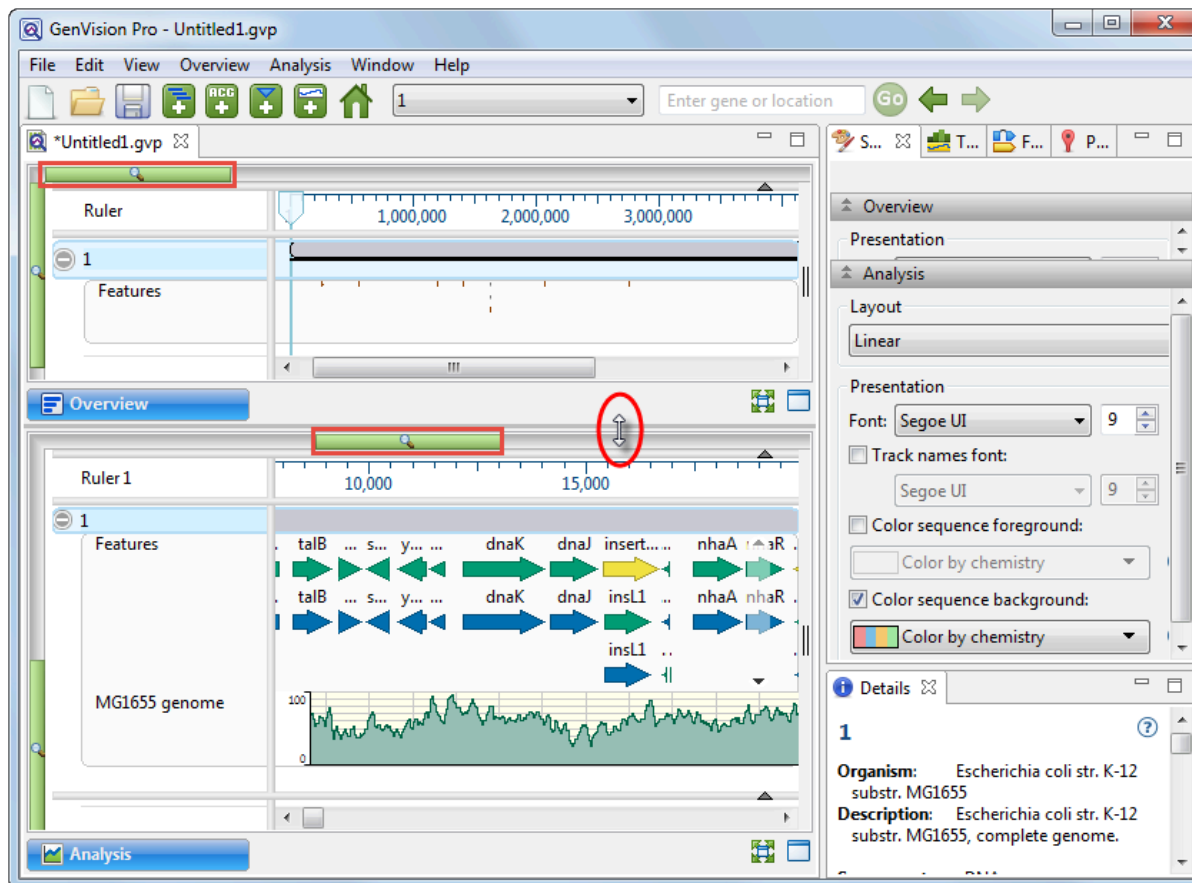
The following tutorial uses free data from the DNASTAR website to demonstrate a typical workflow in GenVision Pro. The tutorial is in four parts, which should be done in order.

Begin with [Part A: Start a new session and rename a sequence using data fields](#).

Part A: Start a new session and rename a sequence using data fields

In this first part of the GenVision Pro tutorial, you will start by downloading and extracting the tutorial data from the DNASTAR website. Next, you will begin a new session and add an *E. coli* assembly produced by DNASTAR's [SeqMan NGen](#). You will then create a custom label for the sequence based on the accession number and sequence description.

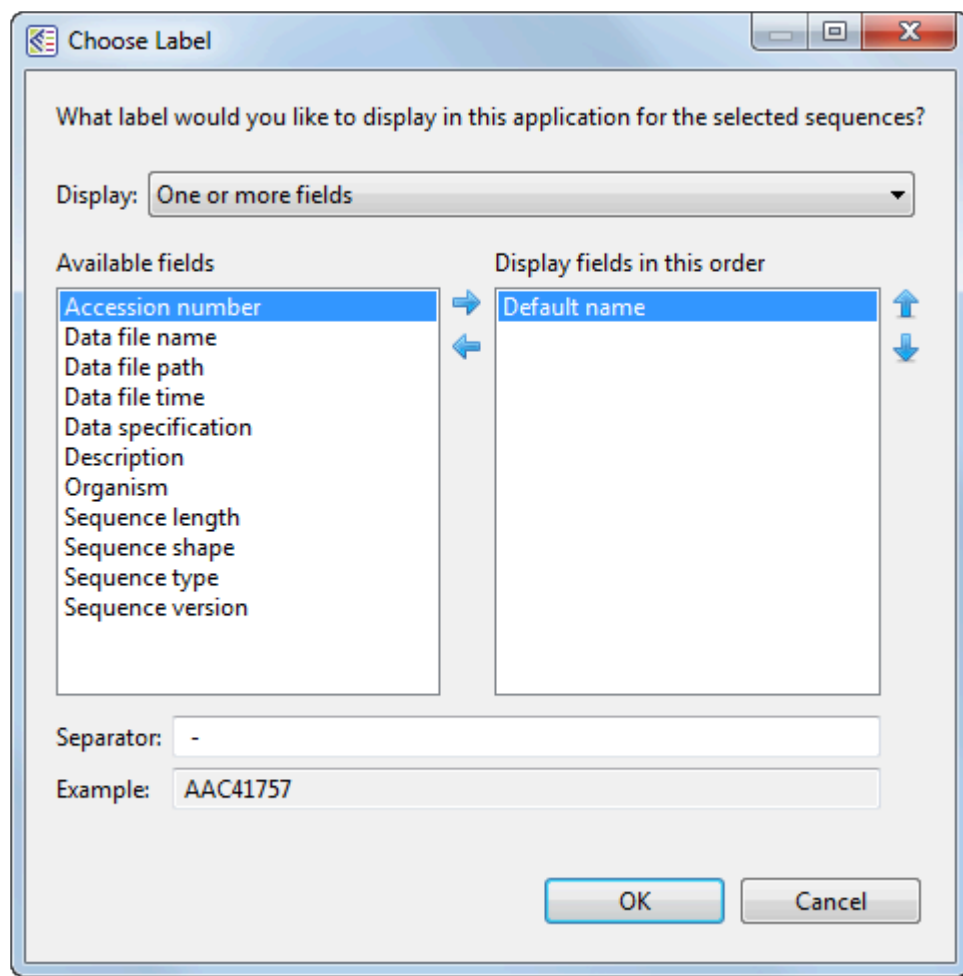
1. [Download the tutorial data](#) extract the folder to any suitable location (e.g., your desktop).
2. If a GenVision Pro project is already open, choose **File > New GenVision Pro Session**. Otherwise, launch GenVision Pro.
3. Add file *MG1655_genome.assembly* to the session using either of the following methods:
 - Use **File > Add Assemblies** or press the **Add Assemblies to project** button (). Select the assembly, and then press **OK**. Note that double-clicking is not supported in this dialog.
 - Drag & drop the assembly on the GenVision Pro window.
4. Drag the pane dividers and the horizontal zoom sliders until the view looks approximately like the image. Drag the horizontal pane divider upwards, if necessary, until the [Analysis view](#) is about twice as tall as the [Overview](#).



Note that the name of the active sequence is '1.' In the next steps, you will be changing this name to something more useful.

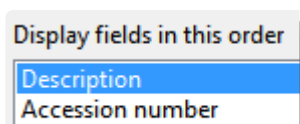
- Right-click on sequence '1' in either view and choose **Rename with Fields**. This opens the Choose Label dialog.

Note that the **Display** is set to **One or more fields**. This setting lets you automate the naming process for any number of selected sequences using fields such as sequence length, organism, or description.



The left pane shows available fields, and the right pane shows fields that will be displayed as part of the sequence name. Initially, **Default name** is the only field listed in the right pane.

6. Select and organize the fields to display as part of the sequence name:
 - a. Click on the left arrow (←) to remove **Default name** from the right-hand pane.
 - b. Use **Ctrl/Cmd+click** to select **Accession number** and **Description** from the list on the left. Click the right arrow (→) to move them to the right-hand pane.
 - c. Click on **Description** on the right to select it. Then use the up or down arrows on the right (↑↓) to move **Description** to the top of the list.



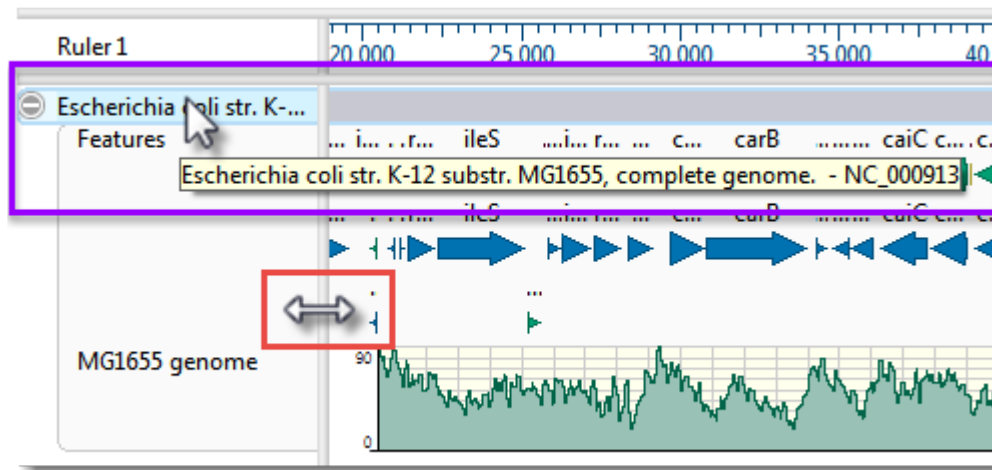
- d. Click **OK** to save changes and exit from the dialog.

The sequence name in both the Overview and Analysis view has changed from '1' to:

Escherichia coli str. K-12 substr. MG1655, complete genome. - NC_000913

However, you may only be able to see the first part of the name.

- To see a tooltip displaying the full name, hover your cursor over the visible portion of the name (see area boxed in purple, below).



- To view the entire name, drag the pane divider (boxed in red, above) to the right. Then return the pane divider to its original position for ease of viewing the sequence section in the next part of the tutorial.

✿ **Note:** Even if the full name is not visible when viewed in the GenVision Pro window, it will be shown in the [Details panel](#), the Navigation bar's chromosome selector (the drop-down menu) and in printouts of the views.

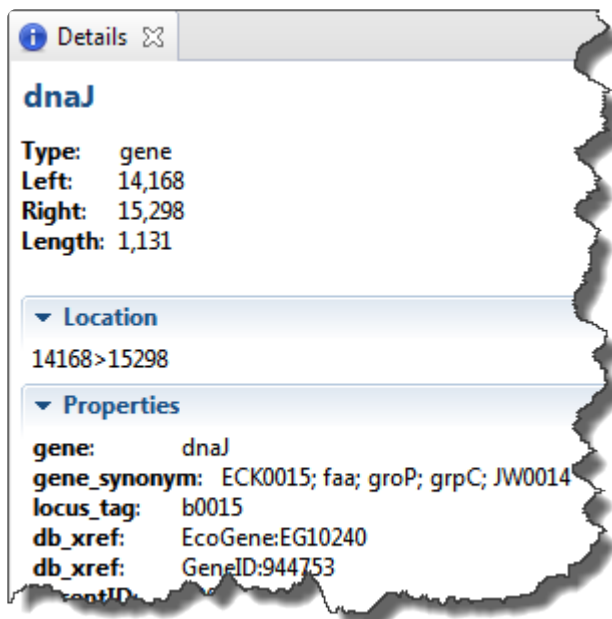
- To edit the name field manually, right-click on the name and select **Rename**. This opens the same dialog as before, but **Display** is now set to **Custom label**. The current name appears in the **Label** field. In that field, change "Escherichia" to "E." and remove the comma and the words "complete genome." Click **OK**.

Proceed to [Part B: Work with feature tracks](#).

Part B: Work with feature tracks

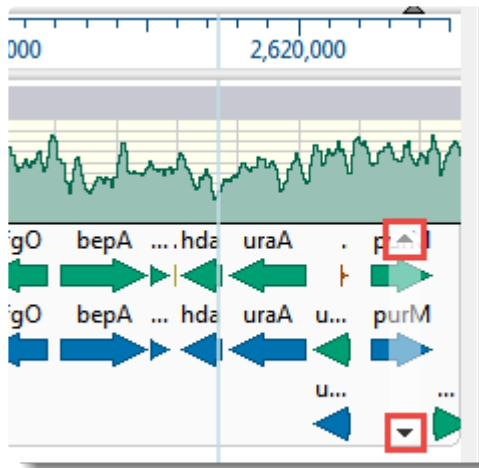
Features are displayed as colored arrows in the [Overview](#) and the [Analysis view](#). In this part of the tutorial, you will learn to toggle between displaying/hiding features, and to view features that are not currently visible.

1. To see an information balloon for any feature, hover over the feature. Try clicking on the feature. This displays the same information in the Details panel on the right, where it can be copied and pasted into a text document.



✿ **Note:** *If you can't see the Details panel, click *View > Reset Panel Layout.

2. Right-click on the word Features in either view and select **Show Track Options**. This command opens both the [Tracks panel](#) and the [Options section](#) associated with the selected track type; in this case, Features.
3. Note that there are two "Feature" check boxes in the Tracks panel; one under **Overview details** and one under **Sequence details**. Experiment with unchecking and rechecking these two **Features** boxes to toggle feature display in the views. Check both boxes before moving to the next step.
4. The GenVision Views display several rows of features, by default. If you wish to see additional rows of features, use the up/down triangles near the right end of the features display. These arrows are connected by a semi-transparent blue bar.



An alternative is to hover the mouse over the bottom of the track, then grab the resize bar and drag it downward.

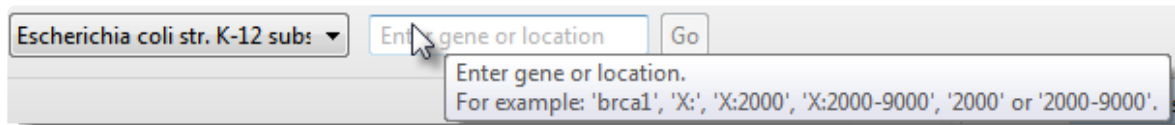


Proceed to [Part C: Investigate sequence coverage](#).

Part C: Investigate sequence coverage

GenVision Pro's navigation tools consist of a “sequence selector,” a text box, and a **Go** button. In this part of the tutorial, you will use the navigation tools to go to a particular region of low coverage that begins around 4,314,000.

1. In the [navigation tools](#) area near the top of the window, hover your cursor over the sequence selector (drop-down menu) and the navigation field text box, in turn. Note that each provides tool tips.

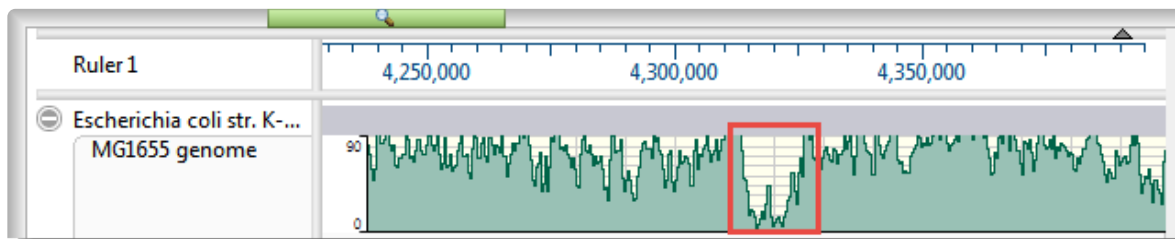


2. Enter **4314000** into the text box. (Alternatively, depending on your locale and computer settings, you could enter **4,314,000** or **4.314.000**.)

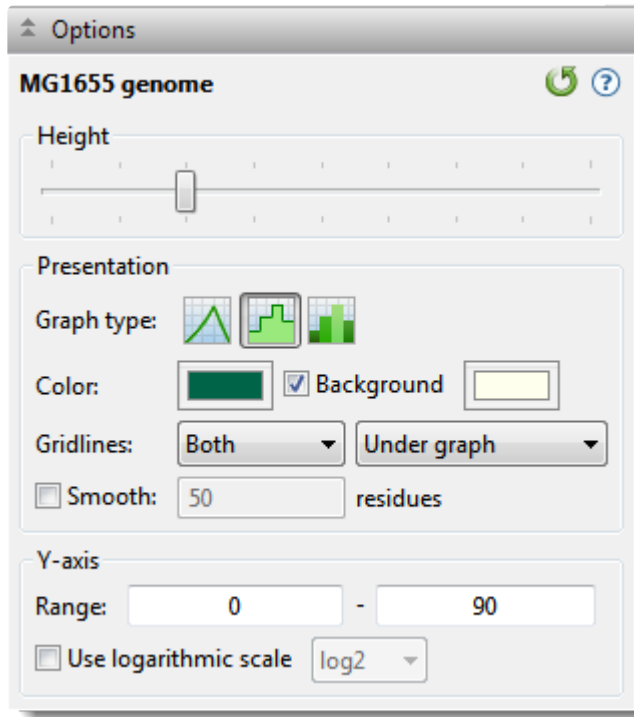




Press **Go** or **Return/Enter**.

3. In the Analysis View, slide the horizontal zoom slider until the Coverage track (entitled “MG1655 genome”) roughly matches the image below. Note the obvious area of low coverage (boxed in red, below).



4. To optimize the Coverage track options, right-click on the name of the track and choose **Show Track Options**.



- a. Next to **Graph type**, click the bar graph icon () . Note that low-coverage areas like the area found above now appear in dark green, making them easier to recognize.
- b. Experiment with other available options. For example, try changing the **Height** slider and/or the **Y-axis Range**, select a different **Graph type** or **Color**, and experiment with the **Gridlines** drop-down menus. Check the **Use logarithmic scale** button and observe how the Coverage track changes.
- c. When you are finished, revert to the default values using the **Restore default settings** tool ().

Proceed to [Part D: Work with region tracks](#).

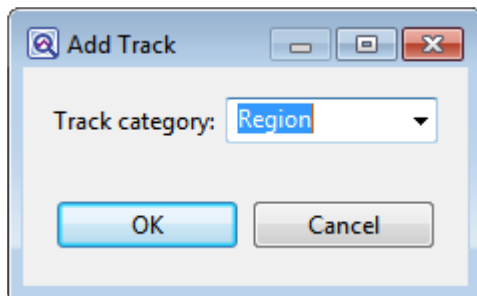
Part D: Work with region tracks

In this part of the tutorial, you will load two BED files associated with the *E. coli* assembly.

- *MG1655_m56_v3.prophage-regions.bed*. contains ten regions or intervals corresponding to the locations of prophages within the genome of this particular strain of *E. coli*.
- *MG1655_m56_v3.Sigma32_regulon.bed* contains regions corresponding to genes that are known to be induced by heat shock (i.e., high temperatures).

Each BED file will appear as a separate [Region track](#) in GenVision Pro, just like the Features and Coverage tracks discussed in earlier parts of this tutorial.

1. BED files must be added one at a time. Select **File > Add Track**. Navigate to and double-click on *MG1655_m56_v3.prophage-regions.bed*.
2. Leave the **Track category** set to **Region** and press **OK**.



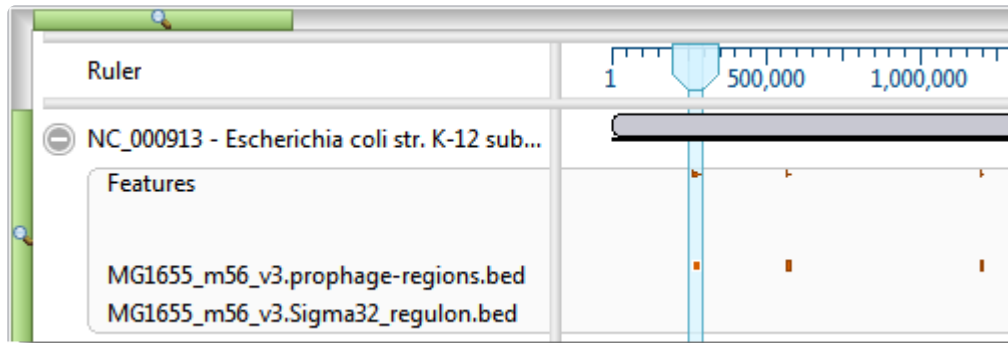
3. Repeat the above steps to add *MG1655_m56_v3.Sigma32_regulon.bed*.

✿ **Note:** Tracks can be renamed by right-clicking on their names in the [Tracks panel](#) (*not* in the views) and choosing **Rename** or **Rename with Fields**. This is the same basic procedure used to rename sequences in [Part A](#) of this tutorial. You can rename the tracks if you wish, but it is not necessary for this tutorial.

Now that the tracks are loaded into the session, the next step is to find regulon members that reside within prophages. One way to do this is to use the [Overview](#) to manually navigate to each of the ten prophage regions in the BED file and visually check whether any regulon regions overlap prophage regions.

4. In the Overview, move the horizontal zoom slider to the left, if it is not already there. Even zoomed out the whole way, you should be able to see 10 orange regions in the *MG1655_m56_v3.prophage-regions.bed* track.

- In the [Analysis view](#), move the horizontal [zoom](#) slider until the [viewport](#) (the semi-transparent vertical bar in the Overview) is narrower than 1 cm in width. Then drag the Viewport so that it is over the left-most orange region.



In the Analysis view, adjust the horizontal [zoom](#) slider so that the entire CP4-6 prophage region is visible. Note that the regulon track below it does not contain any data at this point, indicating that there are no overlapping regulons in this region.

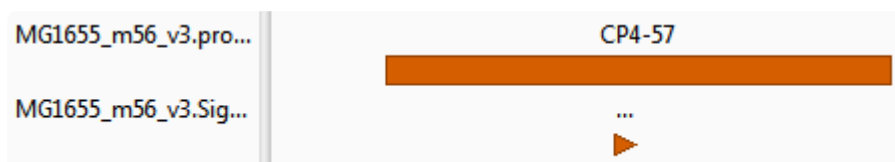


- Repeat the previous step for each of the other nine prophage regions. You should see overlapping regulons at two of them.

One is the fifth prophage from the left (“Qin”):



The other is the ninth from the left (“CP4-57”):



- Under CP4-57, click on the orange arrow to see the regulon member’s region name and coordinates in the [Details panel](#).

Details ⓘ

rnIA_b2630

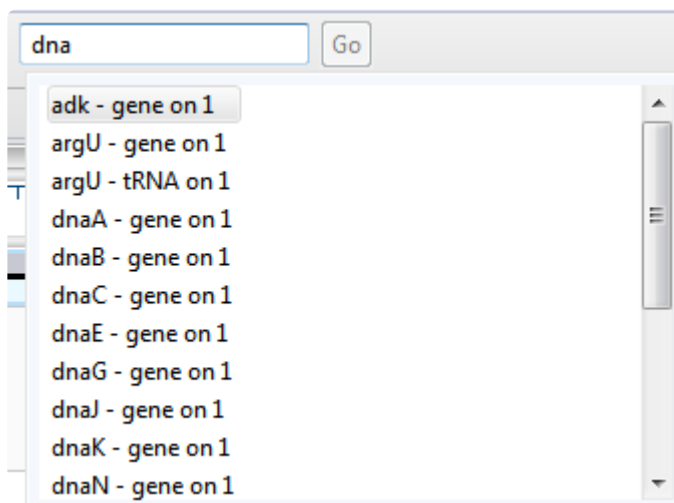
Type: Region
Left: 2,765,918
Right: 2,766,991
Length: 1,074

▼ **Location**
 2765918>2766991

▼ **Properties**
region_name: rnIA_b2630
score: 0

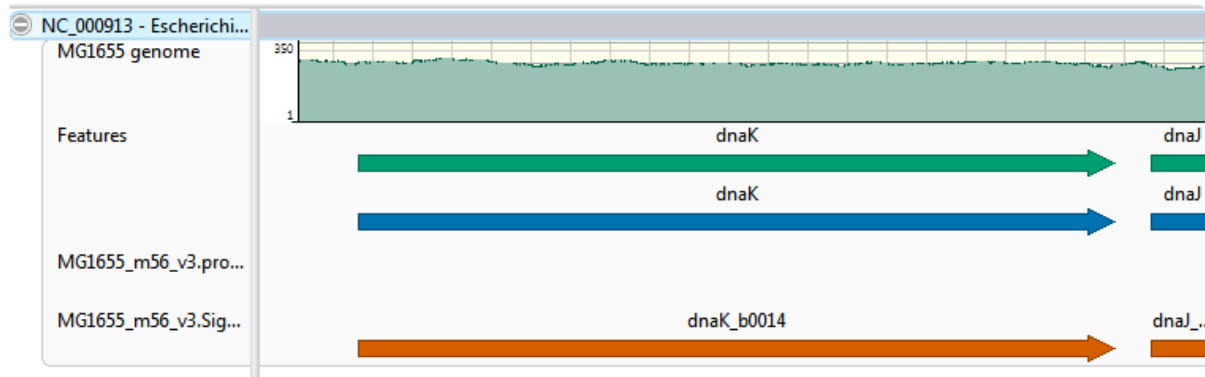
Imagine you are interested in the gene **dnaK**, and want to see if it is a member of the regulon.

8. In the navigation area at the top of the window, start typing **dnaK**. As you type, a list of matches appears.



You can select **dnaK** from the list by double-clicking on it. Or simply finish typing the name manually and press **Go** or **Enter/Return**.

In the Analysis view, you can see that **dnaK** is indeed a member of the regulon.



Congratulations on completing the tutorial!

Create or Open a Session

Because GenVision Pro does not store data when you close it, the information shown in the interface is called a “session,” rather than a “project.” Once you open GenVision Pro, you can open one or many sessions. Each session is displayed in a separate tab and is initially assigned a unique name (Untitled[#].gvp).

For more information, see the following topics:

- [Create a new session](#)
- [Open an existing session](#)
 - [Change the default application for opening files](#)
- [Launch a session from within ArrayStar](#)
- [Make a session active](#)

Create a new session

To create a new, untitled GenVision Pro [session](#) :

Choose **File > New GenVision Pro Session** or press **Ctrl/Cmd+N**.

Once you open a session and [add sequences or assemblies](#), the information is shown in two views: the [Overview](#) and [Analysis view](#). The appearances of the views are determined by options in the [Style panel's Overview](#) and [Analysis](#) sections.

To open an additional GenVision Pro window:

Select the **Window > New Window** command.

Open an existing session

To open an existing GenVision Pro (.gvp) [session](#) :

Use the **File > Open** command or press **Ctrl+O** (Win) or **Cmd+O** (Mac).

Once a project is open in GenVision Pro, you can open additional sessions using the same command.

If you moved or renamed any of the assembly projects, the track file(s) or index file (if any) prior to reopening a session, you may be prompted to supply the new name(s) or location(s) of those files.

If you always want to open `_.gvp_` files using GenVision Pro, see [Change the default application for opening files](#).

Change the default application for opening files

Windows 7 and Windows 8:

1. Open the **Control Panel**.
2. Go to **Programs > Default Programs > Associate a file type or protocol with a specific program**.
3. Select extension you wish to change in the **Extensions** list and then click the **Change program** button.
4. Click the **Browse** button in the Open With dialog box.
5. Navigate to and select the application you want the files to open in. (Lasergene applications are located by default in **C:\Program Files\DNASTAR\Lasergene 'x'** or **C:\Program Files (x86)\DNASTAR\Lasergene 'x'**, where 'x' represents the version number).
6. Click **Open**.
7. Click **OK** to close the Open With dialog box, and then click **Close**.

Macintosh:

1. Select a file of the type you wish to change in Finder.
2. Go to **File > Get Info**.
3. Click the dropdown arrow in the **Open With** field, and navigate to the application you want the files to open in. (Lasergene applications are located by default in **Applications:DNASTAR:Lasergene 'x'**, where 'x' represents the version number).
4. Click the **Change All** button to make the application you selected the default for all files of this type.

Launch a session from within ArrayStar

To view and analyze a selected entry from ArrayStar:

1. Create or open a project in DNASTAR's [ArrayStar](#) application.
2. Open any table and locate a row with a position of interest. Select the row and choose **File > Send Selection To > GenVision Pro** or right-click on the row and choose **Send Selection To GenVision Pro**. GenVision Pro will launch and load the corresponding contig(s) or chromosome(s). If your project contains multiple experiments, all experiments will be loaded into GenVision Pro.
3. (optional) To move to a new location on the sequence in GenVision Pro, repeat Step 2 using a different table row.

The following video shows this workflow in action:

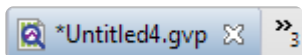
This next video shows an RNA-Seq workflow that begins with assembly in SeqMan NGen, proceeds to downstream analysis in ArrayStar, and then uses ArrayStar's **Send Selection to GenVision Pro** command to open the results in GenVision Pro. Once in GenVision Pro, the Sashimi track is applied. (GenVision Pro section begins at 2:41).

Make a session active

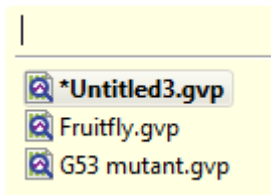
To make a [session](#) active:

Do any of the following:

- Click+ on any session tab to make that session active.
- Click on the **Window** menu and choose the name of the session from the list.
- Press **Ctrl+**; (Win) or **Cmd+**; (Mac) to open a “session chooser.” You may also open the session chooser by pressing the >> icon that appears to the right of the session tabs. This icon is displayed when multiple sessions are open and the GenVision Pro window is too small to display each one in an individual tab.

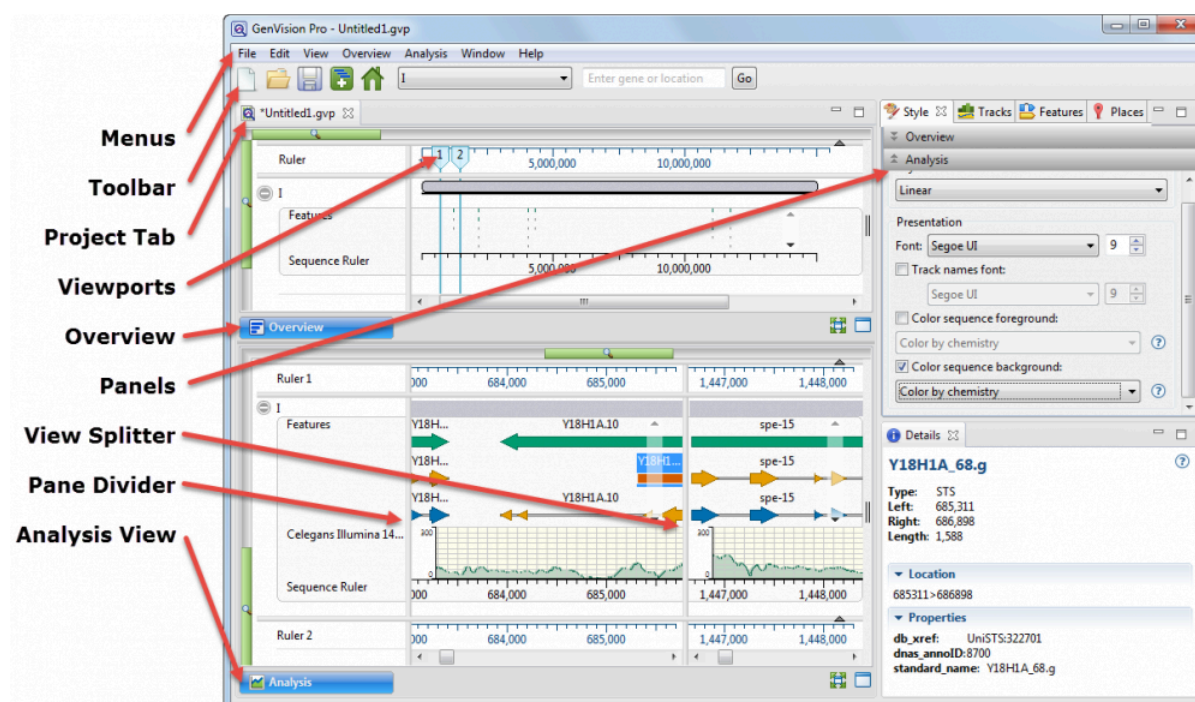


The session chooser appears as a yellow popup with a line for typing in text at the top, and a list of open sessions below. Use your mouse to click on the session you want to make active. If you do not have a mouse, make a selection using the keyboard arrow keys, then press **Enter**.



To instead search for a session using a filter, type text into the text field and press **Enter**. The text field supports the “?” and “*” wildcards.

GenVision Pro Interface



The following table describes components of the GenVision Pro user interface, along with links to more in-depth information about each item:

Item	Description
Menus	The GenVision Pro menus are: GenVision Pro (available only on Macintosh), File , Edit , View , Overview , Analysis , Window and Help . Some menu commands can also be initiated by keyboard shortcuts, button tools, navigation tools, or right-click options.
Button tools	The GenVision Pro button tools are above the Overview on the left.
Navigation tools	The GenVision Pro navigation tools are above the Overview, to the right of the button tools.
Sessions	In GenVision Pro, each session is displayed in a separate tab with a .gvp extension.
Overview	The Overview allows you to navigate or visualize the genome or an individual chromosome.
Analysis view	The Analysis view shows a reference sequence and enabled tracks .
Panels	The Style , Tracks , Features , Places and Details panels provide details about the views on the left, or affect what is displayed there.
View splitter	The view splitter is used to divide the Analysis view or Overview vertically into multiple panes.
Header/Footer	A header and footer are collapsible sections above and below the selected reference sequence. The Overview provides a header, and the Analysis view provides a header and footer.

Sequence Ruler	Sequence rulers pertain only to the sequences just above them.
Show/Hide icons	The gray circles to the left of each label in the Analysis view and Overview contain a plus or minus sign. These toggle between displaying or hiding the detail tracks.

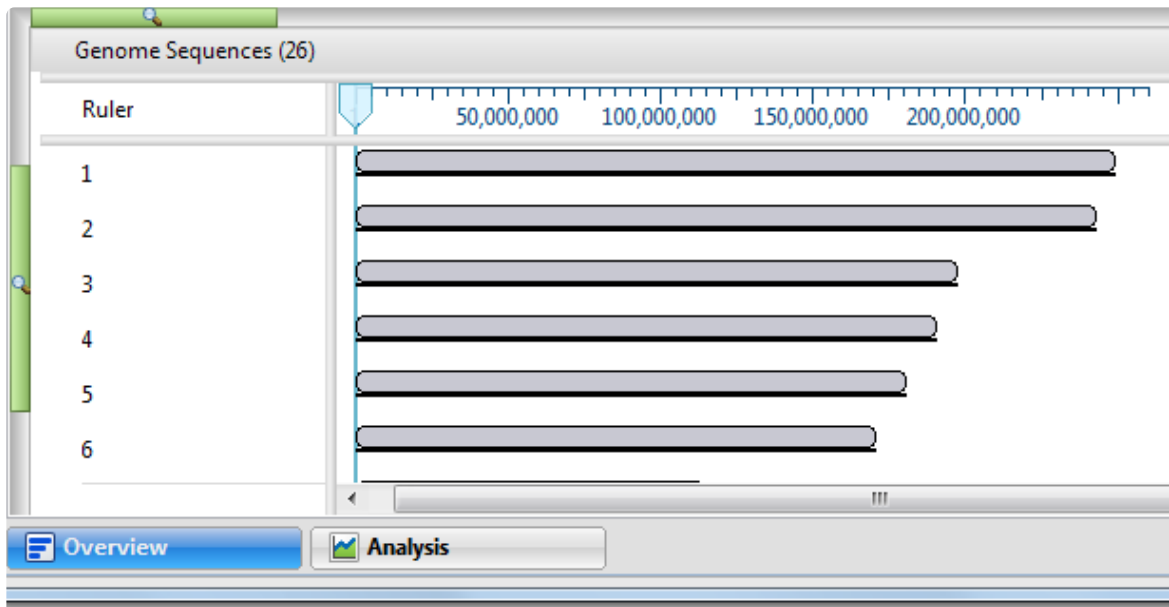
Views

By default, the GenVision Pro interface displays two views: the [Overview](#) and the [Analysis view](#).

If desired, you can [customize the look and layout](#) and of these views.

Overview

To access the view, click on the **Overview** tab (the dark blue part of the image, below) or use **View > Overview**.



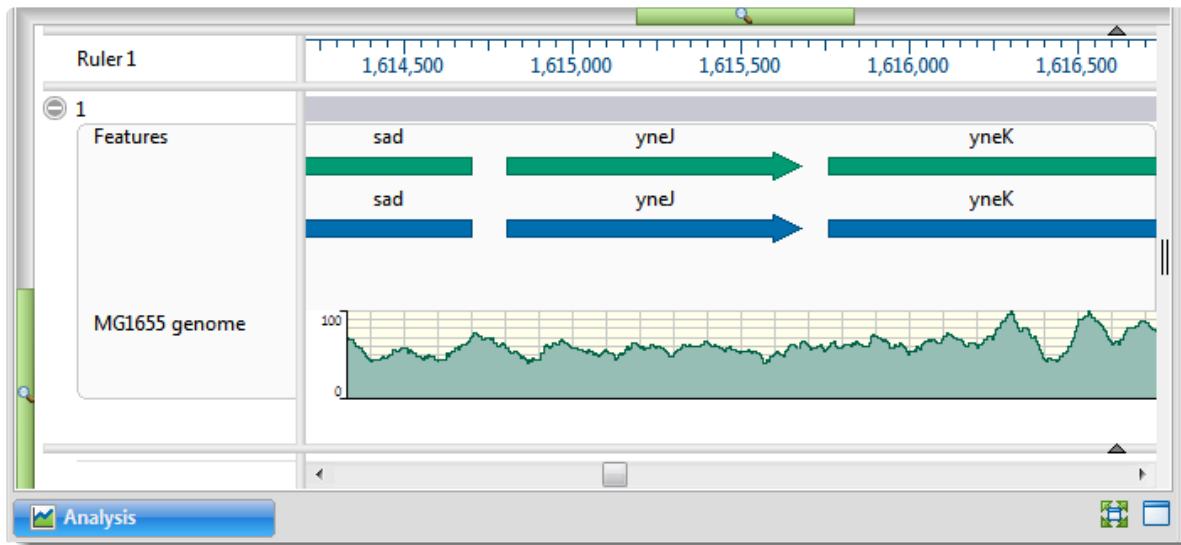
The Overview has two modes:

- No active chromosome or contig – When you first add an assembly, or when you select **(Genome)** using the [navigation tools](#), the Overview displays a header, followed by one or more sequences with labels to their left (see image above). Each sequence is depicted as a “sequence block” of length proportional to the length of the entire sequence. The Overview displays all the sequences in the genome until you navigate to one sequence by double-clicking on its name.
- When a chromosome or contig has been selected – When the project contains a single sequence or after you have selected one sequence by navigating to it or double-clicking on its name, the Overview displays the single sequence. Display of optional [data tracks](#) is also enabled.

Analysis view

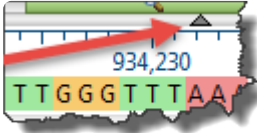
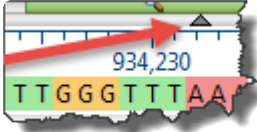
The Analysis View shows tracks for a single sequence. The view is empty unless the session contains only one sequence; or until a single sequence has been chosen in the [Overview](#) or by using the [navigation tools](#) or [Places panel](#) bookmarks. At that point, the Analysis view appears automatically and is populated with data.

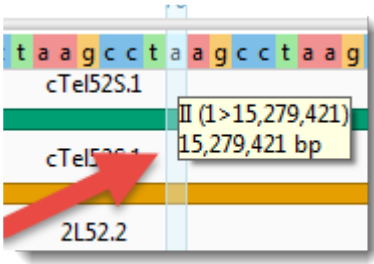
To access the Analysis View at any time, click on the **Analysis** tab, the dark blue tab in the image below, or use **View > Analysis**.



By default, the Analysis view displays a header and footer, along with a sequence and its corresponding [data tracks](#). The Analysis view has a different appearance depending on the [zoom](#) level.

The following table shows ways to customize the Analysis view:

Task	How To
Show the header & footer	Click on the small dark gray arrows near the upper right corners of each section. 
Hide the header & footer	Click on the small dark gray arrows near the upper right corners of each section. 

<p>Show a vertical guideline</p>	<p>Click Analysis > Show Guideline. The presence of a check mark directs GenVision Pro to display the guideline. A vertical guideline is displayed by default, and is a navigational aid to help in guiding your eye between sequences and tracks.</p> 
<p>Hide a vertical guideline</p>	<p>Click Analysis > Show Guideline. The absence of a checkmark means that only an abbreviated version of the guideline will remain visible in the header and footer.</p>

Panels

Settings panels allow you to optimize the look, contents and layout of the GenVision Pro view. To learn what can be done within each panel and their “areas” (expandable sections within each panel), click the links below:

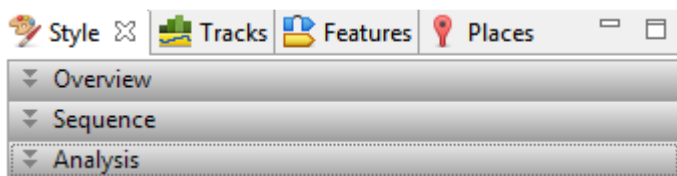
- [Style](#)
- [Tracks](#)
- [Features](#)
- [Places](#)
- [Details](#)

Style panel

The Style panel lets you customize view formatting and layout.

To open this panel, do any of the following:

- Click on the **Style** tab ().
- Use the **View > Style > Style** command.
- Right-click within a view and choose **Show Style Panel**.

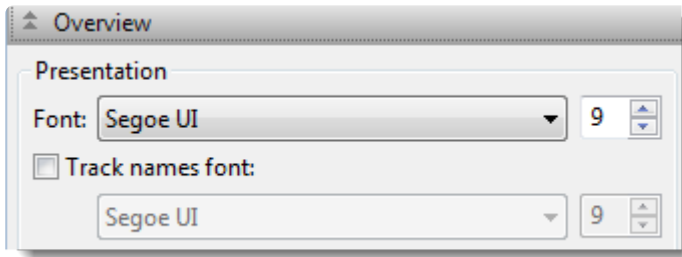




This panel consists of two expandable sections:

- The [Overview section](#) contains options affecting the Overview.
- The [Sequence section](#) contains options affecting the Analysis view.
- The [Analysis section](#) contains options affecting the wrapping used in the Analysis view.

Overview section

The Overview section contains options affecting the [Overview](#). To access this section, click on the [Style panel](#) expand bar entitled **Overview**, or choose **View > Style > Overview**.



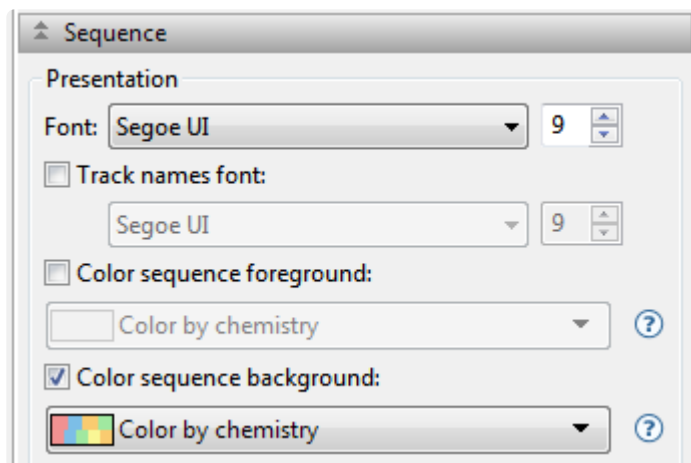
- To change font options for the ruler numbers in the Overview, use the **Font** drop-down menu to choose a font for the ruler numbers in the Overview. Recently selected fonts (if any) appear at the top of the menu, and other available fonts appear below the row of dashes. Enter the preferred font size by typing a number between 4-72 in the box at right, or by using the corresponding up and down arrows (). See note in the row below for additional clarification.
- To select a different font for sequence and track labels in the Overview, first check the box next to **Track names font**. If desired, use the corresponding drop-down menu to change the font from the current value. Enter the preferred font size by typing a number between 4-72 in the box at right, or by using the corresponding up and down arrows ().



Note: When **Track names font** is unchecked and tracks are open, **Font** and **Font size** (described above) affect everything in the view. When **Track names font** is checked and tracks are open, **Font** and **Font size** affect only the rulers, while **Track names font** and **Track names font size** affect sequence labels and track labels.

Customization for font style and size applies to all text in the Overview. Individual rows cannot have different styles or sizes.

Sequence section

The Sequence section contains options affecting the [Analysis view](#). To access this section, click on the [Style panel](#) expand bar entitled **Sequence**, or choose **View > Style > Sequence**.



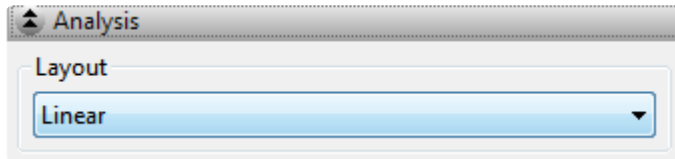
- To specify font options for the ruler numbers in the Analysis view, use the **Font** drop-down menu. Recently selected fonts (if any) appear at the top of the menu, and other available fonts appear below the row of dashes. Enter the preferred font size by typing a number between 4-72 in the box at right, or by using the corresponding up and down arrows ()
- To select font options for other items in the Analysis view, first check the box next to **Track names font**, then use the corresponding drop-down menu to change the font from the current value. Enter the preferred font size by typing a number between 4-72 in the box at right, or by using the corresponding up and down arrows ()

Customization for font style and size applies to all text in the Analysis view. Individual rows cannot have different styles or sizes.

- To change the [sequence letter color scheme](#) in the Analysis view, check the **Color foreground** box. To change the background color (boxes around each letter), check the **Color background** box. Then make selections from the corresponding drop-down menus.

Analysis section

The Analysis section contains options affecting the wrapping style for rows in the [Analysis view](#). To access it, click on the [Style panel](#) expand bar entitled **Analysis**, or choose **View > Style > Analysis**.



Use the **Layout** drop-down menu to select the preferred line wrapping style:


- **Linear** – All information for a sequence appears on a single row with no line breaks. A horizontal scrollbar is provided.
- **Automatic wrapping** – The alignment is wrapped to fit within the view. Wrapping adjusts automatically if the view's width changes. Note that [vertical splits](#) are not available in either type of wrapped view. However, any existing splits are restored if **Automatic wrapping** is turned off.
- **Fixed wrapping** – The alignment is wrapped at the specified number of residues. Enter a number in the Size box to wrap after a different number of residues.

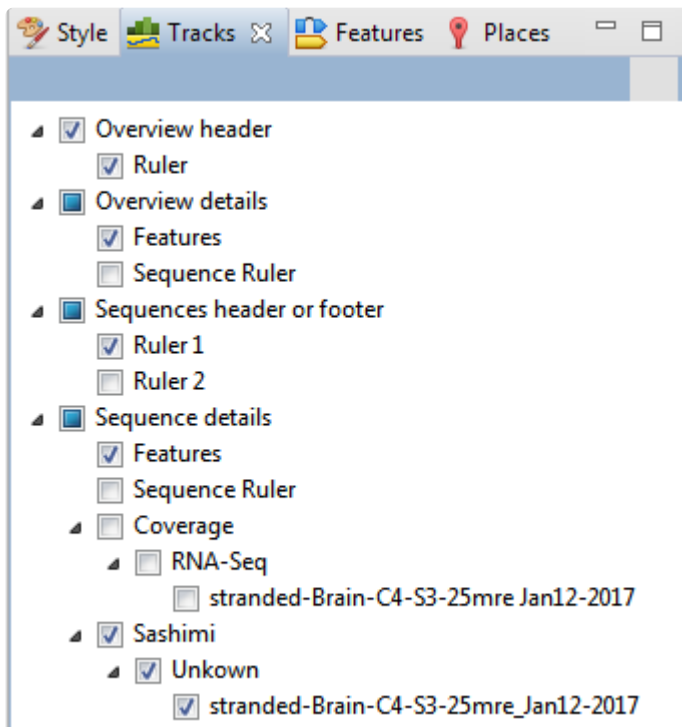


Tracks panel


The Tracks panel lets you manage [tracks](#) displayed in the views.

To open this panel, do either of the following:


- Click on the **Tracks** tab ( Tracks).
- Use the **View > Tracks > Tracks** command.



The uppermost part of the Tracks panel lets you specify which tracks are visible, and configure their options and appearance. Put check marks next to available tracks that you wish to display, and remove check marks next to tracks that you wish to hide. For information about each track type, including user-editable options for the track, see [Work with Tracks](#).

 **Note:** Tracks are added to the views in the same order in which their boxes are checked in the Tracks panel. This means that the position of a track may change when its box is unchecked and then checked again.

To move up or down the list of tracks, either use the mouse wheel or use the vertical scrollbar on the right.

To see the detail tracks that have been checkmarked for display, expand one or more rows in the [Overview](#) and/or [Analysis view](#) by clicking the relevant plus sign icon (.

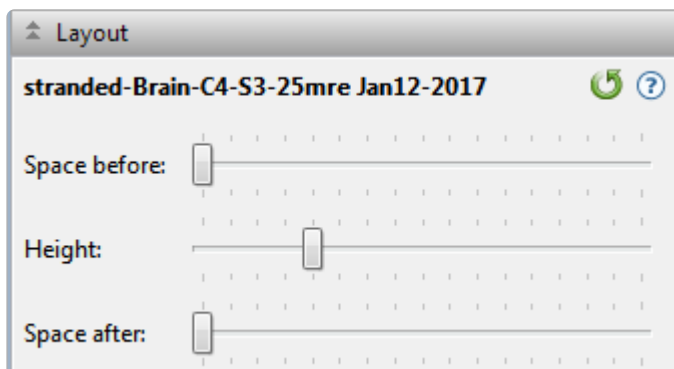
Below the list of tracks are two expandable sections:

- [Layout](#) lets you change the height of a track and create blank space above and/or below the track.
- [Options](#) lets you optimize how tracks appear in the Overview and Analysis view.

Layout section

The Layout section lets you change the height of a track and the space above and/or below a track. Changes made in this section are applied to all currently selected tracks.

Access this section by clicking on the [Tracks panel](#) expand bar entitled **Layout**, or by choosing **View > Tracks > Layout**.



- To control the amount of blank space above and/or below each of the selected track(s), use the **Space before/after** sliders.
- To control the heights of the selected tracks, use the **Height** slider. This option is enabled only when all selected tracks support user-scalable height.
- To return the sliders in this dialog to their default settings, click the **Restore default settings** tool (🔄).

Options section

The Options section is used to edit settings for the track type currently selected in the [Tracks panel](#), and varies in appearance depending upon the selection. Access the Options section by clicking on the Tracks panel expand bar entitled **Options** or by choosing **View > Tracks > Options**.


See the following topics for discussions of each track type and its corresponding Options section.

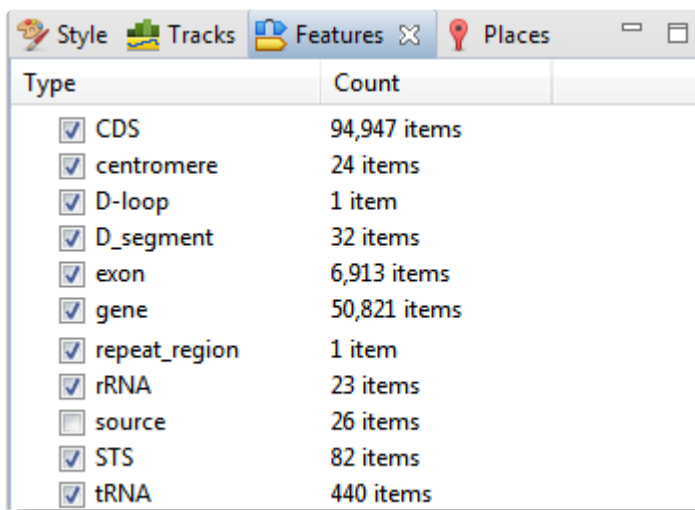
- [Ruler tracks](#)
- [Feature and Region tracks](#)
- [Numeric tracks](#)
- [Sashimi tracks](#)

Features panel

The Features panel lets you specify which feature types should be visible in the [Overview](#) and the [Analysis view](#) when the feature and region [tracks](#) are visible.

To open this panel, do any of the following:

- Click on the **Features** tab ( **Features**).
- Use the **View > Features** command.
- Right-click within a view and choose **Show Features Panel**.



Type	Count
<input checked="" type="checkbox"/> CDS	94,947 items
<input checked="" type="checkbox"/> centromere	24 items
<input checked="" type="checkbox"/> D-loop	1 item
<input checked="" type="checkbox"/> D_segment	32 items
<input checked="" type="checkbox"/> exon	6,913 items
<input checked="" type="checkbox"/> gene	50,821 items
<input checked="" type="checkbox"/> repeat_region	1 item
<input checked="" type="checkbox"/> rRNA	23 items
<input type="checkbox"/> source	26 items
<input checked="" type="checkbox"/> STS	82 items
<input checked="" type="checkbox"/> tRNA	440 items

The **Type** column shows the feature type, while the **Count** column shows the number of each feature type in the session. **Count** includes all sequences, whether selected or unselected. By default, all feature types except **Source** are checked.

To display or hide a particular feature type:

Check or uncheck its box in the **Type** column.


To display or hide all features:

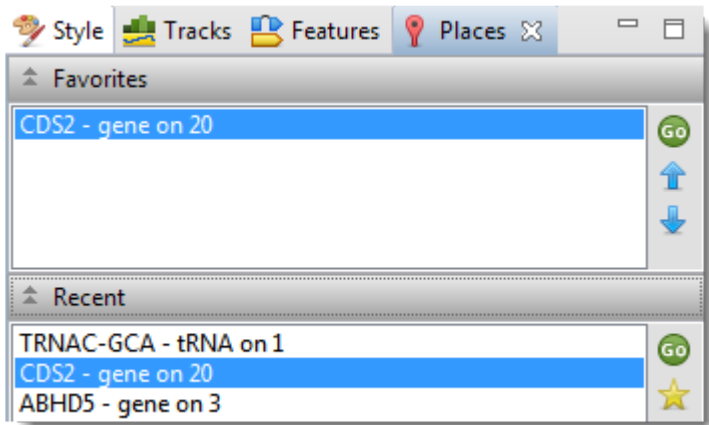
Right-click anywhere in the Features panel and select **Show All** or **Hide All**.

Places panel

The Places panel and the GenVision Pro [navigation tools](#) work together so you can quickly navigate to a chromosome or sequence range that you have visited before.

To open this panel, do either of the following:

- Click on the **Places** tab ( **Places**).
- Use the **View > Places > Places** command.



This panel consists of two or three expandable sections:

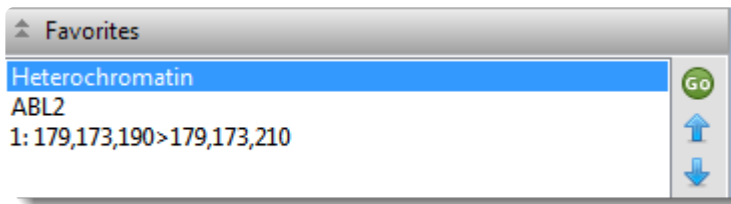
- [Recent](#) lists all locations that you visited after performing a search using GenVision Pro's navigation tools.
- [Received](#) lists data exported to GenVision Pro from ArrayStar (e.g. from ArrayStar's Gene or SNP Tables) using the **File > Send Selection To > GenVision Pro** command. If the GenVision Pro session does not contain items exported from ArrayStar, the Received section is disabled.
- [Favorites](#) is similar to the bookmarks folder for a web browser. It contains a list of previously-visited locations that you have decided you may wish to visit again.

The following video shows the Places panel in action in another DNASTAR application, MegAlign Pro:

Favorites section

The Favorites section is similar to the bookmarks folder for a web browser. It contains a list of previously-visited locations that you have decided you may wish to visit again.

Access this section by clicking on the Places panel expand bar entitled **Favorites** or by choosing **View > Places > Favorites**.



To nominate an entry to the list:

Do any of the following:

- Use the [Recent](#) or [Received](#) sections of the [Places panel](#).
- Choose **Analysis > Add Place to Favorites**.
- Right-click within the Analysis view and choose **Add Place to Favorites**.

Favorites are listed in the same order in which they were added, by default, though you can change the order manually (see table below). The Favorites list is saved whenever you save a session.

The following table shows tasks that can be done from within the Favorites section:

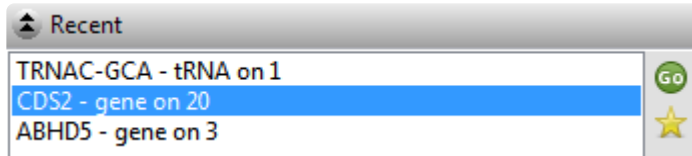
Task	How To
To return to a location in this section	Double-click on the item or make a selection from the list and press the Go to this gene or location button (Go).
To move a bookmarked location further up the Favorites list	Make a selection from the list and press the Move this place up arrow (↑).
To move a bookmarked location further down the Favorites list	Make a selection from the list and press the Move this place down arrow (↓).
To rename a selected item	Click on an item in the Favorites section to select it. Then right-click on the same item and choose Rename Favorite . Type a name into the box and click OK .
To remove a selected item	Click on an item in the Favorites section to select it. Then right-click on the

from the Favorites list	same item and choose Remove Favorite from This List .
To remove all items from the list	Right-click in the Favorites section and select Clear Favorites .

Recent section

When you perform a search for a gene, feature or numerical sequence location using the [navigation tools](#) or the **Edit > Go to Place** command, each found location is automatically stored in the Recent section of the [Places panel](#).

Access this section by clicking on the Places panel expand bar entitled **Recent** or by choosing **View > Places > Recent**.



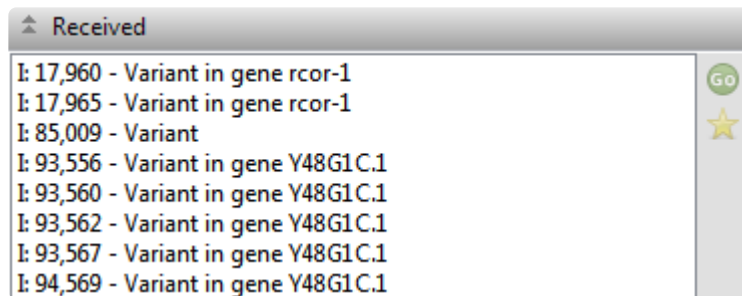
Recent locations are listed in the same order in which they were added, and the list is saved whenever you save a session.

- To return to a location on the list, make a selection from the list and press the **Go to this gene or location** button (Go).
- To save a location on the list to the [Favorites section](#) (similar to bookmarking a page on the Internet), make a selection from the list and press the **Add this place to Favorites** button (★). Alternatively, make a selection from the list, then right-click on the item and choose **Add This Place to Favorites**.
- To remove **all** items from the Recent list, right-click in the Recent section and select **Clear Recent**.

Received section

After opening a SeqMan NGen assembly in DNASTAR's ArrayStar application, you can send up to 100 data rows from its Gene Table or SNP Table directly to GenVision Pro using the **File > Send Selection To > GenVision Pro** command. When you do this, each row exported from the ArrayStar table is automatically stored as a "bookmark" in the Received section of the [Places panel](#).

Access this section by clicking on the Places panel expand bar entitled **Received** or by choosing **View > Places > Received**.




Received locations are listed in the same order in which they were added, and the list is saved whenever you save a session.

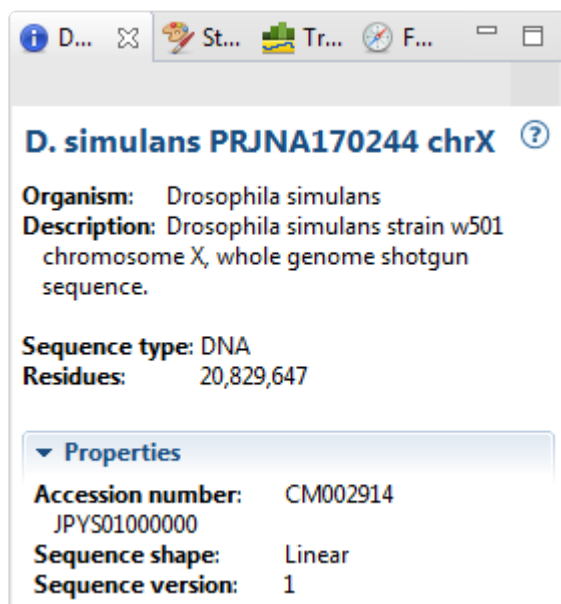
- To return to a location on the list, make a selection from the list and press the **Go to this gene or location** button (Go).
- To save a location on the list to the [Favorites section](#) (similar to bookmarking a page on the Internet, make a selection from the list and press the **Add this place to Favorites** button (★). Alternatively, make a selection from the list, then right-click on the item and choose **Add This Place to Favorites**.
- To remove all items from the Received list, right-click in the Recent section and select **Clear Received**.

Details panel

The Details panel shows details of the application, selection or session. Details are available for all [tracks](#) in the [Overview](#) and [Analysis view](#), as well as the [Tracks panel](#).

To open this panel, do any of the following:

- Click on the **Details** tab ().
- Use the **View > Details** command.
- Right-click within a view and choose **Show Details Panel**.



The appearance of this panel varies according to the situation:

- [When no session, or a blank session, is open](#)
- [When a non-empty session is open](#)
- [When one sequence is selected](#)
- [When a portion of a sequence is selected](#)
- [When multiple sequences are selected](#)
- [When one track is selected](#)
- [When multiple tracks are selected](#)
- [When one feature is selected](#)
- [When multiple features are selected](#)

Text in the Details panel can be copied using [basic editing commands](#) and pasted into a text editor, etc.

When no session, or a blank session, is open

When no [session](#), or only a blank session, is open, the [Details panel](#) displays links to help you get started in GenVision Pro.

Heading	Getting Started in GenVision Pro Create a new project Open a file Add assemblies Watch a training video	Click on the links to: * Create or open a session * Add assemblies to the session * Watch a training video
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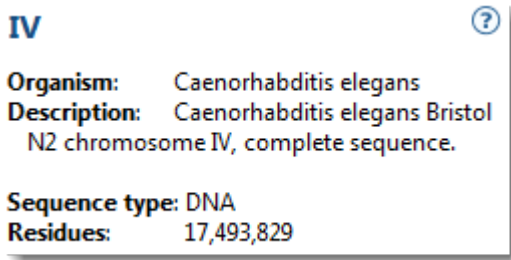
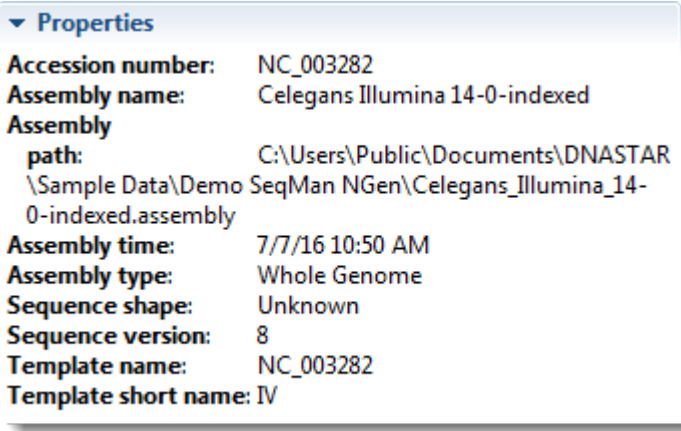
When a non-empty session is open

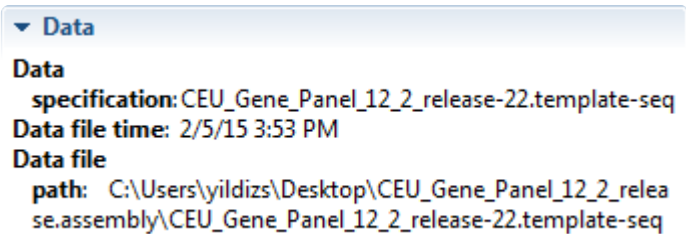
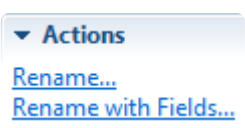
If a [session](#) is open and [data has been added](#), the [Details panel](#) contains the following information:

Heading	CEU gene panel assembly.gvp Sequence type: DNA	The session file name, in blue.
Sequences	<div> ▼ Sequences Sequences: 26 Sequence type: DNA Min. sequence length: 16,569 Max. sequence length: 249,250,621 </div>	<ul style="list-style-type: none"> * Sequences – Number of sequences in the assembly. * Sequence type – Type of sequences in the assembly (DNA or RNA). * Min. and Max. sequence lengths – Lengths of the shortest and longest sequences.
Actions	<div> ▼ Actions Add assemblies Add tracks </div>	<ul style="list-style-type: none"> * Add assemblies – Shortcut to menu command File > Add Assemblies. * Add tracks – Shortcut to menu command File > Add Track.

When one sequence is selected

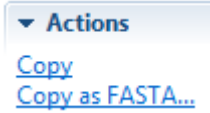
If a single sequence has been selected in any view, the [Details panel](#) may contain a subset of the following information:

Heading		<p>The label used in the Analysis view and Overview, in blue.</p> <ul style="list-style-type: none"> * Organism – The organism containing the chromosome, if available. * Description – A description of the selected chromosome, if available. * Sequence type – Type of sequences in the assembly (DNA or RNA). * Nucleotides/Residues – Number of nucleotides or residues in the selected chromosome.
Properties		<p>Note that the Properties for a sequence show information about a single assembly (not all assemblies) loaded into the session. The information here pertains to the first loaded assembly that covered the chromosome of interest.</p> <ul style="list-style-type: none"> * Accession number – The NCBI accession number of the selected sequence. * Assembly name – The name of the assembly where the sequence or chromosome is located. * Assembly path – The file path to that assembly. * Assembly time – The time the SeqMan NGen assembly finished. * Assembly type – The type of assembly performed in SeqMan NGen, if available (e.g., Exome/Gene Panel). * Sequence shape – Linear or circular, if specified in the reference sequence.

		<p>* Sequence version – The NCBI version number (the part following the decimal after the accession number) for the sequences in the chromosome or contig.</p> <p>* Template name – SeqMan NGen's name for the assembly template, usually the same as its NCBI accession number. Example: In the image shown at left, the Template name is the accession number of the human 'X' chromosome.</p> <p>* Template short name – May match the label displayed in the Overview or the default name originating from the Genome Template Package used to create the assembly.</p>
Data		<p>* Data specification – The name of the sequence file, including extension.</p> <p>* Data file time – The time the sequence file was created or modified.</p> <p>* Data file path – The path to the sequence file in the assembly.</p>
Actions		<p>* Rename – Shortcut to Edit > Rename.</p> <p>* Rename with Fields – Shortcut to Edit > Rename with Fields.</p>

When a portion of a sequence is selected

When a portion of a sequence has been [selected](#) in the [Analysis view](#) (e.g., by double-clicking on a feature, or by dragging across the sequence with the mouse), the [Details panel](#) contains the following information:

Heading	<p>Selected Regions</p> <p>Sequence: 1</p> <p>Residues: 17,230,913</p> <p>Sequence selection: 8>17230891, 17230910>17230938</p>	<p>* Sequence – The name of the sequence from which the region was selected.</p> <p>* Residues – The total number of residues in the selection.</p> <p>* Sequence selection – The inclusive coordinates for the beginning and end of each selection.</p>
Actions		<p>* Copy – Shortcut to the menu command Edit > Copy.</p> <p>* Copy As FASTA – Shortcut to the menu command Edit > Copy As FASTA.</p> <p>See Copy for more information about these commands.</p>

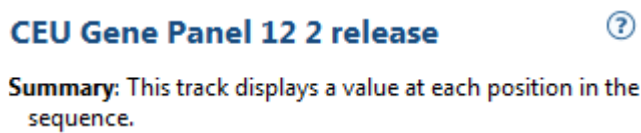
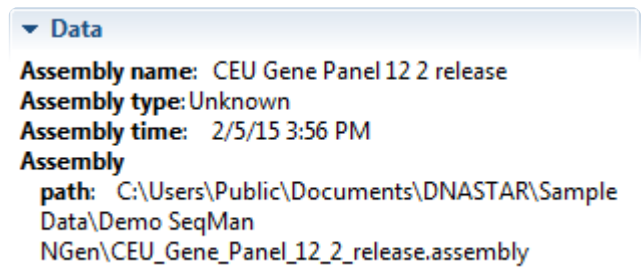
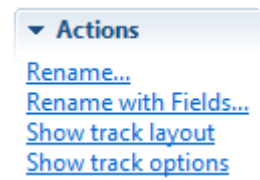
When multiple sequences are selected

If multiple sequences have been [selected](#) in the [Overview](#), the [Details panel](#) contains the following information:

Heading	<p>2 sequences</p> <p>Sequence type: DNA</p> <p>Min. sequence length: 198,022,430</p> <p>Max. sequence length: 243,199,373</p>	<p>* Number of sequences currently selected, in blue.</p> <p>* Sequence type – DNA or RNA.</p> <p>* Min./Max. sequence length – Lengths of the shortest and longest sequences in the current selection.</p>
Actions	<p>▼ Actions</p> <p>Rename with Fields...</p>	<p>* Rename with Fields – Shortcut to Edit > Rename with Fields command.</p>

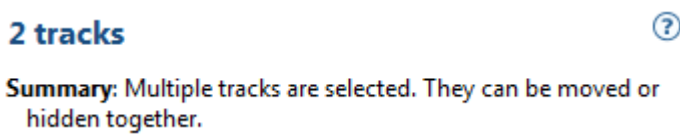
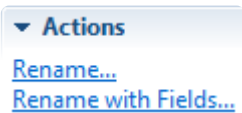
When one track is selected

If a single [track](#) has been [selected](#) in the [Overview](#) or [Analysis view](#), the [Details panel](#) contains the following information.

Heading		<p>The heading contains:</p> <ul style="list-style-type: none"> • Type of track or assembly name, in blue. • Summary – Basic information about what is displayed in the selected track.
Data		<p>Some tracks may have a Data section that includes the source of data.</p> <ul style="list-style-type: none"> • Assembly name – The name of the assembly where the sequence or chromosome is located. • Assembly type – The type of assembly performed in SeqMan NGen, if available (e.g., Exome/Gene Panel). • Assembly time – Date and time the SeqMan NGen assembly finished. • Assembly path – The file path to that assembly.
Actions		<p>Only a subset of links may be available, depending on the selected track.</p> <ul style="list-style-type: none"> • Rename – Shortcut to Edit > Rename. • Rename with Fields – Shortcut to Edit > Rename with Fields. • Show track layout – Shortcut to View > Tracks > Layout. • Show track options – Shortcut to View > Tracks > Options.

When multiple tracks are selected

If two or more [tracks](#) have been [selected](#) in the [Overview](#) or [Analysis view](#), the [Details panel](#) contains the following information.

Heading		<p>The heading contains:</p> <ul style="list-style-type: none"> • The number of tracks currently selected (in blue). • Summary – Description of options available for the multiple track selection.
Actions		<p>The Actions area contains:</p> <ul style="list-style-type: none"> • Rename – Shortcut to Edit > Rename. • Rename with Fields – Shortcut to Edit > Rename with Field.

When one feature is selected

If a single feature has been selected in a track in the [Overview](#) or [Analysis view](#) (e.g., by clicking one time on the feature), the [Details panel](#) contains the following information. Note that the tooltip displayed when you hover over a feature is a subset of the Details panel information for that feature.

Heading	galk Type: CDS Left: 788,054 Right: 789,202 Length: 1,149	The heading contains: <ul style="list-style-type: none"> • The feature name, in blue. • Type – Feature type. • Left and Right – The inclusive coordinates of the beginning and end of the feature range. • Length – Length of the selected feature in nucleotides or residues.
Location	▼ Location 788054<789202	The location of the feature, as a set of one or more segments.
Properties	▼ Properties product: galactokinase gene: galk gene_synonym: ECK0746; galA; JW0740 function: enzyme; Degradation of small molecules; Carbon compounds locus_tag: b0757 protein_id: NP_415278.1 db_xref: GI:16128725 db_xref: ASAP:ABE-0002568 db_xref: UniProtKB/Swiss-Prot:P0A6T3 db_xref: ECOCYC:EG10363 db_xref: EcoGene:EG10363 db_xref: GeneID:945358 codon_start: 1 EC_number: 2.7.1.6 GO_component: GO:0005737 - cytoplasm GO_function: GO:0042280 - cell surface antigen activity, host-interacting GO_process: GO:0016052 - carbohydrate catabolic process; GO:0009242 - colanic acid biosynthetic process; GO:0006012 - galactose metabolic process; GO:0009269 - response to desiccation parentID: b0757 transl_table: 11	This section shows properties of the selected feature. The properties included vary based on the type of feature and the annotations present in the original data file.

Translation	<div>▼ Translation</div> <p>MSLKEKTQSLFANAFGYPATHHTIQAPGRVNLIGEHTD YNDGFVLP CAIDYQTVISCAPRDDRKVRVMAADYE NQLDEFSLDAPIVAHENYQWANYVRGVVVKHLQLR NNSFGGVDMVISGNVPQGAGLSSASLEVAVGTVL QQLYHLPLDGAQIALNGQEAENQFVGCNCGIMDQ LISALGKKDHALLIDCRSLGTKAVSMPKGVAVVIINS NFKRTL VGSEYNTREQCETGARFFQQPALRDVTIE EFNAVAHELDPIVAKRVRHILTENARTVEAASALEQ GDLKRMGELMAESHASMRDDFEITVPQIDTLVEIVK AVIGDKGGVRMTGGGFGGCIVALIPEELVPAVQQAV AEQYEAKTGKETFYVCKPSQGAGQC</p>	<p>This section is displayed only for some CDS features. When present, it displays the NCBI /translate feature qualifier.</p>
Notes	<div>▼ Notes</div> <p>note: ELKS/RAB6-interacting/CAST family member 2; Derived by automated computational analysis using gene prediction method: BestRefSeq, Gnomon.</p>	<p>This section is not available for all features.</p> <ul style="list-style-type: none"> • note – The NCBI feature qualifier of the same name.
Actions	<div>▼ Actions</div> <p>Select Subsequence <i>You can also double-click on this feature.</i></p>	<p>Select Subsequence – * Shortcut to the menu command topic=Menu Commands *Edit > Select Subsequence. Double-clicking on the feature fulfills the same function.</p>

For additional information about working with features, see [Features panel](#).

When multiple features are selected

If two or more features have been selected in a track in the [Overview](#) or [Analysis view](#), the [Details panel](#) contains the following information:












Heading	<p>3 features</p> <p>Type: Region, source, Protein Left: 1 Right: 374 Min. Length: 368 Max. Length: 374</p>	<p>The heading shows:</p> <ul style="list-style-type: none"> • Number of features currently selected, in blue. • Type – List of all feature types represented in the selection. • Left and Right – The inclusive coordinates of the beginning and end of the feature range. • Min. and Max. Length – Lengths of the shortest and longest features in the selection.
Properties	<p>▼ Properties</p> <p>gene: PRR23B db_xref: HGNC:33764, GeneID:389151, HPRD:18392, GI:197927234 parentid: PRR23B</p>	<p>Shows a subset of the qualifiers that all selected features have in common. This section does not show qualifiers that appear elsewhere in the Details panel when a single feature is selected (e.g., /translation and /note)</p>

Button tools

At the top of the GenVision Pro window are eight button-style tools, as well as a set of [navigation tools](#). In the bottom right corner of the view, GenVision Pro offers two additional button-style tools for selecting the screen mode.

You can toggle between showing/hiding the toolbar using the command **View > Show/Hide Toolbar**.


The following table describes the ten button-style tools.

Name	Tool	Keyboard/ Mouse Option	Description
Create a new session		Ctrl/Cmd+N	Shortcut to the File > New GenVision Pro Session menu command.
Open a file		Ctrl/Cmd+O	Shortcut to the File > Open command.
Save session		Ctrl/Cmd+S	Shortcut to the File > Save Session command.
Add assemblies to session		Ctrl/ Cmd+Shift+E	Shortcut to the File > Add Assemblies command.
Add sequences to session		Ctrl/Cmd+E	Shortcut to the File > Add Sequences command.
Download and add a genome to this session			Shortcut to the File > Download and Add Genome command.
Add tracks to session		Ctrl/ Cmd+Shift+T	Shortcut to the File > Add Track command.
Show whole genome			Same as choosing (Genome) from the navigation tools drop-down menu. All available sequences (i.e., the whole genome) will be displayed in the Overview. This is default state of the Overview when a selection has not yet been made.
Full screen		Ctrl/ Cmd+Shift+F	Shortcut to the View > Full Screen command. Undo by clicking the Esc key or the Exit Full Screen icon () at the bottom of the full-screen view.
Show/Remove split			This tool appears under the Overview and Analysis view . It toggles between showing one or two views for this session in the main window.

Navigation tools

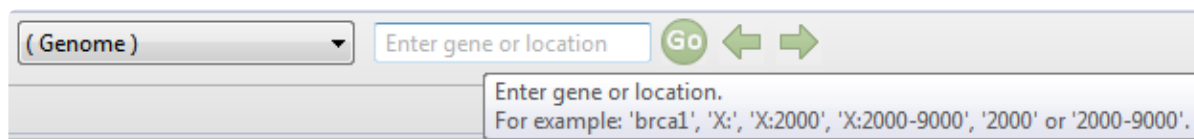
GenVision Pro's navigation tools are located just to the right of the button tools and consist of a "sequence selector" (the drop-down menu), a text box, a **Go** button, and two green arrows. By default, **(Genome)** is shown in the sequence selector, causing the entire genome to be displayed in the [Overview](#). The [Analysis view](#) remains empty until a different selection is made.

To move the cursor to a particular position or range:

Type a position or range into the text box and press the **Go to gene or location specified** button (). See the table below for syntax examples, and the contexts in which they may be used. If you are currently displaying all chromosomes (see above), you may limit the search to a particular one by including it in the query syntax. GenVision Pro will automatically update the drop-down menu to correspond to the chromosome specified by the query.

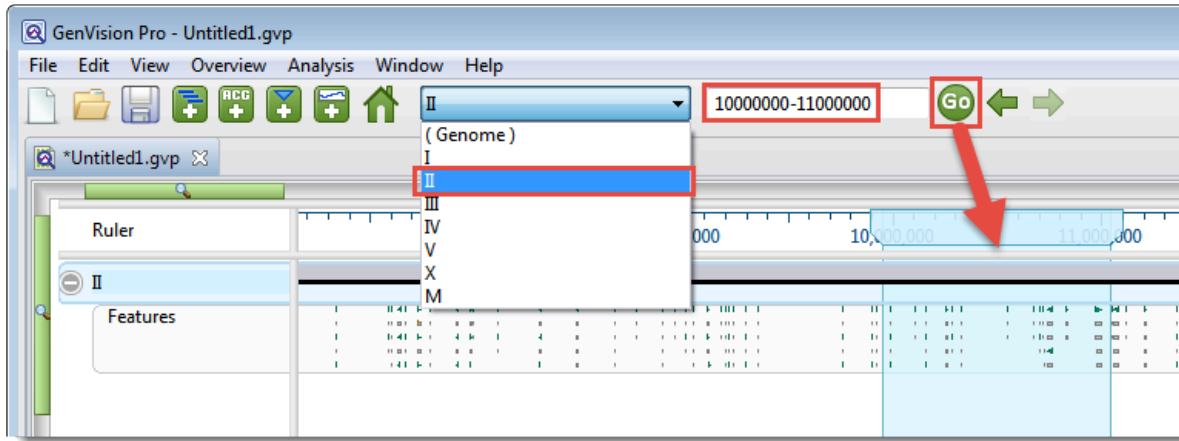
Context	Type...	To go to...
All contexts	chr1:	chromosome 1
	3:	chromosome 3
	chr1:42	position 42 on chromosome 1
	chr2:300-433	range 300-433 on chromosome 2
When viewing a chromosome	451	position 451 of current chromosome
	23-4343	range 23-4343 of the current chromosome
When viewing a genome	3	chromosome or contig 3

If you forget how to enter a query, hover over the sequence selector or text box to reveal a list of sample queries.



A variety of separators (e.g., spaces, < or > symbols) are accepted between the endpoints in a range. For example, all of the following are accepted: 300-433, 300 433, 300..433, 300>43 and 433<300. You can also paste in a range obtained from a variety of external sources, including SeqNinja and the [National Center for Biotechnology Information](#) (NCBI).

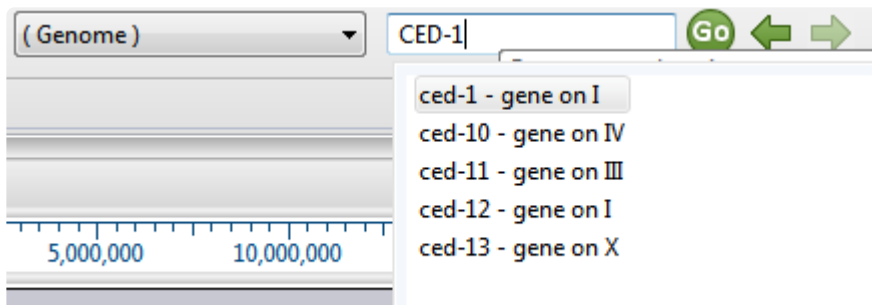
Example: The following image shows an example where both the sequence selector and the text box were used to perform a search.



After pressing the **Go** button, the location will automatically be saved to the [Recent section](#) of the [Places panel](#). This section is similar to the “recent items” cache in other computing contexts, and allows you to return to the same location in the future.

To move the cursor to a particular feature:

Type the feature name into the text box. As you begin typing, possible matches will appear in a list below. To pick one of them, use the up/down arrow keys or the mouse. Press the return key or **Go to gene or location specified** button (Go) to go to the selected item. You can also go to an item by double-clicking on it in the list.




After pressing the **Go** button, the location will automatically be saved to the [Recent section](#) of the [Places panel](#). This section is similar to the “recent items” cache in other computing contexts, and allows you to return to the same location in the future.

To go back to the last recent place:

Click the left arrow (←). The arrow is only enabled if another location was visited prior to the current location. Note that more recently-visited places are higher up on the list.

To go forward to the next recent place:

Click on the right arrow (). The arrow is only enabled if you returned to this location after first visiting another location.

Add Data


Once you have created a GenVision Pro session, the next step is to add data. See the following topics for information:

- [Add sequences](#)
- [Add assemblies](#)
- [Add genomes from NCBI](#)

Add sequences

To add sequences:

To add a genome sequence to the session in Genbank (*.gbk*) or FASTA (*.fasta*) format, do any of the following:


- Use the **Add sequences to project** [button tool](#) ()
- Choose **File > Add Sequences**.
- Press **Ctrl/Cmd+E**

You can add additional sequences at any time. However, once sequences are added, they cannot be deleted from the session. Note that it usually takes longer to add sequences to GenVision Pro than it does to [add assemblies](#).

Add assemblies

To add SeqMan NGen .assembly packages:

Do any of the following:

- Drag & drop one or more assemblies on an open GenVision Pro session
- Press the **Add assemblies to project** [button tool](#) ().
- Choose **File > Add Assemblies**
- Press **Ctrl/Cmd+Shift+E**.

For all but the first option on the list above, you will be prompted to select an assembly (or folder of assemblies) from the file browser. After making a selection, press **OK**. Note that double-clicking is not supported in this situation.

The following table shows warning messages that you might encounter when adding an assembly to a session.

Warning	Explanation
Please pick an assembly or a directory containing assemblies.	The item selected was not an assembly project or a folder containing an assembly project.
Unable to add duplicate data source.	The selected assembly has already been added to the current session.
Most of the sequences being added from the assembly "<assembly name>" do not match those in the document. Add data anyway?	Most contigs or chromosomes in the selected assembly do not match those of assemblies already in the session. Click OK to add the assembly anyway, or Cancel to close the dialog without adding the assembly.
Feature index not found for assemblies. Index features now?	If this prompt appears, we recommend choosing Yes . Choosing Yes simply causes a "feature index" file to be quickly created and added to the original assembly file package. A detailed explanation of "feature index" appears below this table.

"Feature index" description:

During assembly, SeqMan NGen 14.0 (and later) automatically includes a features index file as part of the assembly package. GenVision Pro uses the file for rapid access to features. The presence of a features index allows you to navigate to a gene by name and to view features in the Features panel.

An assembly built in an older version of SeqMan NGen will initially lack this feature index. When you add such an assembly to a GenVision Pro session, this message asks whether you wish to have a feature index

created automatically. If you click **Yes**, a file will be created and stored within the original assembly data. If you click **No**, no file will be created, and the assembly will be added to the session without indexing. This will cause loss of the functionality described in the paragraph above. If you decline to create the feature indices, you may be prompted again when the assembly project is used a different session.


If you add a set of assemblies built using equivalent reference templates, and respond **Yes** to this prompt, a feature index will be created for just one member of the set. In this case, the genome templates for other members of the set are not loaded into GenVision Pro. Note that if you later add one of the non-indexed assemblies to a different GenVision Pro session, you will again be prompted to index, as the new GenVision Pro session will no longer have access to the indexed assembly. Also, if you add assemblies that have additional chromosomes from those added earlier, one of the “expanded” assemblies will also need to be indexed.

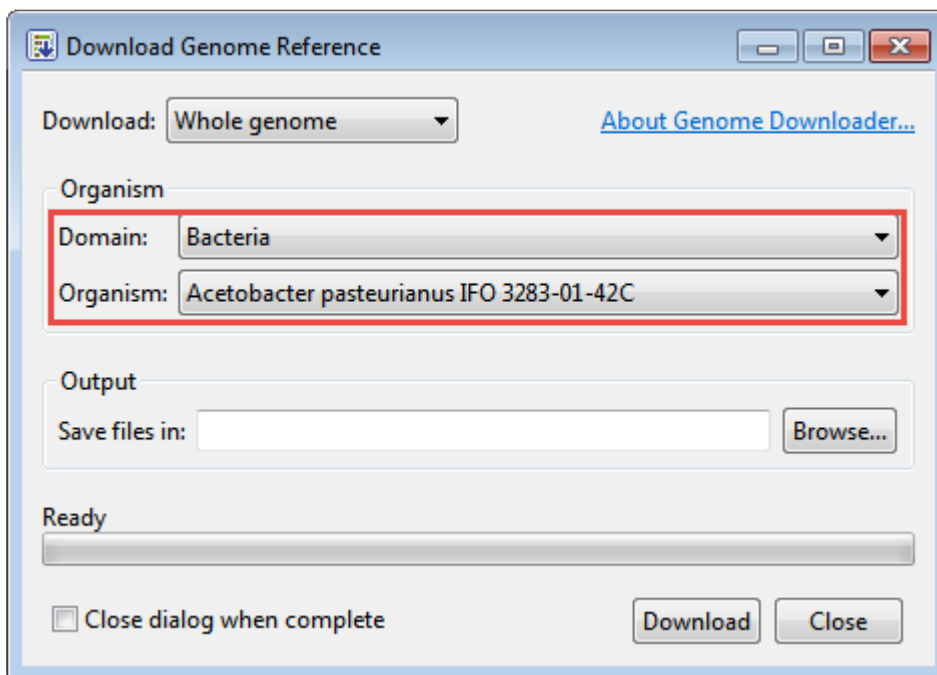
Example: Say you start a GenVision Pro session by adding some human female assemblies from SeqMan NGen v. 13.0. You respond **Yes** to the indexing prompt, and a feature index is created for one of the assemblies. This index will lack feature indexing for the Y chromosome, since all samples so far are female. If you then add human male assemblies that have the additional chromosome Y, one of the male assemblies will need to be indexed.


Note: In order for GenVision Pro to add the index file, you must have “write” permission for the assembly package. If you do not, someone with Administrator status may need to do this step for you. Alternatively, you can copy to the assembly to a location where you have write permission.

Add genomes from NCBI

To import a genome from the [National Center for Biotechnology Information](https://www.ncbi.nlm.nih.gov/) (NCBI) database via organism name or accession number:

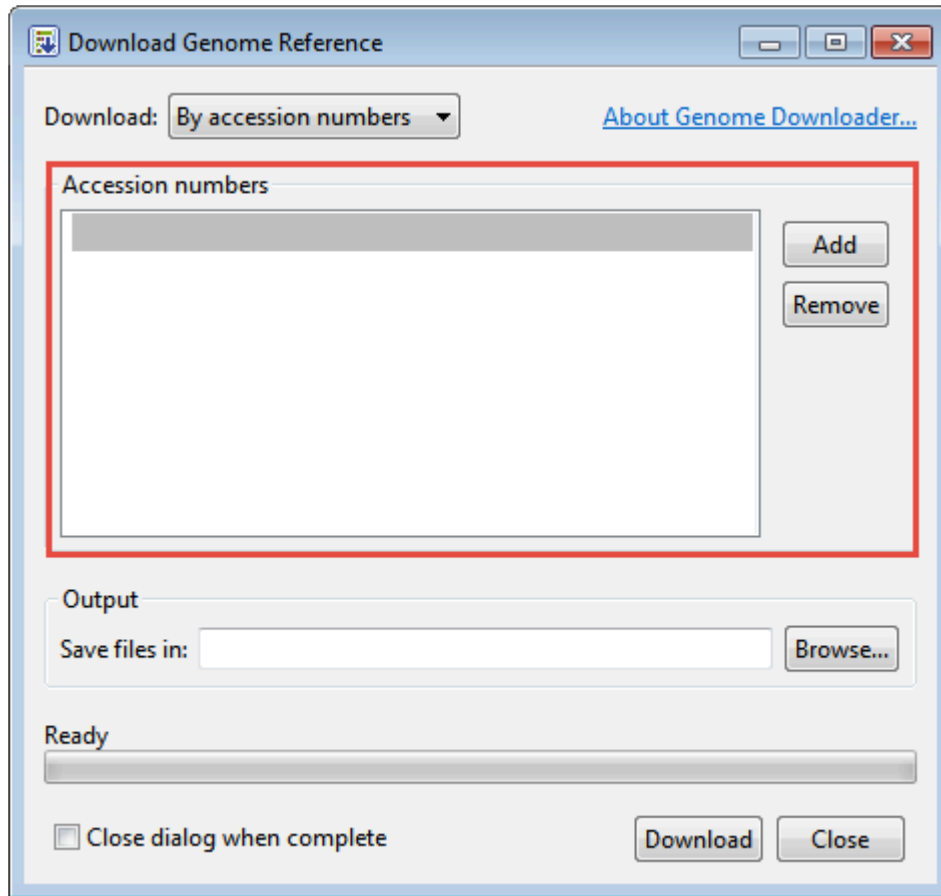
1. Choose **File > Download and Add Genome** or press the **Download and add a genome to the session** [button to](#) .
2. In the Download Genome Reference dialog, use the **Download** dropdown menu to choose between downloading a **Whole genome** or **By accession numbers**.
 - If you select **Whole genome**, GenVision Pro will retrieve the most recent build of the selected genome. Use the next two drop-down menus to select the **Organism type** and **Organism**.



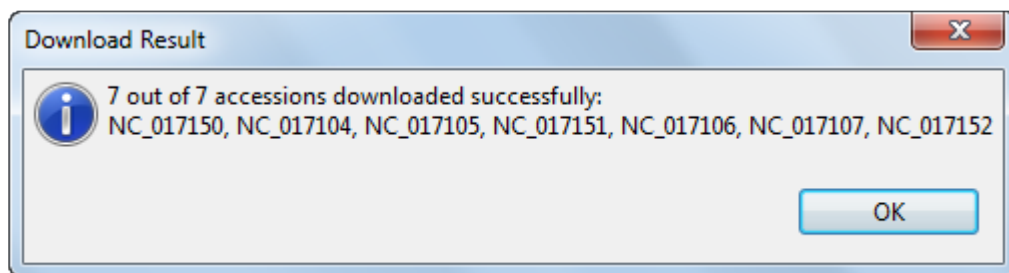
 **Note:** GenVision Pro will download all the reference sequences from the NCBI Entrez Genome Project database for the selected genome. These downloads may include auxiliary genomes such as mitochondria and chloroplasts. They may also include some contigs which have not yet been placed by the genome finishing process.

- If you select **By accession numbers**, the Organism section disappears and is replaced by an Accession numbers entry area. Type an accession number or paste it from your clipboard, then press **Add** to add a number to the list. Continue adding numbers, as desired. Multiple accession numbers should be separated using a space, comma, semi-colon or line break. To remove an

accession number from the list, select it and click **Remove**.



3. Click **Browse** to select a name and location in which to save the downloaded genome files.
4. If you do not need to download additional genomes, you can check **Close dialog when complete**. Otherwise, leave the box unchecked to keep the dialog open after initiating the current download.
5. Press **Download**. Once the download is complete, a message like the one below will appear.



6. Click **OK** to close the dialog and add the accessions to the GenVision Pro session. If you checked **Close dialog when complete**, the Download genome reference dialog will also close. Otherwise, it will remain open so that you can download additional NCBI genomes.




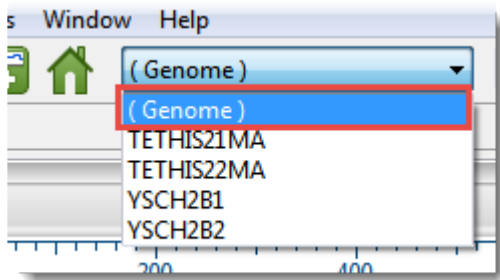
Tip: Some large genomes may take extra time to download. In the meantime, you can work on a different GenVision Pro session by clicking on its tab.

Specify the Data Rows to Display

The [Overview](#) can display one or many chromosomes, contigs or sequences simultaneously. However, only one of these at a time may be displayed in the [Analysis view](#).

To display Overview rows for all uploaded session data:

Either press the **Home** () [button tool](#) or use the [navigation tools](#) to choose **(Genome)** from the drop-down menu.



To display an individual chromosome, contig or sequence in both the Overview and Analysis view:

Either double-click on the name of the chromosome, contig or sequence in the Overview, or use the [navigation tools](#) to make a selection other than **(Genome)** from the drop-down menu.

Rename Sequences

Once you have loaded sequences into GenVision Pro, you can rename them in either of two ways. See the following topics for details:

- [Create names automatically using specified data fields](#)
- [Rename a single sequence manually](#)

Create names automatically using specified data fields

The **Edit > Rename with Fields** command lets you create labels for one or more selected sequences automatically, using specified fields such as sequence length, organism, or description. The custom labels are then displayed for those sequences within the GenVision Pro application.

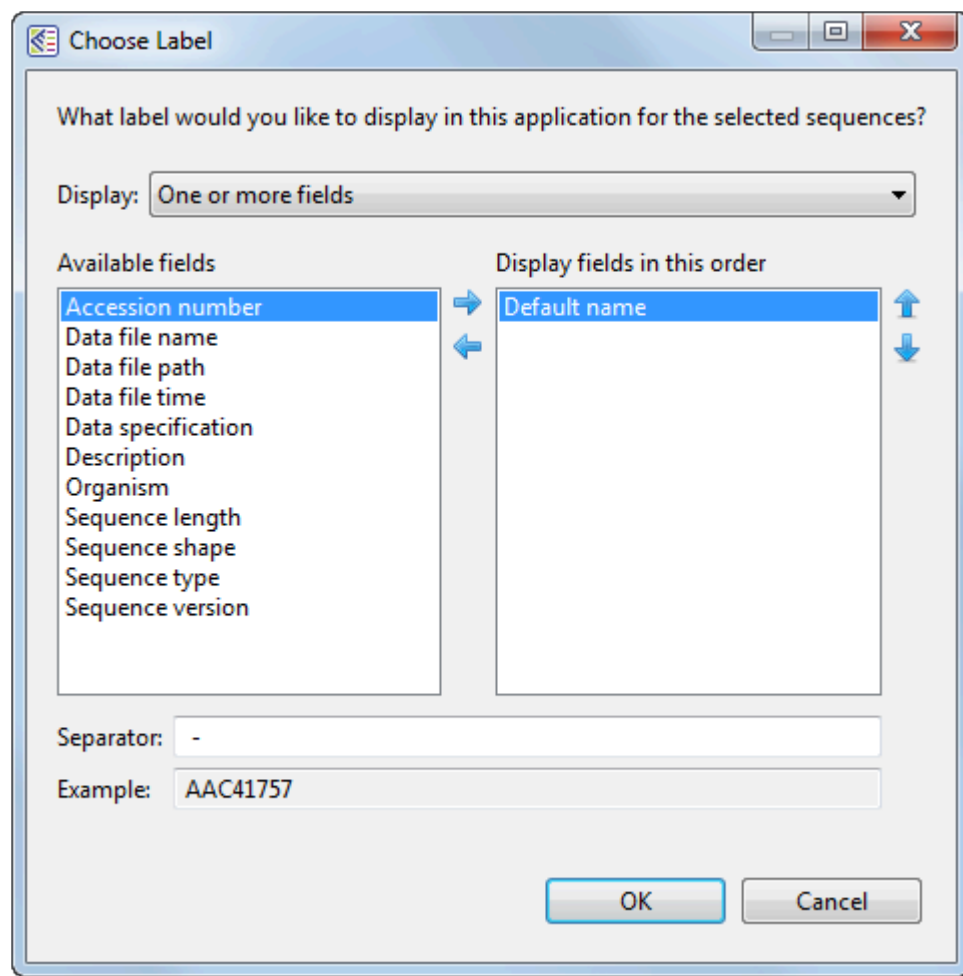
To rename sequences using specified data fields:

1. Select one or more sequence names from any GenVision Pro view.
2. Right-click on the selection and choose **Rename with Fields**, or instead choose **Edit > Rename with Fields** from the main menu. Making no selection prior to using the main menu command is equivalent to selecting all sequences.

The Choose Label dialog opens with the **Display** drop-down menu set to **One or more fields**.



Note: If you selected a single sequence and wish to rename it manually, select **Custom label** from the drop-down. Then follow the instructions in [Rename a single sequence manually](#).



The left pane shows available fields, and the right pane shows fields that will be displayed as part of the sequence name. Initially, **Default name** is the only field listed in the right pane. An example showing the appearance of the name using the specified field(s) appears in the **Example** box at the bottom of the dialog.

3. Select and organize the fields you wish to display as part of the sequence name:
 - To add or remove items, move them between panes using the left and right arrows (←→). Use the up and down arrows on the right (↑↓) to specify the order in which displayed fields should appear.
 - By default, a hyphen (-) is included between each of the displayed fields. If desired, type in a different **Separator**. Or remove all text in the **Separator** box to include nothing between the fields.
 - The **Example** text box shows what the label will look like with the current selections. This text can be manually edited, if desired.
4. When you are satisfied with the choices made in this dialog, click **OK** to save changes and exit from

the dialog. Or click **Cancel** to leave the dialog without saving any changes.

Rename a single sequence manually

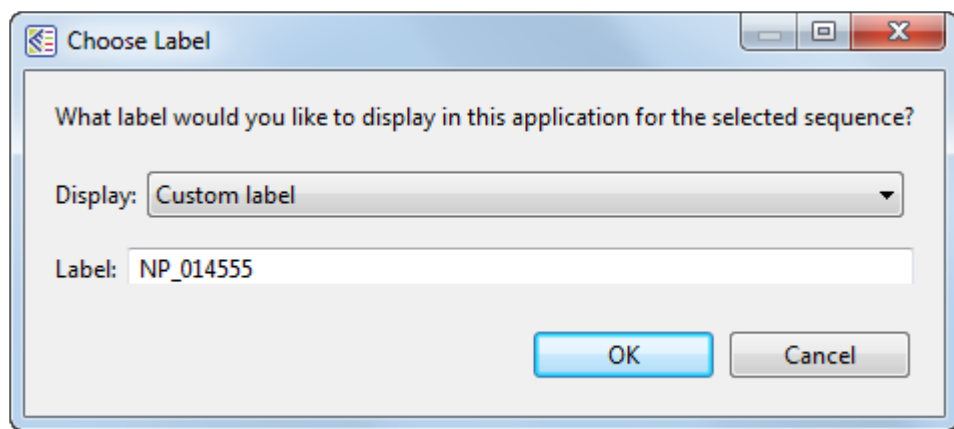
The **Edit > Rename** command lets you manually enter a label (name) to display for those sequences within the GenVision Pro application.

To manually rename a single selected sequence:

1. Select a single sequence name from any GenVision Pro view, then right-click on it and choose **Rename**. Alternatively, select the sequence name and choose **Edit > Rename**.

The Choose Label dialog opens with the **Display** drop-down menu set to **Custom label**.

✱ **Note:** To instead name the sequence using specified data fields, select **One or more fields** from the drop-down. Then follow the instructions in [Creating names automatically using specified data fields](#).



2. Type the desired name into the **Label** text box.
3. Click **OK** to save changes and exit from the dialog, or **Cancel** to leave the dialog without saving any changes.

Customize the Look and Layout

The following topics describe ways in which you can customize the appearance of [views](#) and [panels](#):

- [Change font style and size](#)
- [Change the order of sequences, assemblies or genomes](#)
- [Change the Analysis view color scheme](#)
- [Wrap the Analysis view display](#)
- [Detach or reattach a view](#)
- [Display or hide a vertical guideline](#)
- [Move a view or panel](#)
- [Resize a view, panel or section](#)
- [Scroll horizontally or vertically](#)
- [See a view in full-screen mode](#)
- [Show or hide an element of the interface](#)
- [Split a view horizontally or vertically](#)
- [Zoom in and out](#)
- [Return to the default layout](#)

Change font style and size

The font style and size for text in the views are specified in different sections of the [Style panel](#):

- [Analysis view](#) fonts are customized within the [Sequence section](#).
- [Overview](#) fonts are customized within the [Overview section](#).

Customization for font style and size applies to all text in the view. Individual rows cannot have different styles or sizes.

Change the order of sequences, assemblies or genomes

To move one or more sequence or assembly rows as a group:

Sequence and assembly rows in the [Overview](#) or [Analysis view](#) may be rearranged one at a time or as contiguous groups using drag and drop.

1. Select the desired rows using **Ctrl/Cmd+click** or **Shift+click**.
2. Drag the selected row(s) to the desired location and release the mouse button.

Any ordering changes made to one view are simultaneously made to the other.

Change the Analysis view color scheme

The foreground and background color schemes for the [Analysis view](#) are specified in the [Sequence section](#) of the [Style panel](#). To open the section, click on the expand bar entitled **Analysis**, or choose **View > Style > Analysis**.

To change the letter color in the Analysis View, check the **Color foreground** box. To change the background color (boxes around each letter), check the **Color background** box. Then make selections from the corresponding drop-down menus. Note that the color options are disabled unless a session is open in GenVision Pro.

- **Color by Chemistry** – This is the default color scheme, and matches the colors used in DNASTAR's Protean 3D application. Amino acids are colored according to their side chain chemistry:

Nucleotide
A
C
G
T/U

Side Chain Chemistry - Amino Acids
Aromatic - Phenylalanine (F), Tryptophan (W), Tyrosine (Y)
Acidic (negatively charged) - Aspartate (D), Glutamate (E)
Basic (positively charged) - Arginine (R), Histidine (H), Lysine (K)
Nonpolar (aliphatic) - Alanine (A), Glycine (G), Isoleucine (I), Leucine (L), Methionine (M), Proline (P), Valine (V)
Polar (neutral) - Cysteine (C), Asparagine (N), Glutamine (Q), Serine (S), Threonine (T)

- **Shapely** – This color scheme matches the [RasMol amino acid and RasMol nucleotide color schemes](#), which are, in turn, based on Robert Fletterick's "Shapely models."

Nucleotide
A
C
G
T
U

Amino Acids
Alanine (A)
Arginine (R), Lysine (K)
Asparagine (N), Glutamine (Q)
Aspartate (D), Glutamate (E)
Cysteine (C), Methionine (M)
Glycine (G)
Histidine (H)
Isoleucine (I), Leucine (L), Valine (V)
Phenylalanine (F), Tyrosine (Y)
Proline (P)
Serine (S), Threonine (T)
Tryptophan (W)

- **Taylor** – This color scheme is taken from [Taylor \(1997\)](#) is also used in [JalView \(Waterhouse et al., 2009\)](#).

Nucleotides
A
C
G
T/U

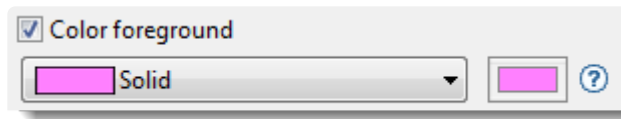
Amino Acids
Alanine (A)
Arginine (R)
Asparagine (N)
Aspartate (D)
Cysteine (C)
Glutamate (E)
Glutamine (Q)
Glycine (G)
Histidine (H)
Isoleucine (I), Leucine (L)
Lysine (K)
Methionine (M)
Phenylalanine (F)
Proline (P)
Serine (S)
Threonine (T)
Tryptophan (W)
Tyrosine (Y)
Valine (V)

- **Zappo** – This scheme colors residues according to their physico-chemical properties, and is also used in [JalView](#) (Waterhouse et al., 2009).

Nucleotide
A
C
G
T
U

Physico-Chemical Property - Amino Acids
Aliphatic/hydrophobic - Alanine (A), Isoleucine (I), Leucine (L), Methionine (M), Valine (V)
Aromatic - Phenylalanine (F), Tryptophan (W), Tyrosine (Y)
Conformationally special - Glycine (G), Proline (P)
Cysteine (C)
Hydrophilic - Asparagine (N), Glutamine (Q), Serine (S), Threonine (T)
Negatively Charged - Aspartate (D), Glutamate (E)
Positively Charged - Arginine (R), Histidine (H), Lysine (K)

- **Solid** – These scheme colors residues with the color shown. After selecting **Solid**, you can specify the color by clicking on the colored box to the right of the menu.



Wrap the Analysis view display

To wrap the display in the Analysis view:

In the Style panel's [Analysis section](#), select **Automatic wrapping** from the **Layout** drop-down menu. The [Analysis view](#) will immediately wrap horizontally.

If you had been using a **Linear** layout and had already [split the sequence portion of the view vertically](#), choosing **Automatic wrapping** will change vertical splits to horizontal ones. Also, the scroll bars will move from the bottom of the view to the right.

When the Analysis view is split, the [Overview](#) provides a separate “[viewport indicator](#)” for each section. Splits are ignored when [printing](#) or [exporting](#) an image, although the layout is preserved.

Detach or reattach a view

To detach the [Overview](#) :

Use **View > Overview > Detach** or right-click on the view tab and choose **Detach Overview View**.

To detach the [Analysis view](#) :

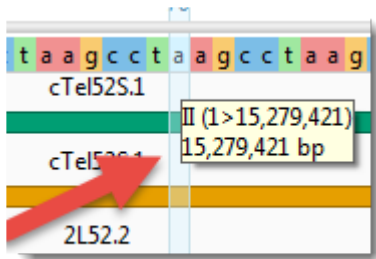
Use **View > Analysis > Detach** or right-click on the view tab and choose **Detach Analysis View**.

To reattach all detached views:

Use, **View > Reattach All Views**.

Display or hide a vertical guideline

To toggle between displaying or hiding a vertical guideline in the [Analysis view](#), click **Analysis > Show Guideline**. A vertical guideline is displayed by default, and is a navigational aid to help in guiding your eye between sequences and tracks.



Move a view or panel

To move a view up or down:

- [Overview](#) – Right-click on the **Overview** tab and choose **Move Overview View Up** or **Move Overview View Down**.
- [Analysis view](#) – Right-click on the **Analysis** tab and choose **Move Analysis View Up** or **Move Analysis View Down**.

To move a tabbed view or panel manually:

Use the mouse to grab the tab, then drag and drop it in the desired location.

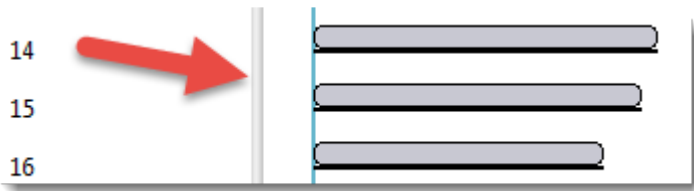
Resize a view, panel or section

To increase or decrease the size of a view or panel:

Do either or both of the following:

- Drag the bottom or left sides of the item using the mouse.
- Drag the light gray divider bar between the panes to the left or right.

Overview:



Analysis view:



To view more of an open section within a panel:

Do either or both of the following:

- Close neighboring sections by clicking on their expand bars.
- Increase the size of the panel.

Scroll horizontally or vertically

To scroll horizontally:

Do any of the following:

- Use the horizontal scrollbar.
- Hold down the **Alt** key (Win) or **Option** key (Mac) and drag the mouse.
- Drag the mouse left or right in the [Overview](#) or [Analysis view](#).

To scroll vertically:

- Use the vertical scrollbar.

To move up or down the list of [tracks](#) :

Either:

- Use the mouse wheel.
- Use the vertical scrollbar on the right.




Note The presence or absence of scrollbars depends upon the reference sequence length and the current [zoom](#) level.

See a view in full-screen mode


To show the active view in full-screen mode:

Either:

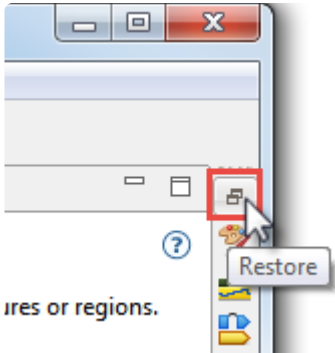






- Press the **Full Screen** tool ()
- Use **Ctrl/Cmd+Shift+F**.

To exit from full-screen mode:

Do any of the following:

- Use the **Exit Full Screen** tool () at the bottom of the full-screen view.
- Press **Ctrl/Cmd+Shift+F**.
- Click the **Esc** key

Show or hide an element of the interface


Interface element type	To show	To hide
Views	<p>If neither view is visible, click the Restore icon.</p>  <p>views or regions.</p> <p>To see both views when only one is displayed, either:</p> <ul style="list-style-type: none"> • Use View > Split. • Press the Split () tool in the bottom right corner of the current view. 	<p>To hide both views, either:</p> <ul style="list-style-type: none"> • Click the Close () or Minimize () icons. • Right-click on a view tab and choose Close, Close Others, Close Tabs to Right, or Close All. <p>To hide one of the two views that is currently displayed, either:</p> <ul style="list-style-type: none"> • Click on the tab of the view you wish to preserve, then use View > Split. • Press the Remove Split () tool in the bottom right corner of the view you wish to preserve.
Panels	<p>Do any of the following:</p> <ul style="list-style-type: none"> • Click on the panel tab • Use the associated View menu command. • Click the Restore icon (see above) 	<p>Do either of the following:</p> <ul style="list-style-type: none"> • Click the Close () or Minimize () icons. • Right-click on a view tab and choose Close, Close Others, Close Tabs to Right, or Close All.
Panel sub-sections	<p>Click on a closed expand bar (medium gray bar) or use the associated View menu command.</p>	<p>Click on an open expand bar.</p>

Split a view horizontally or vertically

To view different sections of sequences, assemblies or genomes simultaneously, you can split the [Overview](#) or [Analysis view](#) into any number of panes.

To split a view vertically:

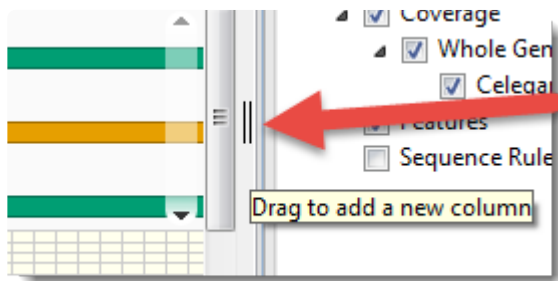
- Use **Overview > Split View** or **Analysis > Split View**. The split can be moved by dragging it left or right with the mouse.

- Drag the vertical splitter tool (), found at the right edge of the view, in a leftward direction.


Overview:



Analysis view:



To split a view horizontally:

Drag horizontal splitter tool (), found at the bottom of the view, in an upward direction.

To automatically remove the right-most vertical split:

Use **Overview > Remove Split** or **Analysis > Remove Split**.

To remove any split:

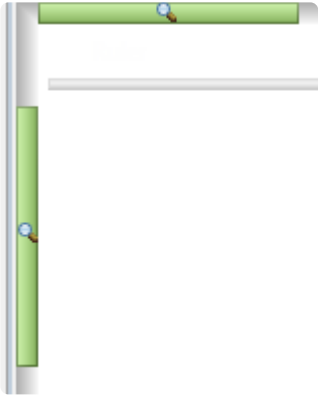
- Drag the divider as far as you can to the side/top/bottom of the view and drop it there.

Notes:

- When the Analysis view is split vertically, the Overview provides a separate “[viewport indicator](#)” for each section.
- Splits are ignored when [printing](#) or [exporting](#) an image, although the layout is preserved.

Zoom in and out

Both the [Overview](#) and [Analysis view](#) have independent vertical and horizontal zoom sliders. Grab any green slider with your mouse and drag left/right or up/down to zoom in or out in the view.



The following table shows the look of the Analysis view sequences and a [numeric track](#) at different zoom levels.

Track	Maximum Zoom	Minimum Zoom
Sequences		
Numeric tracks		

Note that when zooming past the point where a single base corresponds to single screen pixel, the sequence track is shown a gray bar.

Return to the default layout

To return to the default GenVision Pro display:

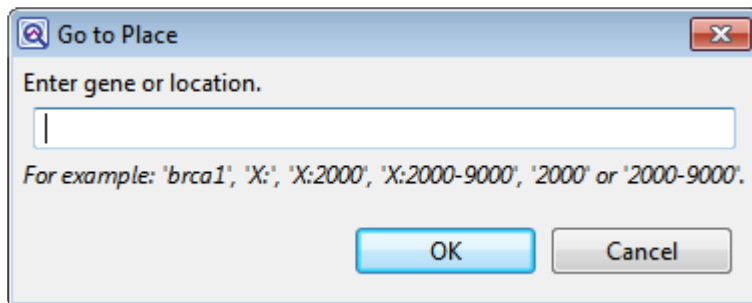
Choose **View > Reset Panel Layout**. This command restores the default layout of panels, including opening any default panels that have been closed; and restoring panels that have been minimized or maximized. It will not reattach a detached view. In that case, use **View > Reattach All Views** instead.

Find a Location

To navigate to a specific spot in the sequence:

To move the cursor to a specific point on the sequence, do any of the following:

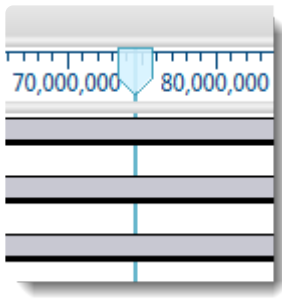
- Use the [navigation tools](#) near the top of the GenVision Pro window.
- Open the [Places panel](#) and double-click on a previously-stored location.
- Use **Edit > Go to Place** or press **Ctrl/Cmd+J**. In some cases, the right-click option **Go to Position** may also be available. In the Go to Place dialog, type the desired text and click **OK**. Using this dialog is equivalent to typing a search query in the navigation area text box and pressing the **Go** button.



The following video shows several of these search functions in action:

To navigate to a general area of the sequence:

The light-blue vertical bar in the [Overview](#), known as the “viewport indicator,” can be used as a navigation tool.



The viewport highlights the portion of sequence displayed in the [Analysis view](#). The shading between the vertical lines of the viewport indicator corresponds to the range of sequence currently visible in the Analysis view.

Here are some examples of how the viewport can be used as a general navigation tool:

- Drag the indicator to scroll the Analysis view along the sequence.
- Double-click on any block in the Overview to center the Analysis view at that position. Once an Overview block has been selected, double-click anywhere on it to move the cursor to that location.
- Once you have centered the viewport in the desired location, use the horizontal [zoom slider](#) in the Analysis view to increase or decrease the width of the view.
- If you split the Analysis view, there will be more than one viewport indicator in the Overview. If you split the Overview, a viewport indicator may appear in more than one of the sub-panes.

Make a Selection

Within the [Analysis view](#), you can select an entire chromosome, a portion of one, or a specific portion of chromosome corresponding to a feature. The active selection is highlighted in light blue. The selection can then be copied to the clipboard in standard or FASTA format.

To select...	Do this...
One or more rows	In either the Overview or Analysis view, click on a row label to make it the active selection, and click again to deselect it. To select multiple rows, use Ctrl/Cmd+click or Shift+click .
The entire active chromosome	Use Edit > Select All .
A portion of the active chromosome	Drag the mouse across residues in the sequence track while holding down the left mouse button.
Only the portion of a single sequence associated with a section of track (e.g. a Gap Fraction peak, etc.)	Drag the mouse across the open track while holding down the left mouse button.
One or more tracks	Click on a track to select it. To add additional tracks to the selection, use Ctrl/Cmd+click or Shift+click .
One or more features and corresponding sequence	Click on a feature to select it. To add additional features to the selection, use Ctrl/Cmd+click .
The portion of a single sequence associated with a feature	Do any of the following: <ul style="list-style-type: none"> Click on the feature to select it, then use Edit > Select Subsequence. Click on the feature to select it, then right-click and choose Select Subsequence. Double-click on the feature under the sequence.
Additional continuous items, when the first endpoint has been selected	Use Ctrl/Cmd+Shift and click on the other endpoint.
Toggle selection of items on or off	Hold down the Ctrl/Cmd key while clicking on the items to toggle on or off. For subsequence selection, hold down the Ctrl/Cmd key while dragging the mouse.
The current selection, but expanded to encompass additional bases	You can extend the length of an existing selection by Shift+clicking on the new endpoint. The selection will expand to use the chosen base as the new endpoint. If there are multiple selected ranges, the one closed to the chosen base will be expanded.



Work with Tracks

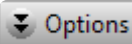
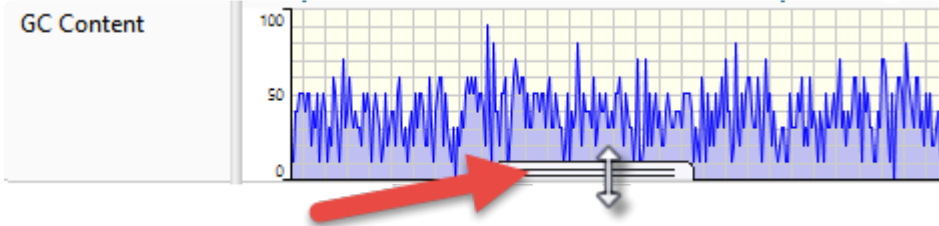
Tracks are rows of information pertaining to a header, footer, or individual sequence row in the [Overview](#) and [Analysis view](#). Tracks may be displayed or hidden, as desired, and some tracks may change in appearance depending upon the [zoom](#) level.

The following tracks can be applied, removed or (in most cases) edited:

- [Ruler](#)
- [Feature and Region](#)
- [Numeric](#)
- [Sashimi](#)


The following table shows tasks that affect the display of tracks within the Overview and Analysis views:

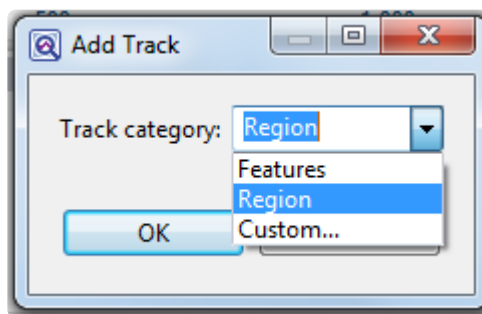
Task	How to...
To create tracks	Track data can be imported manually , imported automatically with some types of sequence data (e.g., Feature and Region tracks), or can be calculated by the application itself (e.g., Ruler and Numeric tracks).
To display tracks in the views	To display any type of track, you must check the box next to the name of the track in the Tracks panel . This is the only condition needed to view a Ruler track. For any type of track other than a Ruler, you must also select a single sequence to display (as opposed to a genome) and expand the track as described below.
To expand/collapse tracks for selected sequences	<p>Do any of the following:</p> <ul style="list-style-type: none"> • Click the plus/minus sign to the left of the sequence name ( / ). • To expand tracks for selected sequences, choose Sequence > Expand Sequence Rows or Overview > Expand Overview Rows; or right-click on the selection and choose Expand. • To collapse tracks for selected sequences, choose Sequence > Collapse Sequence Rows or Overview > Collapse Overview Rows; or right-click on the selection and choose Collapse.
To expand/collapse tracks for all sequences in a particular view	<p>Ensure that no sequences are selected.</p> <ul style="list-style-type: none"> • To expand tracks for all sequences, choose Sequence > Expand All Rows or Overview > Expand All Rows; or right-click in the view and choose Expand All. • To collapse tracks for all sequences, choose Sequence > Collapse All Rows or Overview > Collapse All Rows; or right-click in the view and choose Collapse All.

To hide tracks	<p>Do one of the following:</p> <ul style="list-style-type: none"> • <u>To hide a specific track from all views</u>, uncheck the box next to the name of the track in the Tracks panel. • <u>To hide a specific track in one view only</u>, right-click on the track within that view and choose Hide Track. Alternatively, select a track and use Edit > Delete or press the Delete key. • <u>To hide all tracks in one view only</u>, click the minus sign (⊖) to the left of the sequence name in that view, or use Analysis > Collapse Sequence Rows or Overview > Collapse Sequence Rows. • <u>To hide all tracks in all views</u>, do a combination of the above, or display a genome instead of a single sequence.
To access the options for a particular type of track	<p>Do either of the following:</p> <ul style="list-style-type: none"> • Right-click on a track in either view and choose Show Track Options. • Click View > Tracks > Options or open the Tracks panel and click the Options bar (), then do either of the following to specify the track of interest by clicking on its name in the Tracks panel.
To change the order of all tracks in a view	<p>Open a sequence row to view its track. Then drag a track label (e.g. “Features”) to the desired position among the other tracks and drop it there. Note that if you turn off some tracks in the Tracks panel and add them again later, they will appear in the order in which their boxes were checked.</p>
To increase/decrease the vertical height of a visible track	<p>Hover the mouse over the bottom of the track in the Overview or Sequences view, then grab the resize bar and drag it up or down.</p> 
To see how the zoom level can affect the appearance of tracks	<p>See Zoom in and out.</p>

Import track data

GenVision Pro lets you import an accessory file with track information for one or more assemblies.

1. Choose **File > Add Tracks**, press the **Add Tracks to Project** tool () or press **Ctrl/Cmd+Shift+T**.
2. In the file chooser, navigate to and select the desired file. There are three allowable file types: BED (.bed), GenVision file (.txt; formatted as a histogram or arrow panel) and Wiggle file (.wig). For instance, you could use a targeted region BED file from a SeqMan NGen assembly, or a box file from DNASTAR's original GenVision application. Press **Open**.
3. In the ensuing Add Track dialog, use the drop-down menu to select the **Track category** for the file you chose in the previous step. Choices will include a subset of **Feature**, **Region**, **Coverage** or **Custom**. You can type a custom value directly into the field. Optionally, you can choose the **Custom** menu item to clear the field.



GenVision Pro will use the **Track category** to place the track in the hierarchy in the [Tracks panel](#) and determine default track options.

4. Press **OK** to add the track to the current session.

The following table shows error messages that may occur when attempting to import track data:

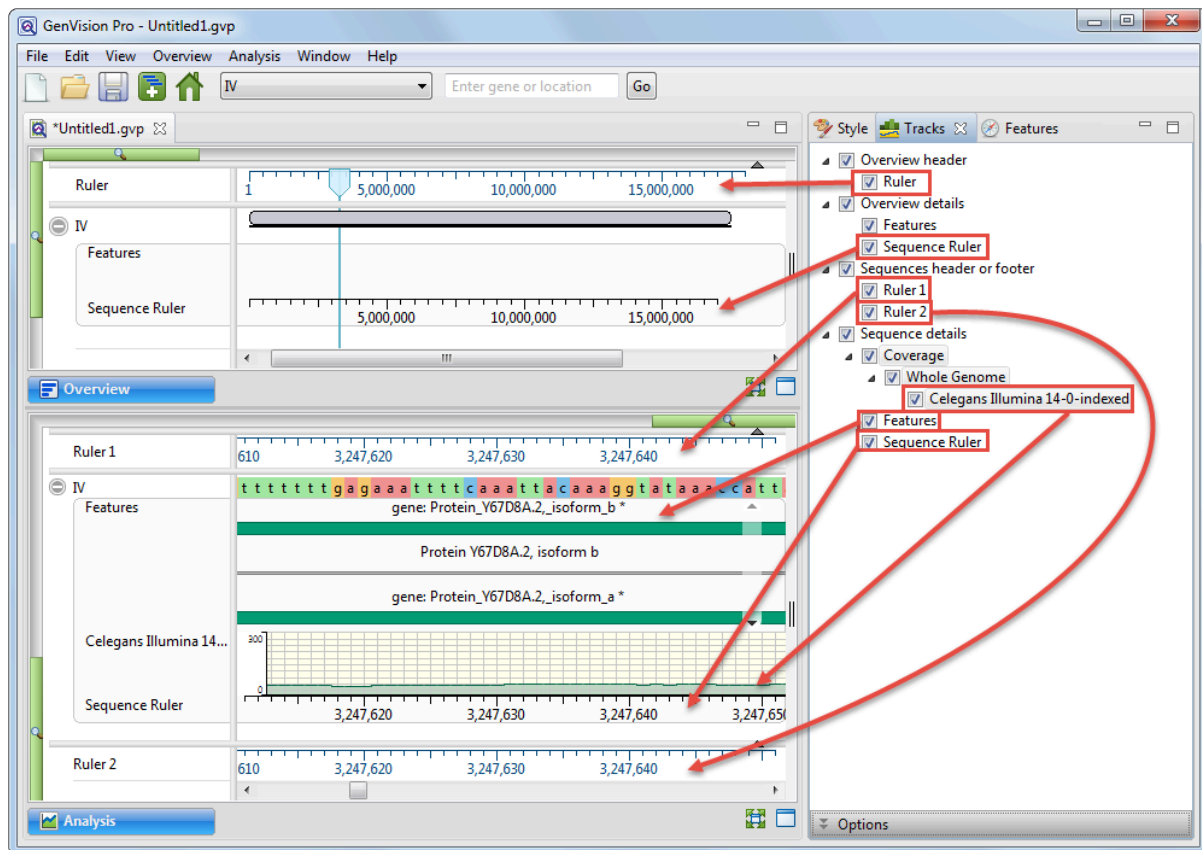
Error Message	Explanation
Some data could not be mapped to document members.	This message appears if some of the sequences identified in the track data could not be matched automatically to sequences in the session.
This file is already loaded in this document.	The selected file has already been added to the current session.
Could not open file.	The file does not contain recognizable track data.

Ruler tracks

Header and footer rulers:

The visibility of header and footer rulers in the [Overview](#) and [Analysis view](#) is dependent on:

- Which boxes you check in the [Tracks panel](#) (see image below).
 - **Ruler** – [Overview](#) header
 - **Ruler 1** – [Analysis view](#) header
 - **Ruler 2** – [Analysis view](#) footer



- Whether or not tracks are visible in the Overview and/or Analysis view. To display tracks, click on the plus sign next to the sequence in the view of interest.

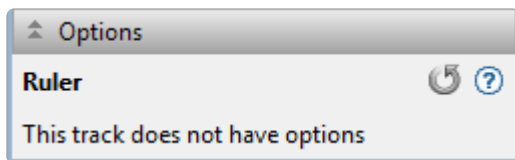
Sequence rulers:

The visibility of sequence rulers in the Overview and Analysis view is dependent on:

- Which boxes you check in the Tracks panel (see image below).
 - **Sequence Ruler** (under **Overview Details**) – Check this box to display sequence ruler tracks in the Overview.
 - **Sequence Ruler** (under **Sequence Details**) – Check this box to display sequence ruler tracks in the Analysis view.
- Whether or not tracks are visible in the Overview and/or Analysis view. To display hidden tracks, click on the plus sign next to a sequence in the view of interest.

Changing Ruler options:

Currently, the Ruler tracks do not have editable options.



However, you can add white space above and/or below the ruler using sliders in the [Layout section](#).

Feature and Region tracks

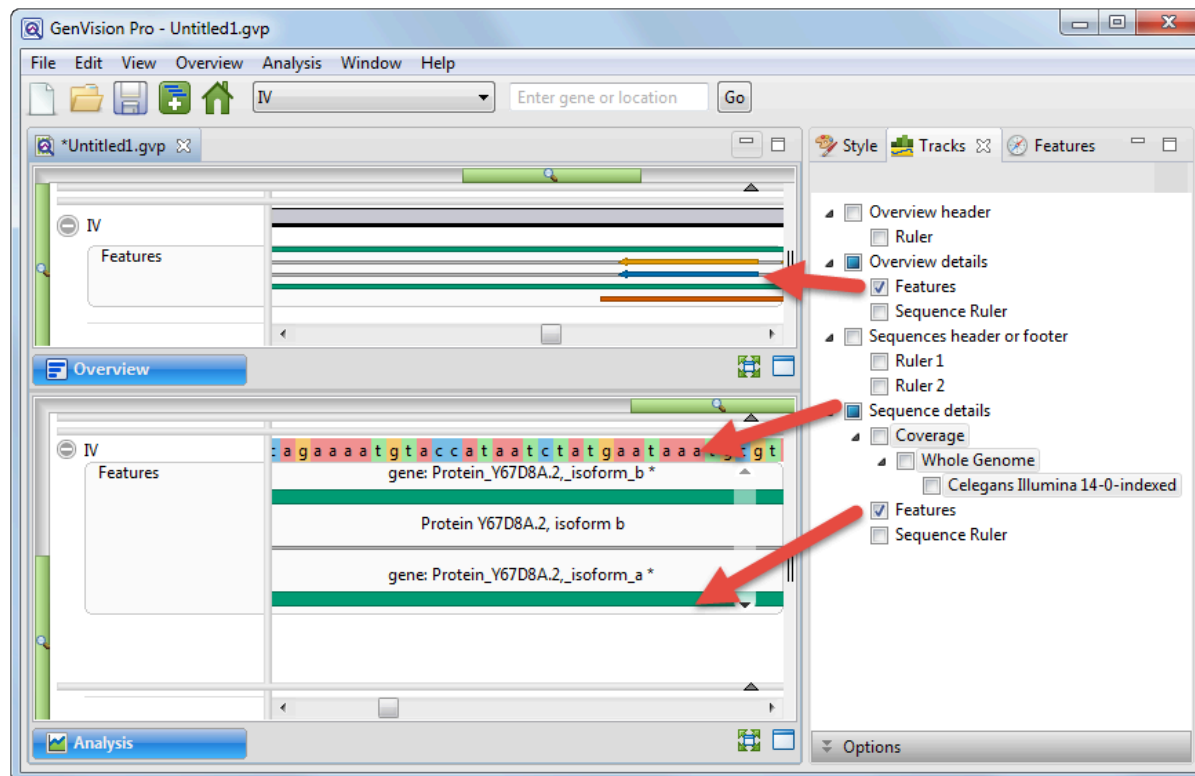
Feature and region tracks may come from the sequences in an assembly, or can be [imported separately](#) using **File > Add Track**.

To display features:

The visibility of feature or region tracks in the [Overview](#) and [Analysis view](#) is dependent on:

- Whether or not tracks are visible in those views. To display hidden tracks, click on the plus sign next to the row of interest in the Overview or Analysis view.
- Whether a track added using **File > Add Track** contains data relevant to the chromosome being viewed.
- Which boxes you check in the [Tracks panel](#) (see image below).
 - **Features** (under **Overview details**) – Check this box to display any available features as Overview [tracks](#).
 - **Features** (under **Analysis details**) – Check this box to display any available features as Analysis view [tracks](#).

✱ **Note:** If **File > Add Track** was used, there may be multiple feature and/or region tracks available. Additional feature and region tracks are placed under the parent items “Features” and “Region,” respectively.



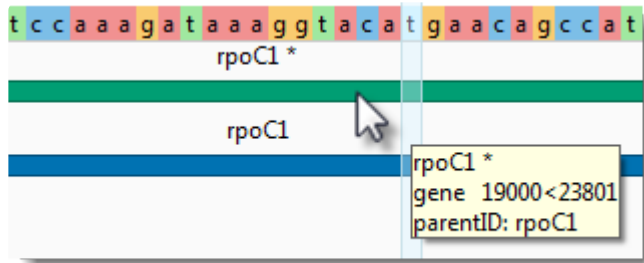
To view a tool tip with details about a region or feature, hover over it with the mouse. Or select one or more features or regions by clicking on them. You can then view information about them in the [Details panel](#).

Features are displayed with the same default color scheme in both GenVision Pro and MegAlign Pro.

Feature Type	Color
gene	green
CDS	blue
RNA	orange
repeat	yellow
transcription	red-purple
all others	orange-red

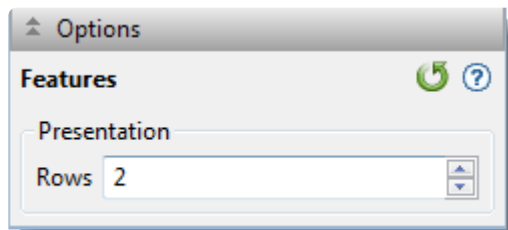
Inferred features:

An asterisk next to a feature name indicates that the feature was inferred by SeqMan NGen. For example, if you assembled data in SeqMan NGen using a template that contained a CDS feature—without a corresponding gene feature—then "gene" would be inferred at that position, and would be displayed in the Feature track. However, the inferred gene would be marked with an asterisk.



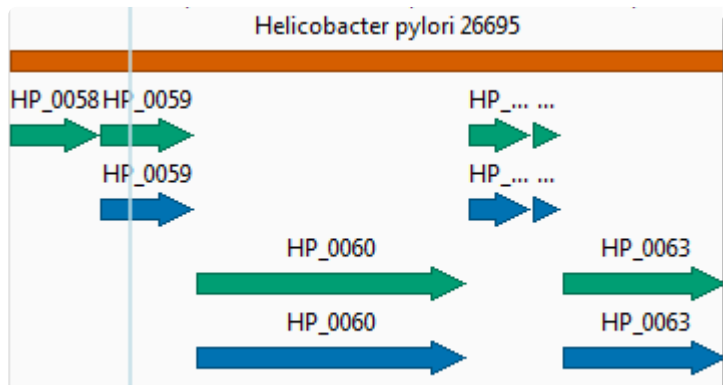
To change feature options:

To learn how to access the options section for this track, see [Options section](#).



Specify the number of feature rows to display by typing a number in the **Rows** box or by using the up/down arrows. If features are overlapping, this indicates a need to increase the number of rows.

The example below displays 5 rows of features.

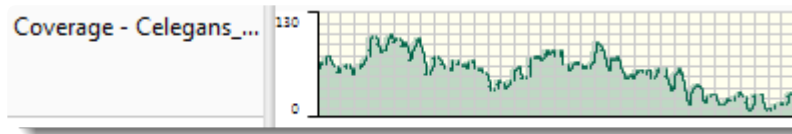


You can also add white space above and/or below features tracks using sliders in the [Layout section](#).

Numeric tracks

Sources of numeric tracks in the [Analysis view](#) :

- Numeric data of any type imported via a Wiggle file using **File > Add Track**.
- Coverage tracks imported with an assembly. This track displays a plot of values along one or more sequences in the session. Values are obtained automatically from assemblies added to the session. When the Coverage track is visible, it consists of a graph showing the depth of sequence coverage for each nucleotide position along the Analysis view.



To display numeric tracks:

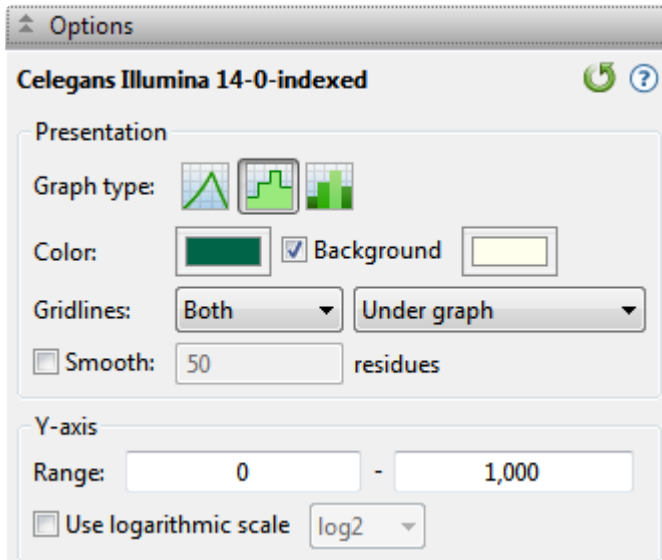
The visibility of numeric tracks in the Analysis view is dependent on:

- Whether or not tracks are visible in the Analysis View. To display tracks, click on the plus sign next to the sequence of interest.
- Whether a track added using [File > Add Track](#) contains data relevant to the chromosome being viewed.
- Whether or not the corresponding box is checked in the [Tracks panel](#).

 **Note:** If **File > Add Track** was used, the Tracks panel may list multiple numeric tracks.

To change numeric track options:

To learn how to access the options section for this track, see [Options section](#).



- Select from three different **Graph types** (**Line**, **Skyline**, **Bar**) by clicking on the corresponding icon.
- By default, numeric graphs are displayed in green with a pale yellow background. To choose another graph color, click on the box to the right of **Color** to make a selection from a color chart. To choose another background color, click the color box to the right of the **Background** checkbox. To turn off the background color, uncheck the checkbox.
- Use the first **Gridlines** drop-down menu to select which grid-lines to display: **Both** (horizontal & vertical), **Horizontal** (only) or **None**. Use the second drop-down menu to choose whether grid-lines should be visible above (**Over graph**) or below (**Under graph**) other parts of the graph.
- Check the **Smooth** box if you wish to average the values over a specified number of residues. Smoothing is computed by averaging values in a sliding window of the specified number of residues. Enter the number of residues in the adjacent text box (maximum=5000). Inputting a high value will smooth the graph curves, while a low value will highlight local differences.
- To change the range of values displayed, enter new y-axis endpoints in the **Range** text boxes. The default range may be too large or too small for some sections, causing the graph to appear empty or peaks to be cut off. You may need to raise or lower the second value, in particular, in order to see the graphical display clearly.
- Check the **Use logarithmic scale** box and select an option from the corresponding drop-down menu if you want to use a logarithmic, rather than a linear scale. Options are **log2** or **log10**.

✿ **Note:** The log of 0 is not defined. Therefore, log values for the track are calculated as follows: For $y > 0$, $y' = \log(y)$; otherwise, it is displayed as a 0.

Click  if you wish to return to the default values.

To change the height of the graph, and the white space surrounding it, use the sliders in the [Layout section](#).

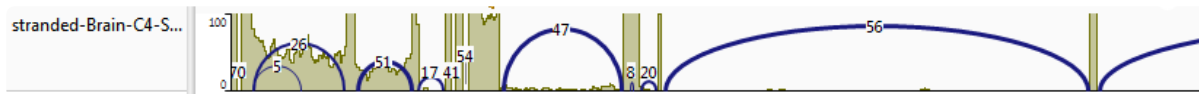
Sashimi tracks

Analysis of mRNA isoform expression is a key aspect of understanding gene expression. For many genes, the change in isoform ratios for a given gene produce a more significant physiological effect than the overall expression level of that gene. Isoforms are typically visualized as Sashimi plots, a way of quantitatively visualizing splice junctions for mRNA sequences aligned to an annotated genomic reference. Sashimi plots allow you to screen differentially spliced exons in genomic regions of interest.

When the Sashimi track is visible in the [Analysis view](#), it consists of two components:

- A bar graph showing the abundance of each exon
- Arcs representing the number of reads split across the junction, also referred to as “junction depth.”

Multiple Sashimi plots from multiple samples can be displayed simultaneously.



Scroll to the bottom of this page to see two videos showing Sashimi tracks in action.

Sashimi track data can come from the sequences in an assembly, or can be [imported separately](#) using **File > Add Track**. When data are available for a given sample, GenVision Pro automatically replaces the [Coverage track](#) with a Sashimi plot, which contains the same Coverage histogram, but also allows for “arcs” to be displayed. The number at the top of each arc represents the number of split reads; the thickness of each arc is proportional to this number. Note that split reads do not necessarily correspond to introns; other types of structural variation can also cause SeqMan NGen to split reads. Annotations are not considered when creating the Sashimi track.

For a brief video showing RNA-Seq data analysis using the Sashimi track, see the second video in [Launch a session from within ArrayStar](#).

To display a Sashimi track:

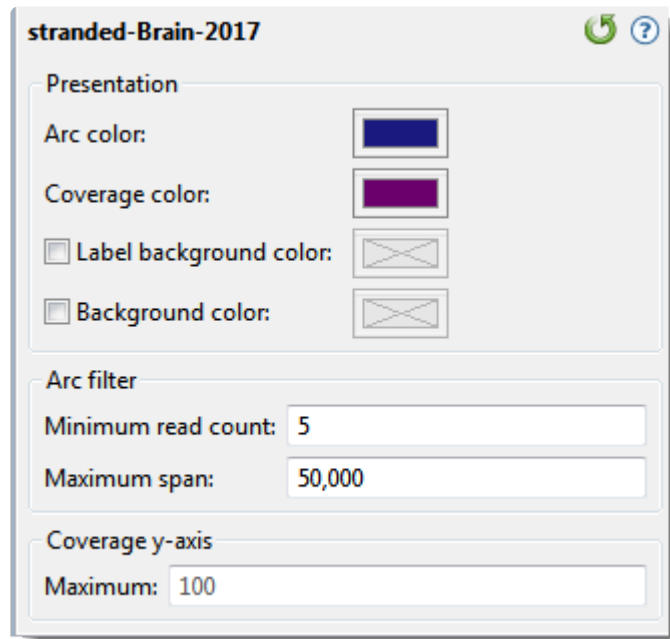
The visibility of Sashimi tracks in the Analysis view is dependent on:

- Whether or not tracks are visible in the Analysis view. To display tracks, click on the plus sign next to the sequence of interest.
- Whether a track added using **File > Add Track** contains data relevant to the chromosome being viewed.

- Whether or not the **Sashimi** box is checked in the [Tracks panel](#). Note that if [File > Add Track](#) was used, the Tracks panel may list multiple Sashimi tracks.

To change Sashimi track options:

To learn how to access the options section for this track, see [Options section](#).



- By default, Sashimi graphs have navy blue arcs and purple coverage histograms. To choose different colors, click on the **Arc color** and/or **Coverage color** box and make a selection from a color chart.
- By default, arc numbers (“labels”) and the Sashimi plot, as a whole, do not have background colors. To add colors, check **Label background color** and/or **Background color**, then click on the corresponding color box and make a selection from a color chart. To turn the colors off again, uncheck either or both check-boxes.
- **Minimum read count** lets you set a threshold for the minimum number of split reads needed to display an arc. If this value is set to zero, no filtering will occur.
- **Maximum span** allows you to set a threshold for the maximum allowable arc length, in bases. To turn off this filter, delete any numbers from the text box, leaving it blank.
- Under Coverage y-axis, set a **Maximum** limit for the height of the y-axis on the coverage graph. This setting is equivalent to the Y-axis range maximum in the [Numeric track options](#).

Click  if you wish to return to the default values.

✿ **Note:** The height of track labels is specified using the presentation **Font** settings in **View > Style > Analysis**. To change the height of the graph and the white space surrounding it, use the sliders in the [Layout section](#).

This video shows how to apply and interpret Sashimi plots in GenVision Pro:

This video shows an RNA-Seq workflow that begins with assembly in SeqMan NGen, proceeds to downstream analysis in ArrayStar, and then uses ArrayStar's **Send Selection to GenVision Pro** command to open the results in GenVision Pro. Once in GenVision Pro, the Sashimi track is applied. (GenVision Pro section begins at 2:41).

Use Basic Editing Commands

The following basic editing commands are available in GenVision Pro:

Command	Keyboard Shortcut	Right-Click Option	Description
Edit > Cut	Ctrl/Cmd+X	Cut	This command is not enabled in GenVision Pro.
Edit > Copy	Ctrl/Cmd+C		To copy text or data to the clipboard. A warning message will appear if you attempt to copy an extremely large amount of data to the clipboard.
Edit > Copy As FASTA	Ctrl/Cmd+Shift+C	Copy as FASTA	To copy text or data to the clipboard in FASTA file format. This command is only available if a subsequence is selected.
Edit > Paste	Ctrl/Cmd+V		To paste text from the clipboard into a text field. This command is disabled in all but a few circumstances.
Edit > Delete	Delete key		To remove selected text from a text box, or to remove one or more selected tracks from the Overview and Analysis view . Using Edit > Delete or pressing the Delete key has the same effect as unchecking the corresponding box(es) in the Tracks panel .
Edit > Select All	Ctrl/Cmd+A		If used in the Overview, selects all chromosomes. If used in the Analysis view, selects all of the active chromosomes in both views.

Copy

In many cases, once you have [selected](#) text, data, sequences or subsequences, you can copy the information to the clipboard. The copy functions described below are accessible using menu commands, context menu commands (i.e., “right-click options”), and/or keyboard shortcuts.

- **Edit > Copy** or **Ctrl/Cmd+C** – Copies the selected text, just as it appears in the view.
 - If a portion of sequence or one or more features are selected, this command copies the selected subsequence(s) as one long string, including the gaps. The subsequence is copied as one long string, without line breaks. If the selection extends across multiple members of the alignment, names are included as prefixes.
 - If a selection is made in the [Style panel](#) and in dialogs, use **Ctrl/Cmd+C**.
- **Edit > Copy As FASTA** – Copies the selected text or data in FASTA format.

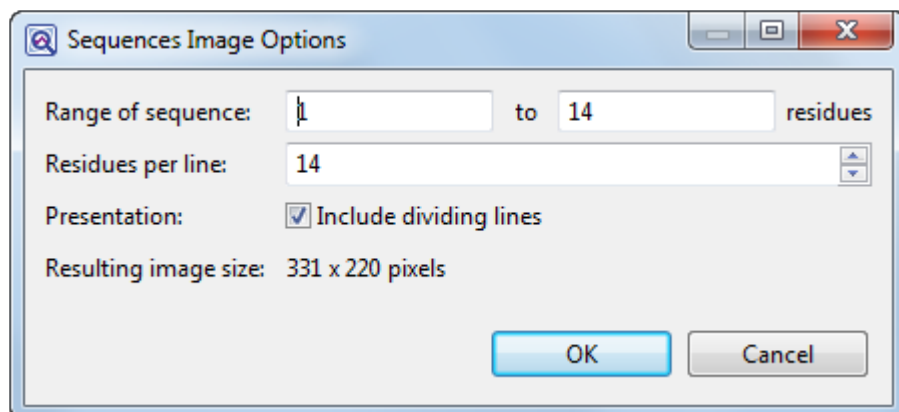
Export

GenVision Pro lets you export an image of either view for use in a text editor or similar program. A separate topic describes how to [edit an exported image using Microsoft Powerpoint](#).

To export an image of the [Overview](#) or [Analysis view](#) :

1. Choose **File > Export Image > Overview** or **File > Export Image > Analysis**.
2. Specify the file name and choose the export format: Adobe PDF (*.pdf*), Microsoft PowerPoint-optimized (*.pptx*), PNG image (*.png*) or JPG image (*.jpg*, *.jpeg*).
 - If you choose Adobe PDF format and a particular font is not supported there, a similar font will be substituted for the original one automatically.
 - If you choose the format that is optimized for use with Microsoft PowerPoint, the GenVision Pro image is converted into an editable set of objects that can be grouped, ungrouped and moved within the target application. To constrain an object (e.g., a GenVision Pro track) within Microsoft PowerPoint to move only vertically, rather than laterally, hold down the **Shift** key.

If exporting the Analysis View, the following dialog appears. If exporting the Overview, an abbreviated version appears.



3. Choose export options.
 - Use the **Range of sequence** boxes to specify the range of residues that should appear in the image. The default is the current viewport range.
 - (“Analysis” only) Type in the number of **Residues per line**. By default, GenVision Pro places the entire range on a single line.
 - (“Analysis” only) Check the **Include dividing lines** box if you wish to include separators

between the header, sequences, and footer.

The **Resulting image size** updates automatically based on the options you choose.

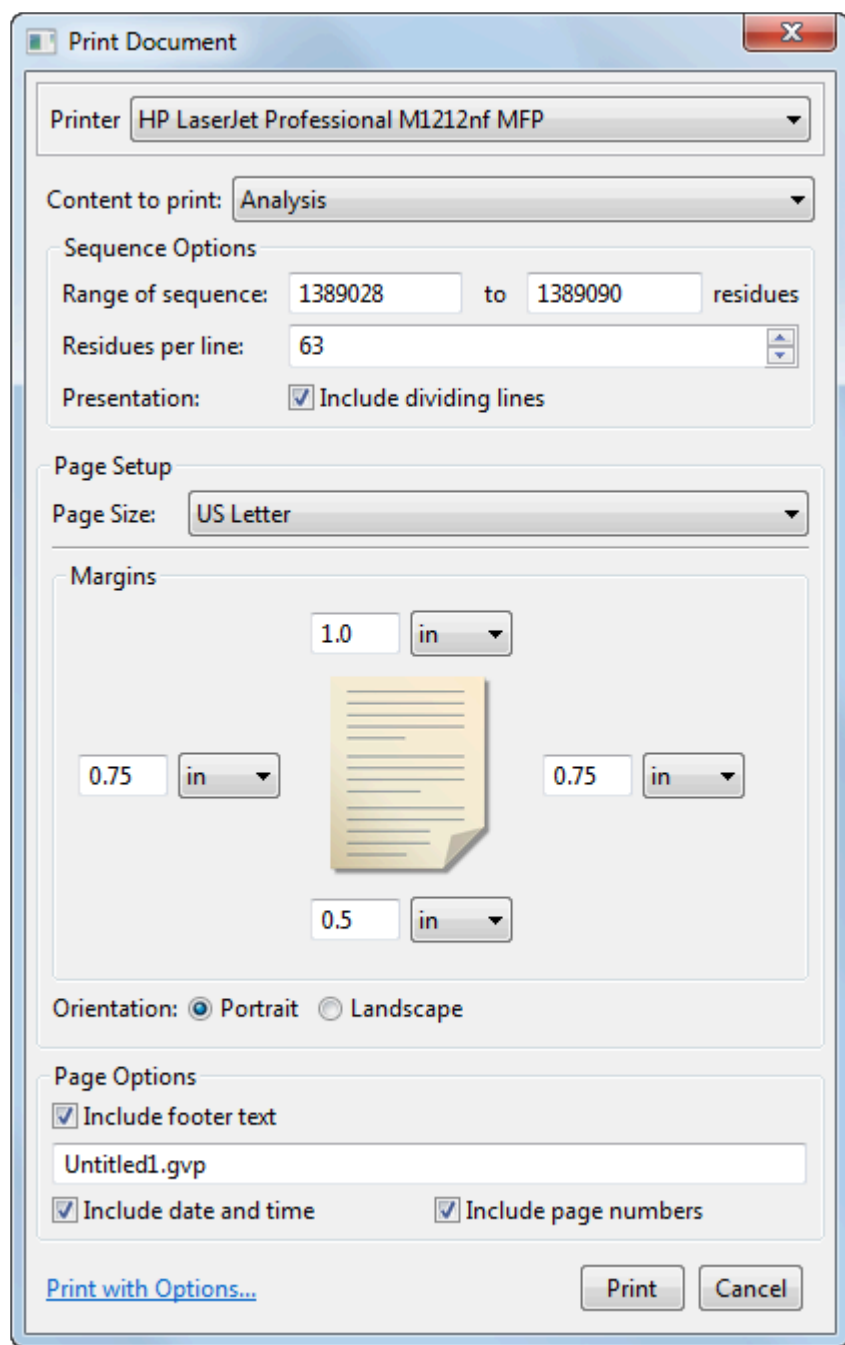
4. Click **OK** to export the image using the specified options or Cancel to close the dialog without exporting.

Edit an exported image in PowerPoint

The following video shows how to edit [exported](#) images of your alignment or genomic tracks within Microsoft PowerPoint:

Print

To print an image of any GenVision Pro view, whether it is currently active or not, choose **File > Print** or press **Ctrl/Cmd+P**. The Print Document dialog opens:



- Use the **Printer** drop-down menu to choose the desired printer from a list of available options.
- Specify the content you wish to print ([Overview](#) or [Analysis view](#)) using the **Content to print** menu. Depending upon the selection, additional options may appear just below this drop-down menu.

- **Overview** and **Analysis View** - To print only a sub-range of the sequence(s), type the left and right residues into the **Range of sequence** boxes.
- **Analysis View** - To specify how many residues to include on one line, type in a number from 1-100 next to **Residues per line**. Check the **Include dividing lines** box if you wish to include separators between the header, sequences, and footer.
- Choose which **Page Size** to print on.
- Specify the top, bottom, left and right **Margins** by typing a number in the associated box and choosing the units (**inches**, **cm**, etc.) from the nearby drop-down menu.
- Choose whether to print in **Portrait** or **Landscape** orientation.
- Under **Page Options**, use the checkboxes to specify what to include in the footer: **footer text**, **date and time** and/or **page numbers**. If you check **Include footer text**, the footer will incorporate the text just below the checkbox. By default, this is the path and GenVision Pro session name (or only the default session name, for unsaved documents), but you may type in any text that you wish.
- Click the **Print with options** link to launch the default Print dialog for your computer.

Choose **Cancel** to exit from the GenVision Pro Print Document dialog without printing. Click **Print** to print using the selected parameters, or **Print with Options** to open the Print dialog for your computer's operating system. The generic dialog can be used to specify additional options, such as the page range and number of copies to print.

Change the default print size

Unless otherwise specified on your computer, the default printing size for all DNASTAR applications is “U.S. Letter” size (8.5 × 11 inches = 21.6 × 28 cm). You can temporarily change to another size, such as A4, from within the application. However, the next time you print, the default size will again be U.S. Letter size.

To correct this issue, you need to change your computer’s default printing size:

On Windows 7 and Windows 8:

1. Open the Control Panel.
2. In the Hardware and Sound category, click on **Printers** or **View devices and printers**.
3. Right-click on your printer and choose **Properties**.
4. In the **General** tab, click on the **Printing Properties** button.
5. In the ensuing **Printing Shortcuts** tab, choose the desired default printing size from the **Printing Sizes** drop-down menu.
6. Click the **Apply** button, then the **OK** button.

On Macintosh:

1. Open System Preferences.
2. Click on **Print & Fax**.
3. Choose the desired size from the **Default paper size** drop-down menu.




Note: Changes to the default printing size will not be applied until after you restart the DNASTAR application.


Save, Close and Exit

To save one or more sessions:

To save one or more sessions or to overwrite a previously saved version of the session in GenVision Pro (.gvp) format

- To save all open sessions, use **File > Save All Sessions** or press **Ctrl/Cmd+Shift+S**.
- To save only the active session, do any of the following:
 - Use the **Save Session** [button tool](#) (). If you want to preserve the earlier version of a session, or store a copy of the session with a different name or location, use **File > Save Session As** instead.
 - Choose **File > Save Session**
 - Press **Ctrl/Cmd+S**.

In all cases, GenVision Pro saves to the desktop by default.

 **Note:** When you add Wiggle files using **File > Add Track**, they are indexed for fast retrieval. When the session is saved, these indices are written to a folder called *<Session Name> .gvp.index*. When you reopen the session, GenVision Pro uses these indices for faster performance. If you move or copy the .gvp file to another location, you can move the .gvp.index folder also; this avoids the need to recompute indices upon reopening the session. Alternatively, you can move just the .gvp file, and the indices will be automatically recomputed.

To close the selected session:

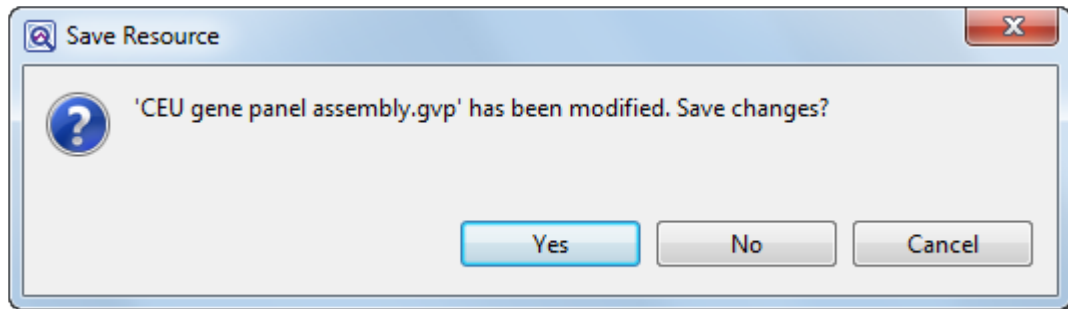
Use **File > Close** or press **Ctrl/Cmd+W**. If multiple sessions are open, first select the tab corresponding to the session you wish to close.

To quit the application:

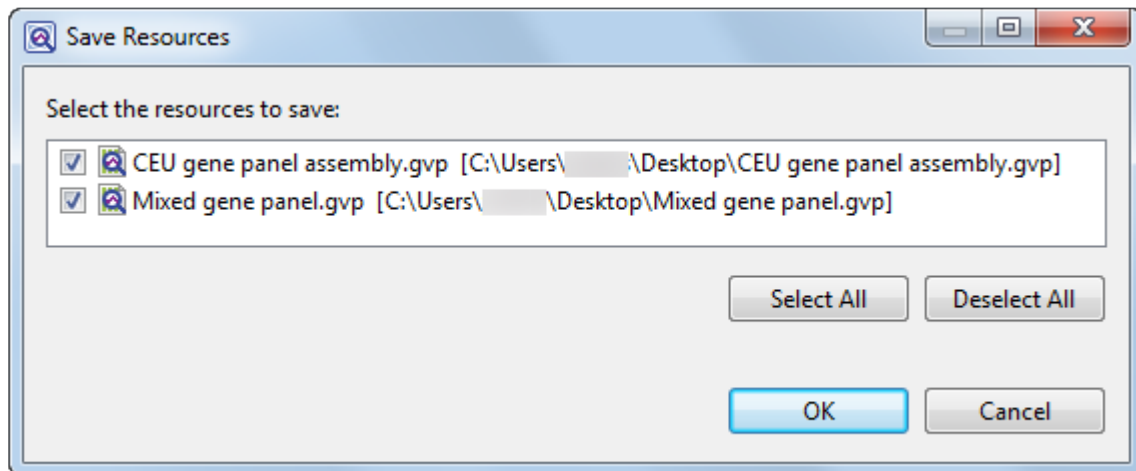
- Windows: Use **File > Exit** or **Ctrl+Q**.
- Macintosh: Use **GenVision Pro > Quit GenVision Pro** or **Cmd+Q**.

Closing or quitting when there are unsaved documents:

If you select **File > Close**, or if you quit GenVision Pro when just one unsaved session is open, GenVision Pro will open the Save Resource dialog. Click **Yes** to save changes, **No** to close/quit without saving changes, or **Cancel** to return to GenVision Pro without closing/quitting.



If you quit GenVision Pro while multiple unsaved sessions are open, GenVision Pro will instead display the Save Resources dialog.



- To save all changed sessions, choose **Select All**. To close all changed sessions without saving the updates, pick **Deselect All**. To save only some of the sessions, add/remove checkmarks individually.
- Click **OK** to save only the checked sessions and to quit GenVision Pro. Click **Cancel** to return to GenVision Pro without saving the checked sessions.

Appendix

The Appendix contains the following topics:

- [View a list of supported file types](#)
- [Set preferences](#) for [displaying help](#), for the [Internet](#) or for [specifying temporary file locations](#).
- View [IUPAC codes](#)
- See the [installed Lasergene file locations](#)
- [Turn off usage logging](#)
- [Troubleshoot the error](#)
- [Clean cached files on startup](#)
- See the list of [research references](#) related to this application

Supported file types

For a list of file formats supported by this DNASTAR product, please see the [File Formats](#) page of our website.

Set preferences

You can set preferences in GenVision Pro for [help](#), [Internet](#), and [temporary files](#).

To open the Set Preferences dialog:

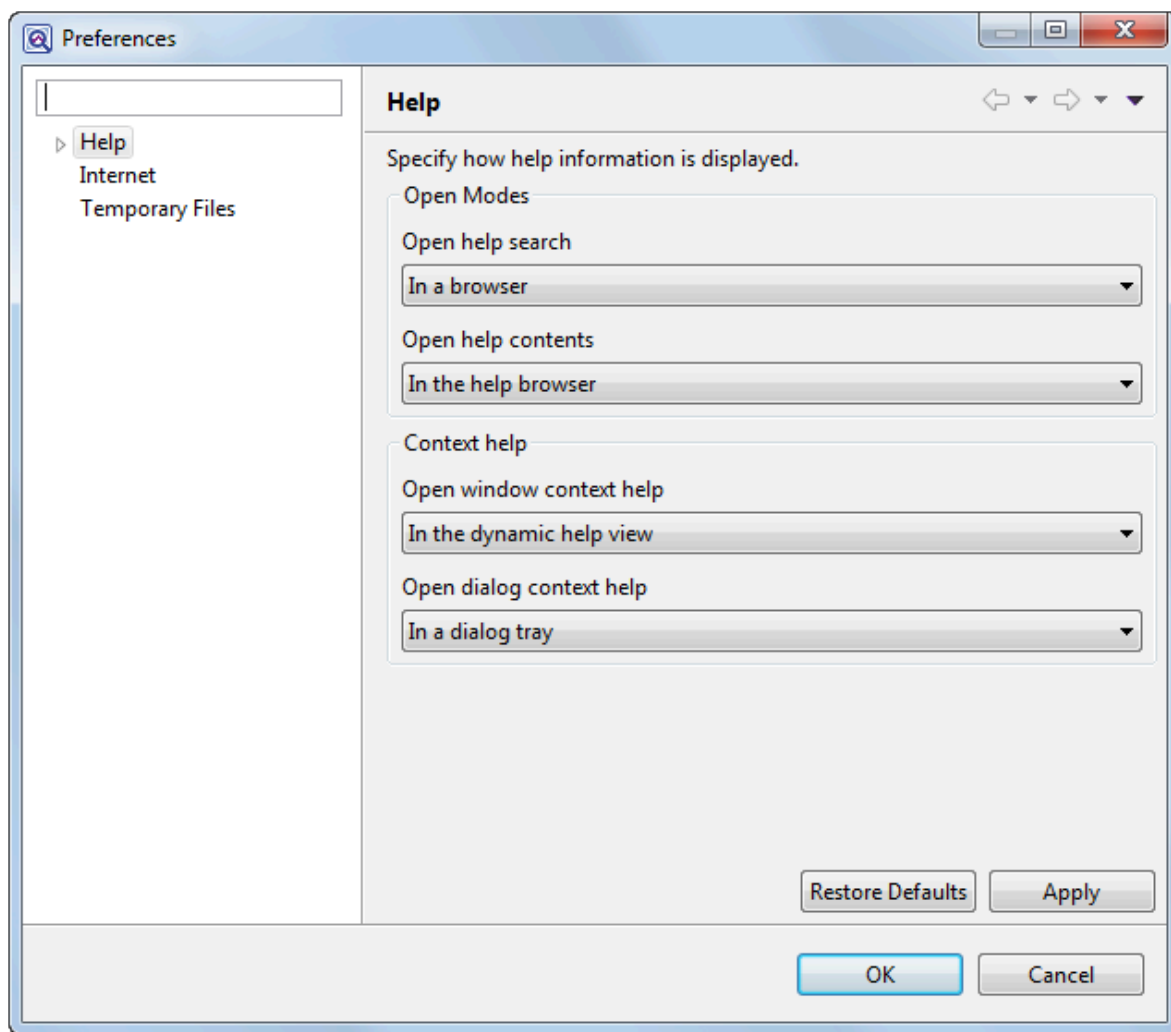
On Macintosh, choose **GenVision Pro > Preferences**. On Windows, choose **Edit > Preferences**.

Set help preferences

The Help Preferences dialog controls how help documentation is displayed when you use the **Help > Help Contents** command.

The dialog is accessed via the command **Edit > Preferences** (Win) or **GenVision Pro > Preferences** (Mac). If the Help section is not already active, click on the word "Help" on the left.

✿ **Note:** There is no need to use the expand arrow to the left of "Help." Its only sub-menu item, "Contents," is disabled in GenVision Pro.



- Specify the browser used to display the Protean 3D Help search results by selecting one of the following options from the **Open help search** menu:
 - **In the dynamic help view** – To display the GenVision Pro Help search results in a new section of the Help interface. This is the default setting.

- **In a browser** – To display the GenVision Pro Help search results in your default web browser.
- Choose how to display the GenVision Pro Help contents by selecting one of the following options from the **Open help contents** menu:
 - **In the help browser** – to display the GenVision Pro Help content in a new section of the Help interface. This is the default setting.
 - **In an external browser** – to display the GenVision Pro Help content in your default web browser.



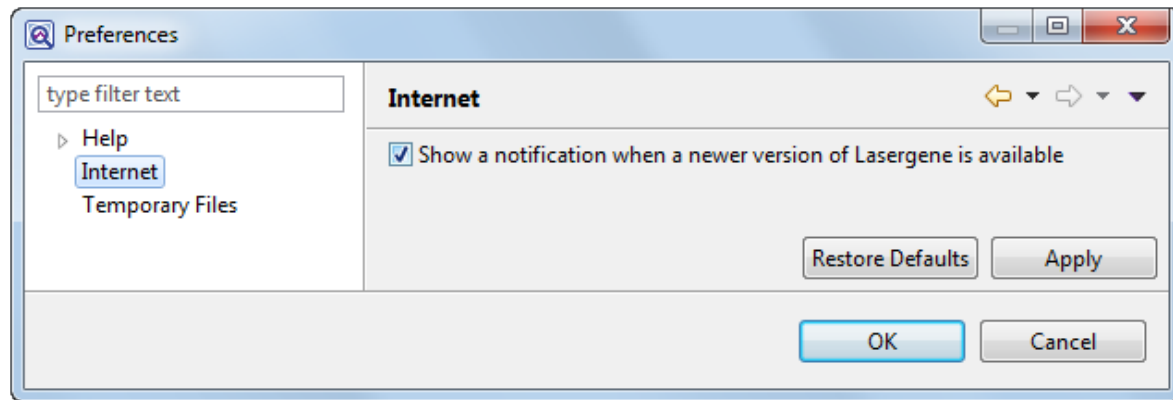
Note: The ContextHelp options in the lower half of the dialog are not applicable to GenVision Pro.

Click **Apply** to save your changes while keeping the preferences dialog open, or **Apply and Close** to save the changes and exit from the dialog. If you instead wish to return to default settings for all four drop-down menus, click **Restore Defaults**. To leave the dialog without applying changes, choose **Cancel**.

Set Internet preferences

The Internet Preferences dialog lets you choose whether you wish to be notified about Lasergene updates.

To access the dialog, use **Edit > Preferences** (Win) or **GenVision Pro > Preferences** (Mac). If the Internet section is not already active, click on the word "Internet" on the left.



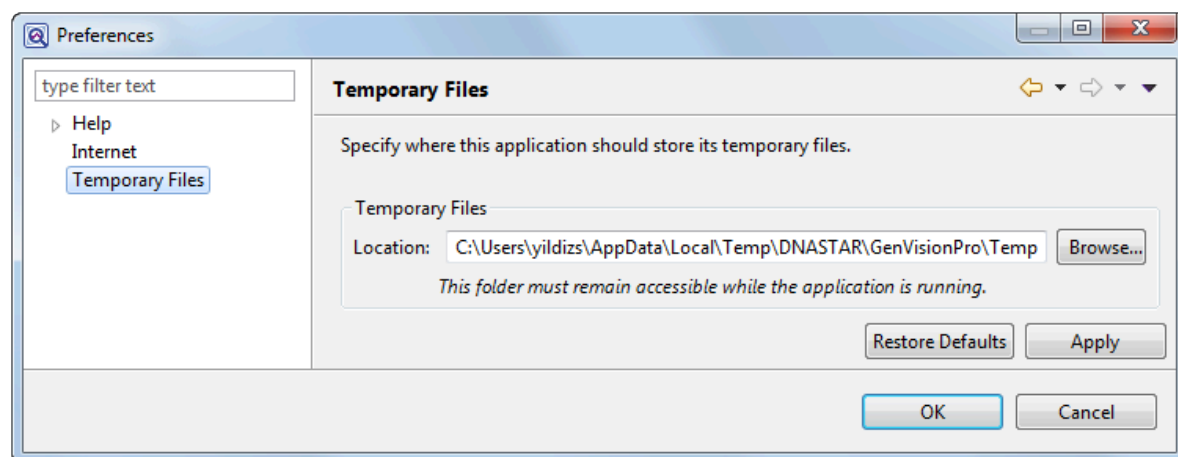
- Check the box if you would like GenVision Pro to display a notification when a newer version of Lasergene is available. Uncheck the box if you do not wish to receive this notification.

Click **Apply** and **OK** to save your changes or **Cancel** to ignore any changes. Click **Restore Defaults** to return to the default settings for all four drop-down menus.

Set temporary file preferences

GenVision Pro creates and uses temporary files while a session is open. The need for temporary file space grows with the number and length of the sequences and track data in open sessions. If you expect the temporary files will be too large to fit in the default location, you may specify a different location for these files using the Temporary Files Preferences dialog.

To access the dialog, use **Edit > Preferences** (Win) or **MegAlign Pro > Preferences** (Mac). If the Temporary Files section is not already active, click on the phrase "Temporary Files" on the left.



- To change the temporary file location, close all GenVision Pro sessions and then return to this dialog. Select the **Browse** button, navigate to the new location and click **OK**. As noted in the dialog, the location you choose must remain accessible while GenVision Pro is running. The new location will be used for all sessions that are subsequently created or opened.

Click **Apply** and **OK** to save your changes or **Cancel** to ignore any changes. Click **Restore Defaults** to return to the default (temporary) storage location.

IUPAC codes

IUPAC codes for amino acids:

1-Letter Code	3-Letter Code	Amino Acid
A	Ala	Alanine
B	Asx	Aspartic Acid or Asparagine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
J	Xle	Leucine or Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
O	Pyl	Pyrrolysine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
U	Sec	Selenocysteine
V	Val	Valine
W	Trp	Tryptophan
X	Xaa	Unspecified or unknown
Y	Tyr	Tyrosine
Z	Glx	Glutamic Acid or Glutamine

IUPAC codes for nucleotides:

Symbol	Description	Bases Represented			
A	adenosine/adenine	A			
C	cytidine/cytosine		C		
G	guanosine/guanine			G	
T	thymidine/thymine				T
U	uridine/uracil				U
W	weak	A			T
S	strong		C	G	
M	amino	A	C		
K	keto			G	T
R	purine	A		G	
Y	pyrimidine		C		T
B	not A		C	G	T
D	not C	A		G	T
H	not G	A	C		T
V	not T	A	C	G	
N or -	any base (not a gap)	A	C	G	T



The non-standard nucleotide codes “I” (Inosine) or “X” (xanthine) are supported in DNASTAR’s PrimerSelect and EditSeq applications only.

Installed Lasergene file locations

The following file names use 'x' to represent the version number.

File Category	Application	Path
Application ²	ArrayStar	Windows: C:\Program Files (x86)\DNASTAR\Lasergene x\ArrayStar
	SeqNinja (command line)	Windows: C:\Program Files (x86)\DNASTAR\Lasergene x\SeqNinjaCL
	All others	Windows: C:\Program Files (x86)\DNASTAR\Lasergene x Macintosh: /Applications/DNASTAR/Lasergene x
Data Manager ² (<i>DMx</i> , <i>DMx.exe</i>)	SeqBuilder Pro, Protean 3D, GeneQuest, MegAlign, MegAlign Pro, PrimerSelect	Windows: C:\Program Files (x86)\DNASTAR\Lasergene x Macintosh: /Applications/DNASTAR/Lasergene x
Data Manager State File	SeqBuilder Pro, Protean 3D, GeneQuest, MegAlign, MegAlign Pro, PrimerSelect	Windows: C:\Program Data\DNASTAR\DataManager Macintosh: ~/Library/Application Support/DNASTAR/DataManager, ~/Library/Preferences/DNASTAR/DataManager
License Manager ²	All	Windows: C:\Program Files (x86)\DNASTAR\License Manager Macintosh: /Applications/DNASTAR/License Manager
Server License File (<i>Iservrc</i>), Server License Manager ² , <i>Server Executables</i> (<i>_Iserv</i> , <i>Iservnt.exe</i>)	All	Windows: C:\Program Files (x86)\DNASTAR-LicenseServer\Server Macintosh: ~/Library/DNASTAR-LicenseServer
Standalone & Trial Licenses (<i>*.license</i>), License Server Client License (<i>*.lshost</i>), Key	All	Windows: C:\Program Data\DNASTAR\Licenses

Server Client License (*.keyhost)		Macintosh: ~/Library/ Application Support/ DNASTAR/Licenses
Preferences	Protean 3D, Navigator, SeqNinja (DNA*), GenVision Pro	Windows: C:\Users\<user>\DNASTAR Macintosh: ~/Library/ DNASTAR
	ArrayStar	Windows: C:\Users\<User>\AppData\ Roaming\DNASTAR\ ArrayStar
	All others	Windows: C:\Users\<user>\AppData\ Local\DNASTAR\ Macintosh: ~/Library/ Preferences



AppData is a hidden folder in Windows. To unhide the folder, go to **Organize > Folder and Search Options > View > Show Hidden files and folders**.

Turn off usage logging

By default, [usage logging](#) is enabled in Lasergene version 11 and later. To opt out of usage logging, launch the DNASTAR Navigator and go to **View > Preferences > Lasergene** (Win) or **DNASTAR Navigator > Preferences > Lasergene** (Mac). Uncheck the box and click **Apply** and then **OK**.

Troubleshoot the error “A different version is running”

If you receive the error “A different version of Lasergene is running” when you try to launch a Lasergene application, but another version of Lasergene actually isn’t running, there may be a lingering .state file from another version that needs to be deleted.

The solution is to locate and delete files named *STARDM*.state*, ...where ‘*’ represents the version number.

These files may exist in the following directories:

Windows 7 and Windows 8:

- *C:\Users\username\AppData\Local\DNASTAR\DataManager*
- *C:\ProgramData\DNASTAR\DataManager*

Macintosh:

- *Hard Drive:Library:Preferences:DNASTAR:DataManager*
- *Hard Drive:Users:username:Library:Preferences:DNASTAR:DataManager*

If you find any of the .state files listed above, delete them. Once the files are deleted, the error should no longer appear.

Clean cached files on startup

If you are a Windows user, you may execute a “-clean” in the unusual event that cached data has become corrupted:

1. Close GenVision Pro if it is currently open.
2. Launch the Command Line (C:\Windows\system32\cmd.exe).
3. Type the path to the GenVision Pro application, followed by a space and the *-clean* command.

C:\Program Files (x86)\DNASTAR\DNASTAR\Lasergene 15\GenVision Pro.exe -clean

Research references

Taylor WR (1997). “Residual colours: a proposal for aminochromography.” Protein Engineering vol.10 no.7 pp.743 – 746. (See the [PDF file](#).) [“Taylor” color scheme]

Waterhouse AM, Procter JB, Martin DMA, Clamp M and Barton GJ (2009). “JalView version 2: a multiple sequence alignment and analysis workbench.” Bioinformatics 25:1189-1191. (See on [PMC](#).) [Discusses methodology later used to create the “Taylor” and “Zappo” color schemes]