User Guide to



DNASTAR

GenVision Pro

DNASTAR, Inc. 2022

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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**.

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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.

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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.

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

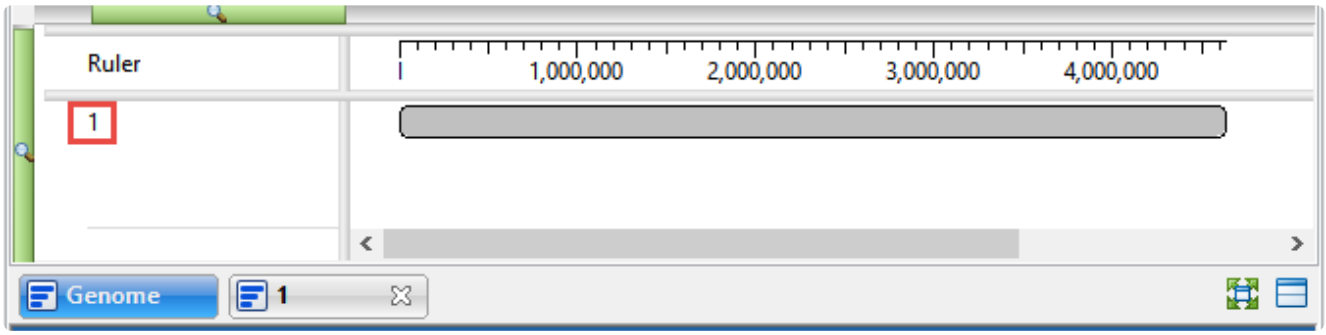
In this first part of the GenVision Pro tutorial, you will start by downloading and extracting the tutorial data from the DNASTAR website. Next, you will begin a new session and add an *E. coli* assembly produced by DNASTAR's SeqMan NGen. You will then create a custom label for the sequence based on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

1. Download the tutorial data extract the folder to any suitable location (e.g., your desktop).

2. Launch GenVision Pro, which will open at the Welcome screen.

3. Drag the newly-extracted project *MG1655_genome.assembly* and drop it on the GenVision Pro window.

4. Click on the **Genome** tab.

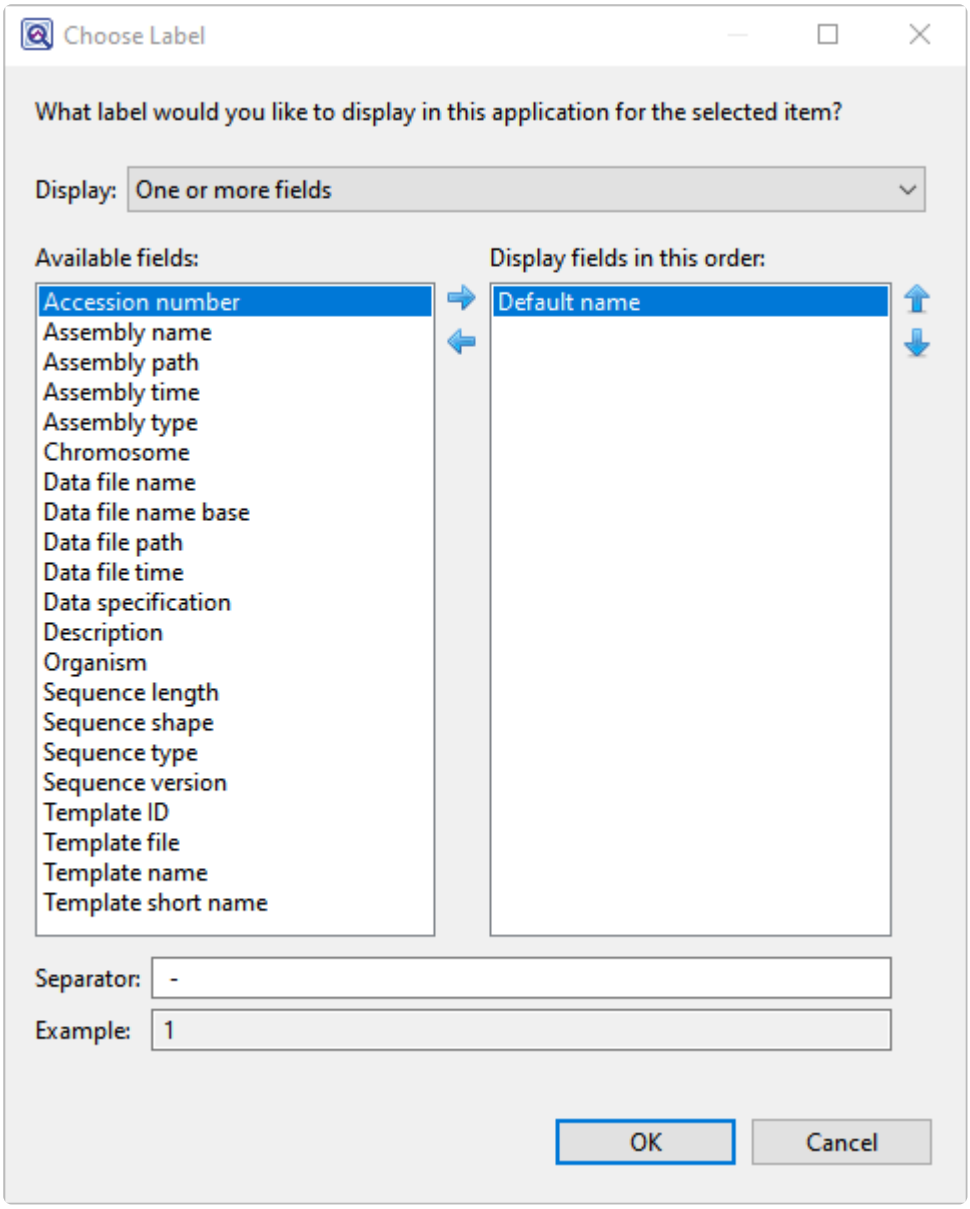


   Note that the name of the active sequence is '1.' In the next steps, you will be changing this name to something more useful.

5. Right-click on sequence '1' 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.

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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.

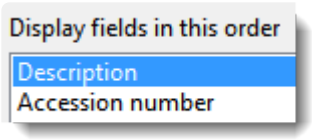
6. Select and organize the fields to display as part of the sequence name:

    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.

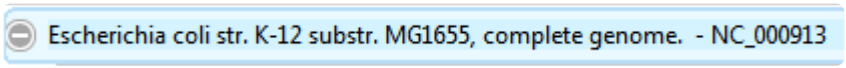
    c. Click on **Description** on the right to select it. Then use the up or down arrows on the right ( ) to move **Description** to the top of the list.

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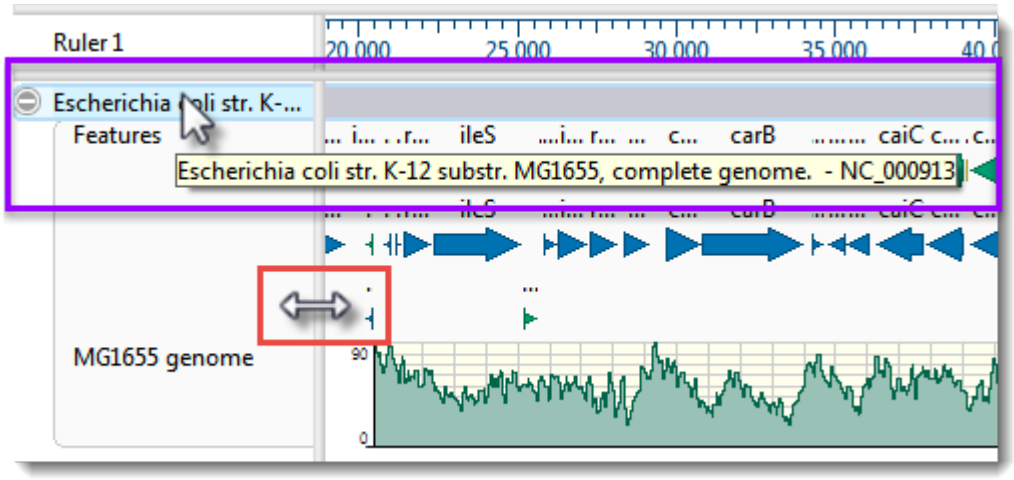
d. Click **OK** to save changes and exit from the dialog.

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



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

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



8. 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.

9. 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**.

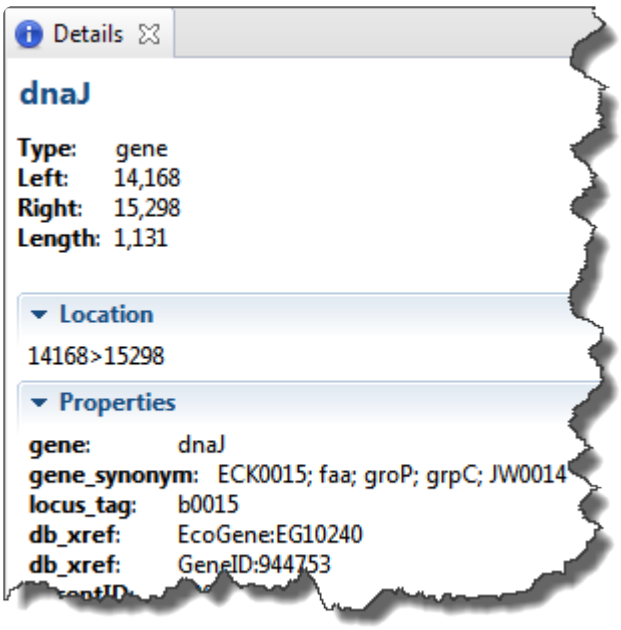
Proceed to Part B: Work with feature tracks.

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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.



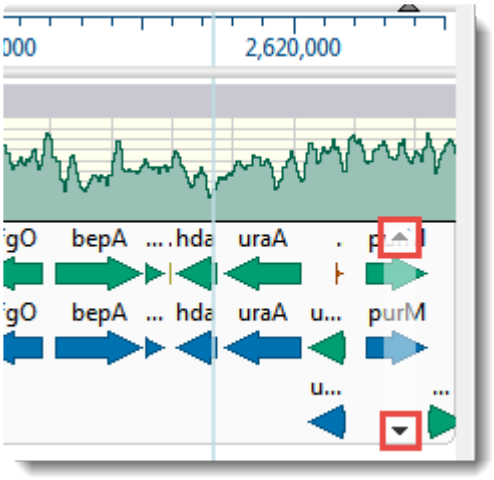
> **Note:*If you can't see the Details panel, click *View > Reset Panel Layout.**

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.

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



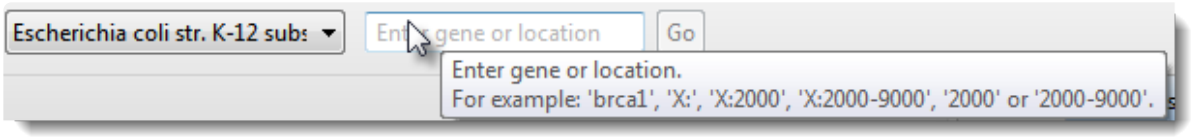
Proceed to Part C: Investigate sequence coverage.

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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.

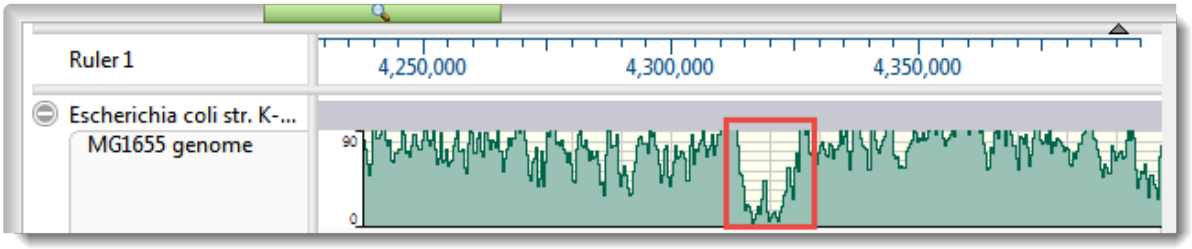


2. Enter **4314000** into the text box. (Alternatively, depending on your locale and computer settings, you could enter **4,314,000** or **4.314.000**.)



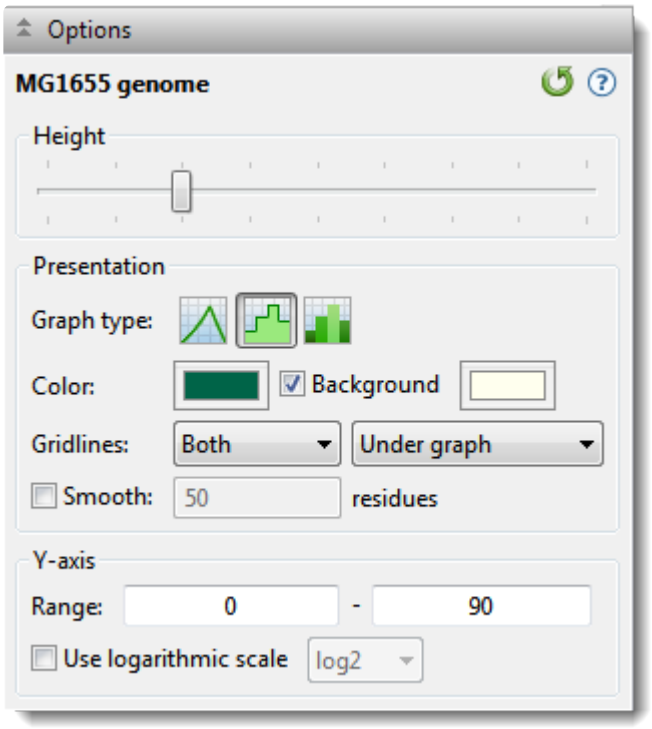
   Press **Go** or **Return/Enter**.

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**.

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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.

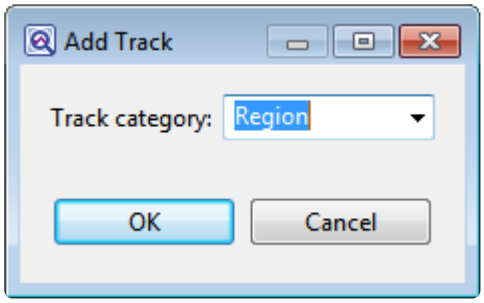
Part D: Work with region tracks

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*.

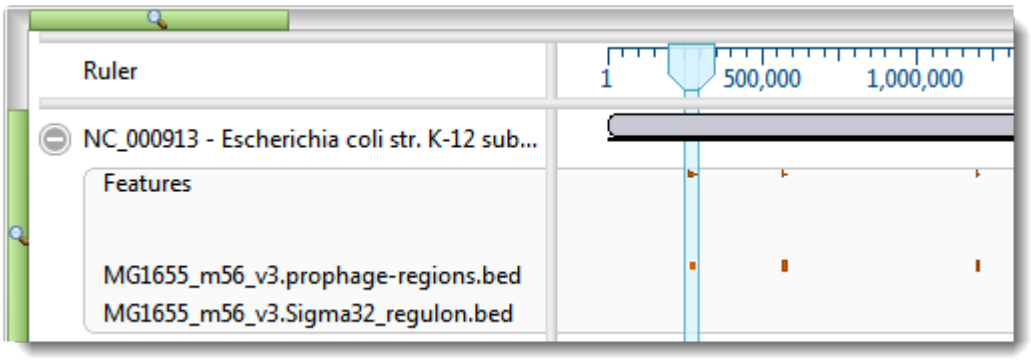
> **Note:** Tracks can be renamed by right-clicking on their names in the Tracks panel (*not* in the views) and choosing **Rename** or **Rename with Fields**. This is the same basic procedure used to rename sequences in Part A of this tutorial. You can rename the tracks if you wish, but it is not necessary 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.
5. In the Analysis view, move the horizontal zoom slider until the viewport (the semi-transparent vertical

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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.



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

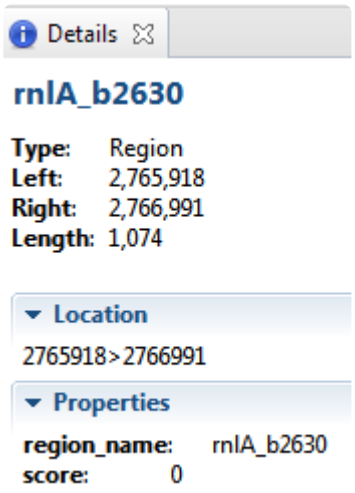
   One is the fifth prophage from the left (“Qin”):



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

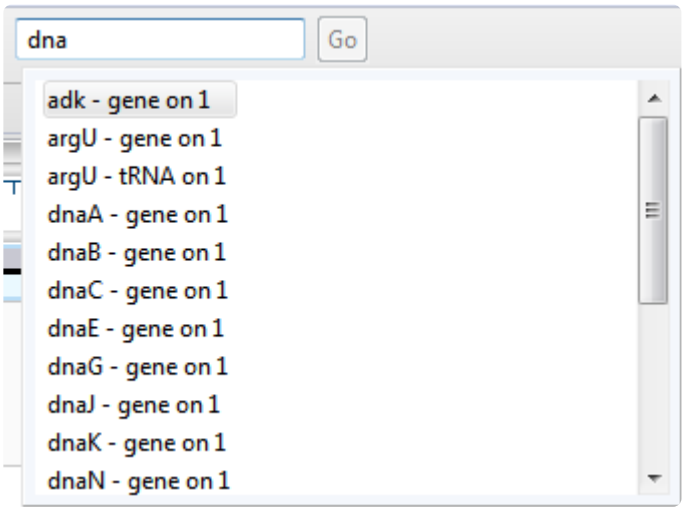


7. Under CP4-57, click on the orange arrow to see the regulon member’s region name and coordinates in the Details panel.



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

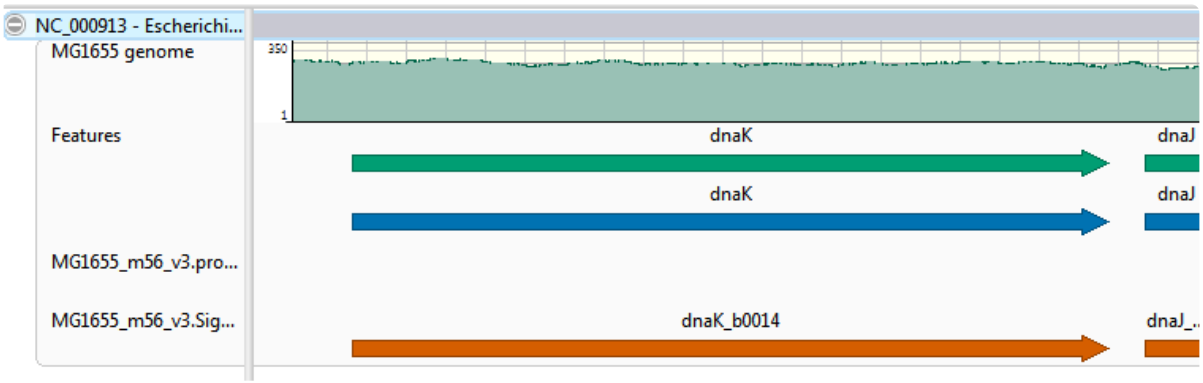
8. In the navigation area at the top of the window, start typing **dnaK**. As you type, a list of matches appears.



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.

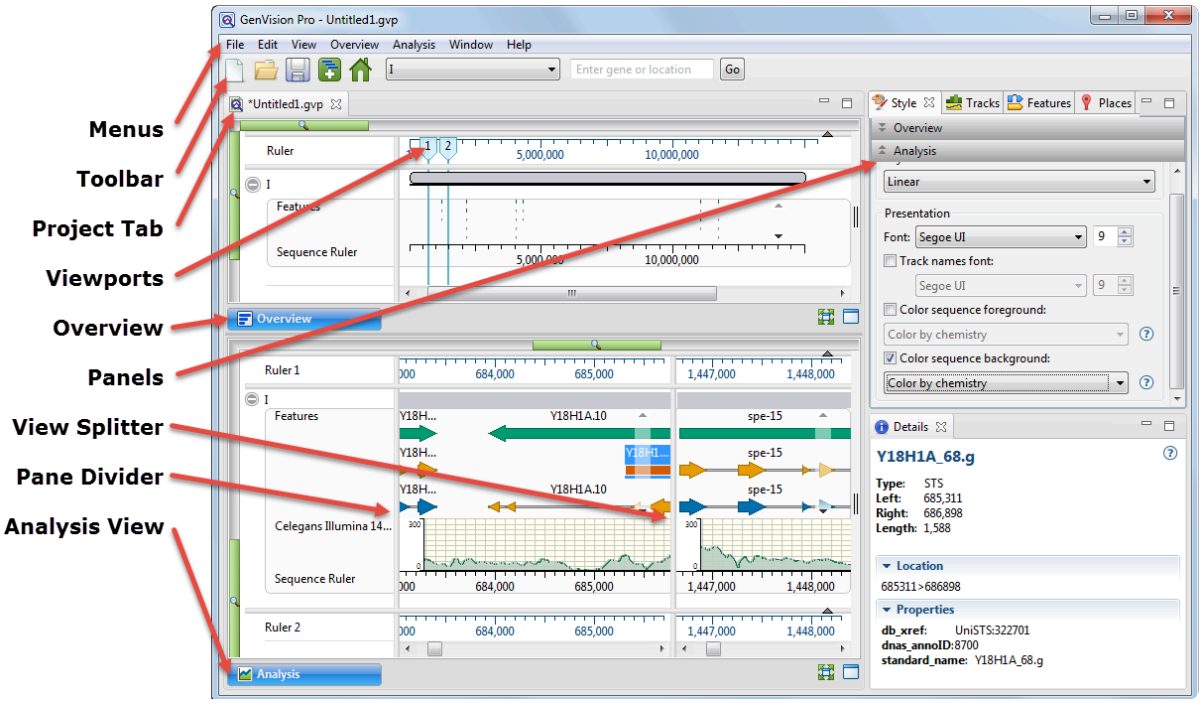
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Congratulations on completing the tutorial!

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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	Displays any enabled tracks, including a ruler and features.
Genome view	Lets you choose the chromosome (or other item) to analyze in the other views.
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,

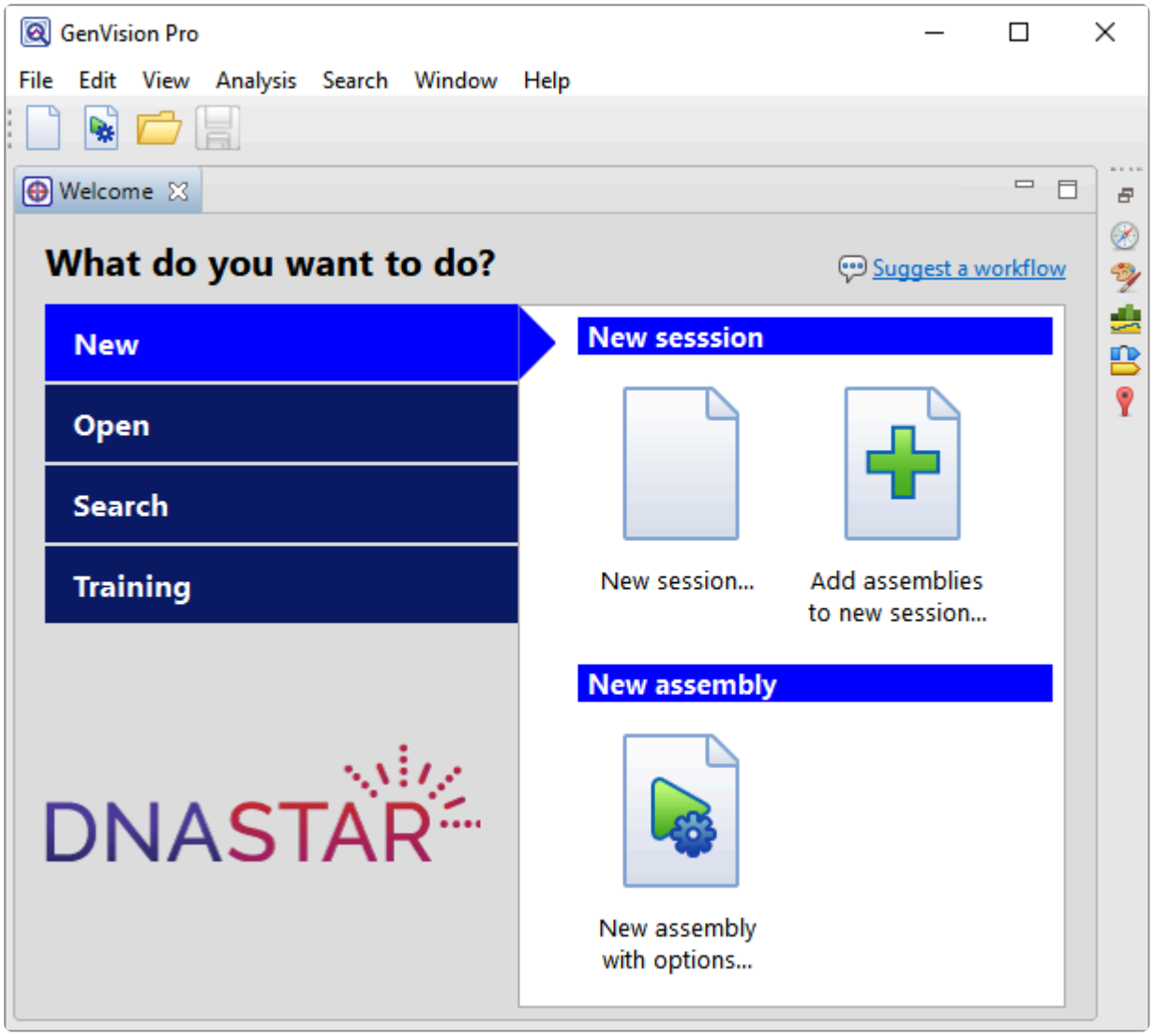
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	or affect what is displayed there.
View splitter	The view splitter is used to divide the Analysis view or Overview vertically into multiple panes.
Header/ Footer	A header and footer are collapsible sections above and below the selected reference sequence. 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.

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Welcome screen

The Welcome “project” opens when you launch GenVision Pro and is a central location for opening or creating sessions or accessing help. As you open sessions, the Welcome “project” will remain as the leftmost tab unless you manually move or close it. We recommend leaving the Welcome tab in place, since it has time-saving shortcuts to useful commands.



Tab on left	Option on right	Shortcut to this menu command:
New	New session	**File > New GenVision Pro Session**. See Create a new session.
	Add assemblies to new session	**File > New GenVision Pro Session** followed by **File > Add Assemblies**. See Create a new session and Add assemblies.

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	New assembly with options	**File > New Assembly with Options**. This launches SeqMan NGen at the Workflow screen. Choose a workflow and proceed through the SeqMan NGen wizard to create a new assembly that can be opened in GenVision Pro. See Create a new assembly using SeqMan NGen.
Open	**Open previously-saved session**	**File > Open**. See Open an existing session.
	Recent documents	**File > Recent Documents**.
Search	**Search**	**Search > Search**. See Search for sequence matches.
	Search for text in NCBI Nucleotide	**Search > Search for Text In > NCBI Nucleotide**. See Search for sequence matches.
	Search for text in NCBI Protein	**Search > Search for Text In > NCBI Protein**. See Search for sequence matches.
Training	**User guide**	**Help > User Guide**. Opens this User Guide.
	Tutorials	**Help > Tutorials**. Opens this User Guide at the topic GenVision Pro Tutorials.

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Views

GenVision Pro views are the large windows on the left of the interface. The following views may be available depending on circumstances. For instance, you may need to select something or perform a search of the BLAST or Entrez databases before a particular view is available.

- Genome view
- Analysis view
- Overview
- Text view
- Table view
- Console view

You can use the Style panel and other methods to customize the look and layout of these views.

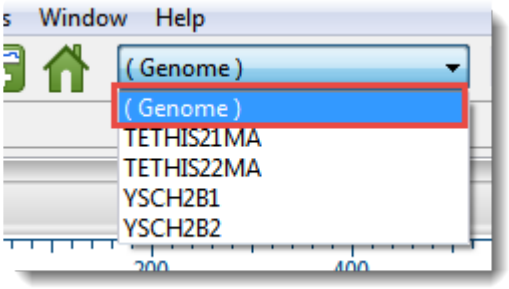
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Genome view

The Genome view can display multiple experiments, chromosomes, contigs or sequences simultaneously.

To access the Genome view, do any of the following:

- Press the **Home** ( ) button tool.
- Use the **View > Genome > Show** command.
- Click on the **Genome** tab.
- Use the navigation tools to choose **(Genome)** from the drop-down menu.



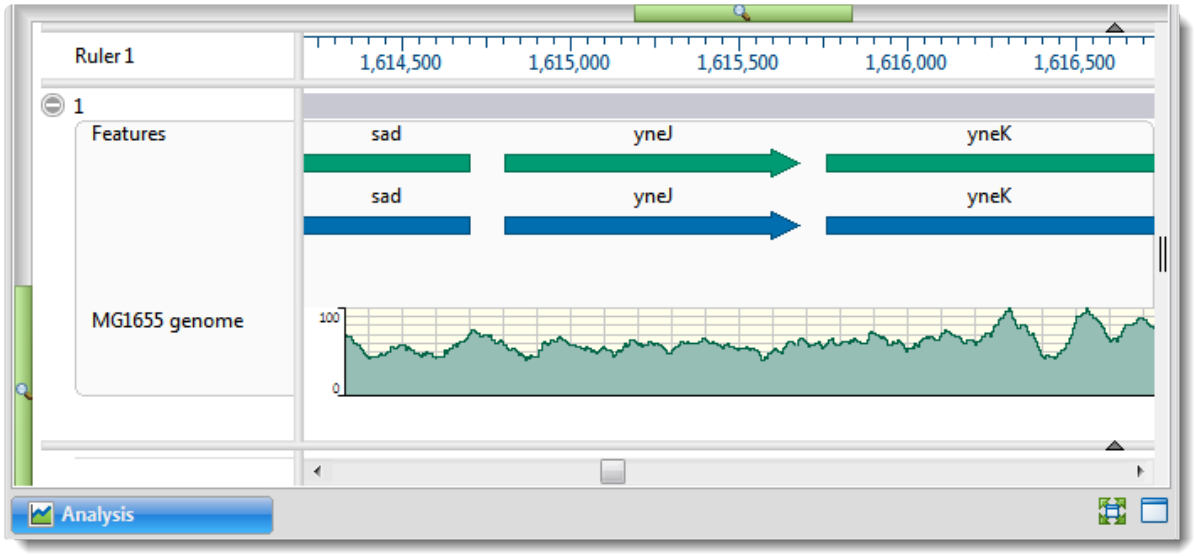
Double-click on an item in this view to display it in the Analysis view and Overview.

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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**.



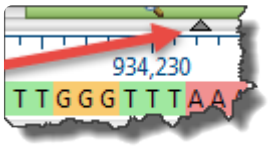
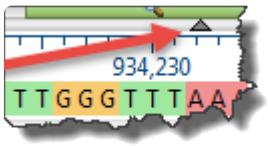
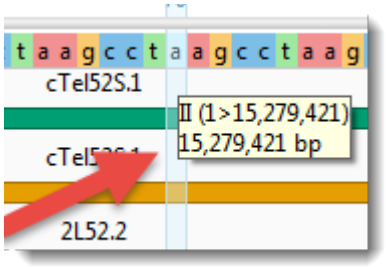
By default, the Analysis view displays a header and footer, along with a sequence and its corresponding data tracks. The Analysis view has a different appearance depending on the zoom level. See the lowermost table on Customize the appearance and layout of views for examples.

To export an image of a view, use the **Export image** tool ( ) in the top right corner of the view.

The following table shows ways to customize the Analysis view:

Task	How To
Change the color scheme, font, or layout	**Use the Style panel's Sequence section and/or Analysis section.**
Show the header & footer	Click on the small dark gray arrows near the upper right corners of each section.

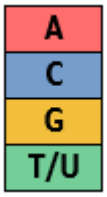
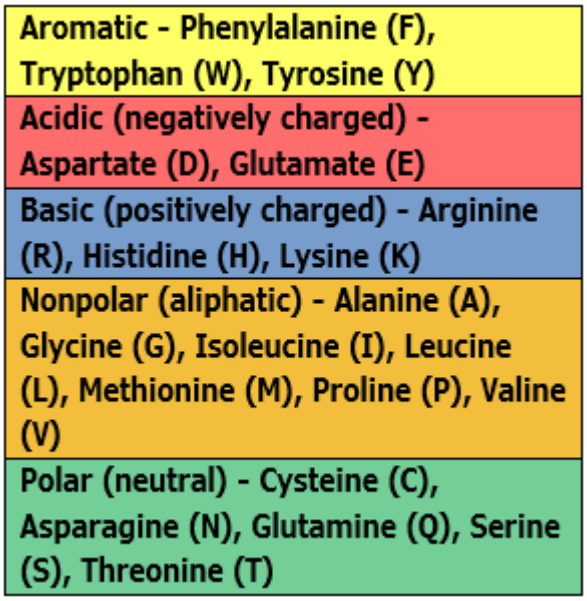
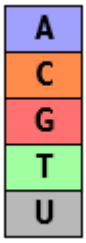
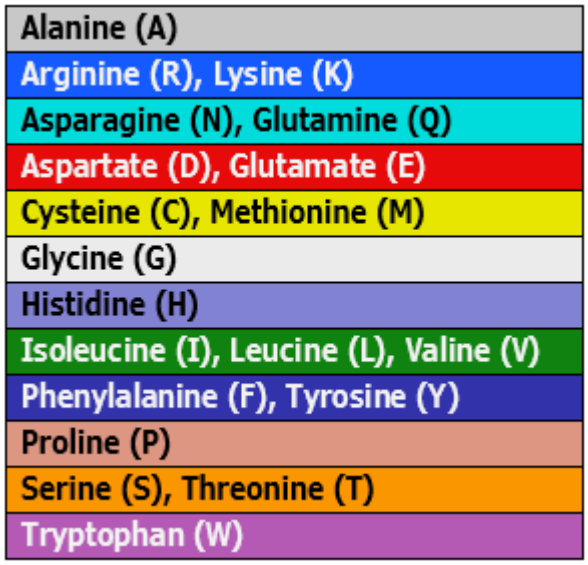
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Hide the header & footer	Click on the small dark gray arrows near the upper right corners of each section. 
Show a vertical guideline	Click **Analysis > Show Guideline**. The presence of a check mark directs GenVision Pro to display the guideline. A vertical guideline is displayed by default, and is a navigational aid to help in guiding your eye between sequences and tracks. 
Hide a vertical guideline	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.

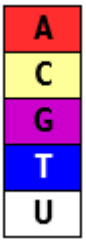
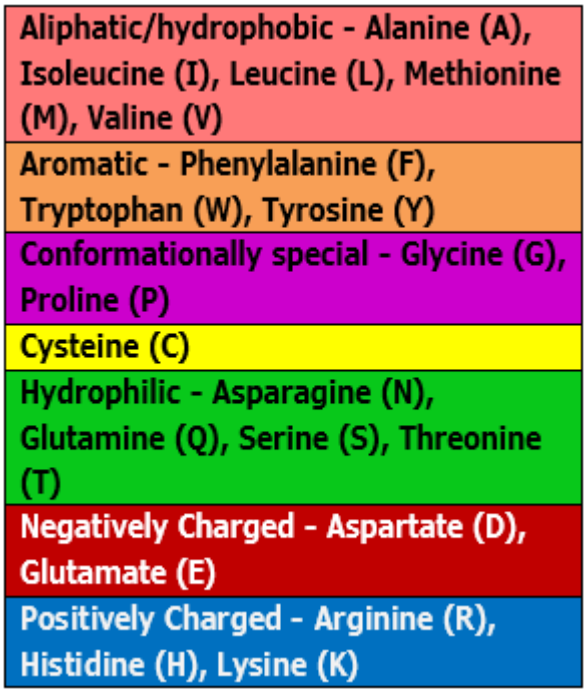
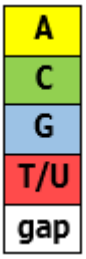
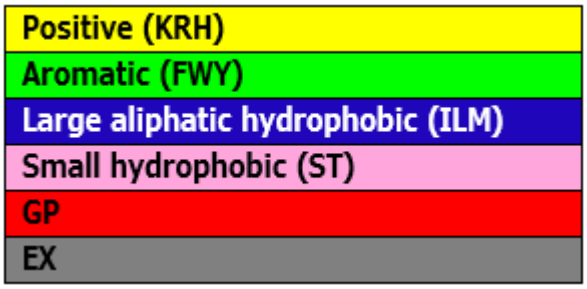
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Change the Analysis view color scheme

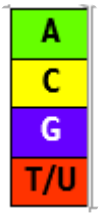
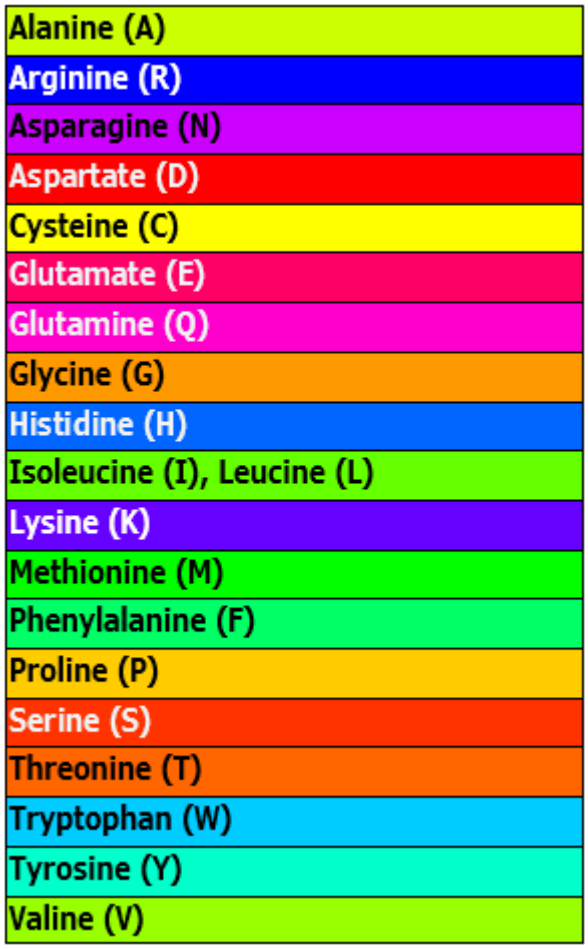
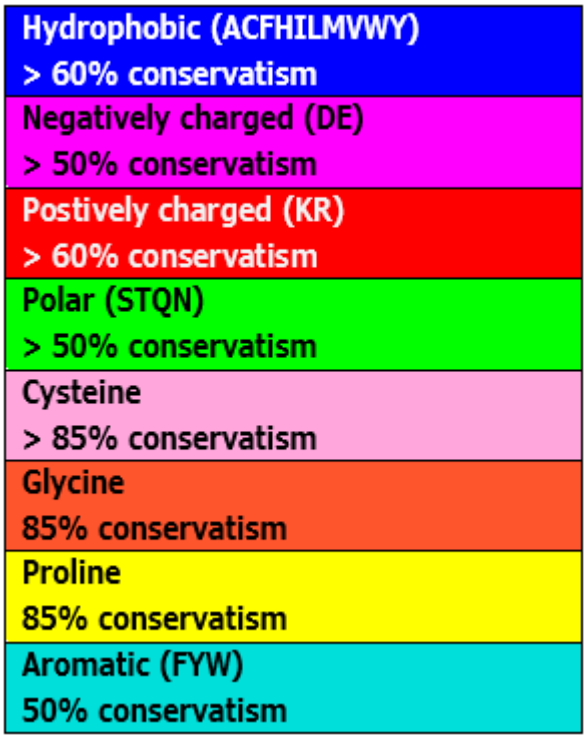
The foreground and background color schemes for the Analysis view are specified in the Analysis section of the Style panel. To open the section, click on the expand bar entitled **Analysis**, or choose **View > Style > Analysis**. Each available color scheme is described below:

Color Scheme	Description	Nucleotide Legend	Amino Acid Legend
Color by Chemistry	The default color scheme used by multiple DNASTAR applications. Amino acids are colored according to their side chain chemistry. While Color by Chemistry can be used for nucleotide sequences too, we recommend instead using a **Solid** background color for nucleotides and then selecting a **Comparison** like **Color only non-conserved residues**, **Color only differences from reference**, etc.		
Physiochemical: Shapely	Matches the RasMol amino acid and RasMol nucleotide color schemes, which are, in turn, based on Robert Fletterick's "Shapely models."		

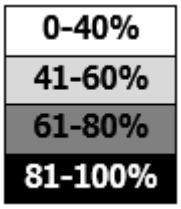
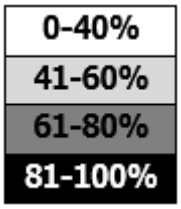
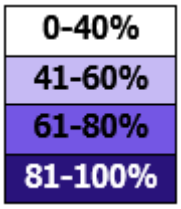
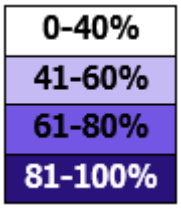
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Physiochemical: Zappo	Colors residues according to their physico-chemical properties, and is also used in JalView (Waterhouse et al., 2009).		
Physiochemical: UGene	Unipro UGENE coloring scheme.		

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Spectral Colors: Taylor	Taken from Taylor (1997) and also used in JalView (Waterhouse et al., 2009).		
Clustal X	Taken from Thompson et al. (1994). This color scheme is only available for protein alignments.	N/A	

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Grayscale – Percentage Identity	This option uses only black/white/gray and is suitable for publications requiring grayscale images.		
Percentage Identity	This option uses only shades of slate blue.		

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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.

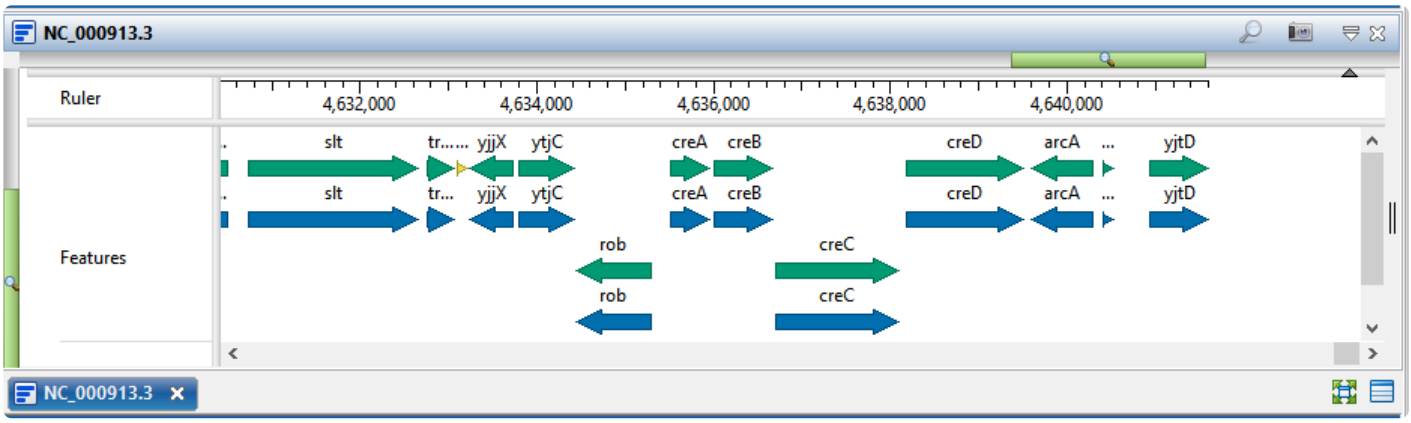
If you had been using a **Linear** layout and had already split the sequence portion of the view vertically, choosing **Automatic wrapping** will change vertical splits to horizontal ones. Also, the scroll bars will move from the bottom of the view to the right.

When the Analysis view is split, the Overview provides a separate "viewport indicator for each section. Splits are ignored when exporting an image, although the layout is preserved.

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Overview

The Overview shows an overview of the currently-selected chromosome (in the Genome view) and its features. To access the view, click on the **Overview** tab (the dark blue part of the image, below) or use **View > Overview > (Name) > Show**.



This view was released in Lasergene 17.3 with the ability only to view a ruler and/or chromosome features. We are developing a variety of very useful tracks for this view that will be available in Lasergene 18.0 and beyond. In the meantime, the Overview primarily serves as a way to view a selected chromosome at a different zoom level than is being used in the Analysis view.

The appearance of a ruler and/or features are controlled through “Overview”-related checkboxes in the Tracks panel. See Work with Tracks for more information.

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Text view

To access the Text view, perform a BLAST search. When the search is complete, the Text and Table views are displayed in a popup window that is separate from the main GenVision Pro window. To reopen the views at a later time, click on the **Status** link in the Jobs panel.

An example Text view is shown below:

```
BLASTN 2.10.0+


Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb
Miller (2000), "A greedy algorithm for aligning DNA sequences", J
Comput Biol 2000; 7(1-2):203-14.



Database: Nucleotide collection (nt)
           71,357,103 sequences; 466,239,233,881 total letters



Query= 1(4636670>4638166)

Length=1497

RID: E6W6KWF8013
                                                                    Score        E
Sequences producing significant alignments:                        (Bits)     Value

CP053604.1 Escherichia coli strain NEB10-beta chromosome, complet...  2765       0.0
CP050289.1 Escherichia coli strain pK19EC149 chromosome               2765       0.0
CP055669.1 Escherichia coli strain RHB30-C19 chromosome, complete...  2765       0.0
CP059137.1 Escherichia coli strain OP50 chromosome                    2765       0.0
CP059043.1 Escherichia coli strain SY3626C1 chromosome, complete ...  2765       0.0
CP058948.1 Escherichia coli strain SY3626C5 chromosome, complete ...  2765       0.0


>CP053604.1 Escherichia coli strain NEB10-beta chromosome, complete genome
Length=4667764

 Score = 2765 bits (1497),  Expect = 0.0
 Identities = 1497/1497 (100%), Gaps = 0/1497 (0%)
 Strand=Plus/Plus

Query  1        ATGGGATATAGCCTGAGGGGCCTGTAATGCGTATCGGCATGCGGTTGTTGCTGGGCTATT  60
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4662782  ATGGGATATAGCCTGAGGGGCCTGTAATGCGTATCGGCATGCGGTTGTTGCTGGGCTATT  4662841

Query  61       TTTTACTGGTGGCGGTGGCAGCCTGGTTCGTACTGGCCATTTTTGTCAAAGAAGTTAAAC  120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4662842  TTTTACTGGTGGCGGTGGCAGCCTGGTTCGTACTGGCCATTTTTGTCAAAGAAGTTAAAC  4662901

Query  121      CGGGCGTGCGAAGAGCAACGGAGGGGACGTTGATCGACACCGCAACGTTGCTGGCGGAGC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

In order, the view shows the following:

- The version of BLAST used in the search (e.g., “BLASTP 2.9.0+”).
- References for the BLAST search engine.
- A description of the BLAST database used in the search, including the number of sequences.
- Information about the Query sequence, including its length and the Request ID (RID) number.
- A table of sequences producing significant alignments.
- Pairwise alignments of each significant match with summary information on the match.

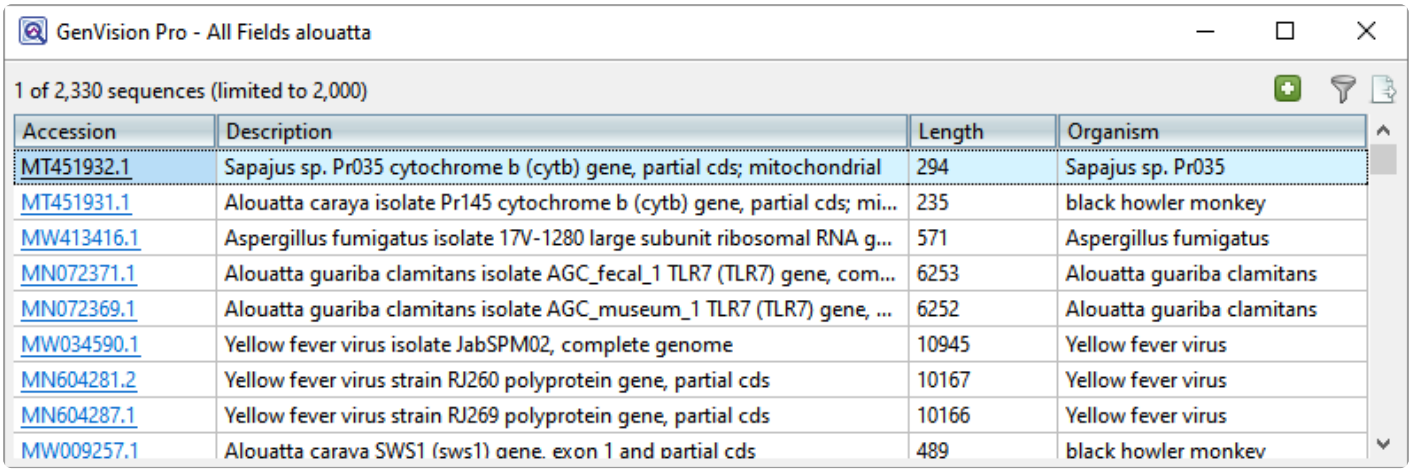
Tasks pertaining to the Text view:

Task	How to…
Make selections in the view	See Make a Selection.
Copy all text	Right-click anywhere in the view and choose **Copy**.
Select all text	Right-click anywhere in the view and choose **Select All**.

Table view

To access the Table view, perform a BLAST search. When the search is complete, the Text and Table views are displayed together in a single popup window that is separate from the main GenVision Pro window. To reopen the views at a later time, click on the **Status** link in the Jobs panel.

If no significant matches were identified, the Table view will be empty. An example of a populated Table view is shown below:



Columns in the view's table are described below. Only a subset of these columns will be available, depending on whether you did a sequence or text search.

Column	Description
Accession	The NCBI "Accession" number for the match. Press the link to open the corresponding page on the NCBI website.
Description	The NCBI "Definition" field text.
Score	The similarity score for the match. (See the NCBI definition for **raw score**). In general, a higher score denotes a better match.
E-Value	The chance that the match is expected to occur by chance. (See the NCBI definition for **E value**). In general, a lower score denotes a better match.
%Coverage	The percentage of the query sequence that aligns to a match in the BLAST database. Example: Query has 596 bases, of which 565 align to a match in the NCBI database. **%Coverage** = 565/596 = 95%.
%Identity	The percentage of bases that match when the query and result sequence are aligned. (NCBI definition). Example: Query has 565 bases that align to the match and 3 bases that don't match. **%Identity**

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	= 562/565 = 99.5%.
Map	Graphic showing areas of agreement between the query and the match.
Length	(Entrez search only) The length of the sequence in bp.
Organism	(Entrez search only) The name of the organism.

Tasks pertaining to the Table view:

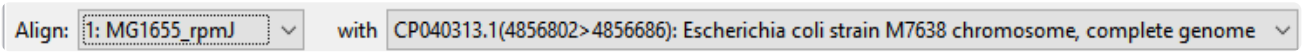
Task	How To…
If a BLAST or Entrez search was performed	
Launch the NCBI page for matching database entry	Click the hyperlink in the table's Accession column.
Copy all information from a search result row	Right-click on the row and choose **Copy**.
Save the sequence match in *.gbk* format	Right-click on the row and choose **Download sequences**. In the ensuing Save As dialog, choose a location in which to save the sequence. By default, the sequence is named using its Accession number.
Add sequences or matches	Use the **Add sequences or matches** tool ( ). Sequences are added back into the host application, not the job's document.
Filter results from a sequence or text search	Use the **Filter results** tool ( ). Learn more about sequence search or text search filtering.
Export data from the view	Use the **Export data** tool ( ), described in the topic Export data from the Text, Table or Pairwise views.
Only if a BLAST search was performed	
To save results	Click the **Save as** tool ( ). A save dialog opens and allows you to save the search results as a *.search* format file. Use the command **Search > Open Search File** to open the search results again in the Table, Pairwise and Text views.
To display a pairwise alignment using a particular search result	If the Table view is open, click on the desired row in the Table view to see the corresponding pairwise alignment in the Pairwise view. As an alternative, open the Pairwise view manually and choose the desired target from the **with** drop-down menu.

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Pairwise view

After the Jobs panel shows the **Status** of a BLAST search or Entrez search is **Done**, pressing the “Done” hyperlink opens the search results simultaneously in the Text, Table, and Pairwise views. All three views are contained in a large pop-up window that is separate from the main GenVision Pro window. The Pairwise view consists of three areas: toolbar, summary, and sequences.

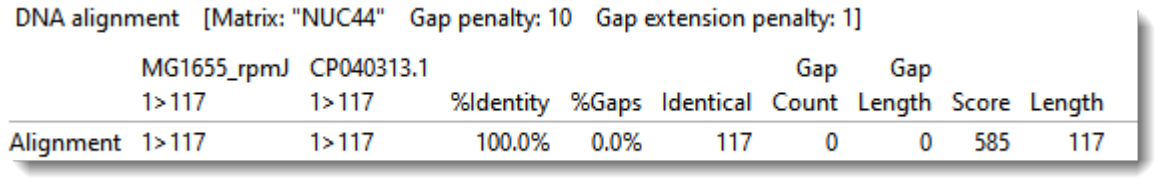
Toolbar area:



This area consists of two drop-down menus and one tool. The **Align** drop-down menu is used to specify the target sequence, which should be the longest sequence of the two. The **with** drop-down menu is used to specify the query sequence. Specifying a different sequence in either menu will initiate a new pairwise alignment.

The Export image* tool (), located on the right of the header, lets you export the summary and sequences areas.

Summary area:



DNA alignment [Matrix: "NUC44" Gap penalty: 10 Gap extension penalty: 1]

	MG1655_rpmJ 1>117	CP040313.1 1>117	%Identity	%Gaps	Identical	Gap Count	Gap Length	Score	Length
Alignment	1>117	1>117	100.0%	0.0%	117	0	0	585	117

The summary area describes the alignment engine and settings that were used to create the pairwise alignment.

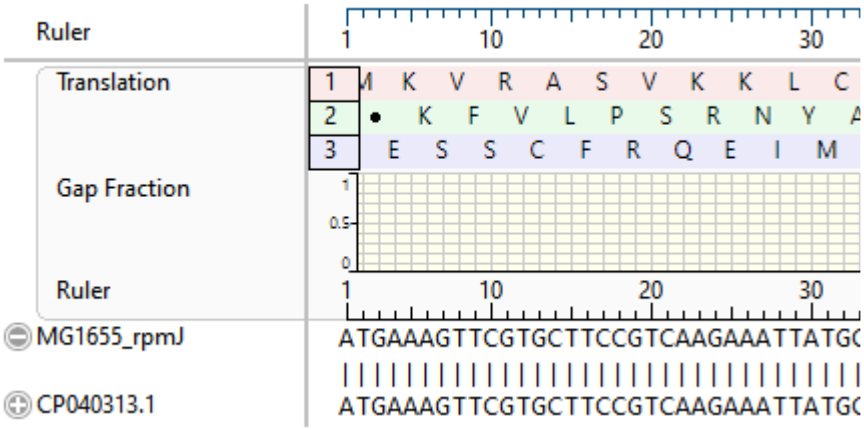
Value	Description
% Identity	Number of matching residues divided by the sum of all residues and gap characters. The quotient is multiplied by 100 to give the similarity as a percent.
% Gaps	The gap length divided by the consensus length. The quotient is multiplied by 100 to give the similarity as a percent.
Identical	Number of residues that are identical in both sequences.
Gap Count	Number of gaps (of any length) in either sequence of an alignment.

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Gap Length	Number of gap characters in an alignment.
Score	The cumulative score for an alignment derived by adding the matrix-derived match scores and subtracting gap penalties.
Length	Number of residues in the consensus, including gaps that match in both sequences.

Sequences area:

The sequences area consists of nucleotide or amino acid codes for each sequence on the right, and their labels on the left. The order is always “target sequence” first, and “query sequence” second. A variety of optional data tracks can be displayed in this section.



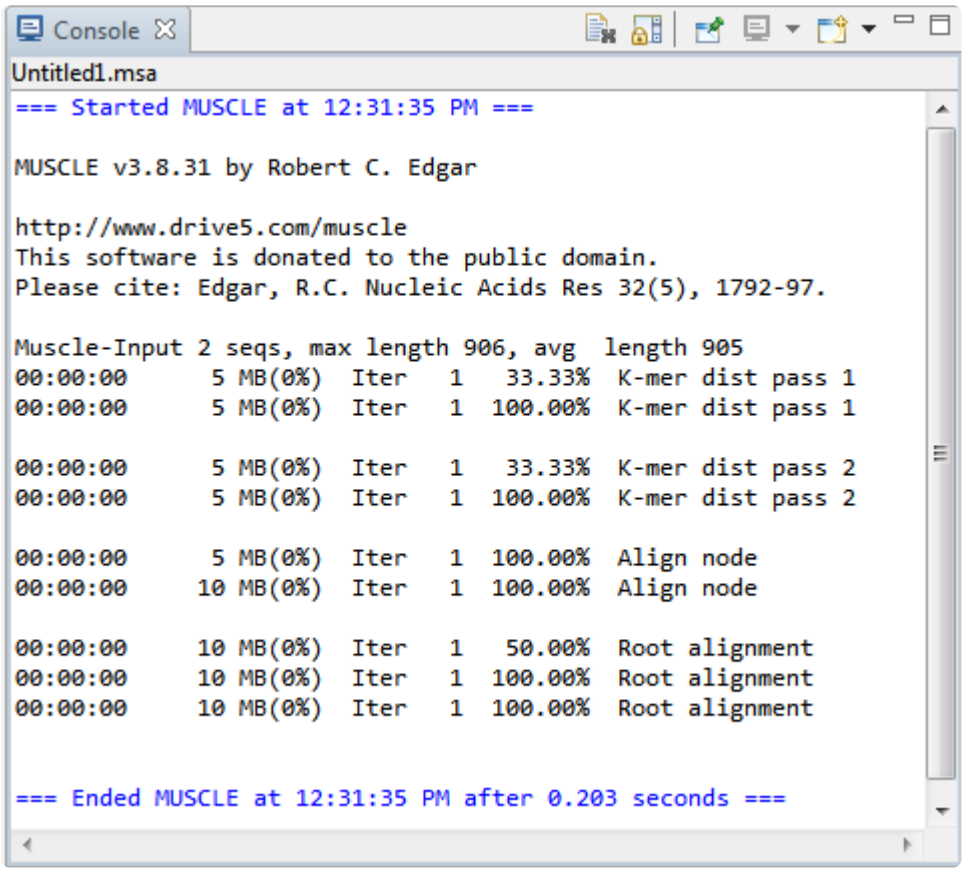
Console view

The Console view displays information, messages and warnings about the operation in progress, or an operation that was recently performed.

To display the console for a particular project:

Click the tab with the project name, then open its console using the **View > Console** command. Each view will have a different console.

To use the Console panel:



Each console has a maximum number of characters. If this maximum is exceeded, the oldest characters disappear in order to make room for new characters.

Right-click on the Console tab to access commands allowing you to move, hide, rearrange, or restore panels and views. (See Customize the layout of other window components).

The following tools are available in the upper right of the Console view:

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Tool	Name	Description
	Clear Console	Clears all text from the active Console.
	Scroll Lock	Stops auto-scrolling caused by alignment output. When alignment output is long, this may fail due to a limit on the amount of text in the console.
	Word Wrap	Controls whether or not lines wider than the console panel should be wrapped.
	Pin Console	Keeps the current Console active even if another project is selected.
	Display Selected Console	Consoles can be displayed for one or more open projects. If more than one alignment is in progress, clicking the arrow to the right of this icon opens a drop-down menu from which the desired Console can be brought to the front.
	Open Console	Opens a new Console. If more than one alignment is in progress at the same time, you can open a new Console and pin it to a particular run using Pin Console (above).
	Minimize	Minimizes the Console.
	Maximize	Maximizes the Console.

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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

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Style panel

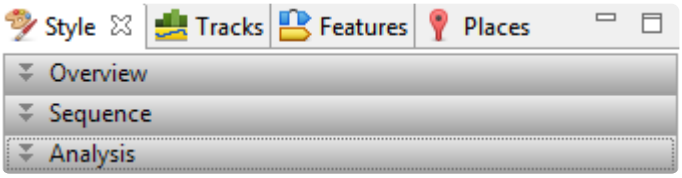
The Style panel lets you customize view formatting and layout.

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**.

To change settings in the Style panel:



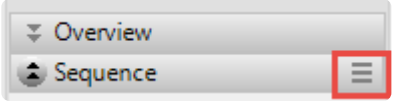
Click the links below to learn about each of the sections in the Style panel:

- 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 and color schemes used in the Analysis view.

To save styles and apply them to future sessions:

Once you have set up styles, you can save them and then apply them to future sessions, either by default or only when you specify that they be applied. You can choose whether to save and apply styles for just one particular view or for all views.

Note that some of the instructions below refer to the “hamburger” menu. To access commands on these menus, click on the expand bar of interest in the Style panel. Then click on the tool consisting of three horizontal lines.



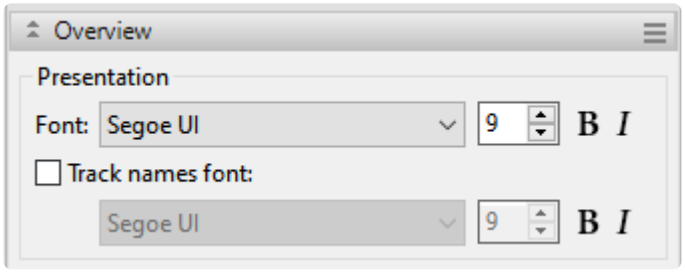
Task	How To

Save all current styles to a file that can be applied to future sessions	Use **View > Document Style > Save Style**.
Save the styles from one particular view to a file that can be applied to that view in future sessions	Click the “hamburger” menu on the right of a Style panel expand bar and choose **Save (Expand bar name) Style**.
Save all current styles to a file that will be applied as the default for future sessions	Use **View > Document Style > Save Style as Default**.
Save the current styles from one particular view to a file that will be applied as the default for that view in future sessions	Click the “hamburger” menu on the right of a Style panel expand bar and choose **Save (Expand bar name) Style as Default**.
Apply styles that were saved earlier to the current sessions	Use **View > Document Style > Apply Style**
Apply styles that were saved for this view previously and apply them to the same view in the current sessions	Click the “hamburger” menu on the right of a Style panel expand bar and choose **Apply (Expand bar name) Style**.
Restore all DNASTAR default styles to the current sessions	Use **View > Document Style > Restore DNASTAR Default Style**.
Restore the DNASTAR default style for one particular view to that view in the current sessions	Click the “hamburger” menu on the right of a Style panel expand bar and choose **Restore DNASTAR Default (Expand bar name) Style**.

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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**.



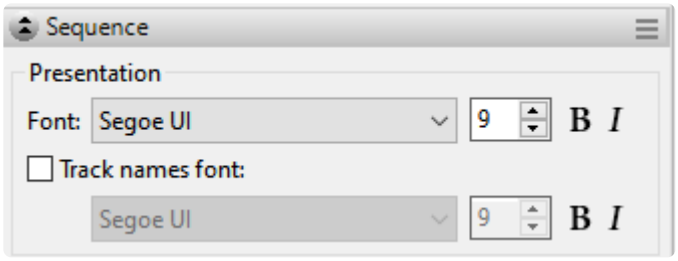
Customization for font style and size applies to all text in the Overview. Individual rows cannot have different styles or sizes.

Task	How 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 ( ). To make the font **Bold** and/or *Italic*, press the **B** and/or ***I*** buttons, respectively.
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.

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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**.



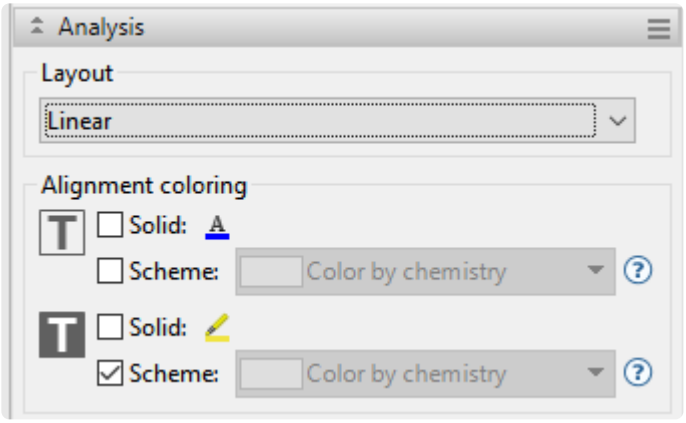
Customization for font style and size applies to all text in the Analysis view. Individual rows cannot have different styles or sizes.

Task	How 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 make the font **Bold** and/or *Italic*, press the **B** and/or ***I*** buttons, respectively.
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 ( ). To make the font **Bold** and/or *Italic*, press the **B** and/or ***I*** buttons, respectively.

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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**.



Task	How to…
Select the preferred line wrapping style	Use the **Layout** drop-down menu: • **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. 
Specify the color of sequence characters	Use the "foreground color" tools to the right of . To display the letters in a single solid color of your choice, check the box next to **Solid**. Then click on the 'A' tool to the right of the checkbox and choose a color from the color picker. To instead choose a preset color scheme, check the box next to **Scheme** and make a selection from the drop-down menu. To learn more about available color schemes, click here.
Specify the background color (boxes	Use the "background color" tools to the right of . To use a single solid color of your choice, check the box next to **Solid**. Then click on the 'highlighter pen' tool to the right of the checkbox and choose a color from the color picker. To instead choose a preset color scheme, check the box next to **Scheme** and make a selection from the drop-down menu. To learn more about

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around each letter)	available color schemes, click here.

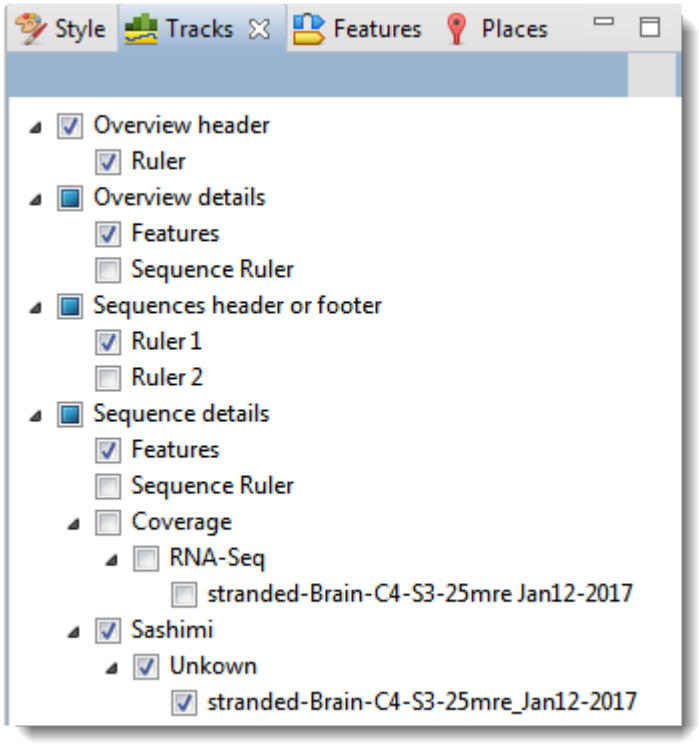
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Tracks panel

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 ( ).

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Below the list of tracks are two expandable sections:

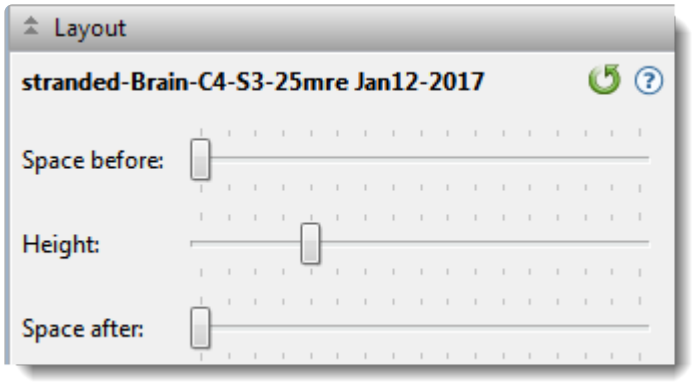
- Layout lets you change the height of a track and create blank space above and/or below the track.
- Options lets you optimize how tracks appear in the Overview and Analysis view.

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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 ( ).|

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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

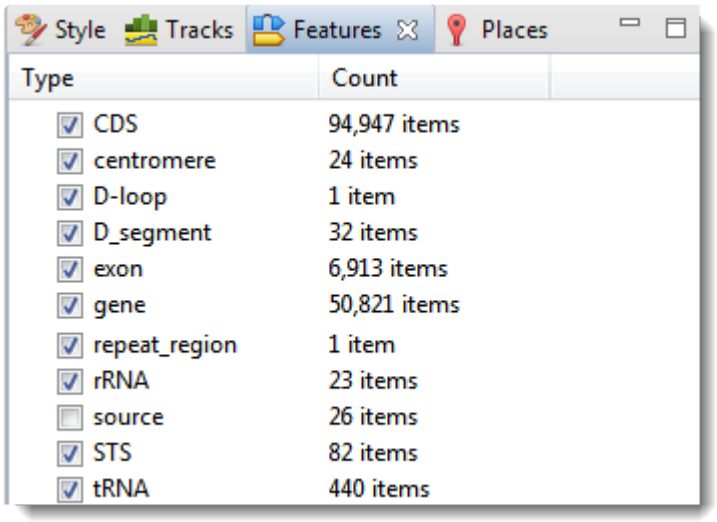
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Features panel

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**.



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**.

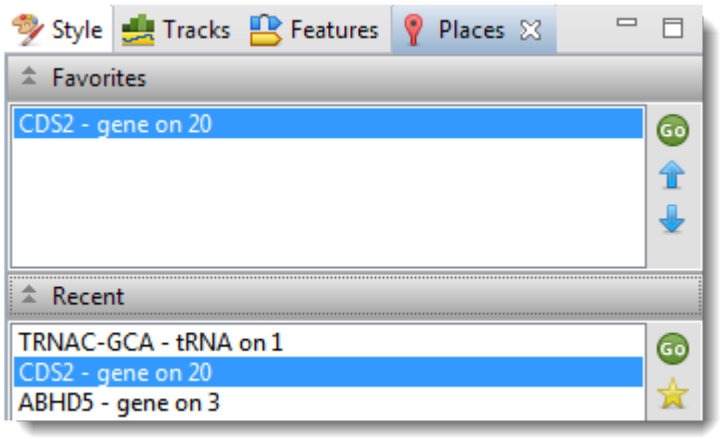
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Places panel

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:

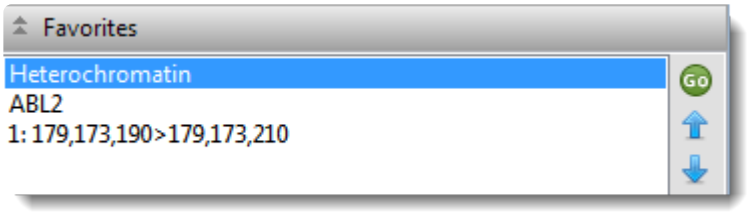
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Favorites section

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. 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.

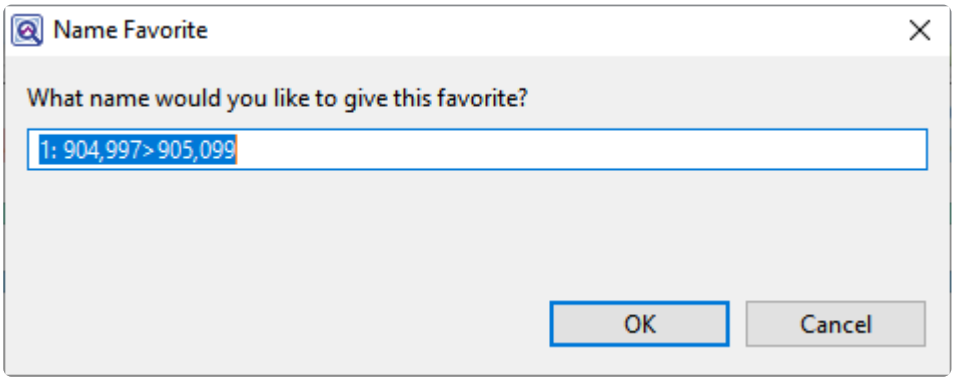
Access this section by clicking on the Places panel expand bar entitled **Favorites** or by choosing **View > Places > Favorites**.



To nominate an entry to the list:

Do any of the following:

- Use the Recent or Received sections of the Places panel. Click the “Recent” and “Received” links to learn more.
- Choose **Analysis > Add Place to Favorites** or right-click within the Analysis view and choose **Add Place to Favorites**. The following popup appears.



The popup shows the selected coordinates. If you would like to give this location a name, you can type it over the coordinates. It’s also fine to keep the coordinates themselves as the name. Press **OK**.

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

Task	How To

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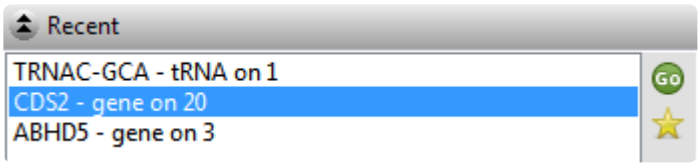
To return to a location in this section	Double-click on the item or make a selection from the list and press the **Go to this gene or location** button ().
To move a bookmarked location further up the Favorites list	Make a selection from the list and press the **Move this place up** arrow ().
To move 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 from the Favorites list	Click on an item in the Favorites section to select it. Then right-click on the 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**.

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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.

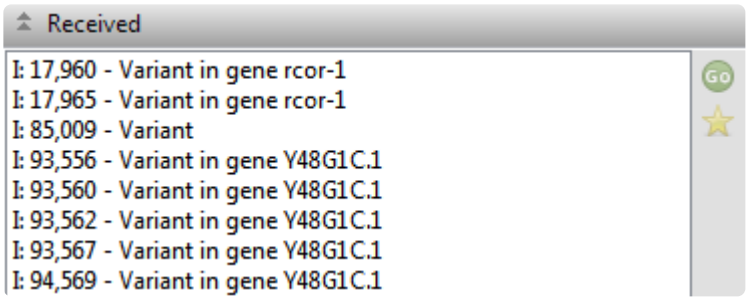
- To return to a location on the list, make a selection from the list and press the **Go to this gene or location** button (Go).
- To save a location on the list to the Favorites section (similar to bookmarking a page on the Internet), make a selection from the list and press the **Add this place to 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**.

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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**.

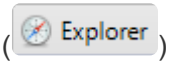


Received locations are listed in the same order in which they were added, and the list is saved whenever you save a session.

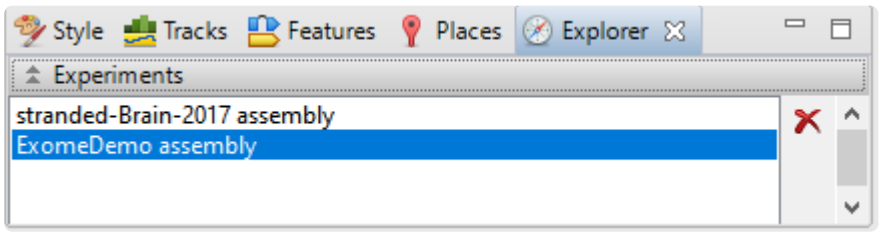
- To return to a location on the list, make a selection from the list and press the **Go to this gene or location** button ( ).
- To save a location on the list to the Favorites section (similar to bookmarking a page on the Internet, make a selection from the list and press the **Add this place to Favorites** 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**.

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Explorer panel

To open the Explorer panel, click on the **Explorer** tab (

) or use the **View > Experiments** command.



The Explorer panel contains two sections.

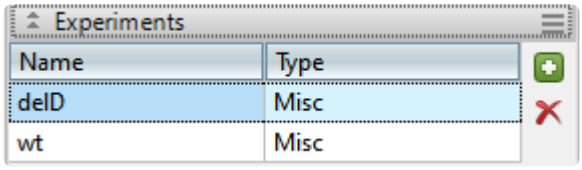
- The Experiments section shows a list of the assemblies or other data sources in the current session.
- The Chromosomes section shows a table of chromosomes in the currently-selected assembly.

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Experiments section

The Experiments section is a section in the Explorer panel. This section lists any *.assembly* files already loaded into the current GenVision Pro session and allows you to add additional files or delete existing ones. Some of the data added here as part of an *.assembly* file is parsed as tracks that you can display in the Analysis view and/or Overview.

Access this section by clicking on the Explorer panel expand bar entitled **Experiments**, or by choosing **View > Explorer > Experiments**.



Column	Description
Name	The name of the assembly or other data source.
Type	If you open an older assembly or session, or if GenVision Pro cannot determine the type, this will appear as **Misc**.

To delete one or more data sources from the session, select them from the table and press the **Remove this data source from session** tool ( ).

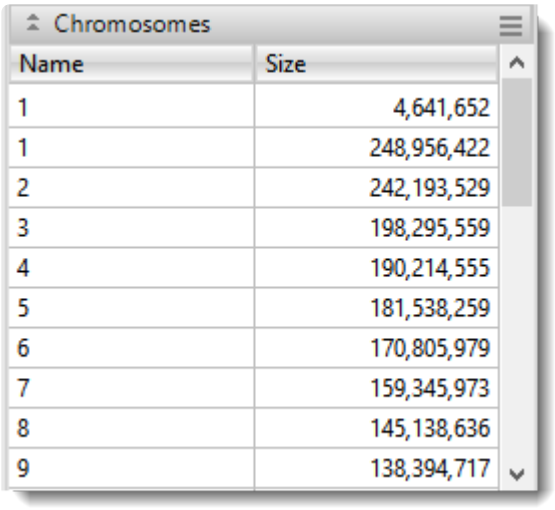
To add a new *.assembly* to the session, press the **Add experiments** tool ( ). To add another data type, see Add Data.

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Chromosomes section

The Chromosomes section is one of two sections in the Explorer panel, and shows a table of chromosomes in the currently-selected assembly. This section allows you to easily maneuver between chromosomes in a multiple sample project.

Access this section by clicking on the Explorer panel expand bar entitled **Chromosomes**. Alternatively, use **View > Explorer > Chromosomes**.



Column	Description
Name	The name or number of the chromosome.
Size	The chromosome length in base pairs.

Double-click on any table row to open an Overview and Analysis view window for that chromosome.

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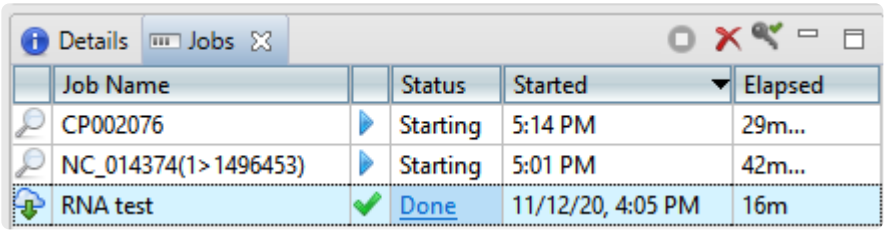
Jobs panel

After initiating an NCBI BLAST or Entrez search, you can monitor its progress and download its eventual output from the Jobs panel. This panel is not visible in a project until you have started running at least one search.

To open the Jobs panel:

Do any of the following:

- Click on the **Jobs** tab.
- Press **Ctrl+Alt+J** (Win) or **Option+Cmd+J** (Mac).
- Use **View > Jobs** or **Search > Show Jobs**.



The Jobs panel consists of a header and a table with the following columns:

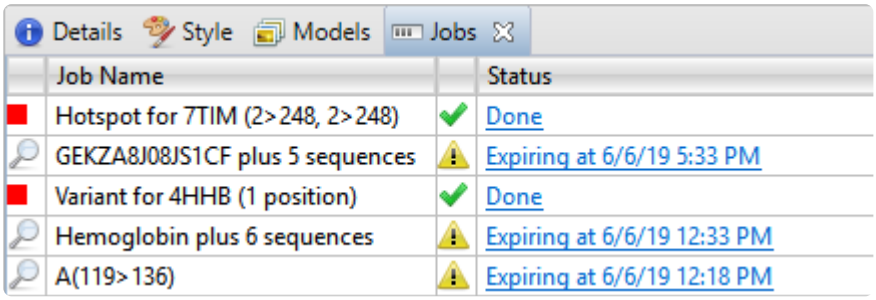
Column	Description
Job Name	Text searches are all named with the field and term of the first search criterion followed by "plus # terms," where # represents the number of additional criteria. Sequence searches use the name specified in the Job screen of the Search wizard. The same **Job Name** can be used for more than one prediction.
Status	A word and icon indicating the status of the search. • **Started** – **Run** or **Run Job** were pressed in the Search wizard • **Queued** – – Submitted and placed into the queue • **Running** – – Running • **Done** – – Job complete; results available • **Failed** – – Job failed • **Stopped** – – Job stopped by user
Started	The date and time the job began.
Elapsed	The total elapsed time between starting and completing the job.

Tasks that pertain to the Jobs panel:

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Task	How To
To open the results of one or more jobs	Click on the **Done** (Done) or **Expiring** links for that job. See below this table for more information on job expiration. You can also open a saved *.search* file using **Search > Open Search File**.
To log into Cloud Assemblies (allows you to see all jobs associated with your username)	Use the **Not logged into Assemblies on the Cloud** tool ( ). If you are already logged in, the tool changes to have a green checkmark ( ).
To stop one or more jobs that are in progress	Select one or more rows with a Status of **Started**, **Queued** or **Running**. Then press the **Stop** tool ( ) in the header above the table. Once stopped, a job cannot be restarted from the Jobs panel. You must instead initiate a new search.
To delete a finished job	Select one or more rows with a Status of **Done**, **Failed** or **Stopped**. Then press the **Delete** tool ( ) in the header above the table.
Top open/reopen the progress dialog for a job	Select one or more rows with a Status of **Started**, **Queued** or **Running**. Then right-click and choose **Open Progress dialog**.

Sequence (BLAST) and text (Entrez) search jobs are intended to be ephemeral and expire after 7 days. The Jobs panel notifies you of upcoming expiration dates.



All jobs are recorded in the location specified in the Temporary File preferences dialog. If you are a Macintosh user and elect to keep the default save location, the operating system may remove jobs after a reboot. To avoid this, we recommend choosing a different location in which to save temporary files.

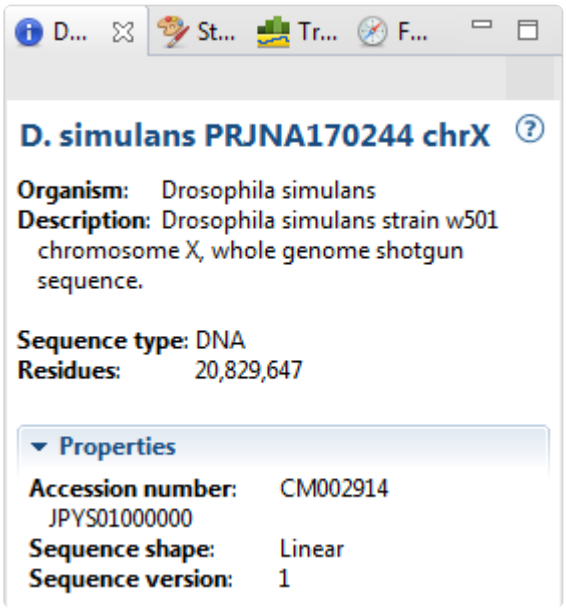
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Details panel

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.

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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

When a non-empty session is open

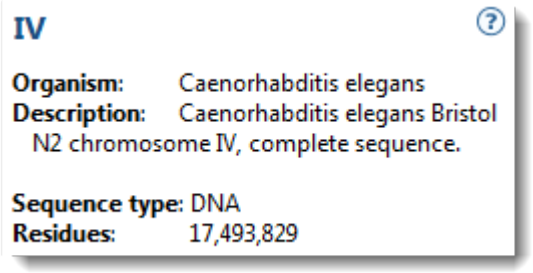
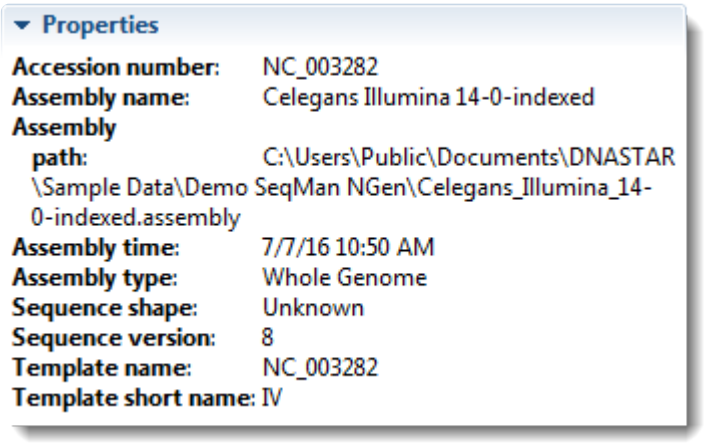
If a session is open and data has been added, the Details panel contains the following information:

Heading	**CEU gene panel assembly.gvp** **Sequence type:** DNA	The session file name, in blue.
Sequences	▼ Sequences **Sequences:** 26 **Sequence type:** DNA **Min. sequence length:** 16,569 **Max. sequence length:** 249,250,621	* **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	▼ Actions Add assemblies Add tracks	* **Add assemblies** – Shortcut to menu command **File > Add Assemblies**. * **Add tracks** – Shortcut to menu command **File > Add Track**.

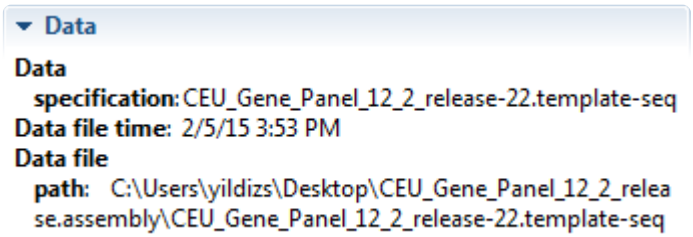
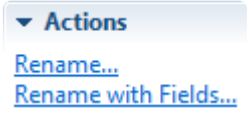
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When one sequence is selected

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

Heading		The label used in the Analysis view and Overview, in blue. * **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		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. * **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

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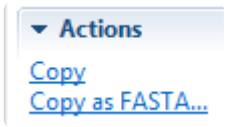
		SeqMan NGen assembly finished. * **Assembly type** – The type of assembly performed in SeqMan NGen, if available (e.g., Exome/Gene Panel). * **Sequence shape** – **Linear** or **circular**, if specified in the reference sequence. * **Sequence version** – The NCBI version number (the part following the decimal after the accession number) for the sequences in the chromosome or contig. * **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. * **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.
Data		* **Data specification** – The name of the sequence file, including extension. * **Data file time** – The time the sequence file was created or modified. * **Data file path** – The path to the sequence file in the assembly.
Actions		* **Rename** – Shortcut to **Edit > Rename**.

		* **Rename with Fields** – Shortcut to **Edit > Rename with Fields**.

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

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When multiple sequences are selected

If multiple sequences have been selected in the Genome view, the Details panel contains the following information:

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

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When one track is selected

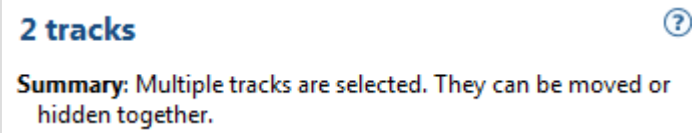
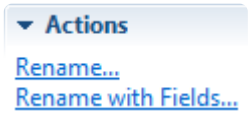
If a single track has been selected in the Overview or Analysis view, the Details panel contains the following information.

Heading	**CEU Gene Panel 12 2 release** **Summary:** This track displays a value at each position in the sequence.	The heading contains: • Type of track or assembly name, in blue. • **Summary** – Basic information about what is displayed in the selected track.
Data	Data **Assembly name:** CEU Gene Panel 12 2 release **Assembly type:** Unknown **Assembly time:** 2/5/15 3:56 PM **Assembly path:** C:\Users\Public\Documents\DNASTAR\Sample Data\Demo SeqMan NGen\CEU_Gene_Panel_12_2_release.assembly	Some tracks may have a **Data** section that includes the source of data. • **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	Actions Rename... Rename with Fields... Show track layout Show track options	Only a subset of links may be available, depending on the selected track. • **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**.

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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		The heading contains: • The number of tracks currently selected (in blue). • **Summary** – Description of options available for the multiple track selection.
Actions		The Actions area contains: • **Rename** – Shortcut to Edit > Rename. • **Rename with Fields** – Shortcut to **Edit > Rename with Field**.

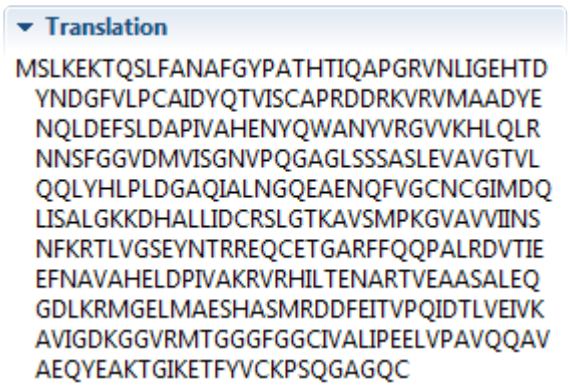
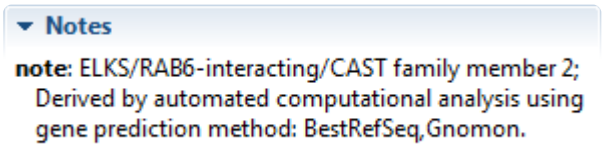
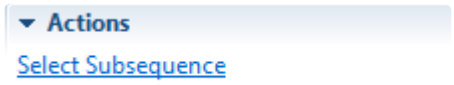
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When one feature is selected

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: • 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.

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Translation		This section is displayed only for some CDS features. When present, it displays the NCBI **/translate** feature qualifier.
Notes		This section is not available for all features. • **note** – The NCBI feature qualifier of the same name.
Actions		**Select Subsequence – * Shortcut to the menu command|topic=Menu Commands *Edit > Select Subsequence**. Double-clicking on the feature fulfills the same function. See Make a Selection for more information.

For additional information about working with features, see Features panel.

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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	**3 features** **Type:** Region, source, Protein **Left:** 1 **Right:** 374 **Min. Length:** 368 **Max. Length:** 374	The heading shows: • 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	▾ Properties **gene:** PRR23B **db_xref:** HGNC:33764, GeneID:389151, HPRD:18392, GI:197927234 **parentid:** PRR23B	Shows a subset of the qualifiers that all selected features have in common. This section does not show qualifiers that appear elsewhere in in the Details panel when a single feature is selected (e.g., **/translation** and **/note**)

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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 each 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		Shortcut to the **File > New GenVision Pro Session** command. See Create a new session for details.	
New assembly with options		Shortcut to the **File > New Assembly with Options** command. See Create a new assembly using SeqMan NGen for details.	
Open a file		Shortcut to the **File > Open** command. See Open an existing session for details.	
Save session		Along with **Ctrl/Cmd+S**, this is a shortcut to the **File > Save Session** command. See Save, Close and Exit for details.	
Add assemblies to session		Shortcut to the **File > Add Assemblies** command. See Add assemblies for details.	
Add sequences to session		Shortcut to the **File > Add Sequences** command. See Add sequences for details.	
Download and add a genome to this session		Shortcut to the **File > Download and Add Genome** command. See Add genomes from the NCBI for details.	
Add tracks to session		Shortcut to the **File > Add Track** command. See Add tracks for details.	
Show whole genome		Same as opening the Genome view or 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	

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		Overview when a selection has not yet been made.
Full screen		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.
Change layout		Lets you choose how many views are displayed and how they are laid out. See Customize the appearance and layout of views for details.

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 Genome view. The Analysis view and Overview remain empty until a different selection is made.

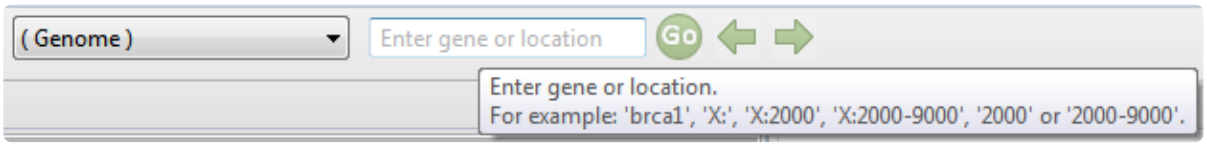
To move the cursor to a particular position or range using the search bar at the top of the GenVision Pro window:

Use the search bar in the header of the GenVision Pro window, just to the left of a round "Go" 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.

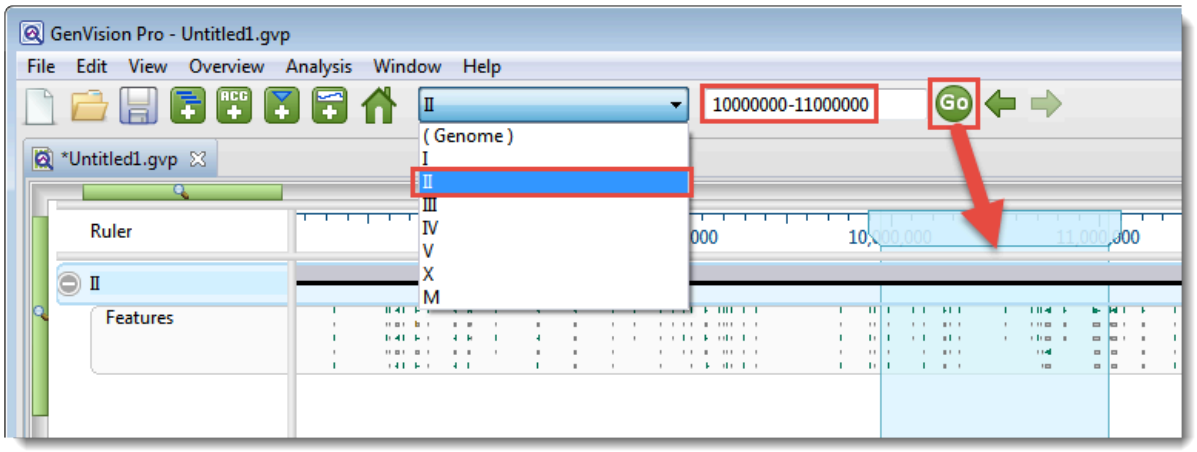


A variety of separators (e.g., spaces, < or > symbols) are accepted between the endpoints in a range. For example, all of the following are accepted: 300-433, 300 433, 300..433, 300>43 and 433<300. You can also paste in a range obtained from a variety of external sources, including SeqNinja and the National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

Example: The following image shows an example where both the sequence selector and the text box were

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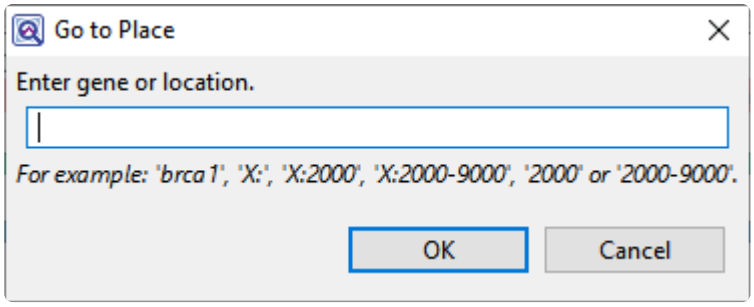
used to perform a search.



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 position or range using a menu command:

Choose **Edit > Go to Place** to open up a popup dialog with a similar search bar.

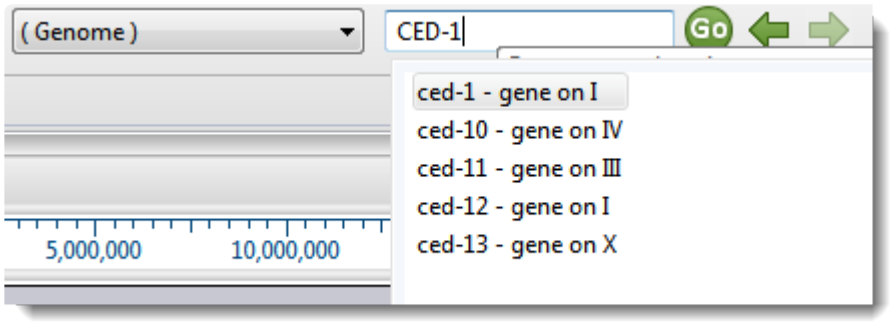


In the popup dialog, type a position or range into the text box (refer to the section above for details) and press **OK**.

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.

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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.

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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

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Create a new session

To create a new, untitled GenVision Pro session :

Do any of the following:

- From the Welcome screen, choose **New session** to open a new blank session; or **Add assemblies to new session** to open a session and add sequences at the same time.
- From the Details panel, click the link **Create a new session**.
- From the menu, choose **File > New GenVision Pro Session**.
- Press **Ctrl/Cmd+N**.

Once you create a session and add sequences or add assemblies, the information is initially shown in the Genome view. Double-click on a chromosome in that view to open its Overview and Analysis view. The appearances of the views are determined by options in the Style panel.

To open an additional GenVision Pro window:

Do either of the following:

- Click on the **Welcome** tab and choose **New session**.
- Use the **Window > New Window** command.

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Open an existing session

To open an existing GenVision Pro (*.gvp*) session :

Do any of the following:

- From the Welcome screen, click the **Open** tab, then click on **Open session**.
- From the Details panel, click the link **Open a session**.
- Use the **File > Open** command.
- 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.

Notes:

- If you created a session in GenVision Pro 17.2.1 or earlier and attempt to open it with version 18.0 or later, read tracks will not be available in the Tracks panel, and a warning may appear. In this case, we recommend closing the session and creating a new session instead.
- 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.

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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.

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Create a new assembly using SeqMan NGen

To create a new assembly from within the GenVision Pro application, do either of the following:

- From the Welcome screen, click the **New** tab on the left and then choose **New assembly with options** on the right.
- From within a GenVision Pro session, click on the **New assembly with options** tool in the top left ().
- Choose the menu command **File > New Assembly with Options**.

All of the above cause SeqMan NGen to launch at the Welcome screen. Choose the desired workflow from the Workflow screen and proceed through the wizard to set up the assembly. For more information, consult the SeqMan NGen User Guide.

The assembly status will appear in GenVision Pro's Jobs panel. Depending on the data type and workflow, the results may launch automatically in SeqMan Ultra once the assembly finishes. If they don't, you can open them in SeqMan Ultra by clicking the blue link in the **Status** column. To learn more about using SeqMan Ultra, consult the SeqMan Ultra User Guide.

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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).

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Make a session active

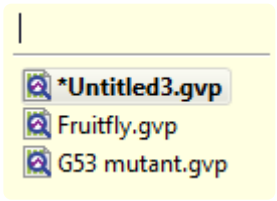
To make a session active:

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.

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Add Data

Once you have created a GenVision Pro session, the next step is to add data.

To add this type of data…	…see this topic	Where data type appears in GenVision Pro	How to view the data
.assembly files created in SeqMan NGen	Add assemblies	Experiments section of the Explorer panel	Double-click on a row to make the selected experiment active in the Analysis view and Overview.
.seq files *.sbd* and *.sbp* files created in SeqBuilder Pro *.msa* files created in MegAlign Pro Reference chromosomes in *.fasta*, *.fas*, *.gb*, or *.gbk* format	Add sequences	Chromosomes section of the Explorer panel	
Genomes from NCBI	Add genomes from NCBI	Chromosomes section of the Explorer panel	
BED files (*.bed*) Wiggle files (*.wig*) GenVision box files (*.txt*)	Add tracks	Tracks panel	Check the box next to the track name to view this data in the Analysis view.

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Add assemblies

You can add a SeqMan NGen *.assembly* package to the session.

To add a SeqMan NGen *.assembly* package:

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**

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.

Each assembly you add will be listed in the Experiments section of the Explorer panel. Double-click on the assembly to view it in the Overview and Analysis view.

Errors when adding assemblies:

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:

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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.

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Add sequences

You can add a sequence to the session if it is in any of the following formats: sequence file (*.seq*), SeqBuilder Pro format (*.sbd*), MegAlign Pro format (*.msa*), Genbank (*.gbk*) or FASTA (*.fas and _.fasta*).

To add sequences:

Do any of the following:

- Drag & drop one or more sequence files on an open GenVision Pro session
- Use the **Add sequences to project** button tool ()
- Choose **File > Add Sequences**.

Each sequence you add will be listed in the Chromosomes section of the Explorer panel. Double-click on the sequence to view it in the Overview and Analysis view.

Note that 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.

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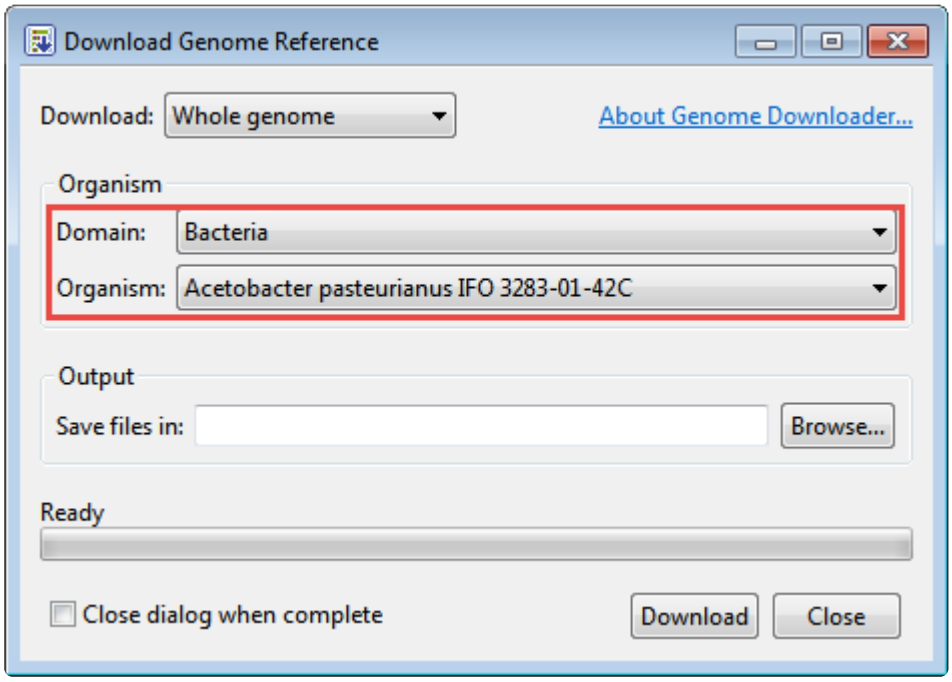
Add genomes from NCBI

To import a genome from the National Center for Biotechnology Information (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**.

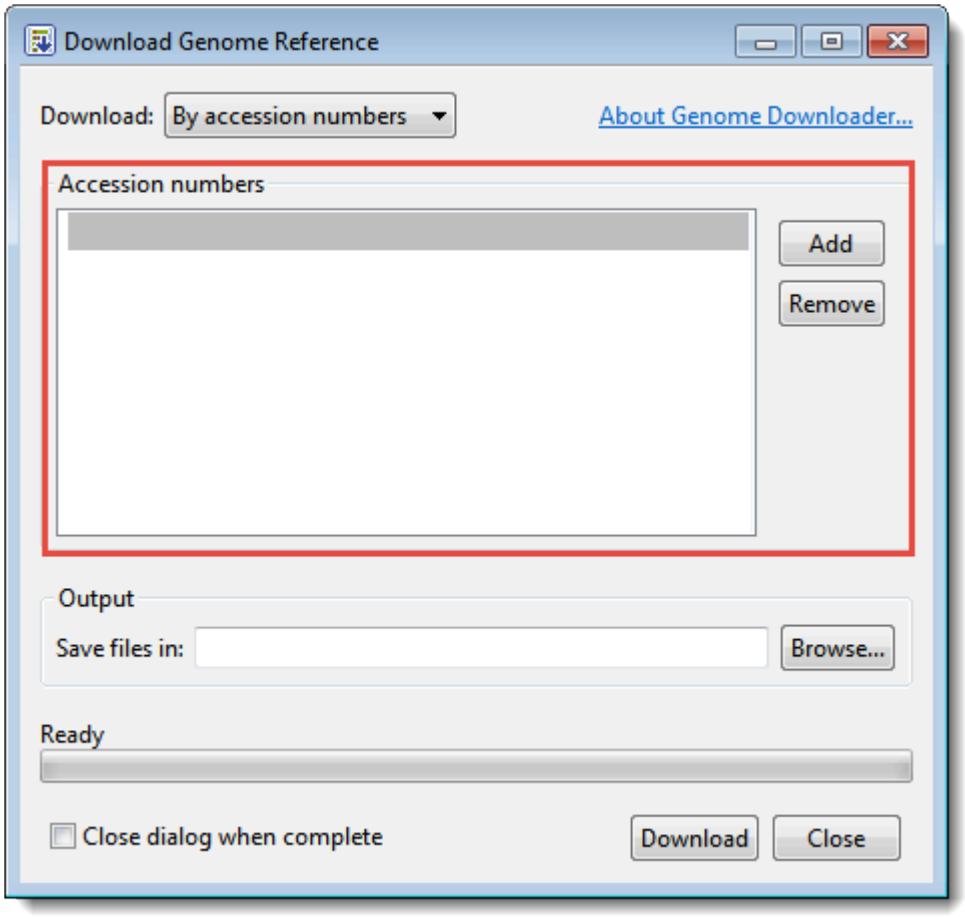
    - If you select **Whole genome**, GenVision Pro will retrieve the most recent build of the selected genome. Use the next two drop-down menus to select the **Organism type** and **Organism**.



      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**.

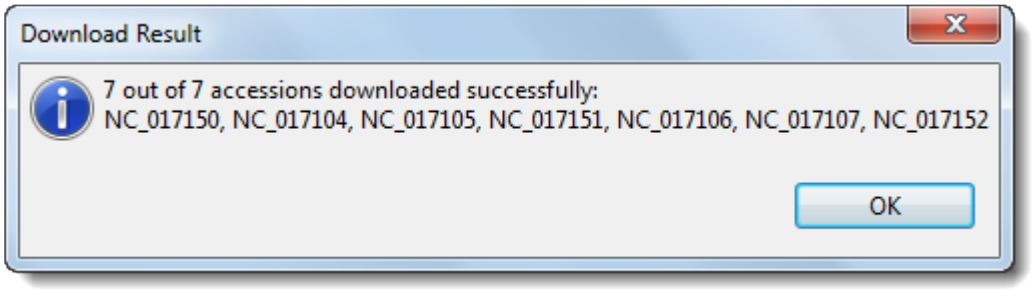
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3. Click **Browse** to select a name and location in which to save the downloaded genome files.

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.

Downloaded genomes will be listed in the Chromosomes section of the Explorer panel. To learn how to view the genome in the Overview or Analysis view, see Work with Tracks.

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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.

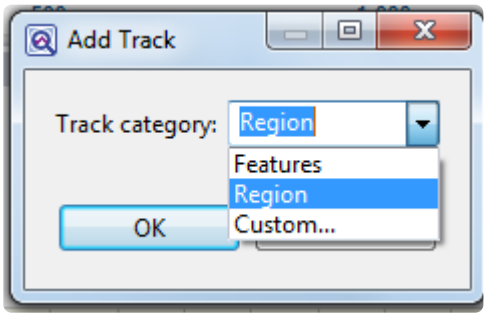
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Add tracks

A data track in BED file (*.bed*), GenVision box file (*.txt*) or Wiggle (*.wig*) format can be imported into a GenVision session.

To add tracks:

1. Do any of the following:
    - Drag & drop one or more track files (see above) on an open GenVision Pro session
    - Use the **Add tracks to project** button tool ( )
    - Choose **File > Add Track**.
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.

To learn how to view track data in the Overview or Analysis view, see Work with Tracks.

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

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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.

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Search for Sequences Online

This application lets you search National Center for Biotechnology Information (NCBI) databases for matches to text or sequence that you specify.

- Query part or all of a nucleotide or protein sequence against one of NCBI's sequence databases using the Basic Alignment Search Tool (BLAST).
- Query text or accession numbers against entries NCBI's Entrez database.

Once a search has been initiated, you can use the Jobs panel to monitor the search, stop an in-progress search, or open search results in the Text and Table views.

Tools available in the Search wizards:

Some or all of the following optional tools may be available in the bottom left corner of the Search wizards:

1. To display the help for this topic, press the question mark icon ().
2. To enter an NCBI Access ID, press the **Set Access ID** () tool. This causes the Access ID dialog to pop up. See Access ID dialog for information.
3. To submit an idea for a new feature, press the **Suggest a feature** () tool.
4. To view information about your service plan, press the **Show service plan details** () tool. For sequence or text search services, the ensuing dialog describes the state of your service plan and any warning or error text messages. The license control has three states: **Active**, **Expiring**, and **Expired**.

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Search for sequence matches (BLAST)

The BLAST Search wizard is used to search a query sequence against one of NCBI's databases. The sequence can be part or all of an active sequence, another sequence file on your computer, or typed/pasted-in text. The wizard consists of four consecutive screens, each described in a separate topic:

- Query screen
- Search screen
- Options screen
- Job screen

To launch the BLAST Search wizard, use one of the following commands or tools. Some commands let you launch the wizard with the workflow pre-selected and the Search list already pre-populated.

Command, shortcut or tool	Description
Search > Search	Launches the wizard at the Query screen.
Use the "Change search strategy" tool ( ) from the Text, Table or Pairwise views	
From the Welcome tab, choose **Search** and then **Search for sequences**.	
Search > Sequence Search with Selection	Launches the wizard at the Query screen, whose table is pre-populated with the currently-selected portion of sequence.
Press **Ctrl/Cmd+B**	
Search > Sequence Search with All Sequences	Launches the wizard at the Query screen, whose table is pre-populated with all sequences in the document.

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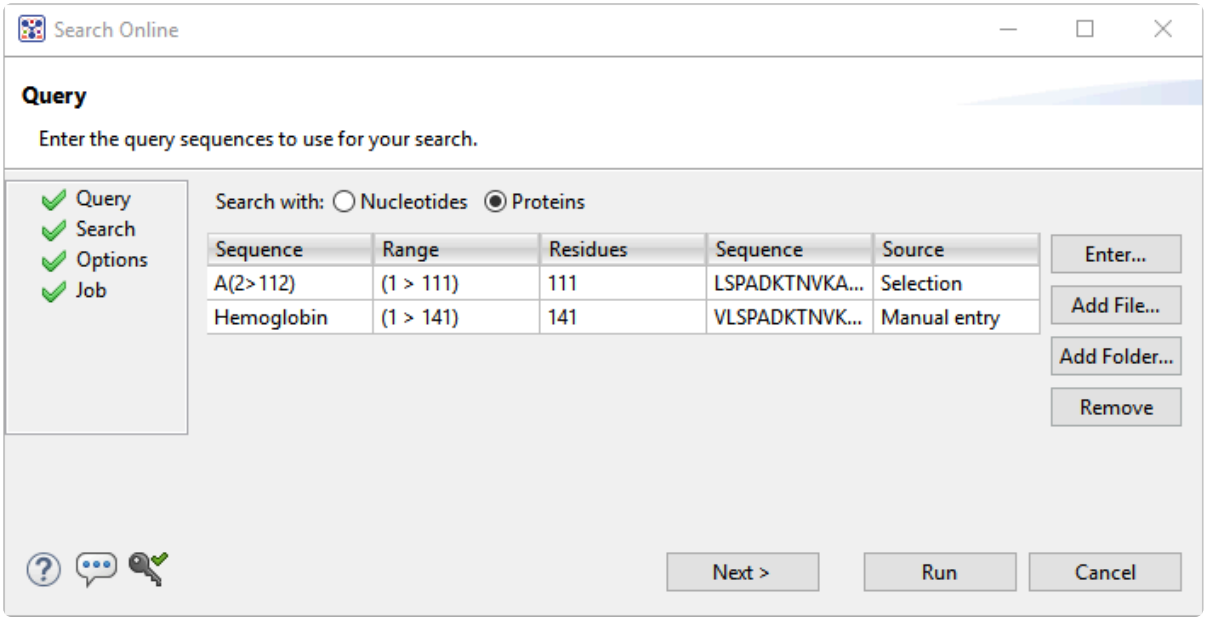
Search wizard: Query

The Query screen is the first of four screens in the BLAST Search wizard. The Query screen is where you add the query sequence, i.e., the sequence for which you wish to locate matches in the NCBI BLAST database.

At the top of the screen, next to “Search with,” select the **Nucleotides** or **Proteins** button.

To add one or more query sequence files or a folder of sequences:

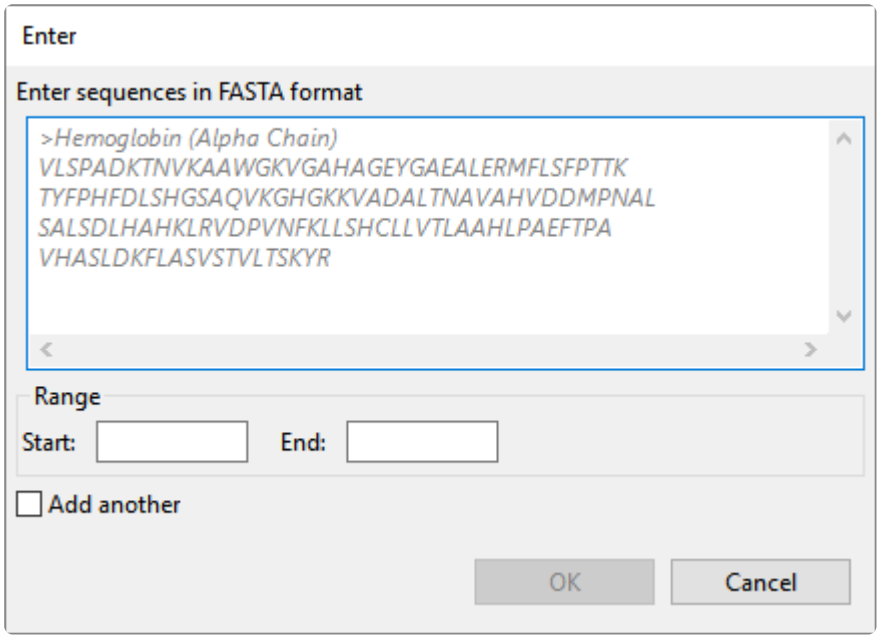
Press the **Add** or **Add Folder** buttons. In the file explorer, navigate to and select the desired file(s)/folder(s), and then click **Open**. If you add a multi-file sequence or multiple sequences, each sequence will appear on a separate row in the table.



To paste or type in the query sequence:

Press **Enter**.

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In the Enter dialog:

1. Type or paste in the desired sequence following the “dimmed” example in the dialog. A header line is optional.

2. (optional) If you wish to use only a range of this sequence, specify the **Start** and **End** positions.

3. (optional) If you want to add another query sequence after this one, check the **Add another** box. After clicking **OK** to the first sequence, a new Enter dialog will open to add the next query. Otherwise, leave this box unchecked.

4. Press **OK**. If you add additional sequences, each sequence will appear on a separate row in the table.

To remove a file that has already been added:

Select the unwanted file from the list and click **Remove**.

To learn about the optional tools in the bottom left corner of the screen, see the bottom of this topic.

Once you have set up the query sequence(s) as desired, do either of the following:

- To choose the BLAST program to use and database to search, press **Next** to continue to the Search screen.

- To run the search directly, press **Run**.

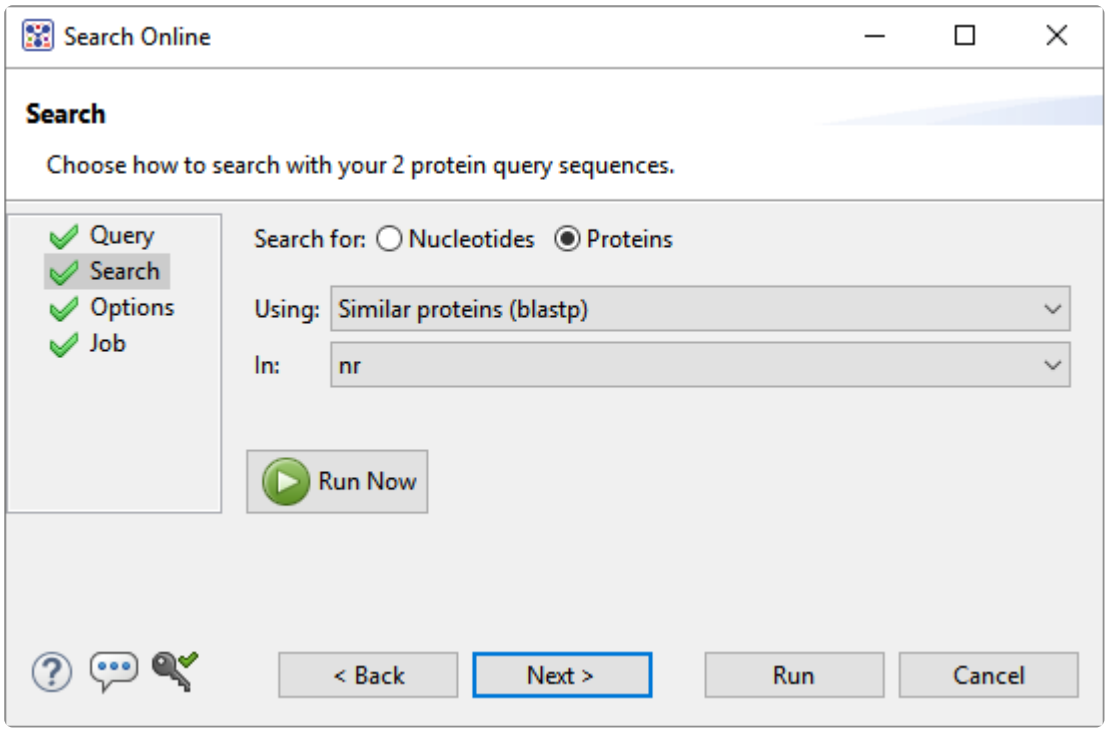
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- To close the Search wizard without starting a search, press **Cancel**.

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Search wizard: Search

The Search screen is the second of four screens in the BLAST Search wizard. The Search screen is used to choose the BLAST program and database.

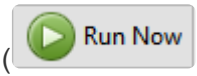


- Specify whether you wish to search for **Nucleotides** or **Proteins**.
- Select the desired BLAST program from the **Using** drop-down menu. For information on the different BLAST programs, see the BLAST Program Selection Guide PDF. Available options depend on the combination of the selections you made in **Search with** (Query screen) and **Search for** (this screen).
    - If you selected **Proteins** on both screens, the **Using** menu contains the unchangeable default of **Similar proteins (blastp)**.
    - If you selected **Nucleotides** on both screens, Choices are **Highly similar sequences (megablast)**, **Similar nucleotides (blastn)**, and **Similar translated nucleotides (tblastx)**.
    - If you selected **Nucleotides** in the Query screen and Proteins in the Search screen, the **Using** menu contains the unchangeable default of **Similar proteins (blastx)**.
    - If you selected **Proteins** in the Query screen and **Nucleotides** in the Search screen, the **Using** menu contains the unchangeable default of **Similar translated nucleotides (tblastn).**
- Select the desired BLAST database from the **In** drop-down menu. Available choices depend on whether you selected **Nucleotides** or **Proteins** in this screen.

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To learn about the optional tools in the bottom left corner of the screen, see the bottom of this topic.

Once you have made the desired selections, do any of the following:

- To go back to the Query screen, press **Back**.
- To add additional parameters to the search, press **Next** to continue to the Options screen.
- To start the search immediately, press the **Run Now** button (

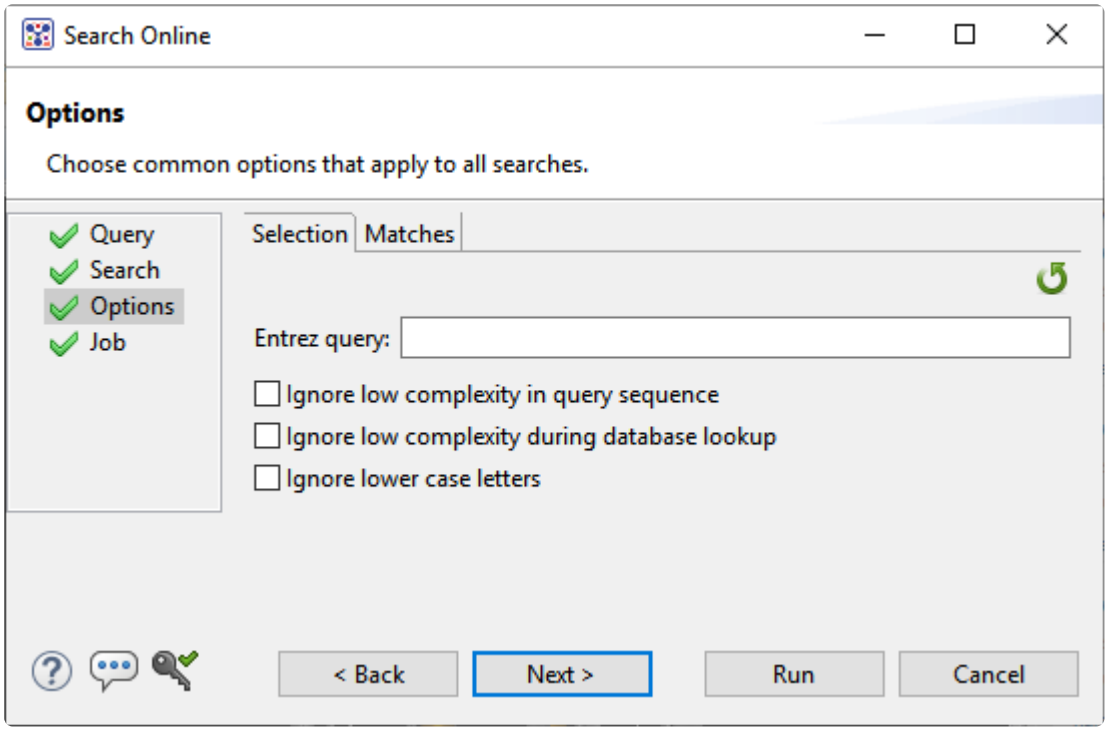
) or **Run** button. The Jobs panel in the application will open and contain information on the status of the search. During the search, a progress dialog is displayed where you can cancel the search using the **Stop** button, hide the dialog using the **Hide** button, or set up another query using the **Settings...** button. Use the Jobs panel to monitor an online search, stop an in-progress search, or open search results in the Text and Table views.
- To close the Search wizard without starting a search, press **Cancel**.

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Search wizard: Options

The Options screen is the third of four screens in the BLAST Search wizard, and has two tabs: **Selection** and **Matches**. These tabs allow you to customize miscellaneous parameters relating to the BLAST search.

- Click the **Selection** tab to make it active.

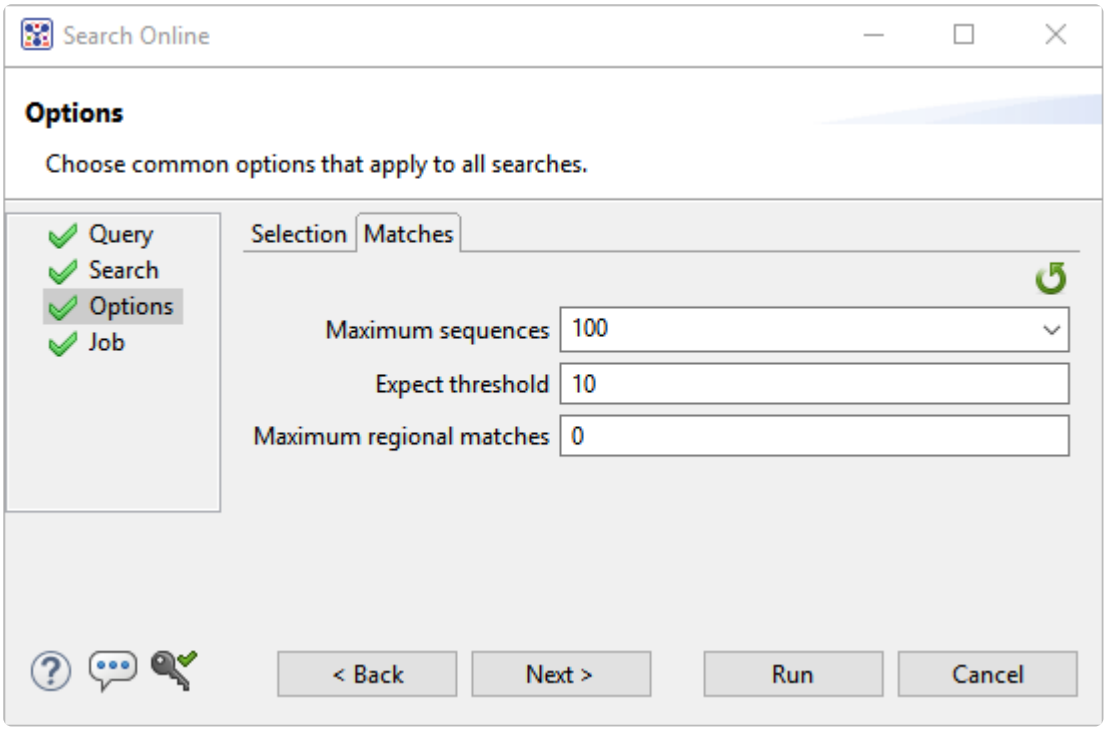


In the **Selection** tab:

  - To filter the database you're searching using a text term, enter a text string in the **Entrez** query field.
  - To filter low-complexity regions in the query, check the box next to **Ignore low complexity in query sequence**. The **blastn** search program will use **DUST** for filtering; all other programs will use **SEG**.
  - To mask the query while producing seeds used to scan database (but not for extensions), check the box by **Ignore low complexity during database lookup**.
  - To mask any letters that were lower-case in the FASTA input, check the box next to **Ignore lower case letters**.

- Click the **Matches** tab to make it active.

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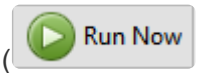


In the **Matches** tab:

- Enter a number next to **Maximum sequences**, the maximum number of aligned sequences to display. The actual number of alignments may be greater than this number. The default is **100**.
- Enter a number beside **Expect threshold**, the expected number of chance matches in a random model. The default is **10**.
- Enter a number next to **Maximum regional matches** to limit the number of matches to a query range. The default is **0**.

To learn about the optional tools in the bottom left corner of the screen, see the bottom of this topic.

Once you have made the desired selections, do any of the following:

- To continue filtering, press **Next** to continue to the Job screen.
- To start the search immediately, press the **Run Now** button (

) or **Run** button. The Jobs panel in the application will open and contain information on the status of the search. During the search, a progress dialog is displayed where you can cancel the search using the **Stop** button, hide the dialog using the **Hide** button, or set up another query using the **Settings...** button. Use the Jobs panel to monitor an online search, stop an in-progress search, or open search results in the Text, Table and Pairwise views.

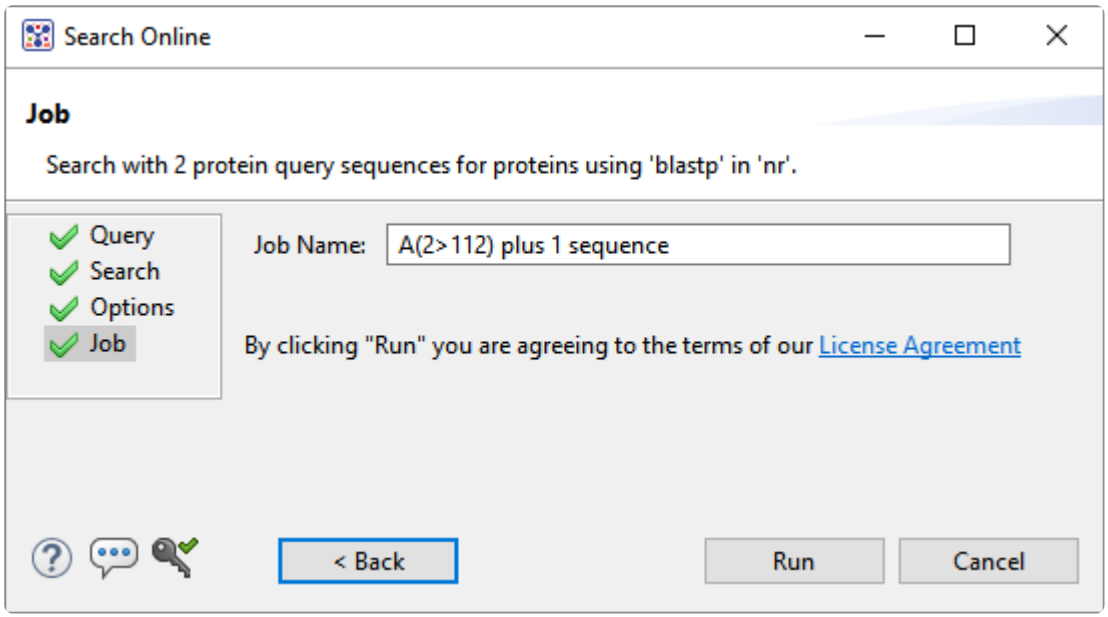
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- To close the Search wizard without starting a search, press **Cancel**.

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Search wizard: Job

The Job screen is the fourth of four screens in the BLAST Search wizard, This screen allows you to overwrite the default search name with a custom name and initiate the BLAST search.



The text box contains an automatically-generated name for the search job. If you wish, you can overwrite this default name with a custom name.

To learn about the optional tools in the bottom left corner of the screen, see the bottom of this topic.

After entering a custom job name (or keeping the default name), do either of the following:

- To start the search , press the **Run** button. The Jobs panel in the application will open and contain information on the status of the search. During the search, a progress dialog is displayed where you can cancel the search using the **Stop** button, hide the dialog using the **Hide** button, or set up another query using the **Settings…** button. Use the Jobs panel to monitor an online search, stop an in-progress search, or open search results in the Text, Table and Pairwise views.

- To close the Search wizard without starting a search, press **Cancel**.

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Search for text or accession number matches (Entrez)

The Entrez Search wizard is used to search a text query or accession number against NCBI's Entrez databases for nucleotides or proteins.

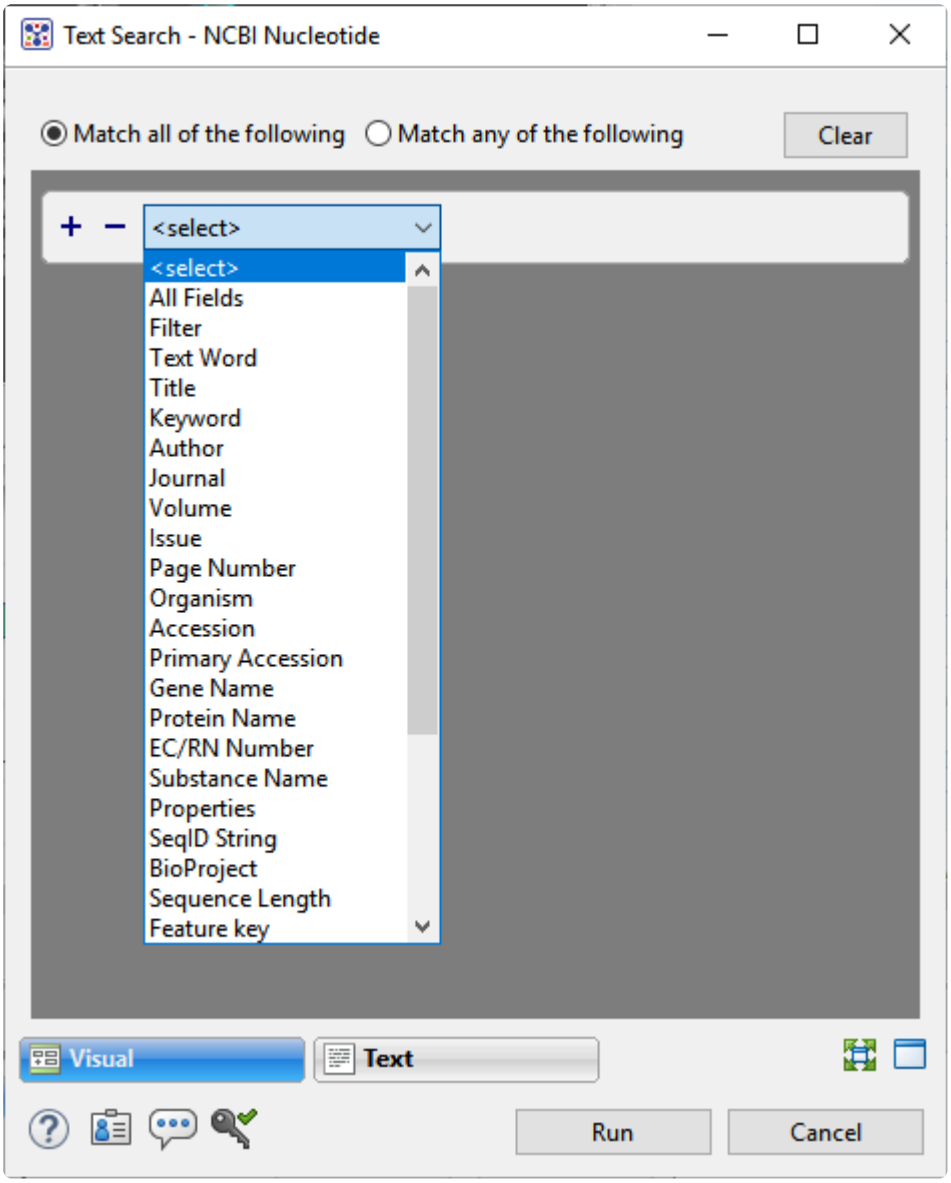
To launch the Entrez search dialog, choose **Search > Text Search in > NCBI Nucleotide** or **Search > Text Search in > NCBI Protein**. Alternatively, open the Welcome tab, choose **Search** and then click either **Search for text in…** link.

The **Visual** view is displayed by default and is described below.

Note: The Visual view is only for non-nested queries using the same type of operator (AND, OR). To perform a more complicated search, press the **Text** tab near the bottom left corner and create the search in the Text view.

1. Use the **<select>** drop-down menu to choose a criterion. The field headings vary depending upon the online database that you are using. Choosing **All fields** will cause the application to search every word of every listing for the query term in the database.

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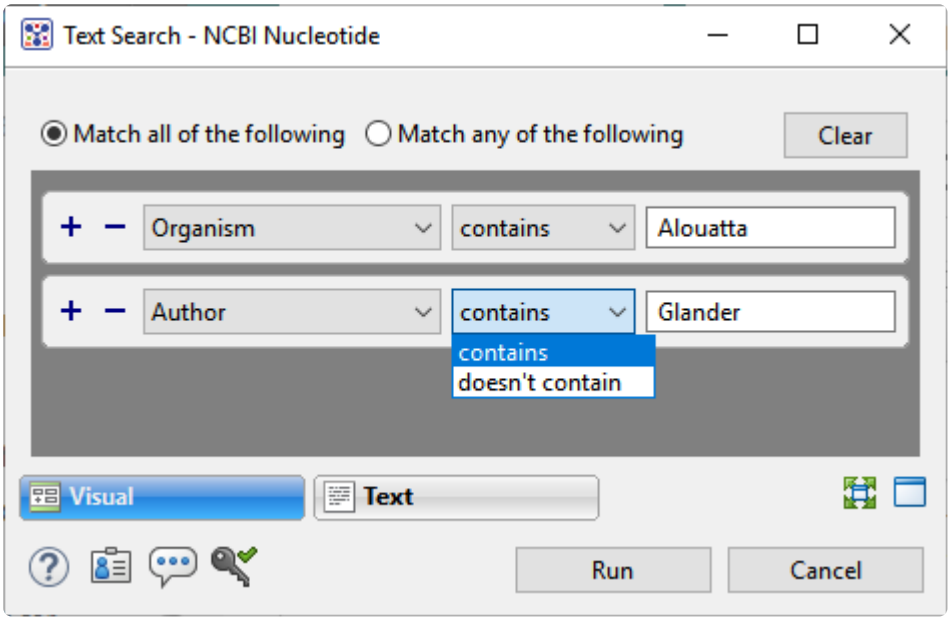


Once you make a selection, a second drop-down menu and an empty text box appear to the right.

- In the second drop-down menu on the row, choose **contains** or **doesn't contain** (see image below).
- In the text box, type the text that should be found in any results (in the case of **contains**) or should not be found in any results (in the case of **doesn't contain**).

2. To add another criterion, press the plus icon (+). To delete a criterion, press the minus icon (−).

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3. Once you have set up all desired criteria, go to the top of the dialog and choose whether to **Match all of the following** or **Match any of the following** criteria.

4. To learn about the optional tools in the bottom left corner of the screen, see the bottom of this topic.

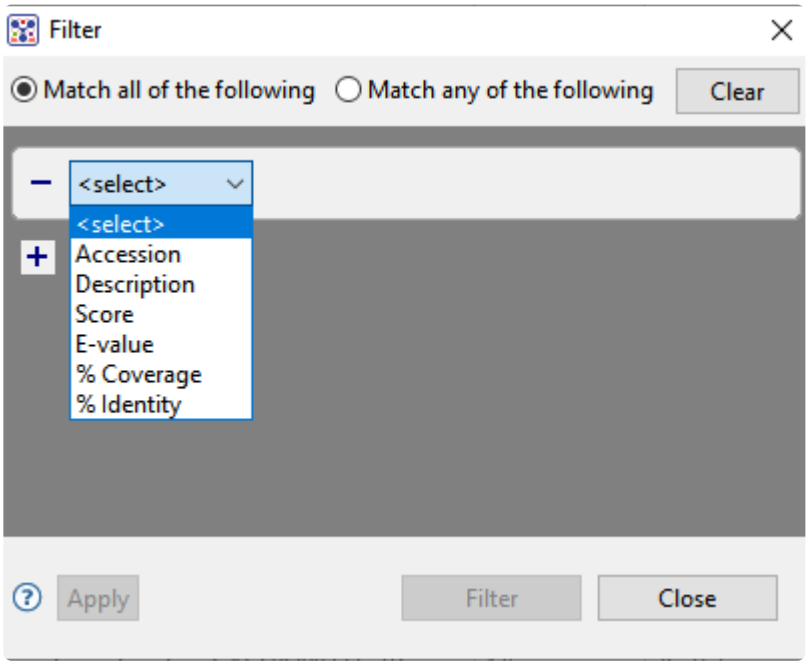
5. Click **Run** to send the query to the database. To instead exit the dialog without searching, press **Cancel**.

During the search, a progress dialog is displayed. Once the search is completed, any matches are displayed in the Jobs panel.

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Filter sequence search results

When you press the **Filter results** tool ( ) in the header above the Table or Pairwise views, there are two options: **Filter** and **Clear Filter**. Clicking on the **Filter** option opens the following dialog:



- Use the **<select>** drop-down menu to choose a filter type, then enter the desired options.

Filter type	Description	Options
Accession	The Accession number.	
Description	The NCBI “Definition” field text.	
Score	The similarity score for the match. (See the NCBI definition for **raw score**). In general, a higher score denotes a better match.	
E-value	The chance that the match is expected to occur coincidentally. (See the NCBI definition for **E value**). In general, a lower score denotes a better match.	
% Coverage	The percentage of the query sequence that aligns to a match in the BLAST database. Example: Query has 596 bases, of which 565 align to a match in the NCBI database. **%Coverage** = 565/596 = 95%.	
% Identity	The percentage of bases that match when the query and result sequence are aligned. (NCBI definition). Example: Query has 565 bases that align to the match and 3 bases that don’t	

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	match. **%Identity** = 562/565 = 99.5%.	

- To add another filter, press the plus icon (+). To delete a filter row, press the minus icon (−).
- Once you have set up all desired queries, go to the top of the dialog and choose whether to **Match all of the following** or **Match any of the following** queries.

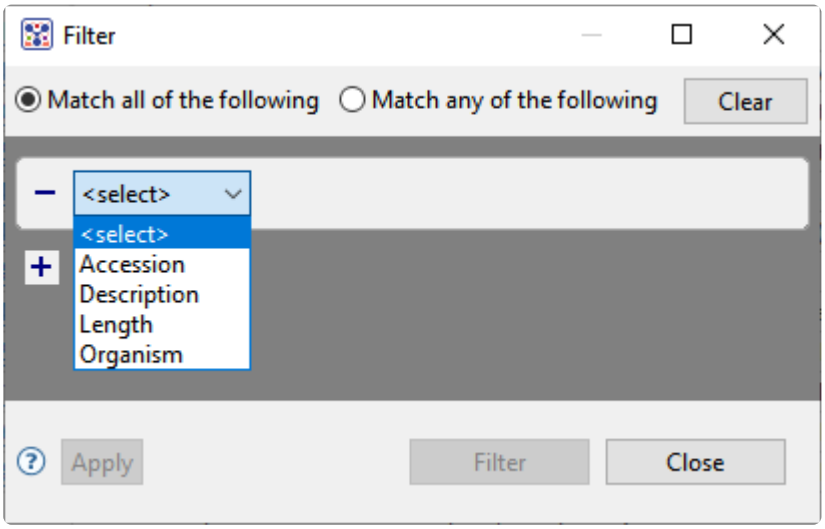
Once you are finished setting up filters, do any of the following:

- To apply the filters, press **Apply** or **Filter**.
- To clear all filters and start over, press **Clear**.
- To exit the dialog without filtering, press **Close**.

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Filter text search results

When you press the **Filter results** tool ( ) in the header above the Table or Pairwise views, there are two options: **Filter** and **Clear Filter**. Clicking on the **Filter** option opens the following dialog:



- Use the **<select>** drop-down menu to choose a filter type, then enter the desired options.

Filter type	Description	Options
Accession	The Accession number.	
Description	The NCBI “Definition” field text.	
Length	The length of the match sequence in bases.	
Organism	The species name.	

- To add another filter, press the plus icon ( ). To delete a filter row, press the minus icon ( ).
- Once you have set up all desired queries, go to the top of the dialog and choose whether to **Match all of the following** or **Match any of the following** queries.

Once you are finished setting up filters, do any of the following:

- To apply the filters, press **Apply** or **Filter**.
- To clear all filters and start over, press **Clear**.
- To exit the dialog without filtering, press **Close**.

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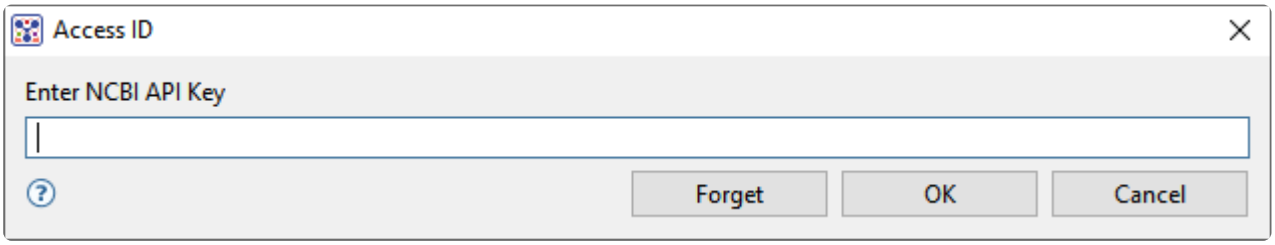
Access ID dialog

As of December 2018, NCBI requires an API key for faster access to NCBI services, or to run more searches concurrently. To get a key, start by setting up an NCBI account. After registering your account, click on your user name and request your key using **API Key Management**. Once you have your key, you can enter it in Lasergene applications to enable NCBI's premium search access.

To add your key to a Lasergene application:

1. Begin an Entrez database search using **Search > Text Search in > NCBI Nucleotide** or **Search > Text Search in > NCBI Protein**.

2. Press the **Set Access ID** ( ) tool in the bottom left corner of the dialog.



- If an NCBI API key is not already present in the text box, enter your key and press **OK**.
- If an NCBI API key is present but you no longer use it, press **Forget** to remove it from the application's memory. Then enter the desired key and press **OK**.
- To exit without saving your changes, press **Cancel**.

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Save and reopen saved search results

To save the Table, Pairwise and Text views for the current search, use the **Save as** tool () in the top right of the Table view. The results are saved in *.search* format.

To reopen saved results, choose **Search > Open Search File** and navigate to the *.search* file.

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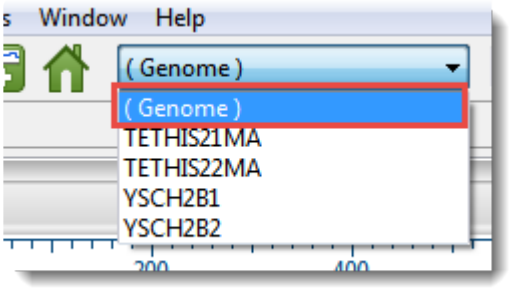
Specify the Experiment or Chromosome to Display

The Genome view can display multiple experiments, chromosomes, contigs or sequences simultaneously. However, only one of these at a time may be displayed in the Analysis view and Overview.

To display Genome view rows for all uploaded session data:

Do any of the following:

- Press the **Home** ( ) button tool.
- Use the **View > Genome > Show** command.
- Click on the **Genome** tab.
- 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:

Do any of the following:

- Double-click on any item in the Genome view.
- Double-click on any item in the Experiments or Chromosomes sections of the Explorer panel.
- Use the navigation tools to make a selection other than **(Genome)** from the drop-down menu.

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Work with Tracks

Tracks are rows of information pertaining to a header, footer, or individual sequence row in certain GenVision Pro views. Tracks may be displayed or hidden by check or unchecking boxes in the Tracks panel.

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

- Feature and Region
- Coverage
- Reads
- Reference
- Ruler
- Sashimi

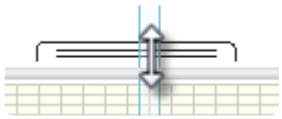
Some tracks may change in appearance depending upon the zoom level.

Where does the data used to build a track come from? When you open an *.assembly* file (or folder of these files) in GenVision Pro, the information contained in the file is parsed out for display as data tracks. For example, as of Lasergene 17.3, GenVision Pro can create the following tracks for each experiment or assembly: a reference sequence, reference ruler, reference features, read tracks, coverage plots, and Sashimi plots (if present). If the assembly project involved BED or WIG files, these are also available as tracks. Track data can also be imported manually or can be calculated by the application itself (e.g., Ruler and Numeric tracks).

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

Task	How to…
Display a track in the views	• To display a specific track in all views, check the box next to the name of the track in the Tracks panel.
Hide one or more tracks in the views	Do one of the following: • To hide a specific track from all views, uncheck the box next to the name of the track in the Tracks panel. • To hide a specific track in one view only, 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.
Change the vertical	In the Analysis view or Overview, hover your mouse over the bottom middle of a track to enable a slider. Grab the slider and pull to reveal more or less of that track.

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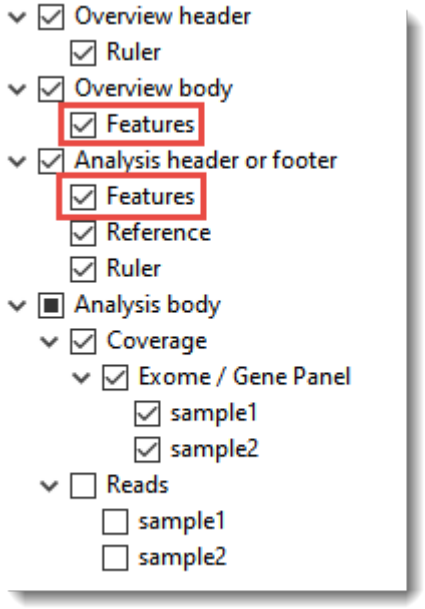
height of a track	
Add white space around a track	To add white space around a track in the Analysis view or Overview, select the track name in the Tracks panel, then use the sliders in the Layout section.
Access the options for a particular type of track	Do either of the following: • Right-click on a track in a view and choose **Show Track Options**. • Click **View > Tracks > Options** or open the Tracks panel and click the Options bar (Options), then specify the track of interest by clicking on its name in the Tracks panel.
Automatically organize tracks in the Analysis view	Use **Analysis > Order Tracks Ascending** (or **Descending**) **By > Category** (or **Name**). These commands are especially useful if you are viewing a large multi-sample project with multiple tracks applied to the view. Sort by **Name** to group tracks by experiment name. Sort by **Category** to group tracks by track type.
Change the order of a selected track in a view	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.

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Feature tracks

One or more Feature tracks can be added to the Overview and/or to the Analysis view header or footer. Feature tracks may come from the sequences in an assembly, or can be imported separately using **File > Add Track**.

For detailed information about applying tracks, see Work with Tracks. These are the Track panel items to check if you want to display one or both Feature tracks:



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

Feature tracks do not have editable options. However, you can add white space above and/or below features tracks using sliders in the Layout section.

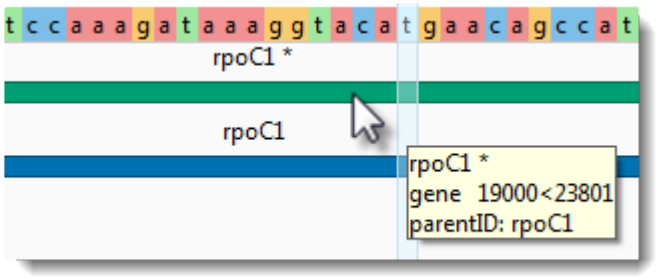
To view a tool tip with details about a region or feature, hover over it with the mouse. Or select one or more features or regions by clicking on them. You can then view information about them in the Details panel.

Inferred features:

An asterisk next to a feature name indicates that the feature was inferred by SeqMan NGen. For example, if

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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.

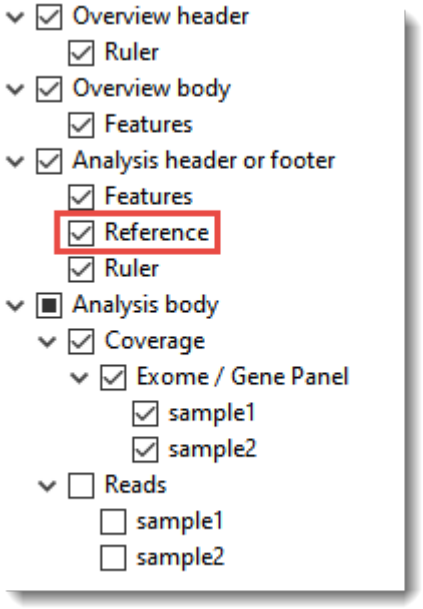


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Reference track

If you are viewing a templated assembly, you can choose to display a Reference track in the Analysis view header or footer.

For detailed information about applying tracks, see Work with Tracks. This is the Track panel item to check if you want to display a Reference track:

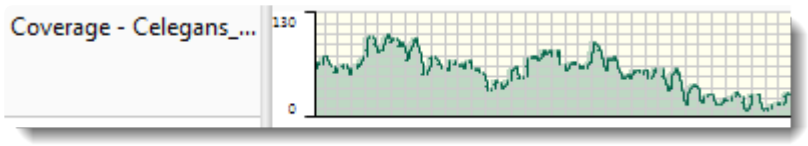


The Reference track does not have editable options. However, you can add white space above and/or below the ruler using sliders in the Layout section.

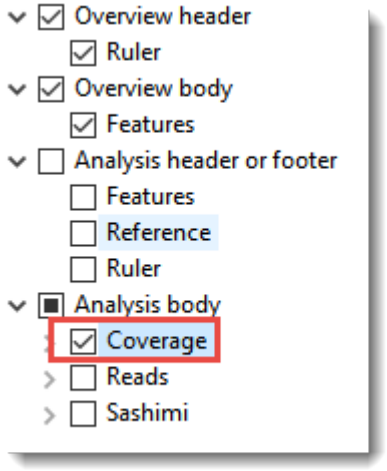
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Coverage tracks

If data are available, you can choose to display a numeric track in the body of the Analysis view. As of Lasergene 17.3, the main numerica track type is the Coverage track.



For detailed information about applying tracks, see Work with Tracks. This is the Track panel item to check if you want to display a Coverage track:



Sources of data for numeric tracks:

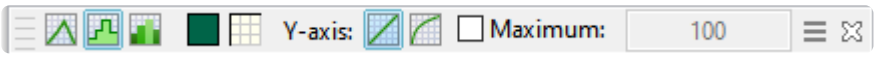
- Numeric data of any type imported via a Wiggle file (*.wig*) using **File > Add Track** (see Add tracks).
- Coverage tracks imported with a SeqMan NGen *.assembly* package (see Add assemblies). This track displays a plot of values along one or more sequences in the session. Values are obtained automatically 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 change Coverage track options:

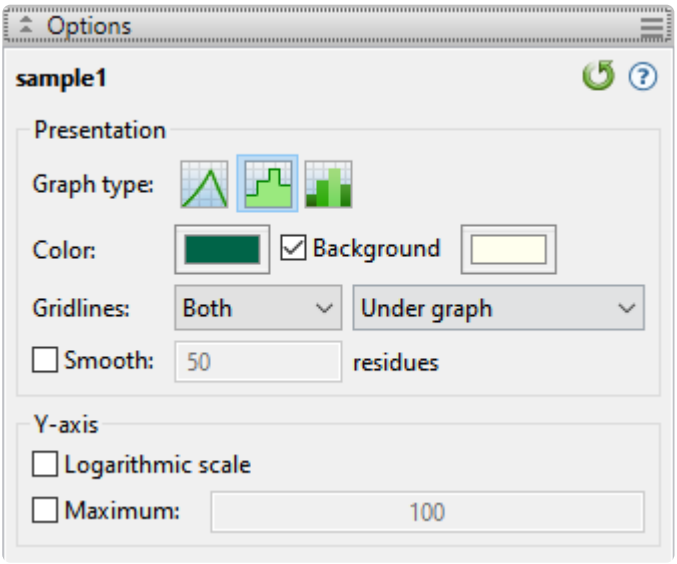
Coverage tracks can be customized using tools that are replicated in two locations. The first location is the Options section. To access it, select the Coverage track in the Tracks panel and then click the Options tab to expand the Options section.

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Once you have checked a Coverage track in the Tracks panel, it is displayed in the Analysis view. The second location where the tools are replicated can be accessed by selecting the Coverage track in that view. A toolbar will pop up to the top-left of the track.



You can use your mouse to grab the popup on its left end and drag it to any desired location in the Analysis view. Options provided in the popup are a subset of all options available in the 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.
- Check the **Logarithmic scale** box if you want to use a logarithmic, rather than a linear scale. 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**.
- If the default display range is not be suitable for a numeric track, you may see an empty graph or a

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graph with the peaks cut off. To correct this, check the **Maximum** box and enter an integer into the associated text box. You may need to try several values before finding the ideal one.

- Click  if you wish to return to the default values.

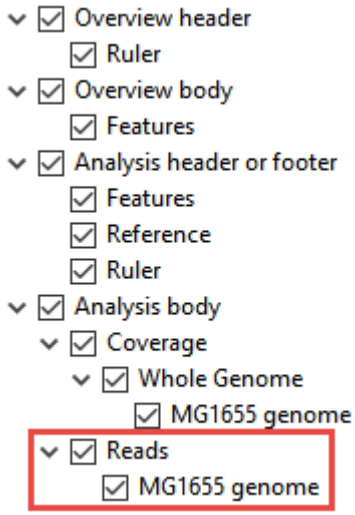
To change the height of the graph, and the white space surrounding it, use the sliders in the Layout section.

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Reads tracks

If you are viewing an assembly created in SeqMan NGen, you can add a track to the Analysis view showing each of the aligned reads in the selected experiment.

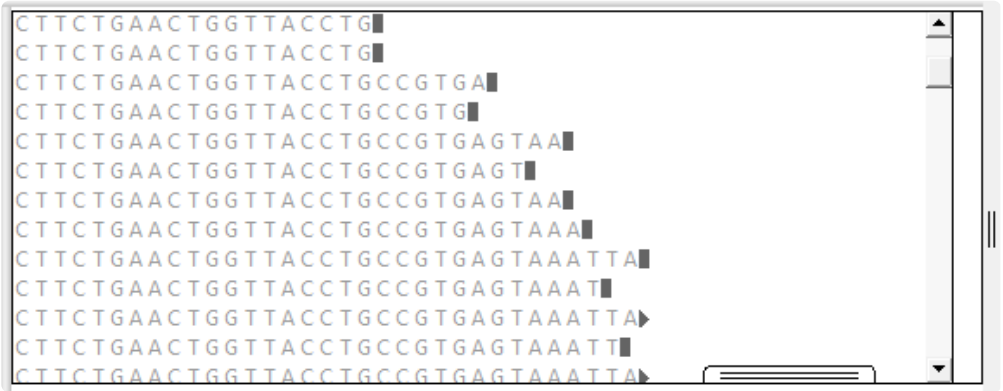
For detailed information about applying tracks, see Work with Tracks. This are the Track panel items to check if you want to display a Reads track. Of course, the actual name you see will match that of the experiment you are viewing.

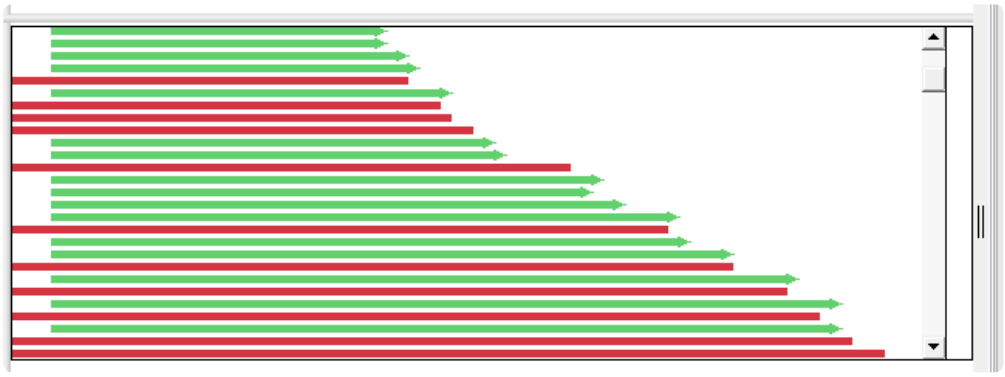


The Reads track does not have editable options. However, you can add white space above and/or below the ruler using sliders in the Layout section.

Viewing the Reads track in the Analysis view:

Once you have checked the reads tracks in the Tracks panel, read data will be displayed in the Analysis view. Depending on the zoom level in the view, the Reads track will show base letters (left) or green and red arrows representing forward and reverse reads, respectively (right).





To resize the track to show more or less data, use the slider that appears if you hover over the bottom middle of the track data. This is visible in the left image above.

Unlike most other track types, Reads tracks have their own tools. To see the read track tools, first apply a read track to the Analysis view, then select the Read track in that view. The toolbar will pop up to the top-left of the track. You can use your mouse to grab the popup on its left end and drag it to any desired location in the Analysis view.

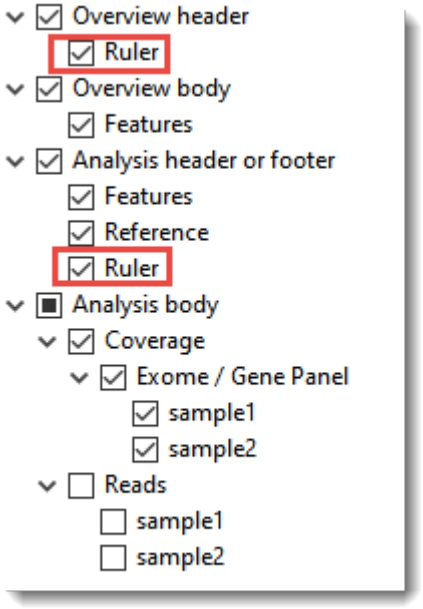
Tool name	Image	Purpose
Quality scores		Choose between **Don't show scores** and **Show scores**. Quality scores are only available for assemblies created using Sanger (*.abi*) reads.
Export data		To export the consensus. See Export the consensus sequence for detailed instructions.
(Hamburger menu)		Choose **Tracks** to open and focus on the Tracks panel. Choose **Layout** to open the Layout section for the reads track.
Close popup		Closes the tool popup.

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Ruler tracks

One or more Ruler tracks can be added to the Overview header and/or to the Analysis view header or footer.

For detailed information about applying tracks, see Work with Tracks. These are the Track panel items to check if you want to display one or both Ruler tracks:



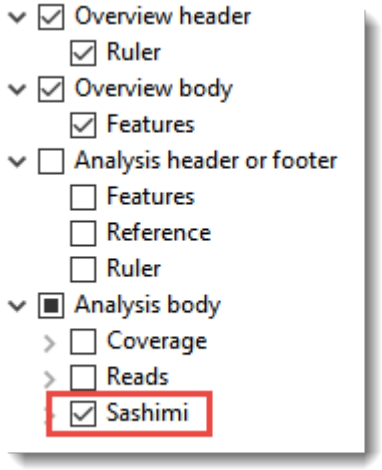
The Ruler tracks do not have editable options. However, you can add white space above and/or below the ruler using sliders in the Layout section.

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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. If data are available, you can choose to display a Sashimi track in the Analysis view.

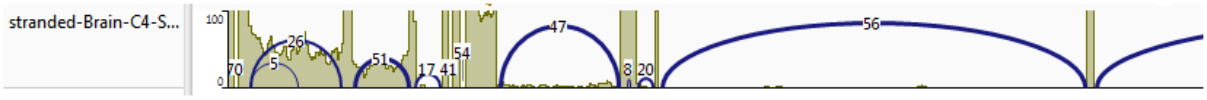
For detailed information about applying tracks, see Work with Tracks. This is the Track panel item to check if you wish to display a Sashimi plot:



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

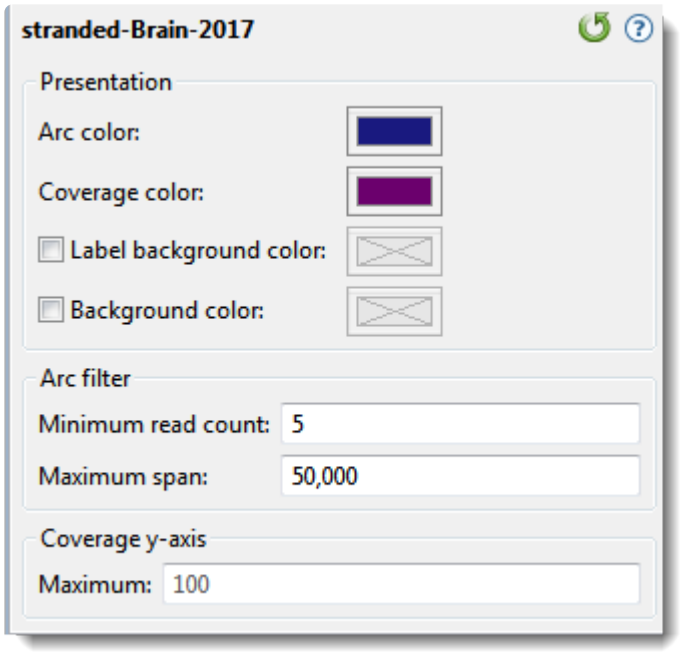
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when creating the Sashimi track.

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 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.

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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).

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Customize the Look and Layout

The following topics describe the many ways you can customize the look and layout of GenVision Pro.

- Use the Style panel to change the look of a view (font styles and sizes, colors, number of decimal places, etc.)
- Customize the appearance and layout of views
- Customize the layout of other window components
- Apply information tracks to a view

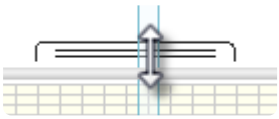
Once you have customized the look and layout as desired, you can:

- Save Styles for individual views and apply them to other sessions
- Save the entire layout and apply it to other sessions

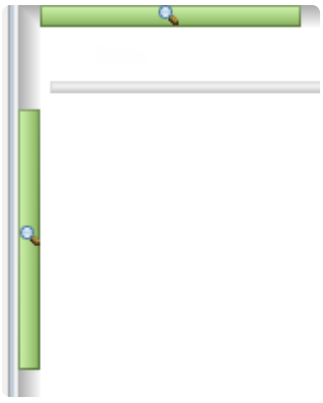
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Customize the appearance and layout of views

The following table lists ways in which you can customize the appearance and layout of views.

Task	How to…
Show a view	Use **View > (View Name) > (chromosome or contig number) > Show**. The third item in the command at left may or may not appear. Example: to see the Analysis view for Chromosome 12, choose **View > Alignment > 12 > Show**.
Resize a track in a view	In the Analysis view or Overview, hover your mouse over the bottom middle of a track to enable a slider. Grab the slider and pull to reveal more or less of that track. 
Add white space around a track in a view	To add white space around a track in the Analysis view or Overview, select the track name in the Tracks panel, then use the sliders in the Layout section.
Change the style (fonts, colors, calculation metrics and more)	Use the Style panel and its subsections. Customization for font style and size applies to all text in a view. Individual rows cannot have different styles.
Move one or more contig rows as a group	In the Overview, you can rearrange contigs one at a time or as contiguous groups using drag and drop. First, select the desired rows using **Ctrl/Cmd+click** or **Shift+click**. Next, drag the selected row(s) to the desired location and release the mouse button.
Detach a view	Only certain views can be detached. To do this, right-click on the view tab and choose **Detach (View Name)**. Alternatively, use **View > (View Name) > (chromosome or contig number) > Detach**. Detaching a view turns it into a free-floating window.
Reattach all detached views to their original locations	Use **View > Reattach All Views**.
Show the active view in full-screen mode	Use the **View > Full Screen** command or the the **Full screen** tool  at the bottom right corner of the view.

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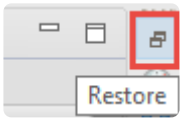
Exit from full-screen mode	Click the **Esc** key, use the **Exit Full Screen** tool ( ) at the bottom of the full-screen view, or press **Ctrl/Cmd+Shift+F**.
Configure the number and location of visible views.	Use the **View > Document Layout** command or the **Change layout** tool (image varies) in the bottom right corner of the view to access possible layouts. The following options are available: • **One** – One – To show only the current view. • **Two Horizontal** (Two Horizontal) – To show the current view on top and one additional view below it. • **Two Vertical** (Two Vertical) – To show the current view on the left, and one additional view to the right. • **Three Horizontal** (Three Horizontal) – To show the current view on top and two additional views below it. • **Three – Left** (Three - Left) – To show the current view on the left and two additional views stacked one on top of the other on the right. • **Three – Right** (Three - Right) – To show the current view on the right and two additional views stacked one on top of the other on the left. • **Three – Top** (Three - Top) – To show the current view on the top and two additional views side-by-side on the bottom. • **Three – Bottom** (Three - Bottom) – To show the current view on the bottom and two additional views side-by-side on the top.
Zoom in or out on a view	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. 
Split a view vertically	Drag the vertical splitter tool ( ), found at the right edge of the view, in a leftward direction. Splits are ignored when exporting an image, although the layout is preserved. To remove a split, drag the divider as far as you can to the right of the view and drop it there.
To view two or	By default, only one session at a time is displayed, even if several sessions are open. To

more sessions simultaneously on a split screen	view two or more sessions simultaneously on a split screen, drag a session tab in a downward, right or left direction. When you see a black arrow, release the mouse button. Sessions can be re-docked in their original positions by reversing this process.
Return to the default window display	Choose **View > Reset Panel Layout**.

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Customize the layout of other window components

Controls for this application's view, panels and expand bars are described in the following table. For information that pertains only to views, also see Customize the appearance and layout of views.

Task	"How To"
Show or open a hidden item	Use the associated **View** menu command, click on a closed expand bar or click the **Restore** icon ().
Show/Hide the side panels	Double-click on the project name to toggle between showing and hiding the side panels on the right of the window.
Display panel sub-sections	Click on a closed expand bar (medium gray bar) or use the associated **View** menu command. If you can't see all the information in an expanded section, close other expanded sections and/or increase the size of the whole panel as described elsewhere in this table.
Hide panel sub-sections	Click on an open expand bar. Alternatively, click the "hamburger menu" ( ) on the right of an expand bar and choose **Collapse All** to close all sections or **Collapse Others** to close all but this section.
Maximize an item	use the **Maximize** icon ( ) .
Change the relative sizes of panes	Drag the divider bar between them to the left, right, up or down.
Hide or close a visible item	Use the **Close** icon ( ) or **Minimize** icon ( ), or click on an open expand bar. To close one or more tabs, right-click on a project, view or panel tab and choose **Close**, **Close Others**, **Close Tabs to Right**, or **Close All**. Some of these options are only available for certain tabs.
Move a view, panel or project to another location	Right-click on the view tab and choose **Move (View Name) to (Location)**. In some cases, you can use your mouse to grab a project, view or panel tab, then drag and drop it in the desired location.
Scroll vertically	Use the vertical scrollbar or the mouse wheel.
Scroll horizontally	Use the horizontal scrollbar, or hold down the **Alt** key (Win) or **Option** key (Mac) and drag the mouse.

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Return to the default side panel layout	Choose **View > Reset Side 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.
Return to the default layout for the entire window	Choose **View > Document Layout > Restore DNASTAR Default Layout**.

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Save a custom layout and apply it to other projects

You can change the layout of GenVision Pro's views and panels as described in Customize the look and layout.

Once you have arrived at a layout you like, you can save it and then apply it to future projects, either by default or only when you specify that it be applied.

Task	How To
Save the current layout to a file that can be applied to future projects	Use **View > Document Layout > Save Layout**.
Save the current layout to a file that will be applied as the default layout for future projects	Use **View > Document Layout > Save Layout as Default**.
Apply a layout that was saved earlier to the current project	Use **View > Document Layout > Apply Layout**.
Restore the DNASTAR default layout to the current project	Use **View > Document Layout > Restore DNASTAR Default Layout**.

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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 a 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.

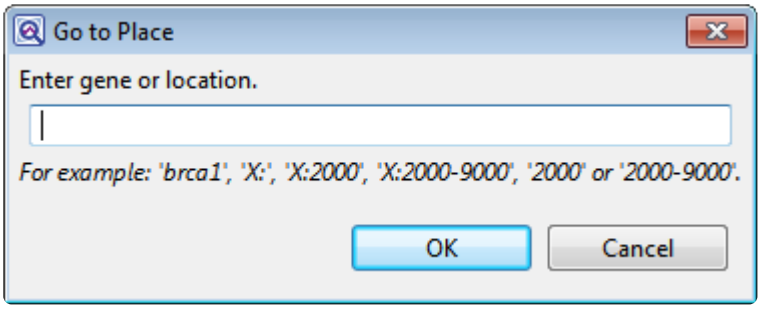
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Find a Location

Navigate to a specific position in the sequence:

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

- Use the navigation tools in the main GenVision Pro header.
- 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.



Navigate to a specific position on the reference sequence:

1. Enable searching in the Overview or Analysis view by pressing the **Search alignment** tool ( ) in the upper right of the view.
2. In the upper left of the same view, choose **Go to reference position** from the **Find** drop-down menu.
3. Type the desired position in the text box to the right of the **Find** menu. Then press either of the green arrows to navigate to the specified location.

The specified reference position will be selected in all views, and the Analysis view will automatically zoom in on that position for a close-up view.

Navigate to features on the reference sequence:

The following procedure allows you to move from feature to feature or gene to gene while zoomed in. If you want to find a specific feature by name, you should instead use the navigation tools in the main GenVision Pro header.

1. Enable searching in the Overview or Analysis view by pressing the **Search alignment** tool ( ) in the

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upper right of the view.

2. In the upper left of the same view, choose **Reference features** from the **Find** drop-down menu. A second drop-down menu appears to the right.

3. In the new drop-down menu, choose from the following search types: **Any enabled type**, **Common search types** (to find RNA, CDS and gene features), **RNA types**, **CDS**, **Gene**, or **Custom**.

4. If you entered **Custom**, enter the search type in the box that opens to the right. Otherwise, go on to the next step.

5. Press either of the green arrows to navigate to the next feature that is upstream or downstream of the current position.

Each time a feature is located, it is selected in all views until you press one of the green arrows again.

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

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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	To expand a selection consisting of one or more features to a selection containing just the sequence corresponding to the feature(s), do any of the following: • 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. • In the Details panel, click on the Action **Select Subsequence**.
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	You can extend the length of an existing selection by **Shift+clicking** on the

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expanded to encompass additional bases	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.

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Rename Assemblies and Tracks

A selected assembly or track can be renamed manually or by using specified data fields. See the following topics for details:

- Create names automatically using specified data fields
- Rename a single sequence manually

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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:

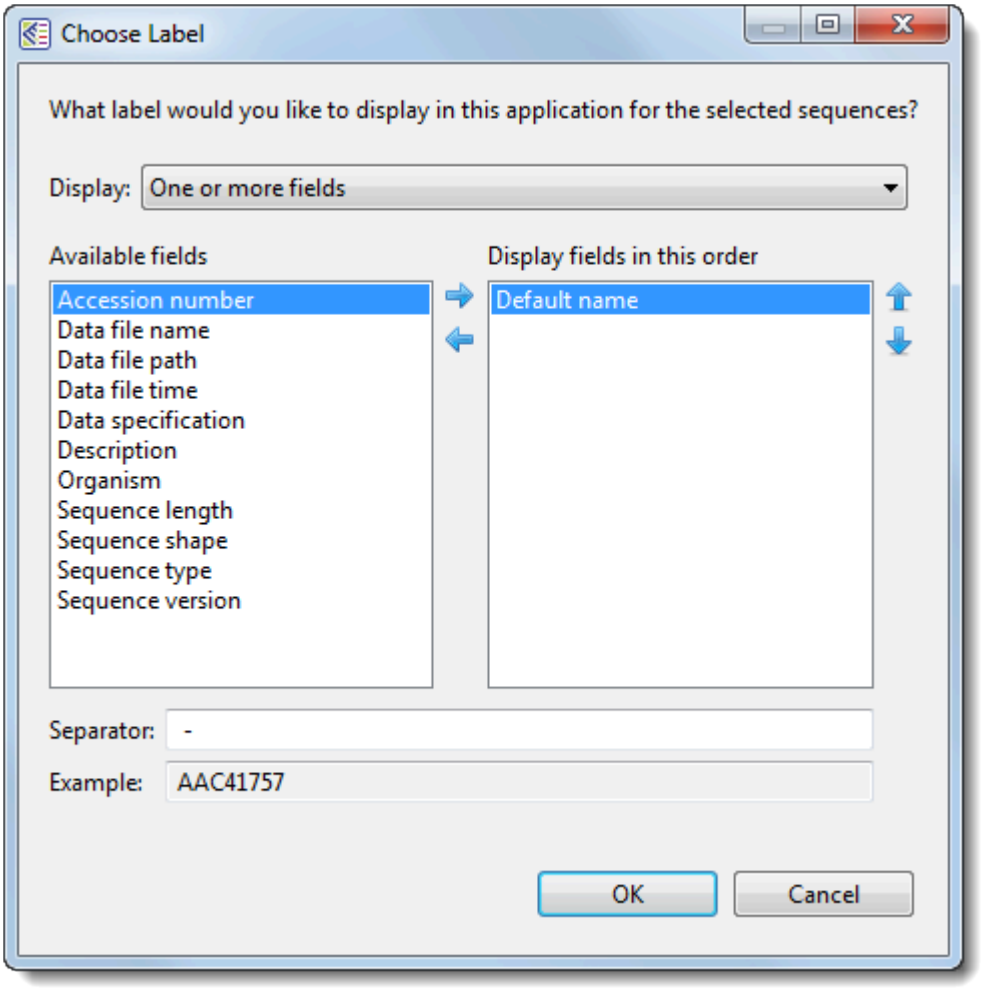
1. Select one or more sequence names from any GenVision Pro view.

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.

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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

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

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Rename a single sequence manually

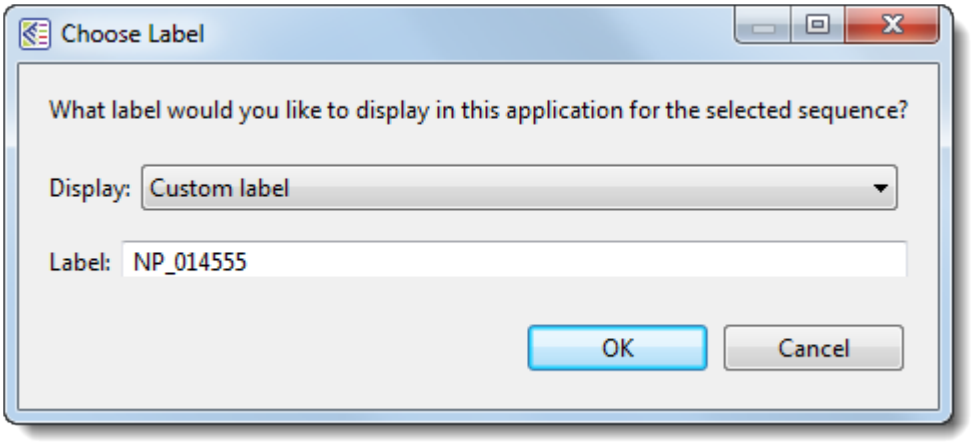
The **Edit > Rename** command lets you manually enter a label (name) to display for those sequences within the GenVision Pro application.

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.

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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.

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Export

For detailed steps on exporting data and images from GenVision Pro, see the following topics:

- Export an image of a view (and edit it in PowerPoint)
- Export data from the Text, Table or Pairwise views
- Export the consensus sequence

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Export an image of a view

GenVision Pro lets you export an image of the Overview or Analysis view for use in a text editor or similar program.

1. Do either of the following:

    - Press the **Export image** tool ( ) in the upper right corner of the view you want to export.

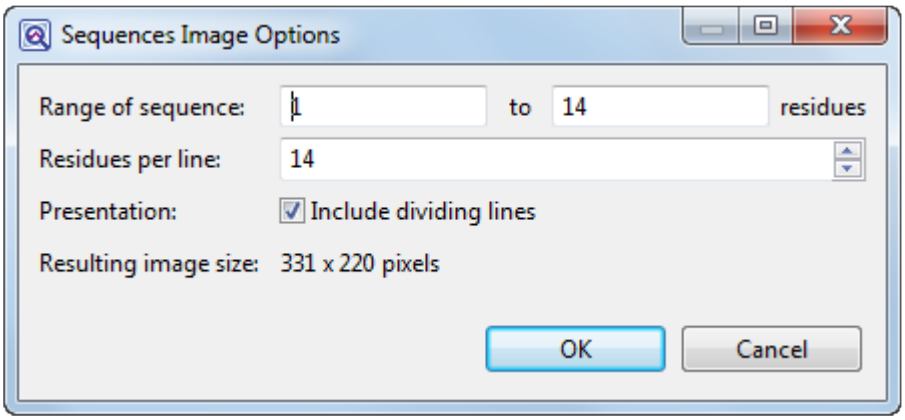
    - Use **File > Export Image > Overview** or **File > Export Image > Analysis**.

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.

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- (“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.

Note: If you saved the image in PowerPoint format, you can edit the image after opening it in PowerPoint. See Edit an exported image in PowerPoint.

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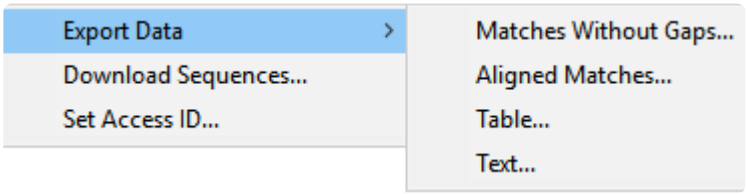
Edit an exported image in PowerPoint

The following video shows how to edit exported images of your alignment or genomic tracks within Microsoft PowerPoint:

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Export data from the Text, Table or Pairwise views

The **Export data** tool ( ), located in the header above the Text, Table or Pairwise views, lets you export data from those views. This tool provides a choice of three options, one of which has four sub-options.



Options include:

- **Export Data >**
    - **Matches without Gaps** – To export an ungapped FASTA (*.fasta*) file consisting of matching regions of displayed matches, but not the query sequence itself.
    - **Aligned Matches** – To export a gapped FASTA (*.fasta*) file with displayed matches aligned against the query.
    - **Table** – To save Table view contents in either Comma- or tab-separated value (*.csv* or *.tab*) formats.
    - **Text** – To save the Text view contents in Text (*.txt*) format.
- **Download Sequences** – To download the selected match sequence in GenBank (*.gbk*) format.

The commands above all launch a Save As dialog. Choose a file name, location and file type (fixed, in some cases) then press **Save**.

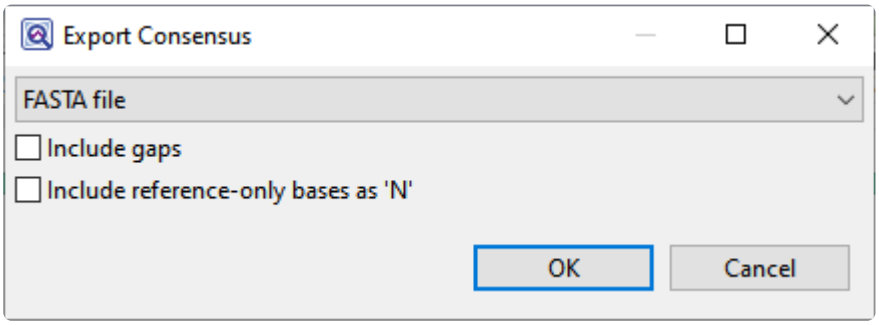
- **Set Access ID** – To launch the Access ID dialog, in which you can specify your NCBI Access ID (optional). See Access ID dialog for information.

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Export the consensus sequence

To export a consensus sequence:

1. From the Tracks panel, check the boxes pertaining to read tracks.
2. In the Analysis view, select a read track. A toolbar pops up at the track's top left corner.
3. Click the **Export data** tool ( ). The Export Consensus popup dialog appears.



   a. Use the drop-down menu to choose from **FASTA file**, **GenBank file** or **Lasergene DNA file** formats.

   b. If you wish to preserve gaps in the consensus, add a checkmark next to **Include gaps**.

   c. If you wish to include bases that were only found in the reference sequence and not in any read sequences, add a checkmark next to **Include reference-only bases as 'N'**.

   d. Press **OK**.

4. When the consensus export is complete, you will see a hyperlink for it in the **Status** column of the Jobs panel. Click the link to download the sequence to your computer.

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

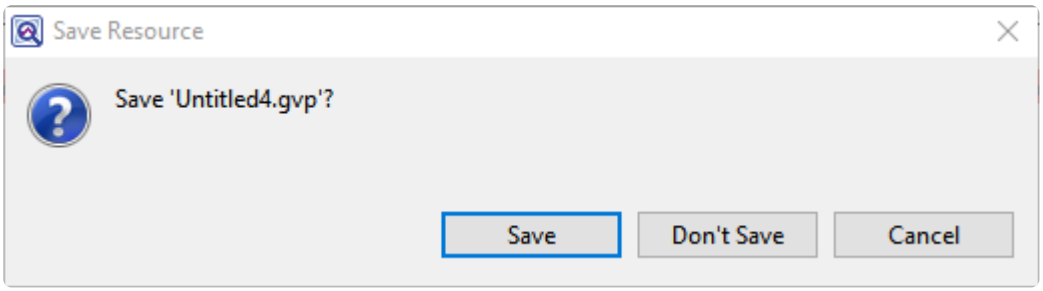
To quit the application:

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

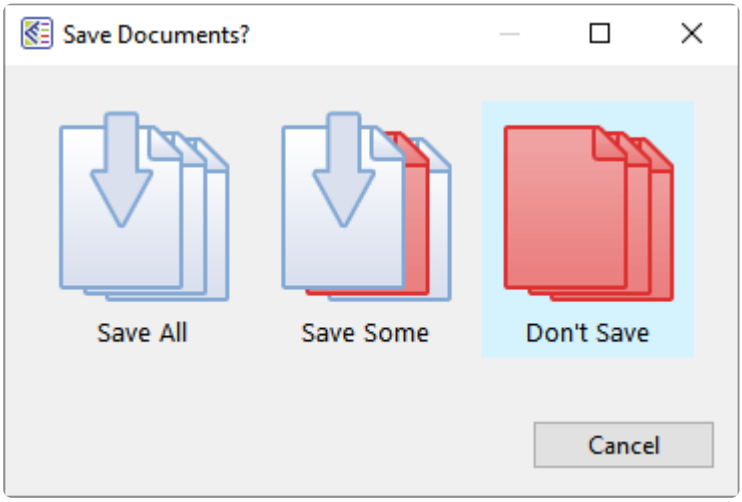
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Closing or quitting when there are unsaved sessions:

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 **Save** to save changes, **Don't Save** to close/quit without saving changes, or **Cancel** to return to GenVision Pro without closing/quitting.



If you select **File > Close**, or if you quit GenVision Pro when multiple unsaved sessions are open, GenVision Pro will open the Save Documents dialog.



To save all changed projects, choose **Save All**. To choose which projects to save, choose **Save Some**. To exit from GenVision Pro without saving any sessions, choose **Don't Save**. Click **Cancel** to return to GenVision Pro without saving the sessions.

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Appendix

The Appendix contains the following topics:

- View a list of supported file types
- Set preferences 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

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Supported file types

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

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Set preferences

To open the Set Preferences dialog on Macintosh, choose **GenVision Pro > Preferences**. On Windows, choose **Edit > Preferences**.

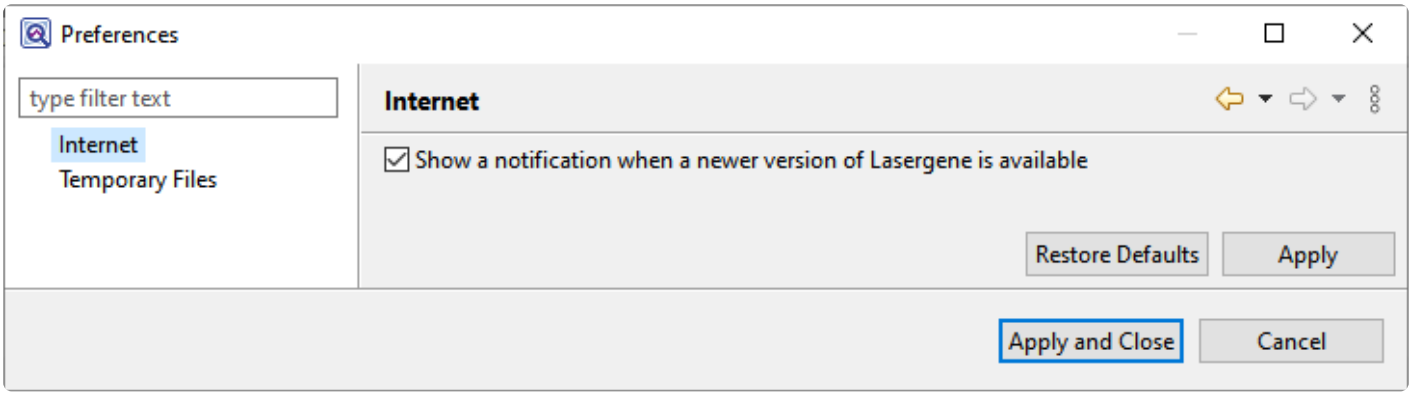
You can set preferences in GenVision Pro for Internet, and temporary files.

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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.

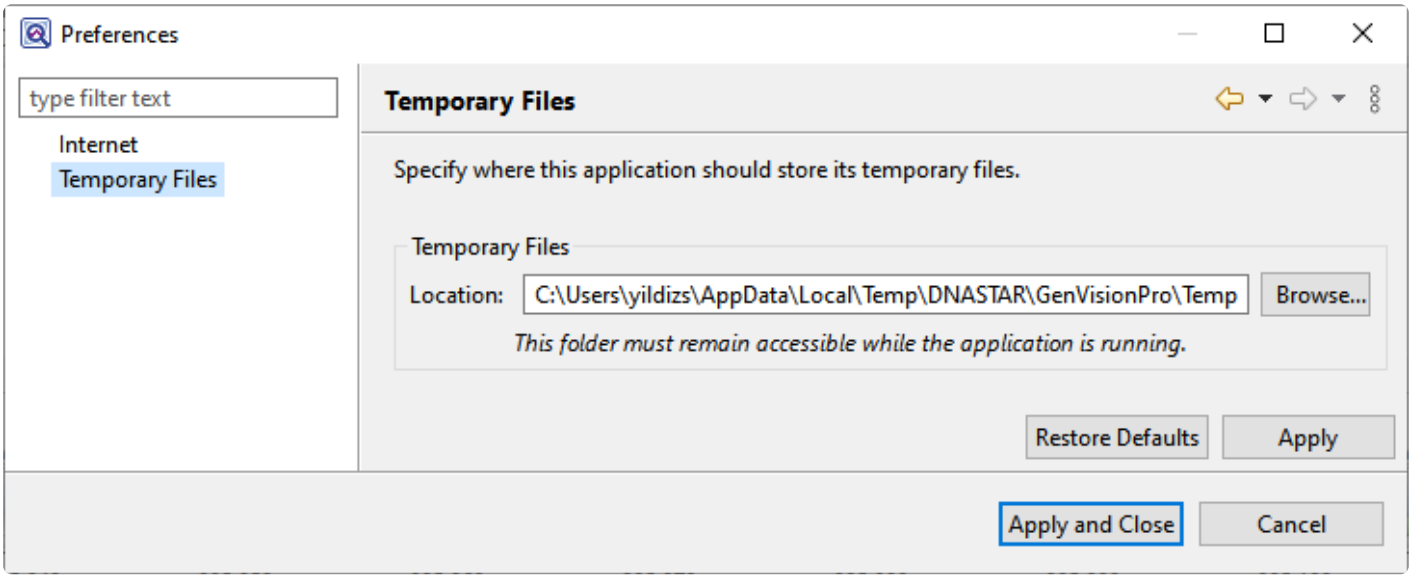
Click **Apply** and **OK** to save your changes or **Cancel** to ignore any changes. Click **Restore Defaults** to return to the default settings for all four drop-down menus.

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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 **GenVision 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.

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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

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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.

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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] (*DMx, DMx.exe)*	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

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Server License File (*lservrc*), Server License Manager [2], *Server Executables (_lserv, lservnt.exe*)	All	Windows: C:\Program Files (x86)\DNASTAR-LicenseServer\Server Macintosh: ~/Library/DNASTAR-LicenseServer
Standalone & Trial Licenses (**.license)*, License Server Client License (**.lshost)*, Key Server Client License (**.keyhost*)	All	Windows: C:\Program Data\DNASTAR\Licenses 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**.

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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**.

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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.

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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

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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]

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