Transitioning from:

- EditSeq to SeqBuilder Pro
- PrimerSelect to SeqBuilder Pro
- MegAlign to MegAlign Pro
- SeqMan Pro to SeqMan Ultra

DNASTAR, Inc. 2020

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Why switch from the applications I currently use?

Why switch from the applications I currently use?

If you are a long-time user of DNASTAR software, you may be wondering why you need to make the switch to our newer applications, SeqBuilder Pro, MegAlign Pro and SeqMan Ultra.

Some of our 32-bit applications—EditSeq, PrimerSelect and MegAlign—were retired with the release of Lasergene 16.0 in mid-2019. Since then, all development efforts and new features related to sequence editing, primer design, and cloning are being focused exclusively on SeqBuilder Pro, while pairwise & multiple sequence alignment efforts are being focused on MegAlign Pro. With the release of Lasergene 17.0 in early, 2020, we replaced 32-bit SeqMan Pro with SeqMan Ultra, which features a modern, intuitive interface. For now, we are including both applications, but will be removing SeqMan Pro in a future release.

All three of the newer applications contain numerous features not found in their classic counterparts, and provide an improved user experience and many new capabilities compared to EditSeq, PrimerSelect, MegAlign and SeqMan Pro.

Try the new apps for yourself online. No download necessary!	Upgrade now to access powerful new functionality
Free Trial	Request a Quote

Why a special guide just for transitioning between applications?

During our preparations to retire three 1990's applications with the Lasergene 16.0 release in 2019, we realized that a substantial number of Lasergene users were still using legacy versions of our applications, despite having had 6 to 14 years in which to switch to their replacements. Are you one of these loyal "classic app" fans? If you haven't yet made the switch, you are in for a treat! Lasergene's modern apps feature sleek, intuitive and customizable interfaces and a whole new world of time-saving functionality. Click the following links to learn how to transition from:

- EditSeq to SeqBuilder Pro
- PrimerSelect to SeqBuilder Pro
- MegAlign to MegAlign Pro
- SeqMan Pro to SeqMan Ultra

About this User Guide:

- For help **INSTALLING** Lasergene, see our separate Installation Guide.
- 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**.

New functionality in SeqBuilder Pro, MegAlign Pro and SeqMan Ultra

Click the bullet-pointed links below to learn about added or improved functionality in the modern application compared to the “classic” versions. These links will take you away from this “Transitioning” guide to the relevant User Guide topic for SeqBuilder Pro or MegAlign Pro.

> **Note:** For illustrated help showing how to perform your current EditSeq, PrimerSelect, MegAlign or SeqMan Pro tasks in the newer applications, see the following topics in this guide: Transitioning from EditSeq to SeqBuilder Pro / PrimerSelect to SeqBuilder Pro / MegAlign to MegAlign Pro or SeqMan Pro to SeqMan Ultra.

SeqBuilder Pro lets you:

- Create a new sequence based on an existing sequence; among others, by using the reverse complement, translation, or a feature, by sampling sequences* Perform virtual cloning
- Auto-annotate sequences with or without first creating a custom feature database
- Easily edit primers by using a mutation/codon change tool, by typing or by changing the primer length
- Customize the appearance of features
- Display the translation of a sequence below the original sequence
- Easily change the appearance of views and the layout of views and panels
- Change the rendering style and font
- Easily create, modify and join features, and show or hide features in the views
- Perform highly customizable agarose gel simulations
- Export a sequence in many different formats

MegAlign Pro lets you:

- Perform multiple alignments using the Clustal Omega, Clustal W, MAFFT or MUSCLE algorithms
- Perform genome-level multiple alignments with Mauve
- Perform pairwise alignments using the Smith-Waterman algorithm, or either of two variations of the Needleman-Wunsch algorithm; then easily perform subsequent pairwise alignments using different parameters or a different combination of sequences.
- Rename a single sequence manually, or one or more sequences automatically, using a customized naming convention
- Analyze results in several graphic-rich views, and customize the view layout
- View details about any selection: one or more sequences, a portion of one or more sequences, one or more tracks or features, or a portion of a pairwise alignment
- Apply detail for rulers, features, a translation, a consensus, the sequence logo, GC content or gap fraction histograms and many more.

- Bookmark a sequence location or range of interest, so you can easily return to it later
- Export data, a phylogenetic tree, or an image of a view

SeqMan Ultra lets you:

- Seamlessly access SeqMan NGen, where you can create and build your assembly.
- Open finished assemblies for downstream analysis
- View information about the currently open assembly or about any selection.
- Work with contigs by organizing them into scaffolds, closing gaps between them and seeing contig information in graphical or tabular views.
- Apply data tracks that provide enhanced information about the contig, consensus and reads.
- View features in graphical, tabular or text format and filter features.
- View, filter and score variants.
- Search for sequences online in NCBI's BLAST and Entrez databases.
- Customize the appearance and behavior of views, tables and the layout itself
- Export the consensus or data from a view.

Timeline for “classic” and modern applications

The following timeline shows the release dates of the “classic” Lasergene applications and their modern counterparts:

- **1988** – **EditSeq** was DNASTAR’s original application for creating and editing sequences and their features.
- **1993** – **PrimerSelect** was DNASTAR’s original application for primer design and primer catalog creation, while **MegAlign** offered pairwise and multiple sequence alignment and the creation of phylogenetic trees.
- **2001** – With increasing popularity of the Internet, **PrimerSelect**, **MegAlign** and **EditSeq** were upgraded to allow searching of NCBI’s BLAST and Entrez databases.
- **2005** – **SeqBuilder** was added to the Lasergene software offering for virtual cloning, PCR primer design, plasmid map creation, and sequence editing.
- **2013** – **MegAlign Pro** was released with Lasergene 11.0 for multiple sequence alignments and visualization.
- **2017** – **SeqBuilder Pro** was released with Lasergene 15.0 and **SeqBuilder** was retired. SeqBuilder Pro featured a beautiful new interface and supported additional cloning methods and agarose gel simulation. To smooth the transition from **EditSeq** and **PrimerSelect**, **SeqBuilder Pro** even featured a button that users could press to make the interface resemble their favorite classic applications.
- **2018** – Pairwise alignment functionality was added to **MegAlign Pro**.
- **2019** – With the release of Lasergene 16.0 in June, **EditSeq**, **PrimerSelect** and **MegAlign** were retired.
- **2020** – With the release of Lasergene 17.0 in February, **SeqMan Ultra** was introduced as a replacement for SeqMan Pro. SeqMan Pro will remain in the package temporarily, but will be removed in a later release.

Transitioning from EditSeq to SeqBuilder Pro

As of Lasergene 16.0, SeqBuilder Pro completely replaced EditSeq. Compared to its co-predecessor, EditSeq, SeqBuilder Pro features a modern, colorful user interface and greatly increased functionality.

This short video is an overview of the SeqBuilder Pro application:

For an illustrated comparison showing how to perform an EditSeq task in SeqBuilder Pro, click any of the links below:

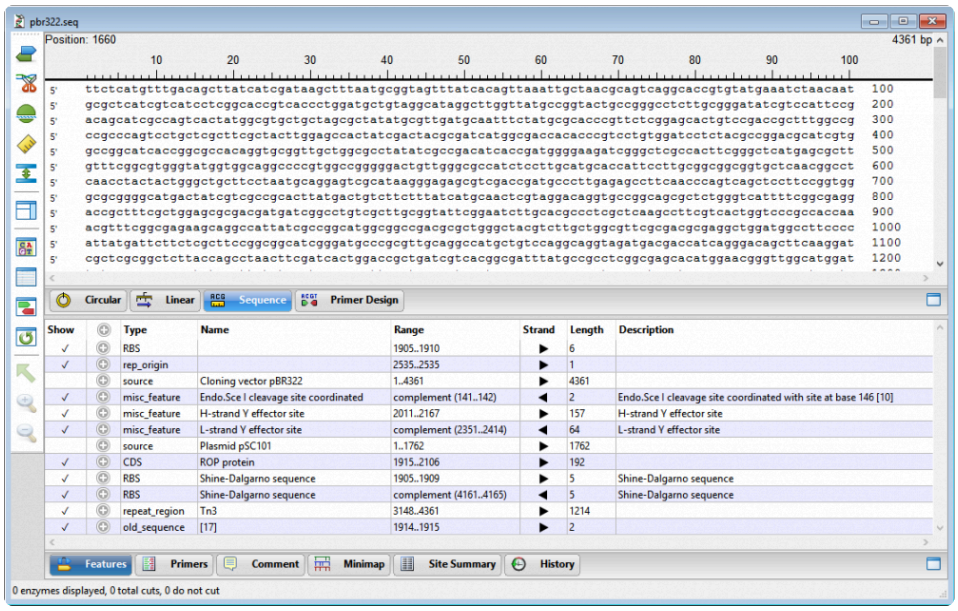
- Edit a sequence
- Trim sequence ends
- Translate a nucleotide sequence
    - Select and edit a genetic code
- Back translate a protein sequence
- Display a sequence and its translation simultaneously
- View sequence statistics
- Work with features
- Save or export a sequence

Make SeqBuilder Pro resemble EditSeq

To make the SeqBuilder Pro layout look similar to EditSeq, press the **Compact EditSeq Layout** tool on the left of SeqBuilder Pro's document window. SeqBuilder Pro will display the Sequence view in the upper half of the Document window, without spacers or rulers, and the Features view in the lower half.

EditSeq application layout:

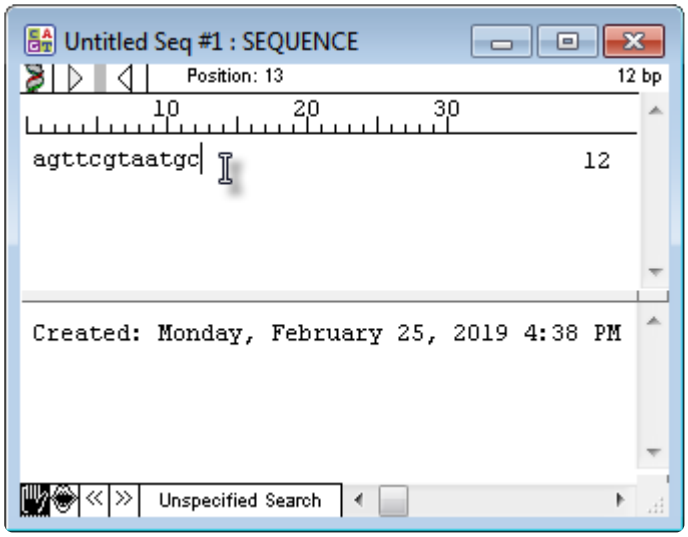
SeqBuilder Pro application using **Compact EditSeq Layout** tool:



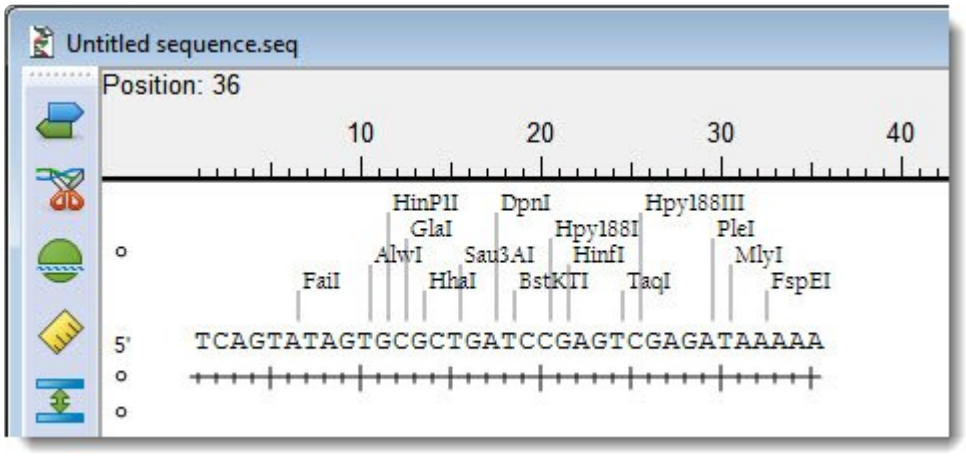
Edit a sequence

To edit a sequence:

- **EditSeq** – Paste or type IUPAC characters into the sequence pane. To delete characters, use the **Backspace** or **Delete** keys.



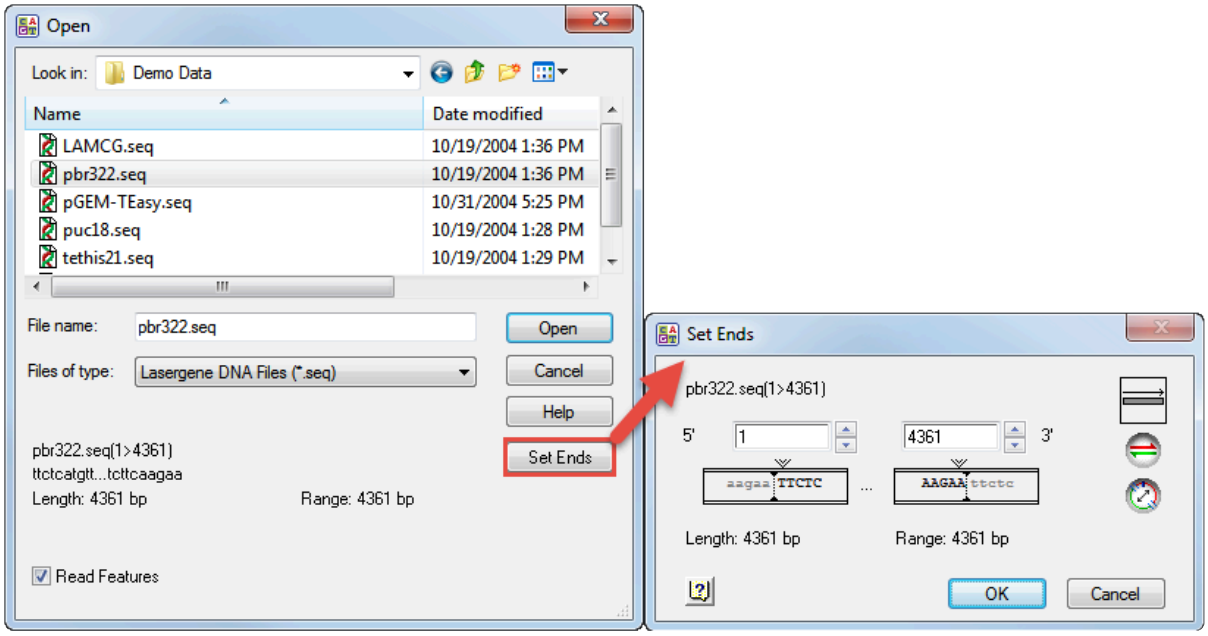
- **SeqBuilder Pro** – Paste or type IUPAC characters into the Sequence view. To delete characters, use the **Backspace** or **Delete** keys. For more information, see the SeqBuilder Pro User Guide topic Use editing commands.



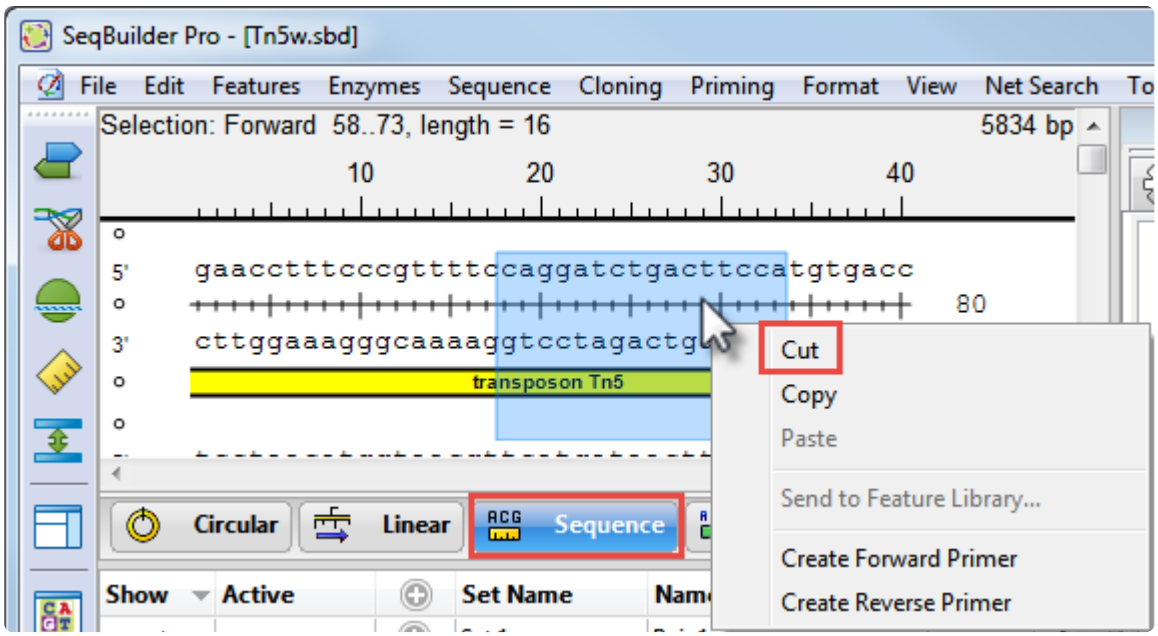
Trim sequence ends

To trim sequence ends:

- **EditSeq** – Use **File > Open** and press the **Set Ends** button, then specify cut points in that dialog.



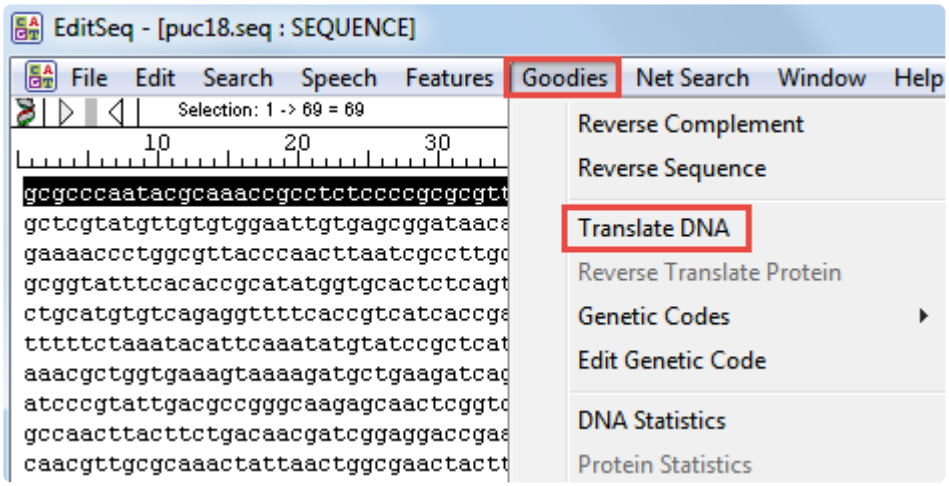
- **SeqBuilder Pro** – Select a portion of an already-open sequence in the the Circular, Linear or Sequence views and use **Edit > Cut**; or right-click on the selection and choose **Cut**. For more information, see the SeqBuilder Pro User Guide topic Use editing commands.



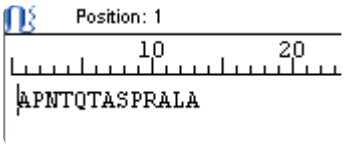
Translate a nucleotide sequence

To create a new document containing the translation of a selected portion of DNA/RNA sequence:

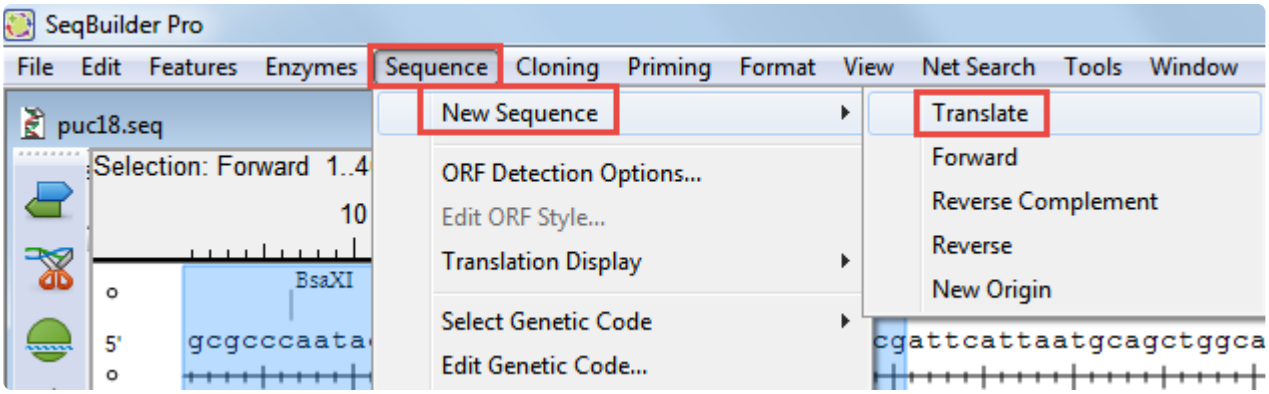
- **EditSeq** – Use **Goodies > Translate DNA**.



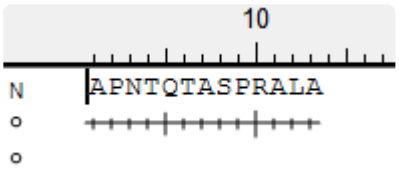
The new document looks like this:



- **SeqBuilder Pro** – Use **Sequence > New Sequence > Translate**. For more information, see the SeqBuilder Pro User Guide topic Create a sequence based on another sequence.



The new document looks like this:



Select and edit a genetic code

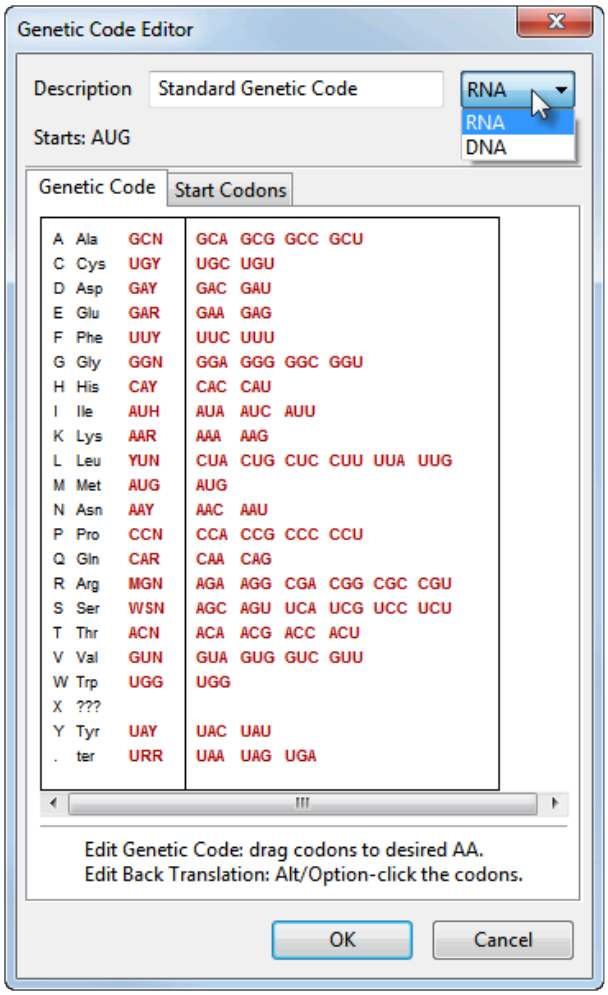
To select a genetic code:

- **EditSeq** – Use **Goodies > Genetic Codes** and choose a code from the list.
- **SeqBuilder Pro** – Use **Sequence > Select Genetic Code** and choose a code from the list. For more information, see the SeqBuilder Pro User Guide topic Choose the genetic code.

To edit a genetic code:

- **EditSeq** – Use **Goodies > Edit Genetic Code**.
- **SeqBuilder Pro** – Use **Sequence > Edit Genetic Code**. For more information, see the SeqBuilder Pro User Guide topic Modify the genetic code.

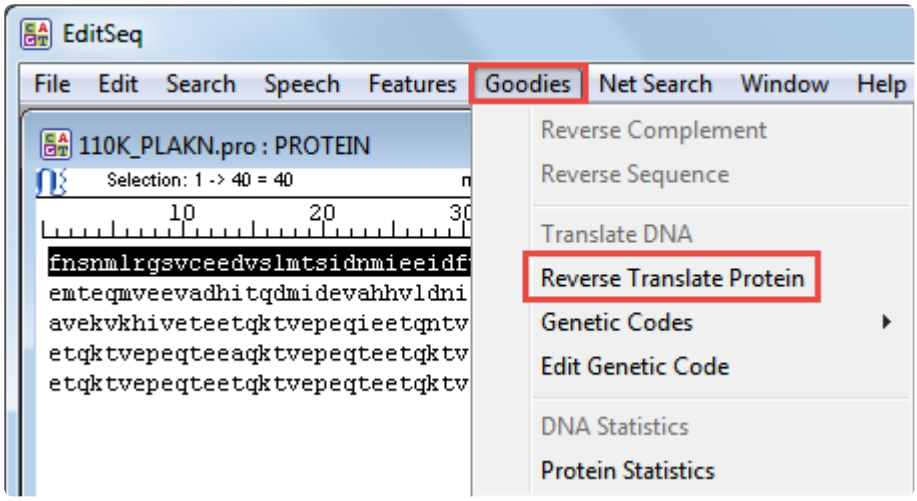
Though the command is in a different menu, the genetic code editor is the same for both applications.



Back translate a protein sequence

To create a new document containing the back translation of a selected portion of protein sequence:

- **EditSeq** – Use **Goodies > Reverse Translate Protein**.



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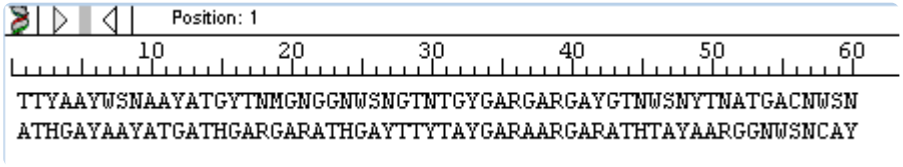
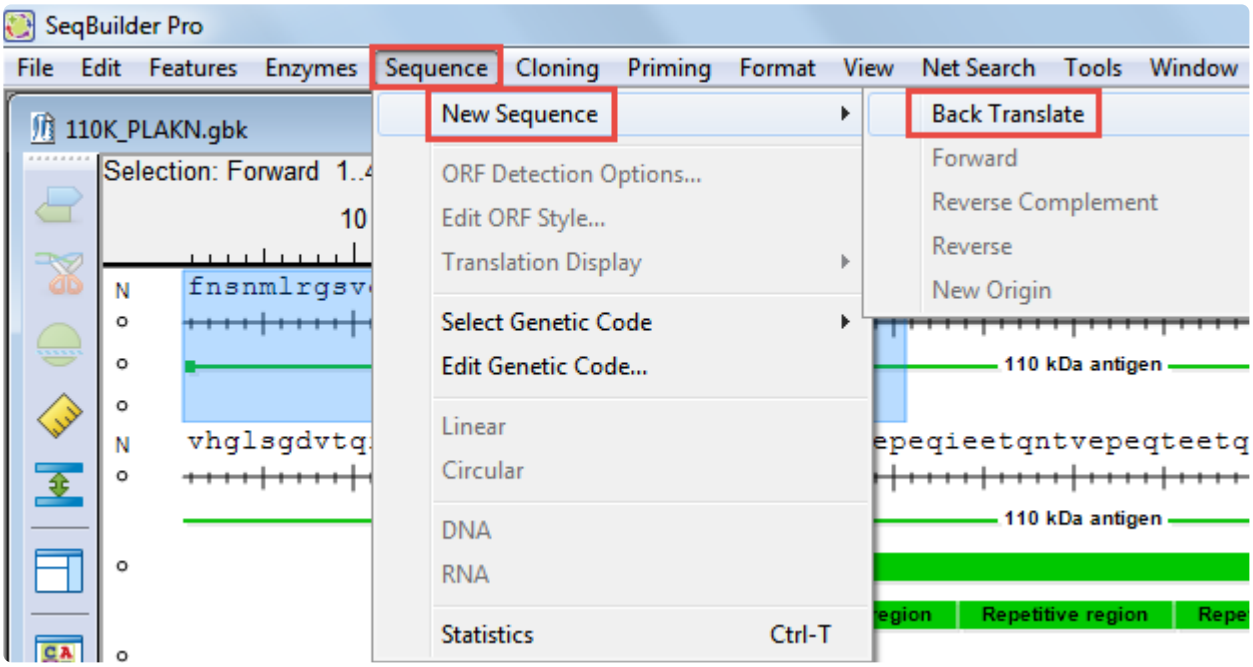
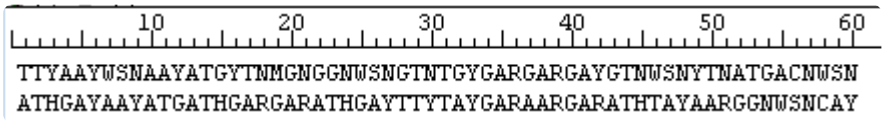


- **SeqBuilder Pro** – Use **Sequence > New Sequence > Back Translate**. For details, see the SeqBuilder Pro User Guide topic Create a sequence based on another sequence.



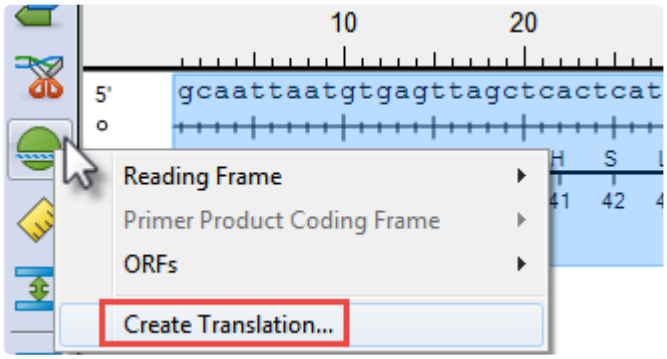
The new document looks like this:



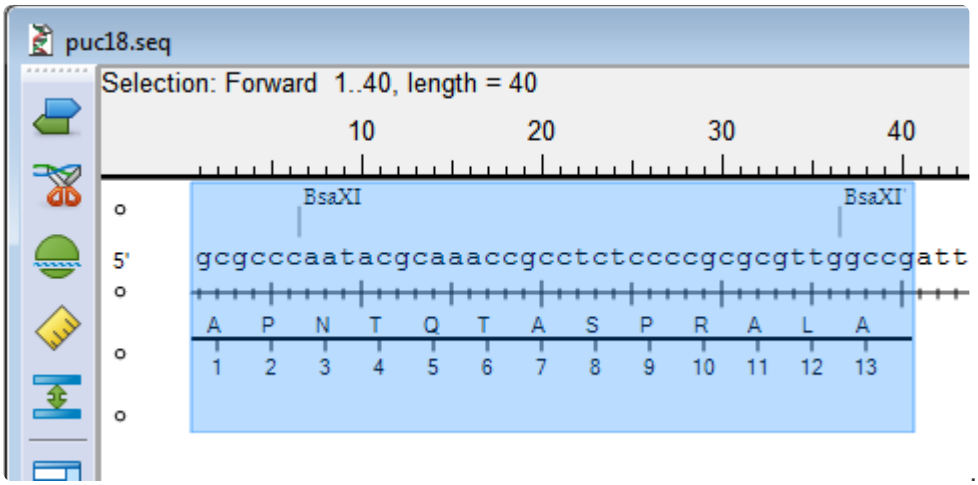
Display a sequence and its translation simultaneously

To display the translation below the nucleotide sequence:

- **EditSeq** – Not available.
- **SeqBuilder Pro** – Select part or all of the sequence, click on the **Translations and ORFs** ( ) tool and choose **Create Translation**. For more information, see the SeqBuilder Pro User Guide topic Translations.



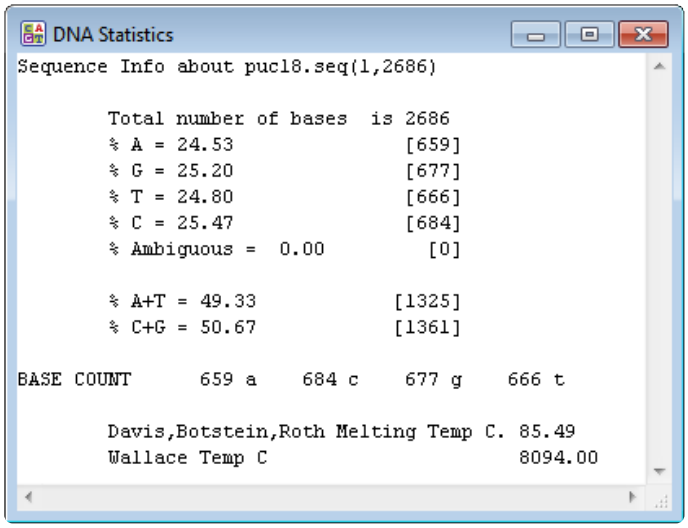
The translation appears below the DNA/RNA sequence.

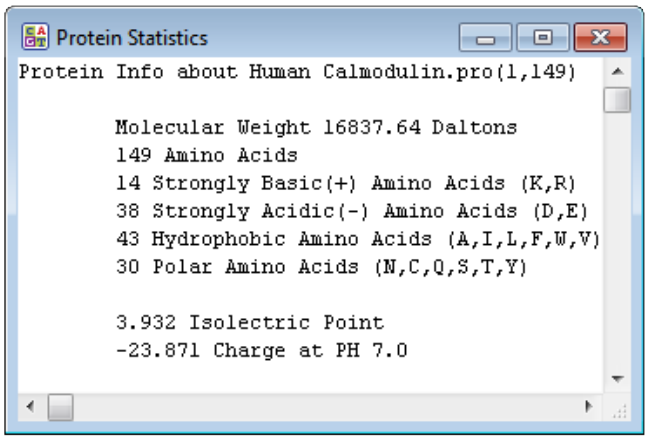


View sequence statistics

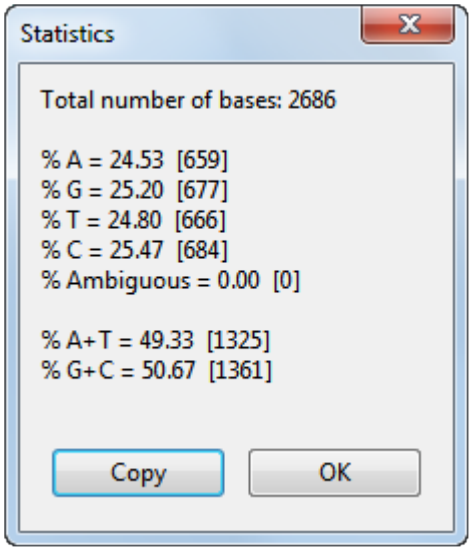
To view sequence statistics:

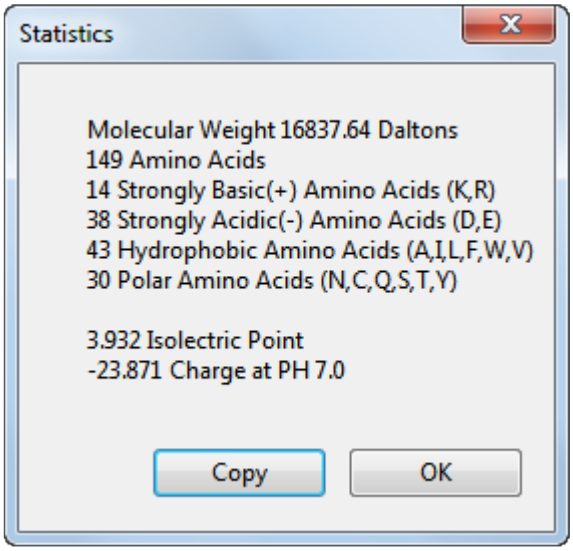
- **EditSeq** – Use **Goodies > DNA Statistics** or **Goodies > Protein Statistics**.





- **SeqBuilder Pro** – Use **Sequence > Statistics**. For more information, see the SeqBuilder Pro User Guide topic Sequence Statistic.

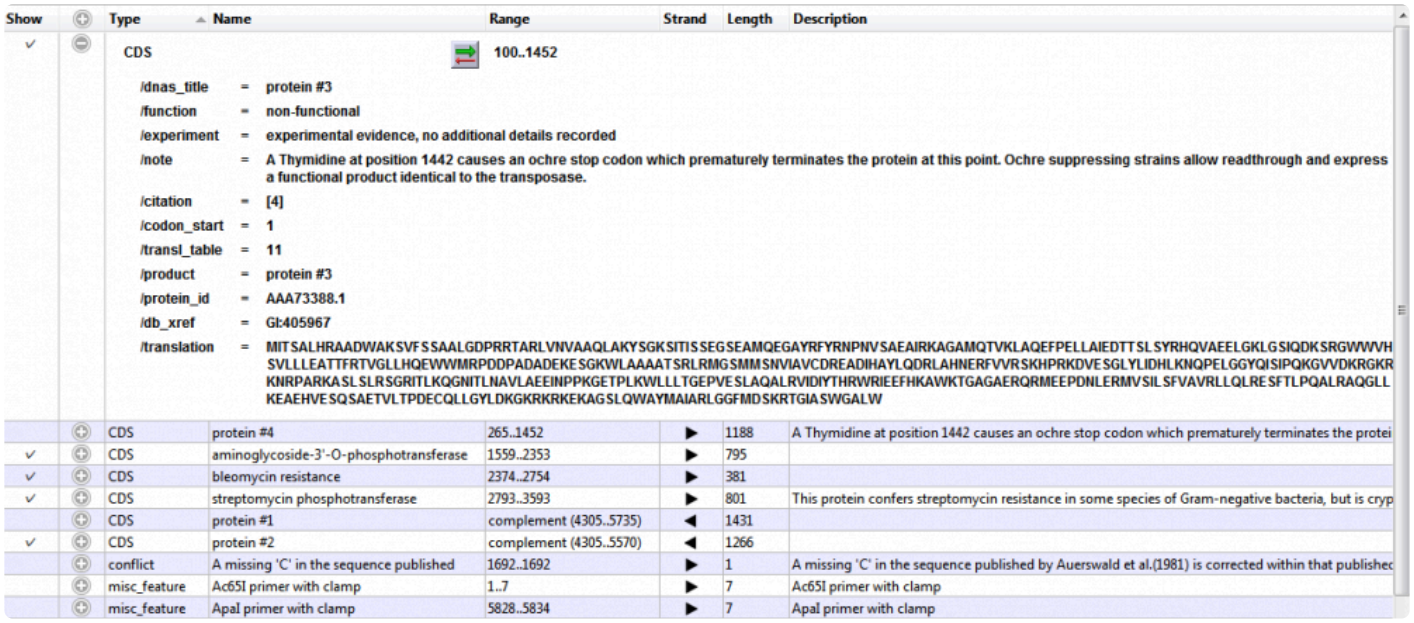




Work with features

Many feature-related commands are the same in EditSeq and SeqBuilder Pro, including **Features > New Feature**, **Features > New Feature with Translation**, and **Features > New Translation**. The EditSeq command **Features > Join Segment** changes to **Features > Join to Feature** in SeqBuilder Pro, but functions identically.

However, SeqBuilder Pro's "Features" view offers feature-related functionality that is not available in EditSeq. For instance, you can reverse the strand the feature is on, add and edit qualifier fields, change the lengths of segments or features, select text to use as the feature name, and much more. For details, see the SeqBuilder Pro User Guide topic Edit information about a feature.



Show		Type	Name	Range	Strand	Length	Description
✓	⊖	CDS		100..1452			
		/dnas_title = protein #3					
		/function = non-functional					
		/experiment = experimental evidence, no additional details recorded					
		/note = A Thymidine at position 1442 causes an ochre stop codon which prematurely terminates the protein at this point. Ochre suppressing strains allow readthrough and express a functional product identical to the transposase.					
		/citation = [4]					
		/codon_start = 1					
		/transl_table = 11					
		/product = protein #3					
		/protein_id = AAA73388.1					
		/db_xref = GI:405967					
		/translation = MITSALHRAADWAKSVFSSAALGDPRRTARLVNVAAQLAKYSGKSITISSEGSEAMQEGAYRFYRNPNVSAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVH SVLLLEATTFRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDRLAHNERFVVRSKHPRKDVESGLYLIDHLKNQPELGGYQISIPQKGVVDKRGKR KNRPARKASLSLRSGRITLKQGNITLNAVLAEEINPPKGETPLKWLLLTGEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLL KEAEHVESQSAETVLTPDECQLLGYLDKGKRKRKEKAGSLQWAYMAIARLGGFMDSKRTGIASWGALW					
	⊕	CDS	protein #4	265..1452	▶	1188	A Thymidine at position 1442 causes an ochre stop codon which prematurely terminates the protei
✓	⊕	CDS	aminoglycoside-3'-O-phosphotransferase	1559..2353	▶	795	
✓	⊕	CDS	bleomycin resistance	2374..2754	▶	381	
✓	⊕	CDS	streptomycin phosphotransferase	2793..3593	▶	801	This protein confers streptomycin resistance in some species of Gram-negative bacteria, but is cryp
	⊕	CDS	protein #1	complement (4305..5735)	◀	1431	
✓	⊕	CDS	protein #2	complement (4305..5570)	◀	1266	
	⊕	conflict	A missing 'C' in the sequence published	1692..1692	▶	1	A missing 'C' in the sequence published by Auerswald et al.(1981) is corrected within that publishec
	⊕	misc_feature	Ac65I primer with clamp	1..7	▶	7	Ac65I primer with clamp
	⊕	misc_feature	ApaI primer with clamp	5828..5834	▶	7	ApaI primer with clamp

Save or export a sequence

To save or export a sequence:

- **EditSeq** offers the following options:
  - To save in Lasergene (*.seq* or *.pro*) file format, use **File > Save As**.
  - To export to Genbank (*.gbk*), FASTA (*.fas*) , or GCG (*.gcg*) file formats, use **File > Export** .
  - To export multiple sequences into a single file with a Genbank (*.gbk*), FASTA (*.fas* or *.fap*) , or DNA Multiseq (*.mseq*) file format, use **File > Export all as one**.
- **SeqBuilder Pro** offers the following options:
  - To save in SeqBuilder Pro (*.sbd*), Lasergene (*.seq* or *.pro*), GenBank (*.gbk*), FASTA (*.fas* or *.fap*), ABI (*.abi*) or EMBL (*.embl*) file formats, use **File > Save As**. For details, see the SeqBuilder Pro User Guide topic Save.
  - To export sequences in *.sbd*, *.seq*, *.gbk*, *.embl*, or *.fas*. formats, use **File > Export Sequence(s) From Project**. For details, see Export sequences to a file.
  - To export sequences to GenVision (*.gnv*) format, use **File > Export As GenVision Project**. For details, see Export sequences to GenVision.

Transitioning from PrimerSelect to SeqBuilder Pro

As of Lasergene 16.0, SeqBuilder Pro completely replaced PrimerSelect. Compared to its co-predecessor, PrimerSelect, SeqBuilder Pro features a modern, colorful user interface and greatly increased functionality.

This short video is an overview of the SeqBuilder Pro application:

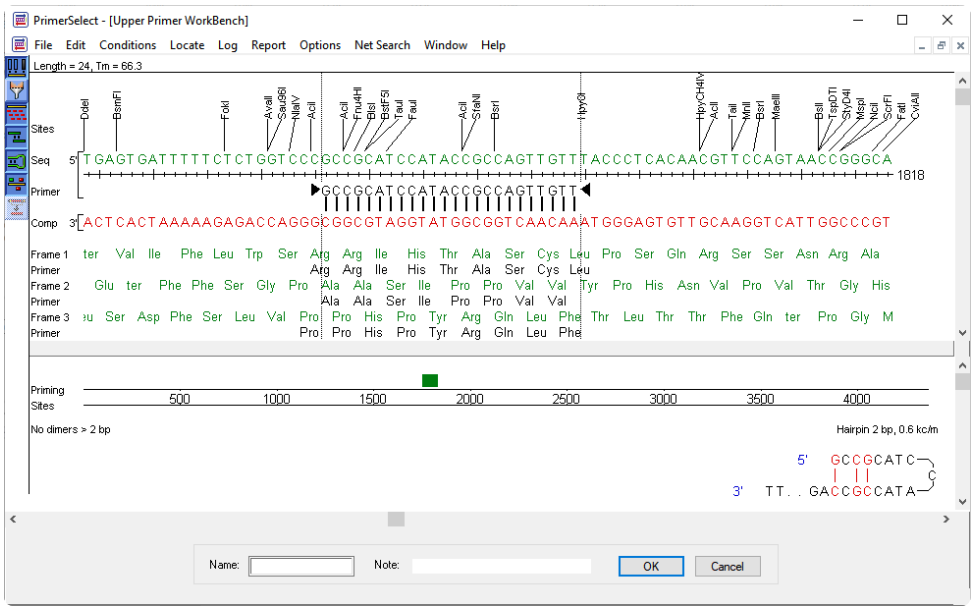
For an illustrated comparison showing how to perform an PrimerSelect task in SeqBuilder Pro, click any of the links below:

- Trim sequence ends
- Locate primers
- View dimers, pair dimers and hairpins
- View general primer statistics
- View information on primer composition and amplfication
- Edit primers
- Import primers from a catalog
- Nominate new primers to a catalog
- Save a primer catalog
- Select and edit a genetic code

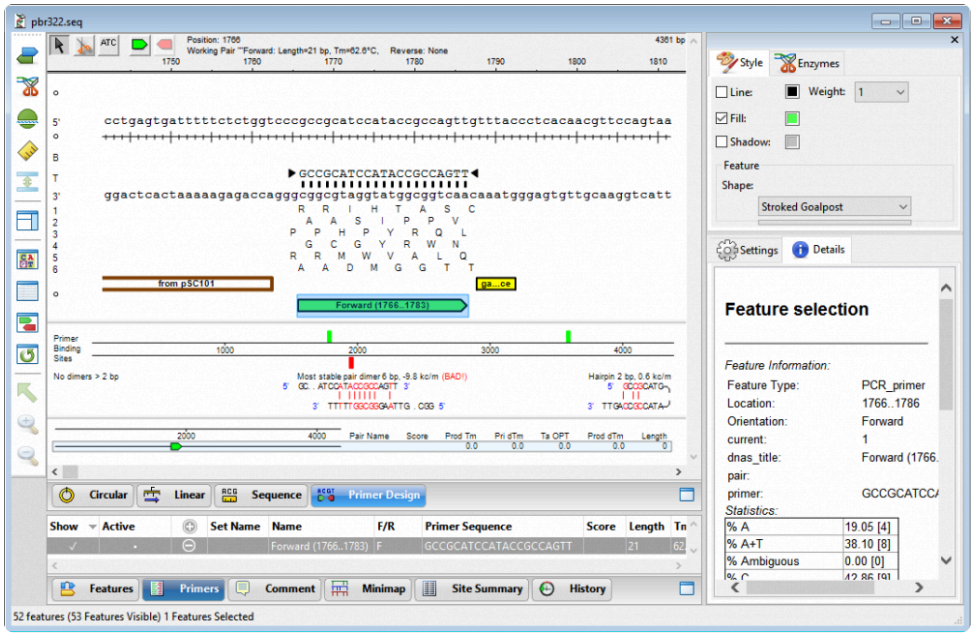
Make SeqBuilder Pro resemble PrimerSelect

To make the SeqBuilder Pro layout look similar to PrimerSelect, press the **Primer Design Layout** tool on the left of SeqBuilder Pro's document window. SeqBuilder Pro will display the Primer Design view in the upper half of the Document window, and the Primers view in the lower half.

PrimerSelect application layout:



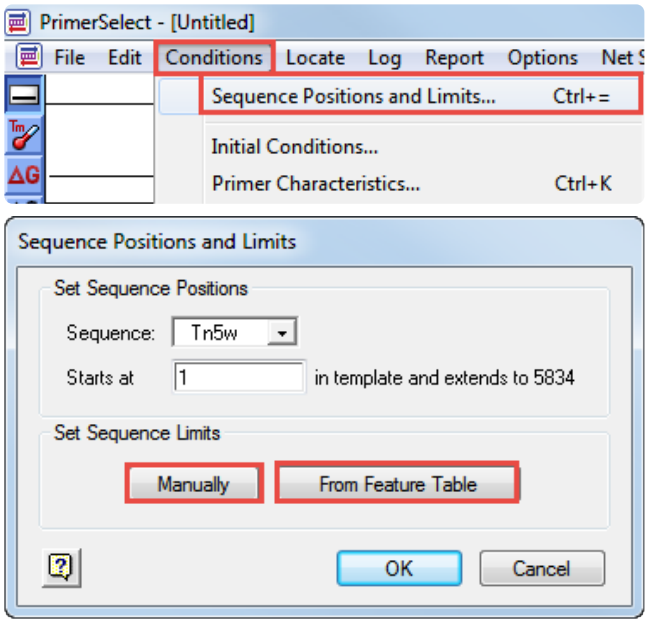
SeqBuilder Pro application using **Primer Design Layout** tool:



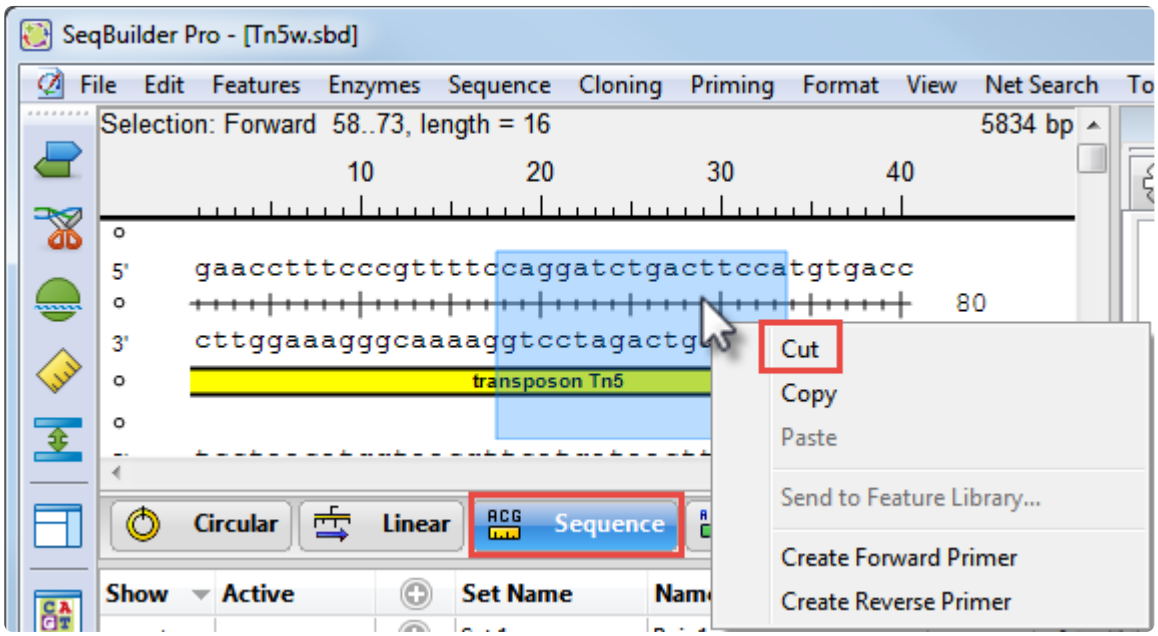
Trim sequence ends

To trim sequence ends:

- **PrimerSelect** – Use **Conditions > Sequence Positions and Limits**. In the dialog box, choose either **Manually** or **From Feature Table** to open another dialog in which you can specify the cut points.



- **SeqBuilder Pro** – Select a portion of an already-open sequence in the the Circular, Linear or Sequence views and use **Edit > Cut**; or right-click on the selection and choose **Cut**. For more information, see the SeqBuilder Pro User Guide topic Use editing commands.

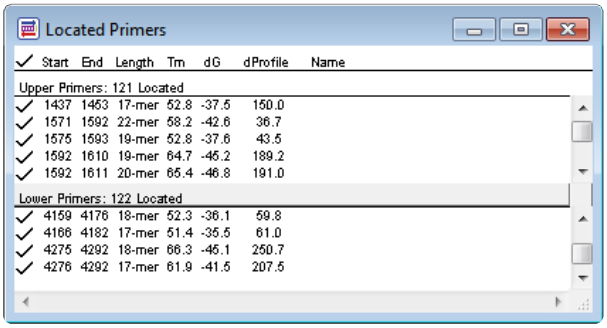


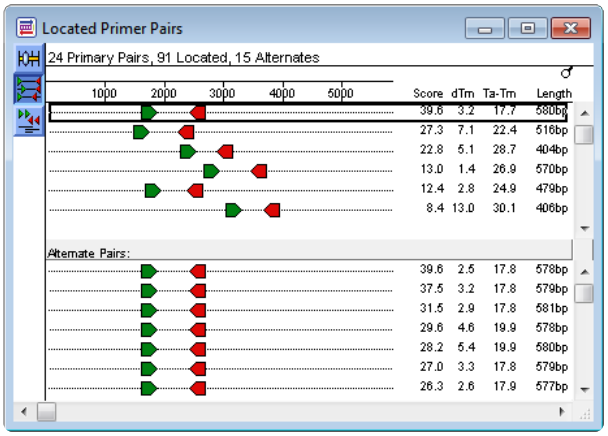
Locate primers

To locate primer pairs automatically:

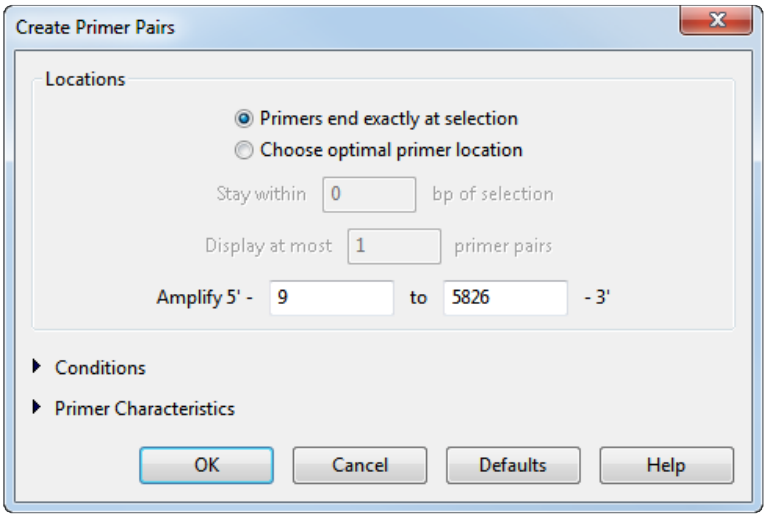
Both the classic and modern applications provide multiple ways to find primers, but there are subtle differences between the commands. The images show the results of using each command when the same sequence feature is selected in each of the applications. A short video is available at the bottom of this topic.

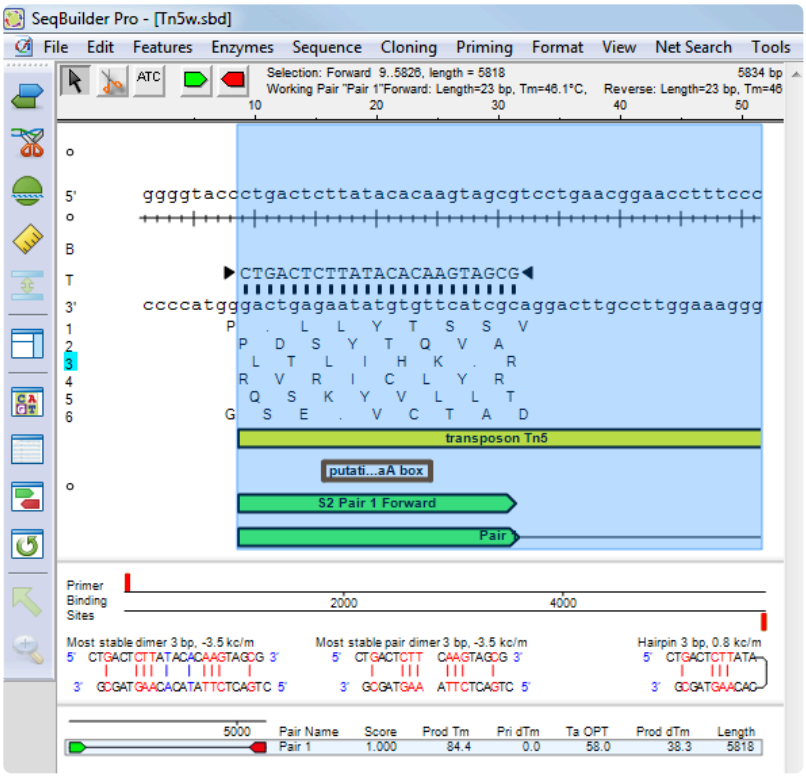
- **PrimerSelect** – To search both template strands for primers or probe sequences meeting specified conditions, use **Locate > Primers & Probes** (left image). To limit the search to only primers contained with the “primer catalog,” use **Locate > Only Catalogued Primers**. To search for compatible pairs required for PCR amplification, use **Locate > PCR Primer Pairs** (right image).



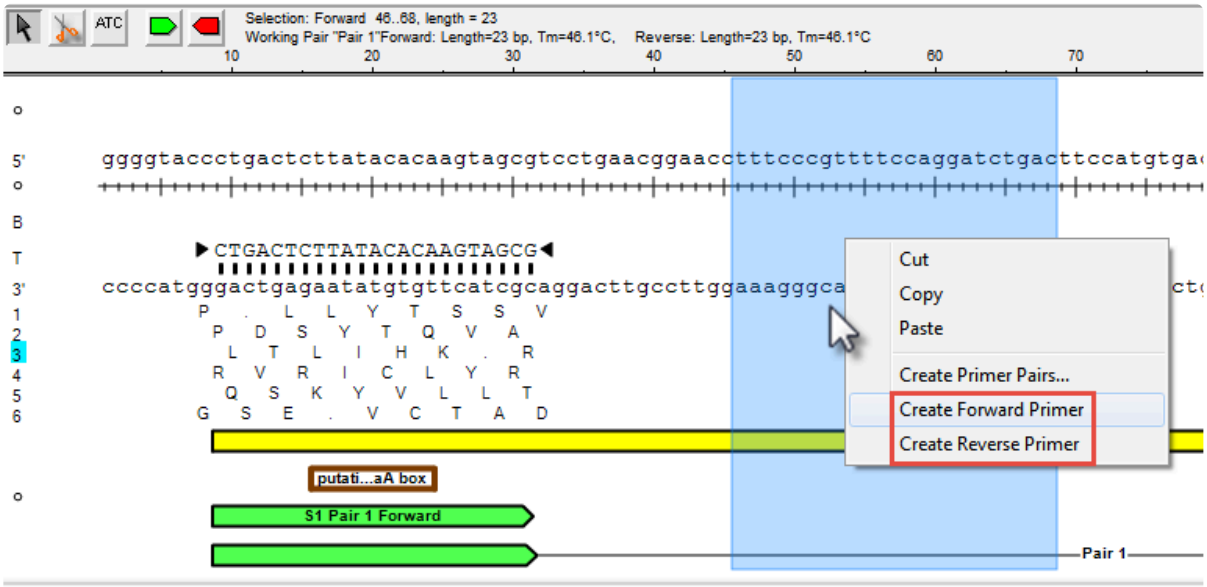


- **SeqBuilder Pro** – For detailed information on primer design, see the SeqBuilder Pro User Guide topic Primers. In brief, to create pairs based around a selected feature or a sequence range, use **Priming > Create Primer Pairs** to open an options dialog (left image). Select the desired options and click **OK** to display the list of primer pairs (right image).





To locate forward & reverse primers separately based around a selected feature or a sequence range, use **Priming > Create Forward Primer** or **Priming > Create Reverse Primer** or the corresponding right-click commands. Both options are only available after using **Priming > Create Primer Pairs** at least once. (In the image below, note the already-found primers to the left of the current selection.)

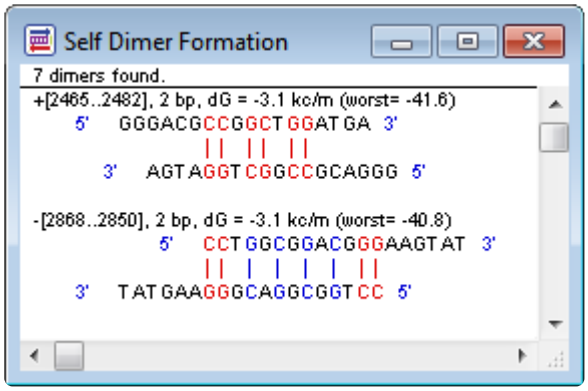


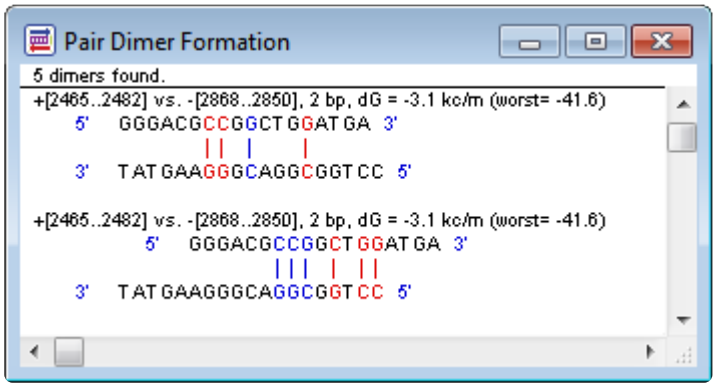
The following video is a brief introduction to primer design in SeqBuilder Pro. For another video on the same topic, see: Primer Design in SeqBuilder Pro.

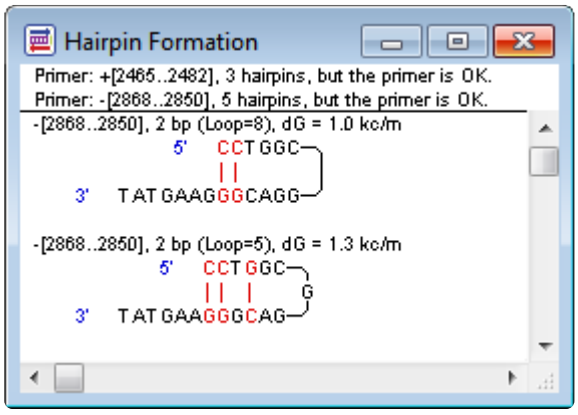
View dimers, pair dimers and hairpins

To view information about dimers, pair dimers, hairpins, and false priming sites:

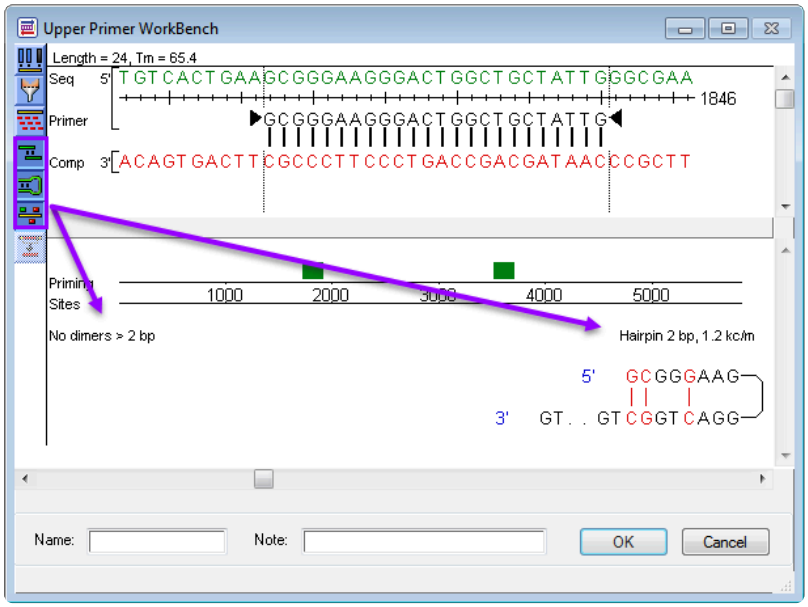
- **PrimerSelect** – Do either of the following:
  - Select a primer pair and choose **Report > Primer Self Dimers**, **Report > Primer Pair Dimers**, and/or **Report > Primer Hairpins**



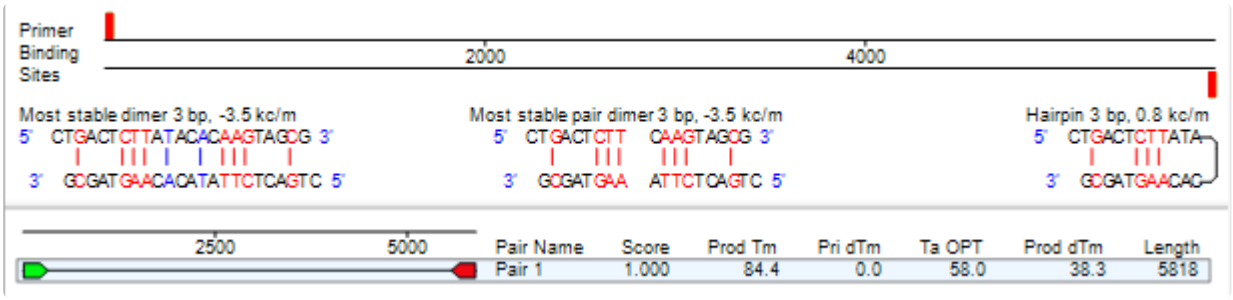




  - Use **Edit > Work on Upper Primer** or **Edit > Work on Lower Primer** to display the primer Workbench. Then use the tools on the left to display self-dimers, hairpins and/or false priming sites.



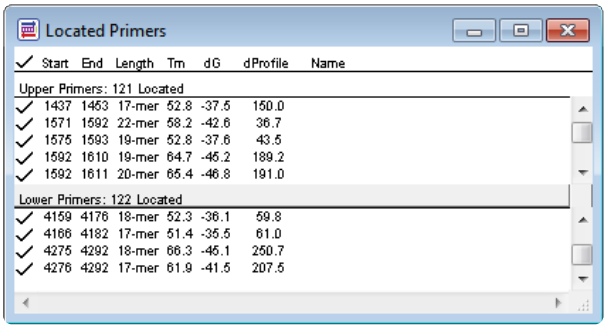
- **SeqBuilder Pro** – This information is displayed automatically in the Primer Design view. To learn how to interpret this information, see the SeqBuilder Pro User Guide topic Primer Design view.



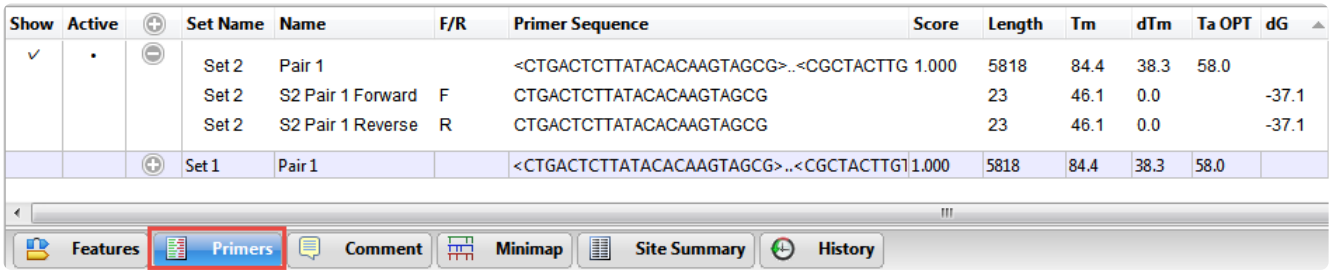
View general primer statistics

To view general statistics about located primer pairs:

- **PrimerSelect** – Use **Report > Located Primers & Probes** to open a window with these statistics.



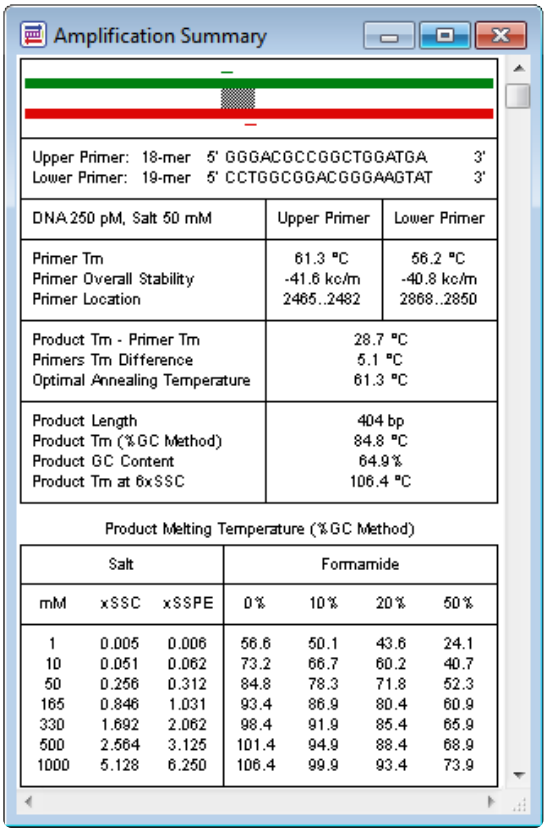
- **SeqBuilder Pro** – Primer statistics are displayed automatically in the Primers view. To learn how to interpret this information, see the SeqBuilder Pro User Guide topic Primers view.

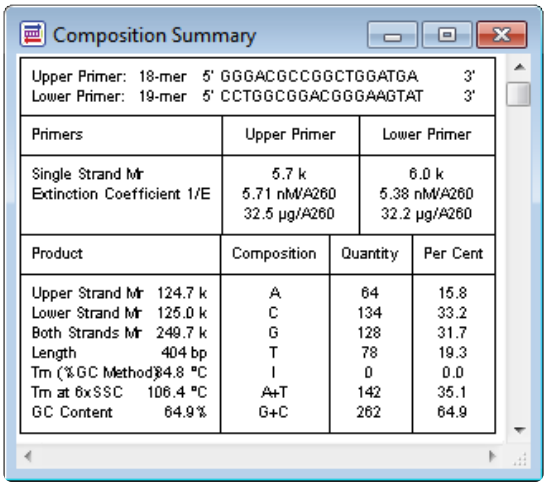


View information on primer composition and amplification

To view information about primer composition and amplification:

- **PrimerSelect** – Select a primer pair and choose **Report > Amplification Summary** or **Report > Composition Summary**.





- **SeqBuilder Pro** – Double-click on a primer in the Primer Design view to view its composition statistics in the Details panel. For more information, see the SeqBuilder Pro User Guide topic Details panel.

Settings | Details

Feature selection

Feature Information:

Feature Type:	PCR_product
Location:	9..5826
Orientation:	Forward
current:	1
pair:	Pair 1
score:	1.000
set:	Set 2

Statistics:

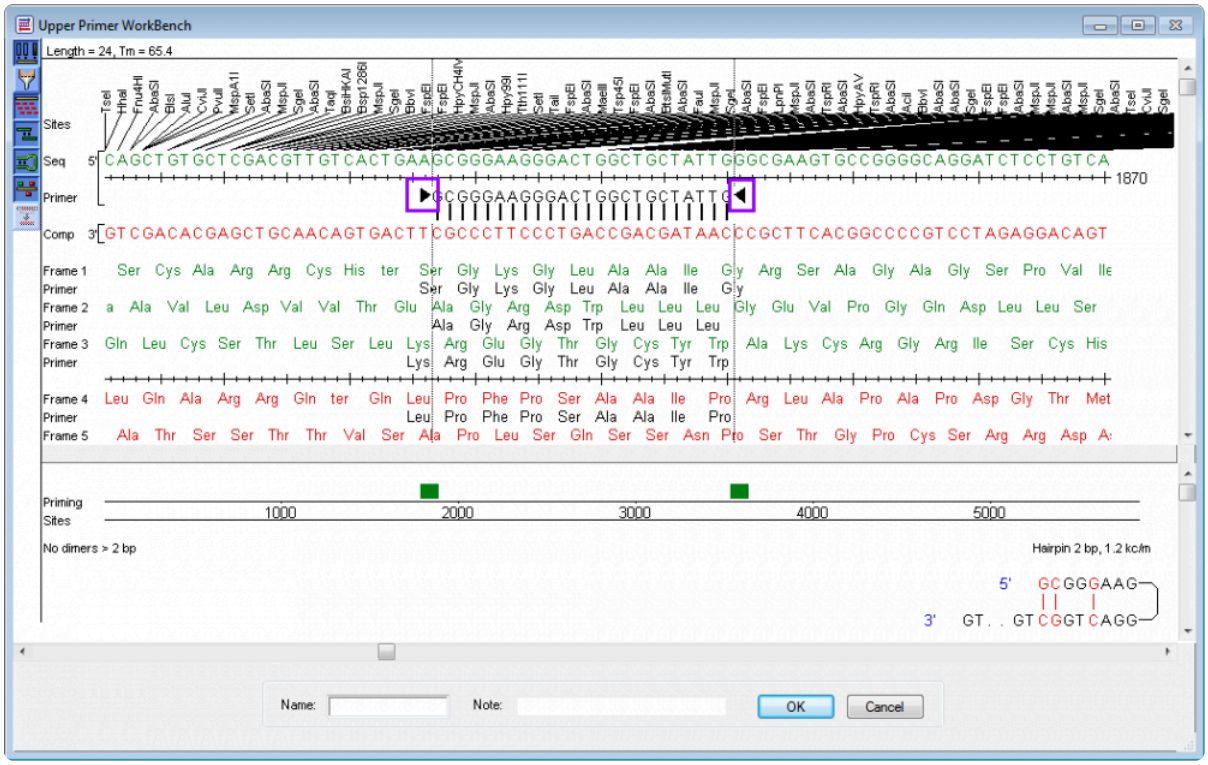
% A	19.34 [1125]
% A+T	39.91 [2322]
% Ambiguous	0.00 [0]
% C	29.55 [1719]
% G	30.54 [1777]
% G+C	60.09 [3496]
% T	20.57 [1197]
% diCG	9.18 [534]
Total number of bases	5818
% AA	4.14 [241]
% AC	4.66 [271]
% AG	5.69 [331]
% AT	4.85 [282]
% CA	6.10 [355]
% CC	7.74 [450]
% CG	9.18 [534]
% CT	6.53 [380]
% GA	6.74 [392]
% GC	10.88 [633]
% GG	8.54 [497]
% GT	4.37 [254]
% TA	2.36 [137]
% TC	6.26 [364]
% TG	7.13 [415]
% TT	4.83 [281]

Amplification information is not available in SeqBuilder Pro.

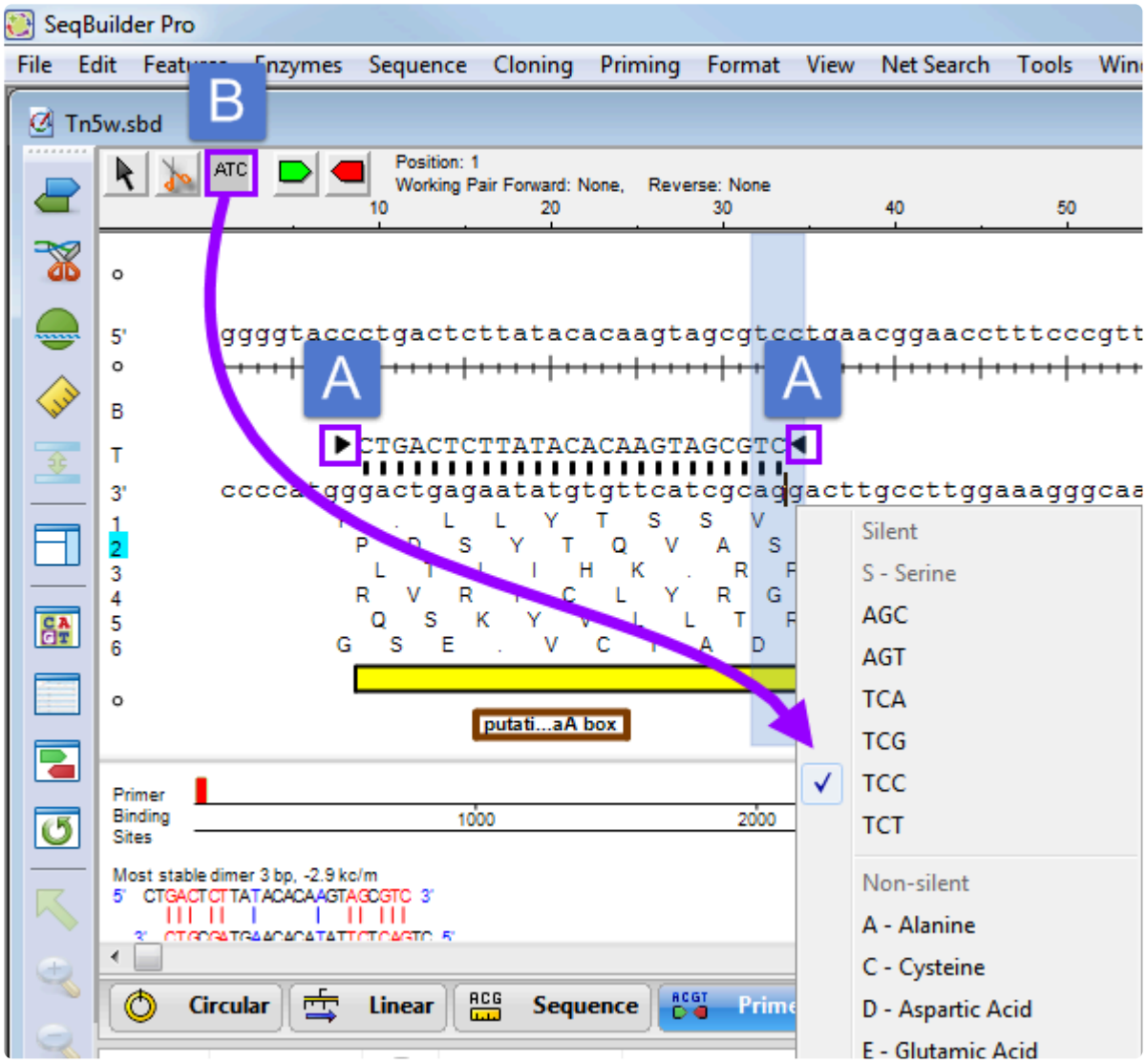
Edit primers

To edit primers:

- **PrimerSelect** – Use **Edit > Work on Upper Primer** or **Edit > Work on Lower Primer**. Drag the black triangles left or right to change the size and location of the primer.



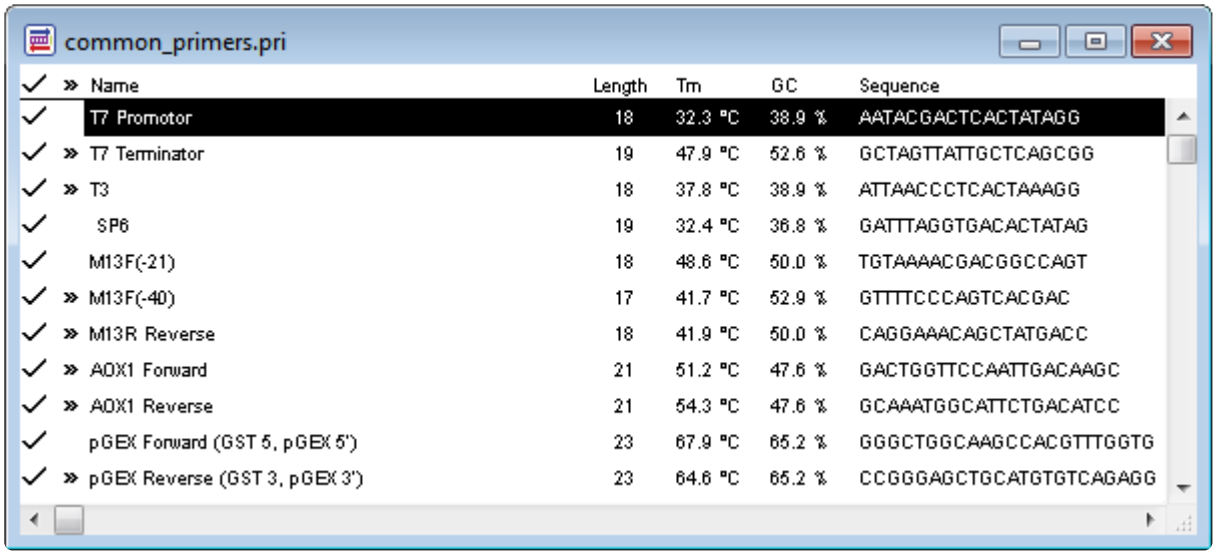
- **SeqBuilder Pro** – In the Primer Design view, either A) drag the black triangles left or right to change the size and location of the primer; or B) use the mutation/codon change tool to select a silent or non-silent mutation for any codon in the primer. For more information, see the SeqBuilder Pro User Guide topic Edit primers.


SeqBuilder Pro
File Edit Features Enzymes Sequence Cloning Priming Format View Net Search Tools
Tn5w.sbd
B
ATC
Position: 1
Working Pair Forward: None, Reverse: None
A
A
putati...aA box
Primer Binding Sites
Most stable dimer 3 bp, -2.9 kc/m
Circular
Linear
Sequence
Silent
S - Serine
AGC
AGT
TCA
TCG
TCC
TCT
Non-silent
A - Alanine
C - Cysteine
D - Aspartic Acid
E - Glutamic Acid

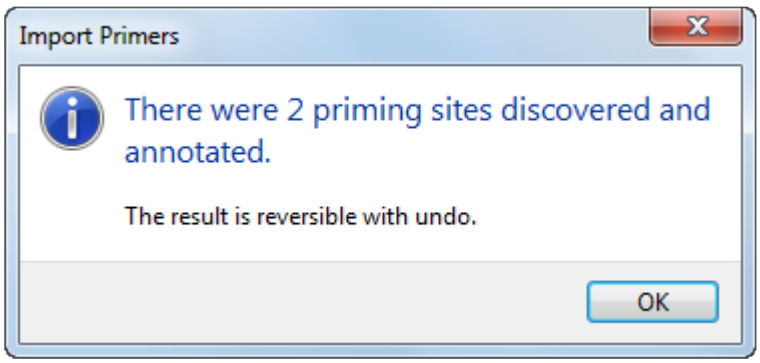
Import primers from a catalog

To import primers from a primer catalog:

- **PrimerSelect** – Use **File > Open** and change the file type to **Primer Catalog (.pri)**. After opening a file with a .pri extension, the primer catalog is displayed as a list.



- **SeqBuilder Pro** – After entering a sequence, use **File > Import Primers from a Catalog** and select a file with a .pri extension. SeqBuilder Pro attempts to locate each primer in the catalog on the current sequence by searching for sites on the template that match at least the 12-mer at the 3' end of the primer. Those that are found are annotated as PCR_primer features and added to the Primers view. If primers were located, a message confirming the new primers will appear.

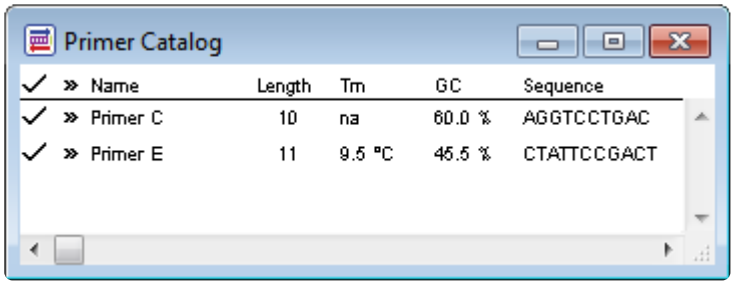


Otherwise, a message appears stating "There were no priming sites discovered." For details on importing primers, see the SeqBuilder Pro User Guide topic Import primers.

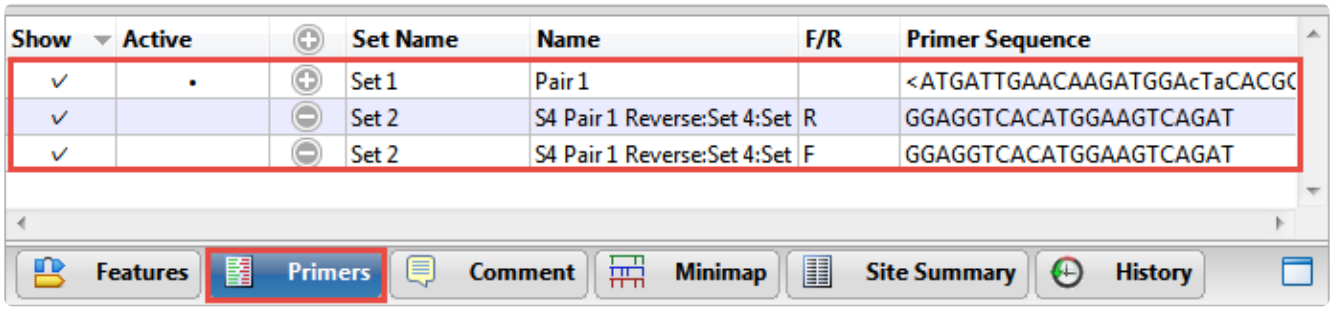
Nominate new primers to a catalog

To nominate new primers to an unsaved primer catalog:

- **PrimerSelect** – Use **File > Enter New Primer** and type in the primer information. After clicking **OK**, the primer is added to the primer catalog, which is displayed with the new entry. To view the catalog at any other time, choose **Log > Primer Catalog**.



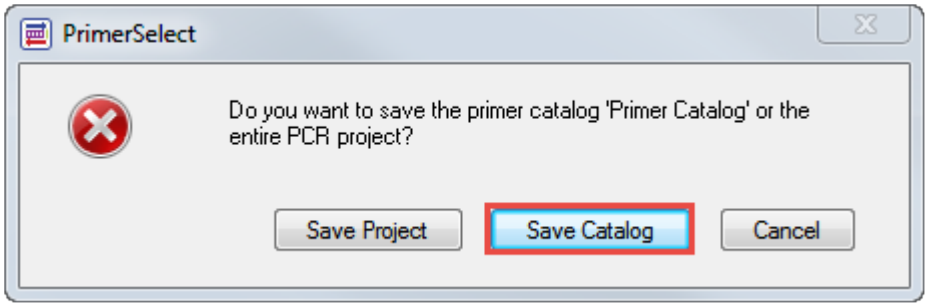
- **SeqBuilder Pro** – Before saving a catalog (below), ensure that only primers you wish to save are displayed in the Primers view.



Save a primer catalog

To save the primer catalog:

- **PrimerSelect** – Use **File > Save**. When prompted, choose **Save Catalog**.



- **SeqBuilder Pro** – Use **File > Save Primer Catalog** to save the primer catalog in *.txt*, *.fas* or *.pri* format. For details, see the SeqBuilder Pro User Guide topic Export primers.

Select and edit a genetic code

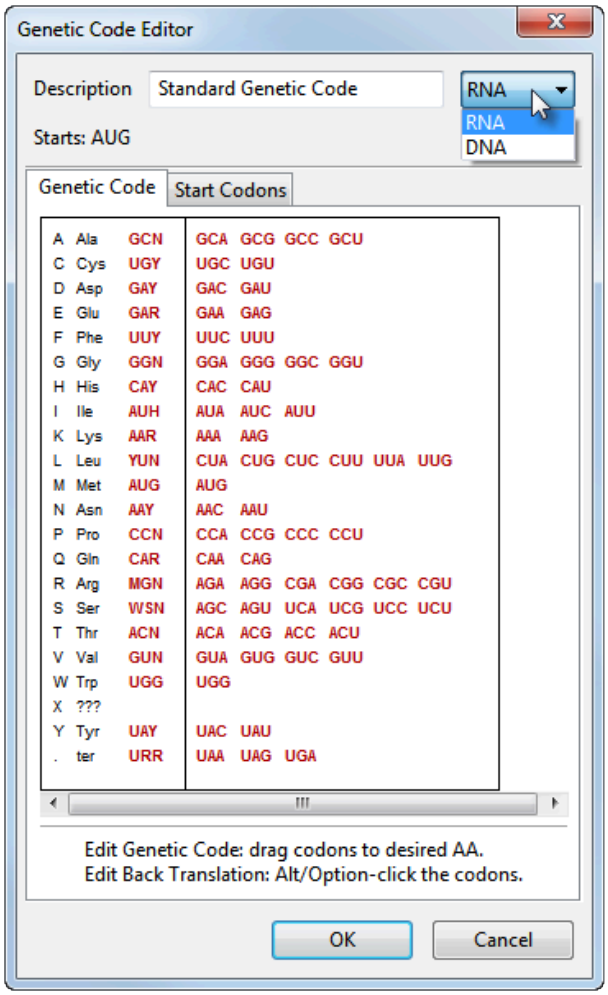
To select a genetic code:

- **PrimerSelect** – Use **Options > Genetic Codes** and choose a code from the list.
- **SeqBuilder Pro** – Use **Sequence > Select Genetic Code** and choose a code from the list. For more information, see the SeqBuilder Pro User Guide topic Choose the genetic code.

To edit a genetic code:

- **PrimerSelect** – Use **Options > Edit Genetic Code**.
- **SeqBuilder Pro** – Use **Sequence > Edit Genetic Code**. For more information, see the SeqBuilder Pro User Guide topic Modify the genetic code.

Though the command is in a different menu, the genetic code editor is the same for both applications.



Transitioning from MegAlign to MegAlign Pro

As of Lasergene 16.0, MegAlign Pro completely replaced MegAlign. Compared to its predecessor, MegAlign, MegAlign Pro features a modern, colorful user interface and greatly increased functionality.

This short video is an overview of the MegAlign Pro application:

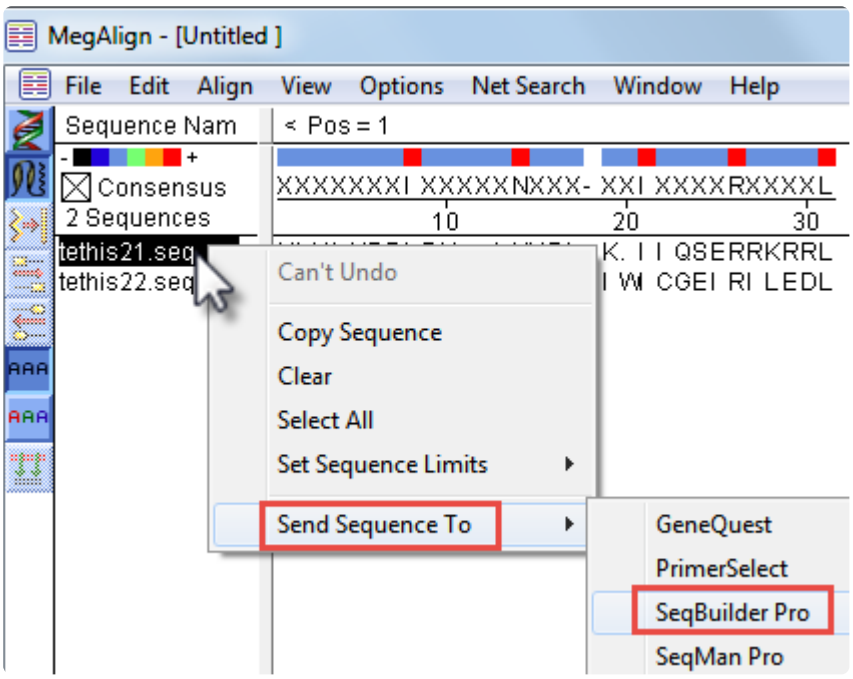
For an illustrated comparison showing how to perform an MegAlign task in MegAlign Pro, click any of the links below:

- Edit a sequence
- Trim sequence ends
- Rename a sequence
- View sequence information
- Translate or back translate a sequence
    - Select and edit a genetic code
- Perform a pairwise alignment
    - View pairwise alignment results
- Perform a multiple alignment
    - View multiple alignment results
    - View sequence distances
    - View phylogenetic tree
    - Create a subalignment
- Find a position
- Locate gaps and disagreements
- Copy and export

Edit a sequence

To edit a sequence:

- **MegAlign** – After entering sequences, select a sequence and use **File > Send Sequence to SeqBuilder Pro**. Edit the sequence and save it in SeqBuilder Pro to automatically update it in MegAlign. There is no need to reload the sequence into MegAlign.

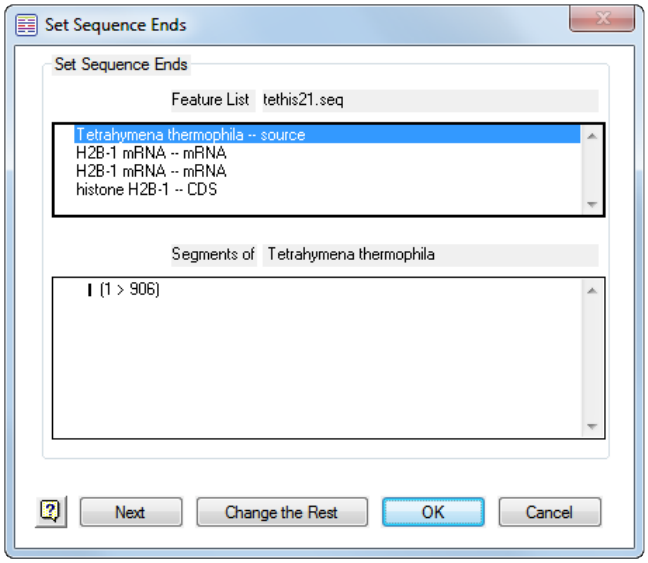


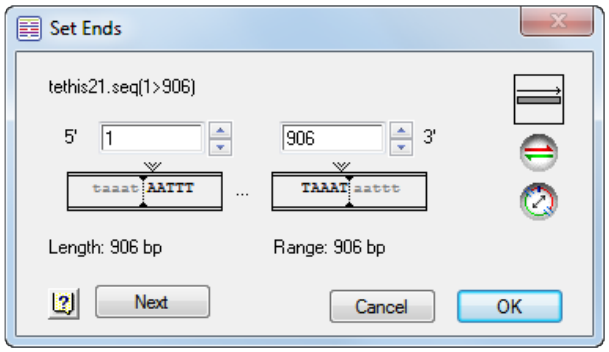
- **MegAlign Pro** – Sequences must be manually opened in SeqBuilder Pro and edited there before entering them in MegAlign.

Trim sequence ends

To trim sequence ends:

- **MegAlign** – Use **Options > Set Sequence Limits > From Feature Table** (left) or **Options > Set Sequence Limits > By Coordinates** (right)





- **MegAlign Pro** – Sequences must be manually opened in SeqBuilder Pro and edited there before entering them in MegAlign.

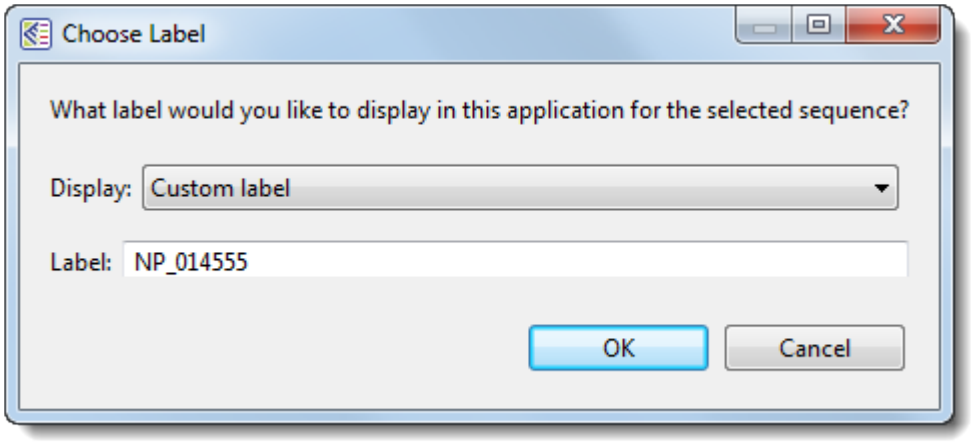
Rename a sequence

To rename a sequence:

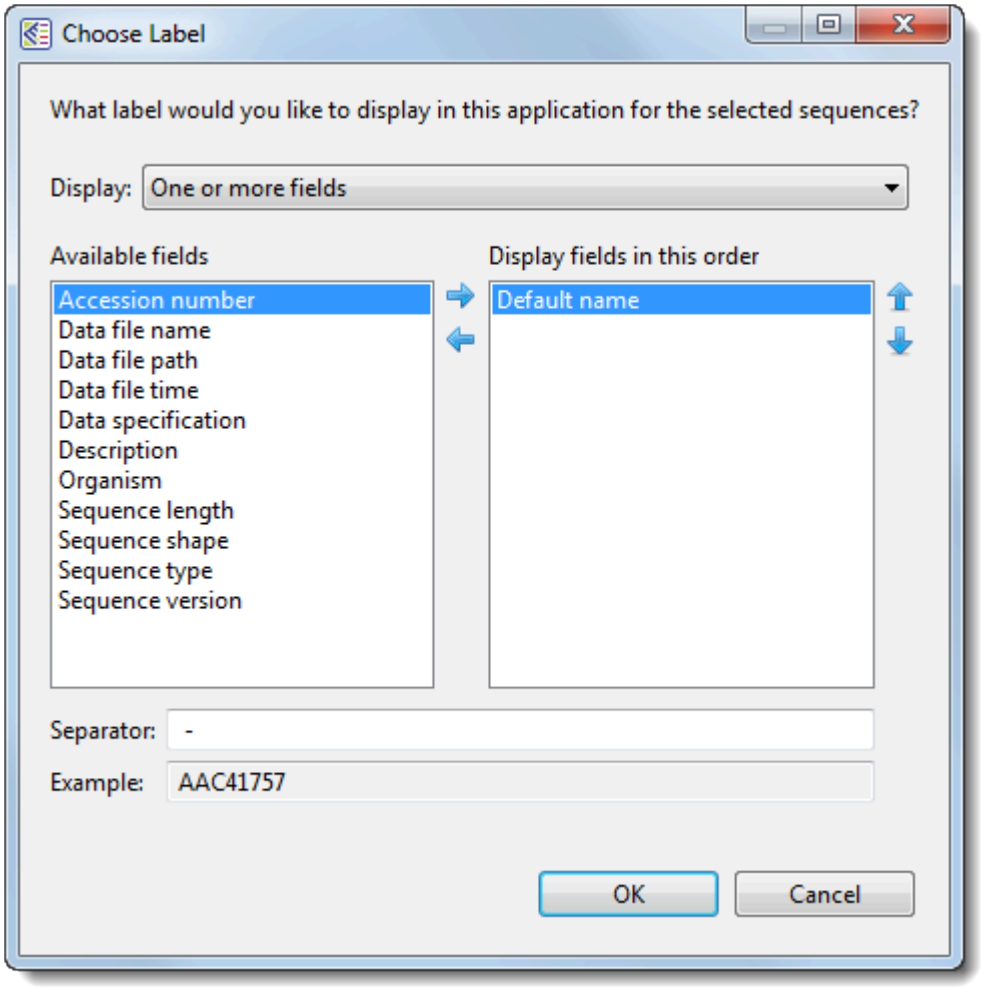
- **MegAlign** – Click for about two seconds on the name of the sequence to allow editing. Then type in a new name.

- **MegAlign Pro** – There are two options for renaming sequences: a manual option, and an automatic option that can rename all selected sequences simultaneously using a specified naming convention.

    - To manually rename a selected sequence, choose **Edit > Rename**. For details, see the MegAlign Pro User Guide topic Rename sequences manually.



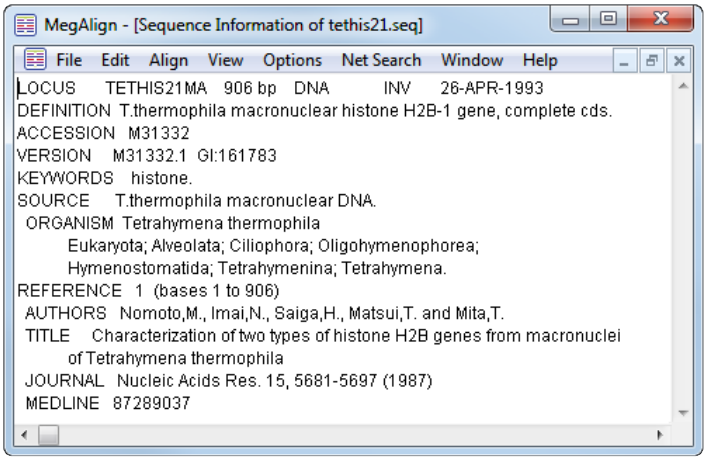
    - To rename one or more selected sequences using specified data fields, use **Edit > Rename with Fields**. For details, see the MegAlign Pro User Guide topic Rename sequences automatically based on specified data fields. The left pane shows available fields, and the right pane shows fields that will 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. Select and organize the fields you wish to display as part of the sequence name



View sequence information

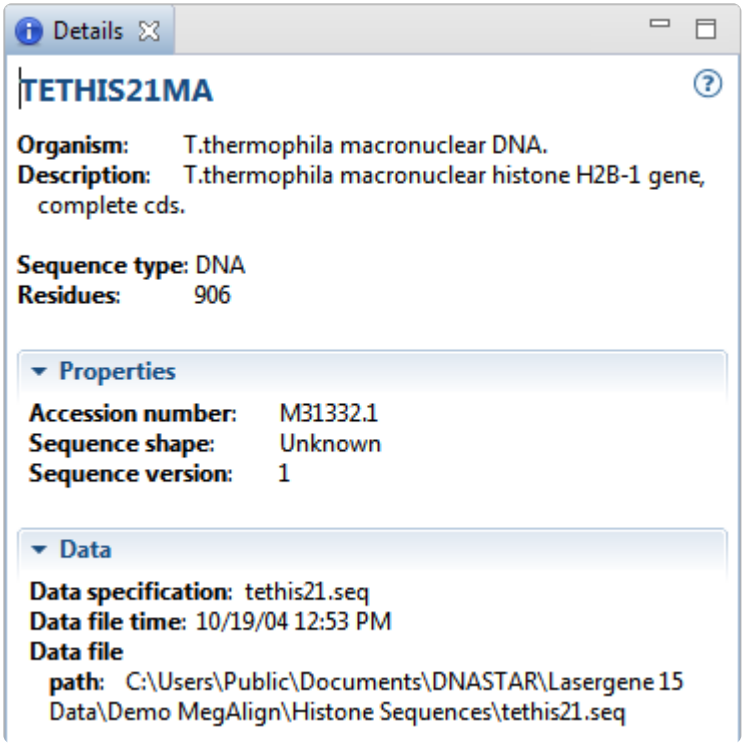
To view information about a selected sequence:

- **MegAlign** – Use **View > Sequence Information**.

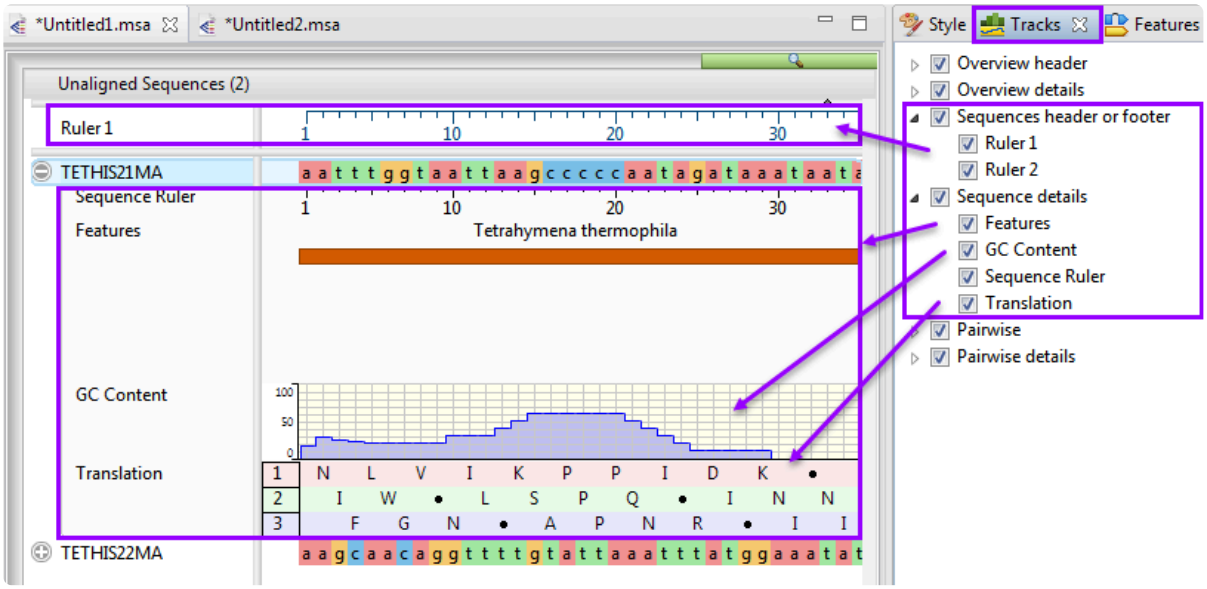


- **MegAlign Pro** – Do either or both of the following:

  - Select a sequence in any view to display its information in the Details panel. To learn more about this panel, which varies according to the current selection, see the MegAlign Pro User Guide topic Details panel.



- Use the Tracks panel to apply tracks to the sequence in the Overview and/or Sequences view. For details, see the MegAlign Pro User Guide topics Tracks panel and Tracks. Track types vary according to whether the sequence is nucleotide or protein, and whether the sequence is part of a pairwise or multiple assembly, or is still unassembled. Tracks may include information about GC content, gap fraction, protein translation, or Sashimi data.

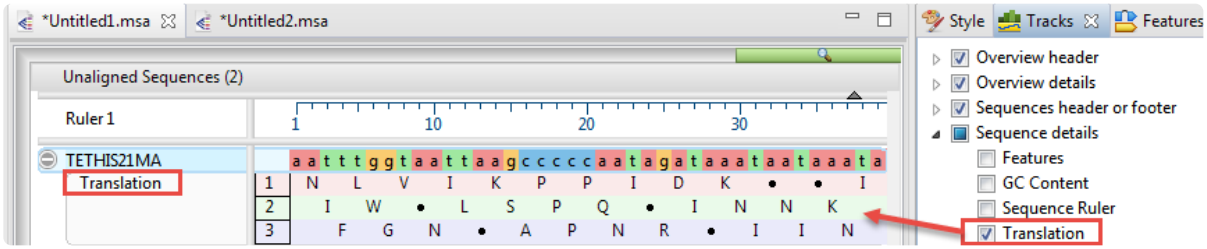


Translate or back translate a sequence

To translate or back translate a sequence:

- **MegAlign** – Use the **Show as DNA** ( ) and **Show as Protein** ( ) tools to toggle between how sequences are displayed on the Worktable. Each command is applied to all sequences on the Worktable.

- **MegAlign Pro** – To display a translation of a nucleotide sequence in MegAlign Pro, use the Tracks panel to apply the **Translation** track. For details, see the MegAlign Pro User Guide topic Translation track.



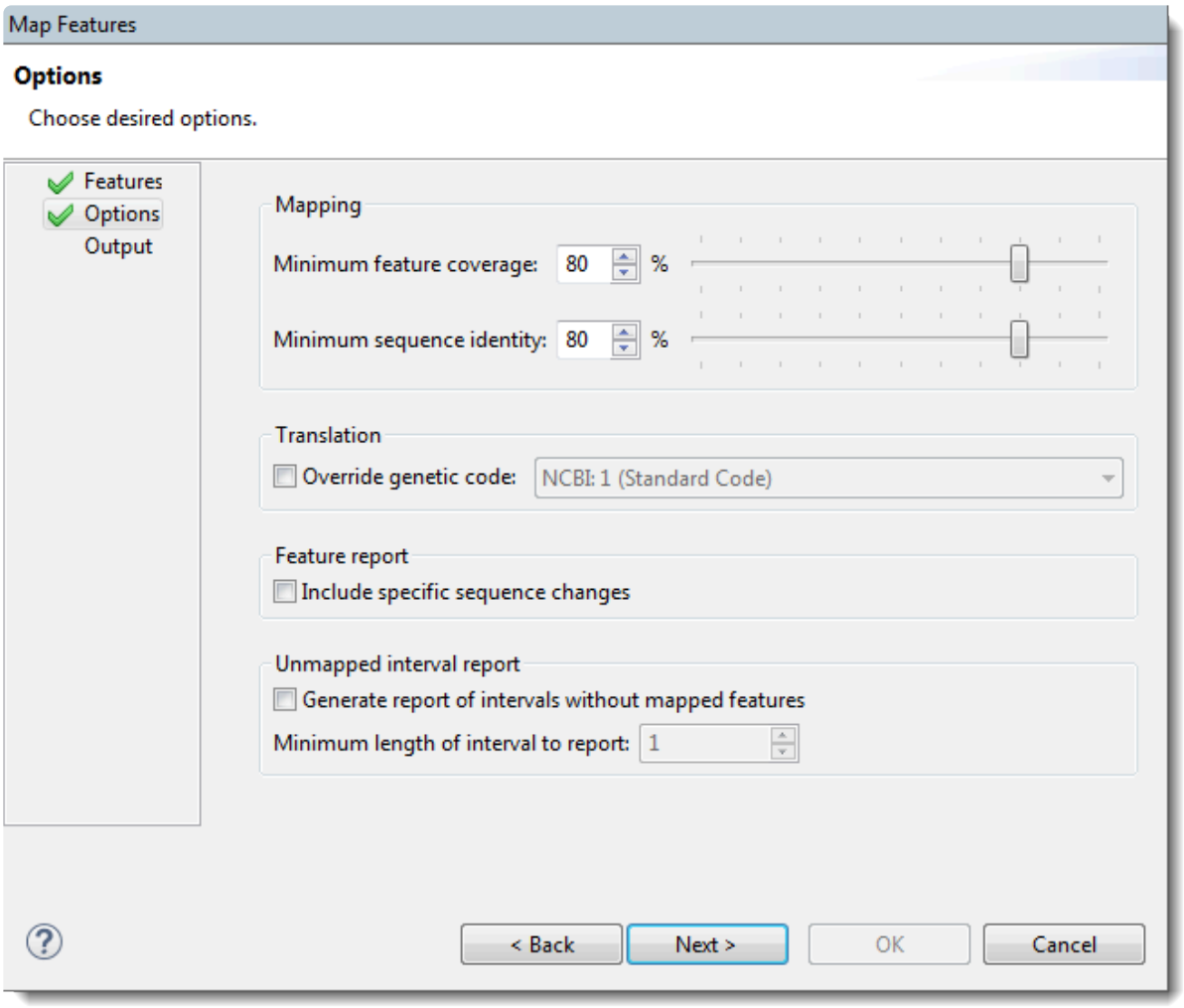
To instead use the translated or back-translated version of a sequence in a MegAlign Pro alignment, first open the sequence in SeqBuilder Pro and change it there there, Then enter the revised sequence in MegAlign.

Select and edit a genetic code

To select a genetic code:

- **MegAlign** – Use **Options > Genetic Codes** and choose a code from the list.

- **MegAlign Pro** – You can choose an alternate genetic code only when mapping features from one sequence to another using **Features > Map Features**. In the **Options** screen, check the box next to **Override genetic code**, then select the desired code from the drop-down list. See the MegAlign Pro User Guide topic Options screen for details.



To see feature mapping in action, see the video Copying annotations between genomes.

To edit a genetic code:

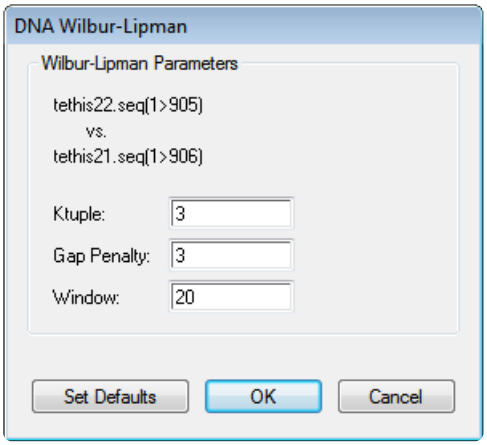
- **MegAlign** – Use **Options > Edit Genetic Code**.

- **MegAlign Pro** – Not available.

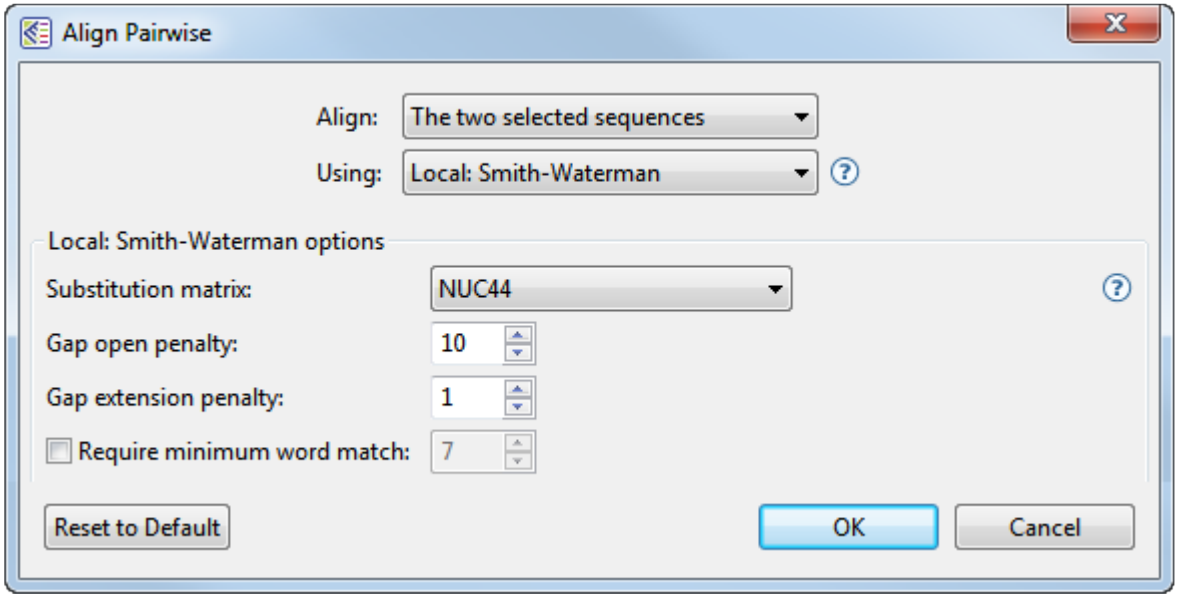
Perform a pairwise alignment

To perform a pairwise alignment:

- **MegAlign** – Select two sequences in the Worktable and use **Align > One Pair > Wilbur and Lipman**, **Align > One Pair > Martinez-NW**, **Align > One Pair > Lipman-Pearson**, or **Align > One Pair > DotPlot**. In the ensuing dialog, make any desired changes to alignment parameters.



- **MegAlign Pro** – Select two sequences any view and use **Align > Pairwise** or press the **Align** tool ( ) and select **Align Pairwise**. In both cases, a dialog opens in which you can select the desired alignment type (**Local: Smith-Waterman**, **Global: Needleman-Wunsch** or **Semi-Global: Needleman-Wunsch**) and make any changes to alignment parameters. For details, see the MegAlign Pro User Guide topic Perform a Pairwise Alignment.

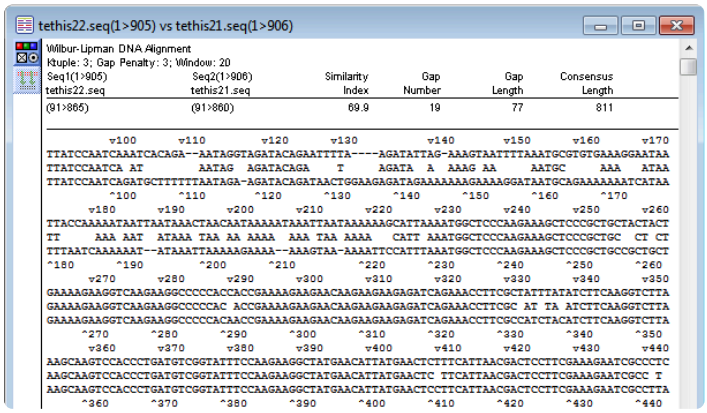


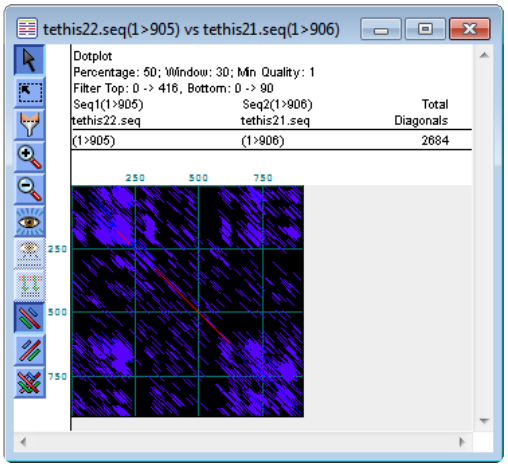
The following brief video is an overview of pairwise alignment in MegAlign Pro.

View pairwise alignment results

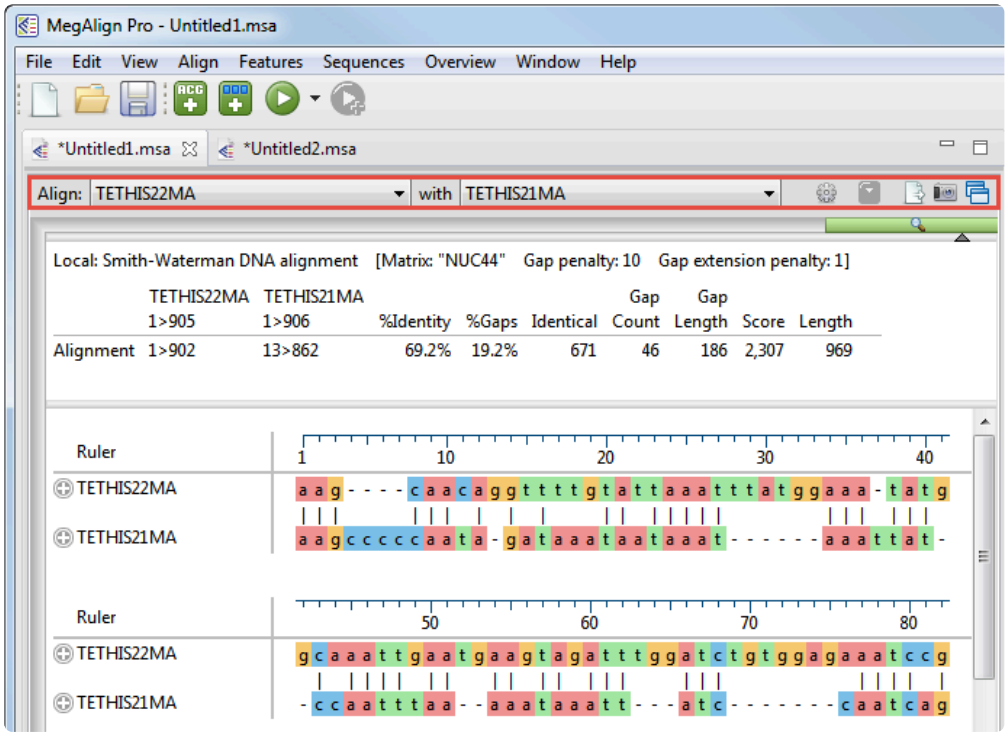
To view pairwise alignment results

- **MegAlign** – Depending on the pairwise alignment method used, results open automatically in the Alignment or DotPlot views.





- **MegAlign Pro** – Results open in the **Pairwise** view, whose appearance is controlled by the **Style** panel's **Pairwise Alignment** section. Tracks, if present, are controlled by which tracks have been checked in the **Tracks** panel. If desired, use the drop-down menus and tools in the top of the view to open additional Pairwise alignment using different combinations of sequences and alignment methods. For more information, see the MegAlign Pro User Guide topics Pairwise view / Pairwise Alignment section and Tracks.

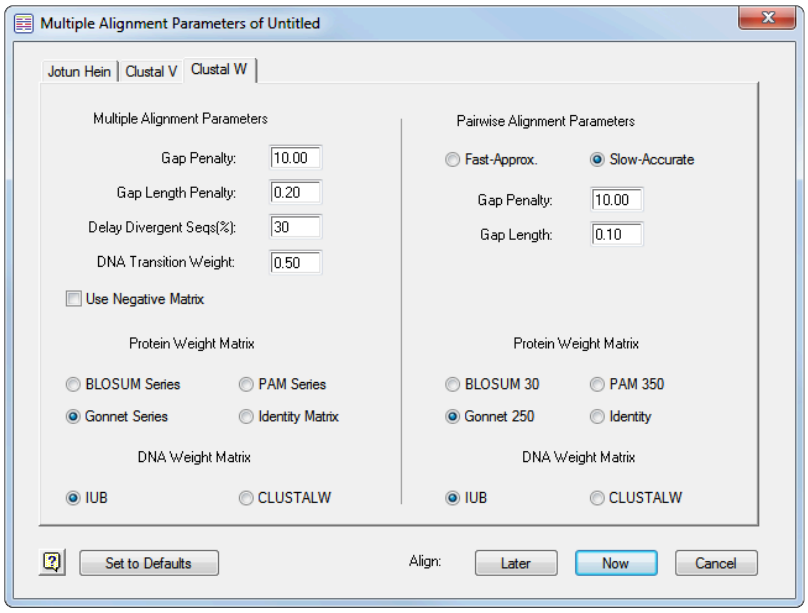


For a brief introduction to using the Tracks panel, see the following video:

Perform a multiple alignment

To perform a multiple alignment:

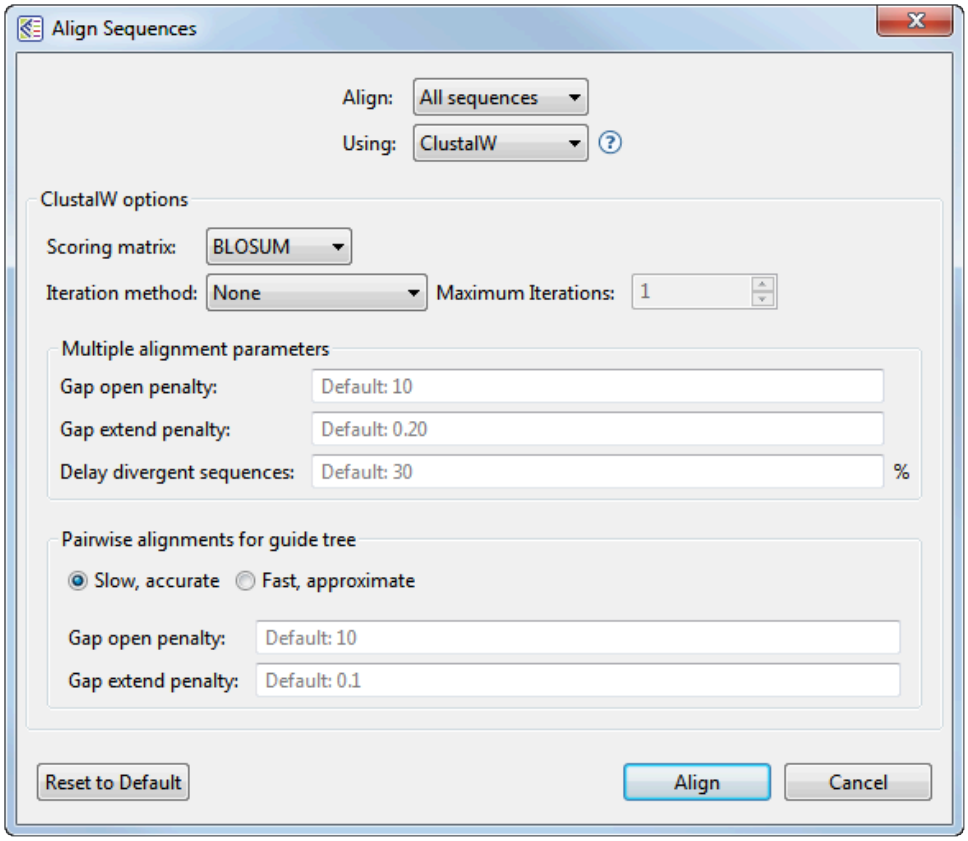
- **MegAlign** – Select the sequences to align and use **Align > By Jotun Hein Method**, **Align > By Clustal V Method**, or **Align > By Clustal W Method**. To change parameters prior to alignment, use **Align > Method Parameters**, choose the tab of interest and make changes, then press the **Now** button.



  To edit a multiple alignment, select a portion of sequence in the Worktable and use the **Straighten Columns** (), **Shuffle Right** () or **Shuffle Left** () tools.

- **MegAlign Pro** – Select the sequences to align and use **Align > Align Using Clustal Omega**, **Align > Align Using Clustal W**, **Align > Align Using MAFFT**, or **Align > Align Using MUSCLE**.

  Alternatively, press the **Align** tool ( ) and choose the option of the same name. To change alignment options, instead use **Align > Align with Options** or press the **Align** tool and choose the option of the same name. Select the desired method using the drop-down menu, then edit the settings and press **Align**. For more information, see the MegAlign Pro User Guide topic Perform an initial multiple alignment.



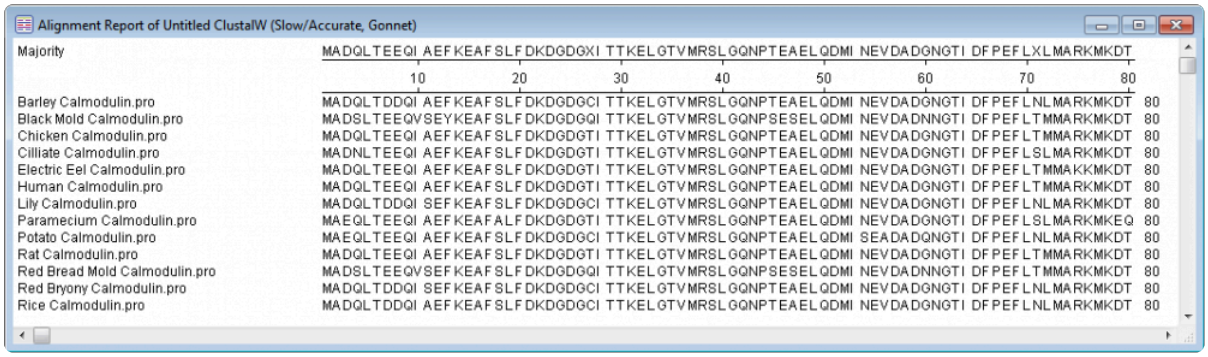
The following brief video is an overview of multiple alignment in MegAlign Pro.

Additional videos highlighting multiple alignment functionality in MegAlign Pro include: Merging and realigning sequences, Aligning genomes using Mauve and Aligning multi-segment files.

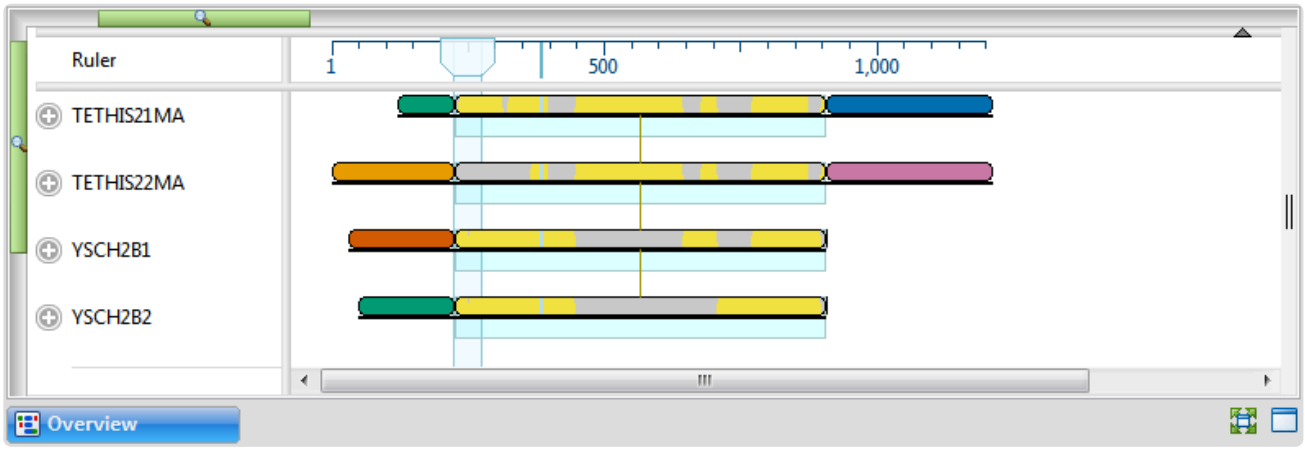
View multiple alignment results

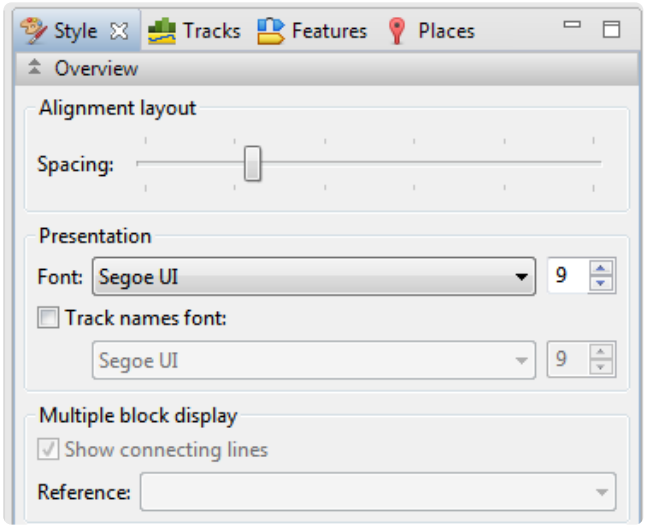
To view multiple alignment results:

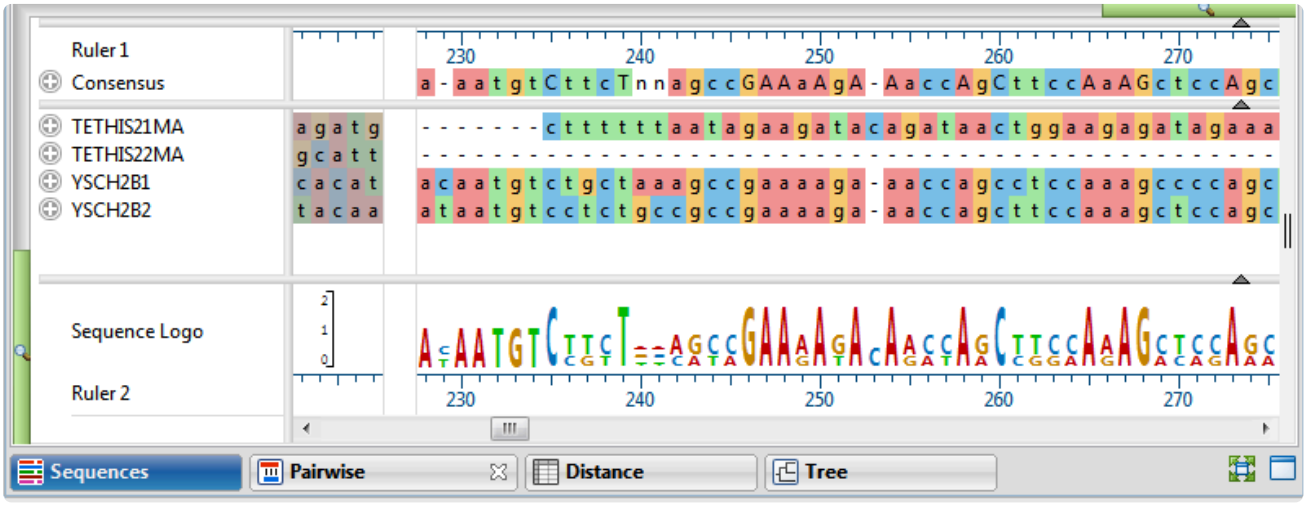
- **MegAlign** – Use **View > Alignment Report**.

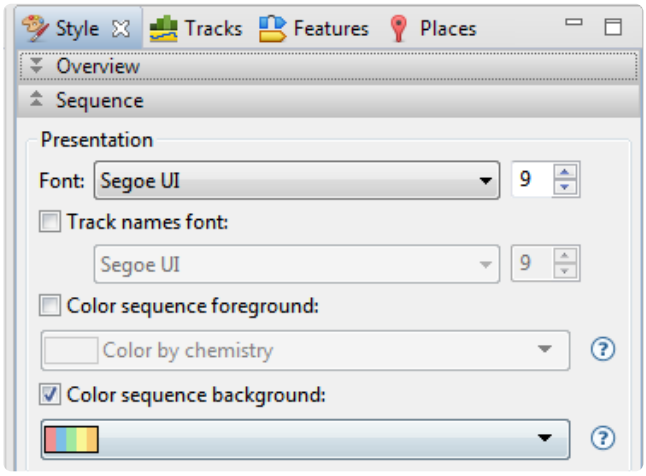


- **MegAlign Pro** – Results are displayed in the **Overview** and **Sequences** view, whose contents and appearances are controlled through the **Style** panel's **Overview** and **Sequence** sections, respectively. Tracks, if present, are controlled by which tracks have been checked in the **Tracks** panel. For more information, see the MegAlign Pro User Guide topics Overview / Overview section, Sequences view / Sequence section, and Tracks.







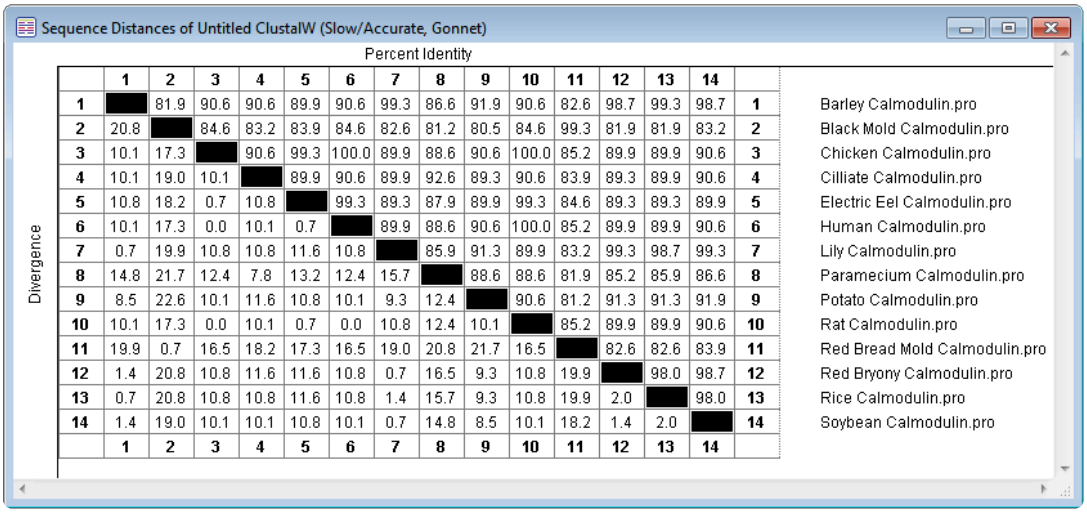


For a brief introduction to using the Tracks panel, see the following video:

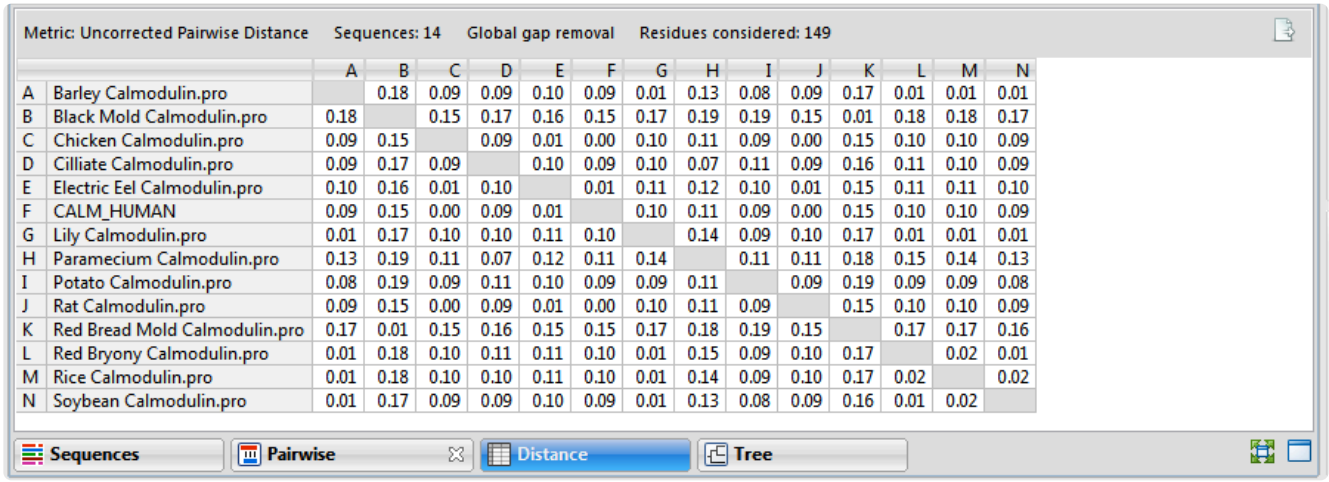
View sequence distances

To view multiple alignment results:

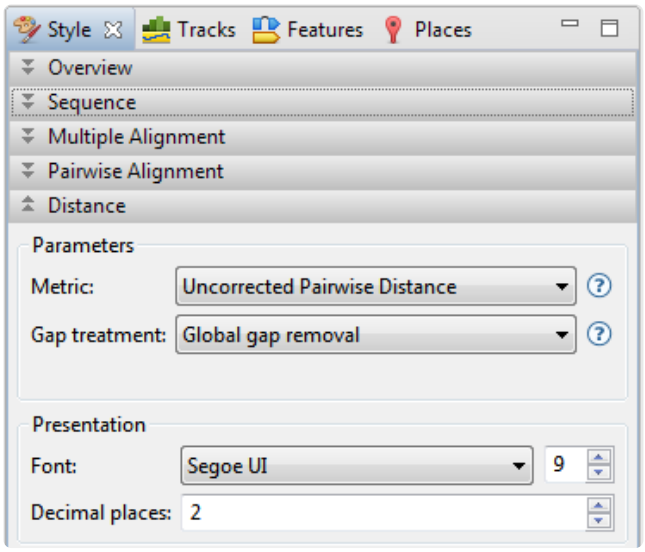
- **MegAlign** – Use **View > Sequence Distances**.



- **MegAlign Pro** – Results are displayed in the **Distance** view, whose contents and appearance are controlled through the **Style** panel's **Distance** section. For more information, see the MegAlign Pro User Guide topics Distance view / Distance section.



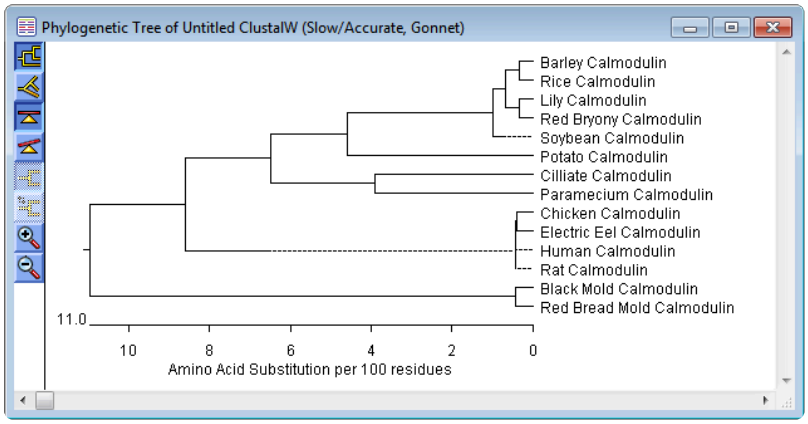
		A	B	C	D	E	F	G	H	I	J	K	L	M	N
A	Barley Calmodulin.pro		0.18	0.09	0.09	0.10	0.09	0.01	0.13	0.08	0.09	0.17	0.01	0.01	0.01
B	Black Mold Calmodulin.pro	0.18		0.15	0.17	0.16	0.15	0.17	0.19	0.19	0.15	0.01	0.18	0.18	0.17
C	Chicken Calmodulin.pro	0.09	0.15		0.09	0.01	0.00	0.10	0.11	0.09	0.00	0.15	0.10	0.10	0.09
D	Cilliate Calmodulin.pro	0.09	0.17	0.09		0.10	0.09	0.10	0.07	0.11	0.09	0.16	0.11	0.10	0.09
E	Electric Eel Calmodulin.pro	0.10	0.16	0.01	0.10		0.01	0.11	0.12	0.10	0.01	0.15	0.11	0.11	0.10
F	CALM_HUMAN	0.09	0.15	0.00	0.09	0.01		0.10	0.11	0.09	0.00	0.15	0.10	0.10	0.09
G	Lily Calmodulin.pro	0.01	0.17	0.10	0.10	0.11	0.10		0.14	0.09	0.10	0.17	0.01	0.01	0.01
H	Paramecium Calmodulin.pro	0.13	0.19	0.11	0.07	0.12	0.11	0.14		0.11	0.11	0.18	0.15	0.14	0.13
I	Potato Calmodulin.pro	0.08	0.19	0.09	0.11	0.10	0.09	0.09	0.11		0.09	0.19	0.09	0.09	0.08
J	Rat Calmodulin.pro	0.09	0.15	0.00	0.09	0.01	0.00	0.10	0.11	0.09		0.15	0.10	0.10	0.09
K	Red Bread Mold Calmodulin.pro	0.17	0.01	0.15	0.16	0.15	0.15	0.17	0.18	0.19	0.15		0.17	0.17	0.16
L	Red Bryony Calmodulin.pro	0.01	0.18	0.10	0.11	0.11	0.10	0.01	0.15	0.09	0.10	0.17		0.02	0.01
M	Rice Calmodulin.pro	0.01	0.18	0.10	0.10	0.11	0.10	0.01	0.14	0.09	0.10	0.17	0.02		0.02
N	Soybean Calmodulin.pro	0.01	0.17	0.09	0.09	0.10	0.09	0.01	0.13	0.08	0.09	0.16	0.01	0.02	



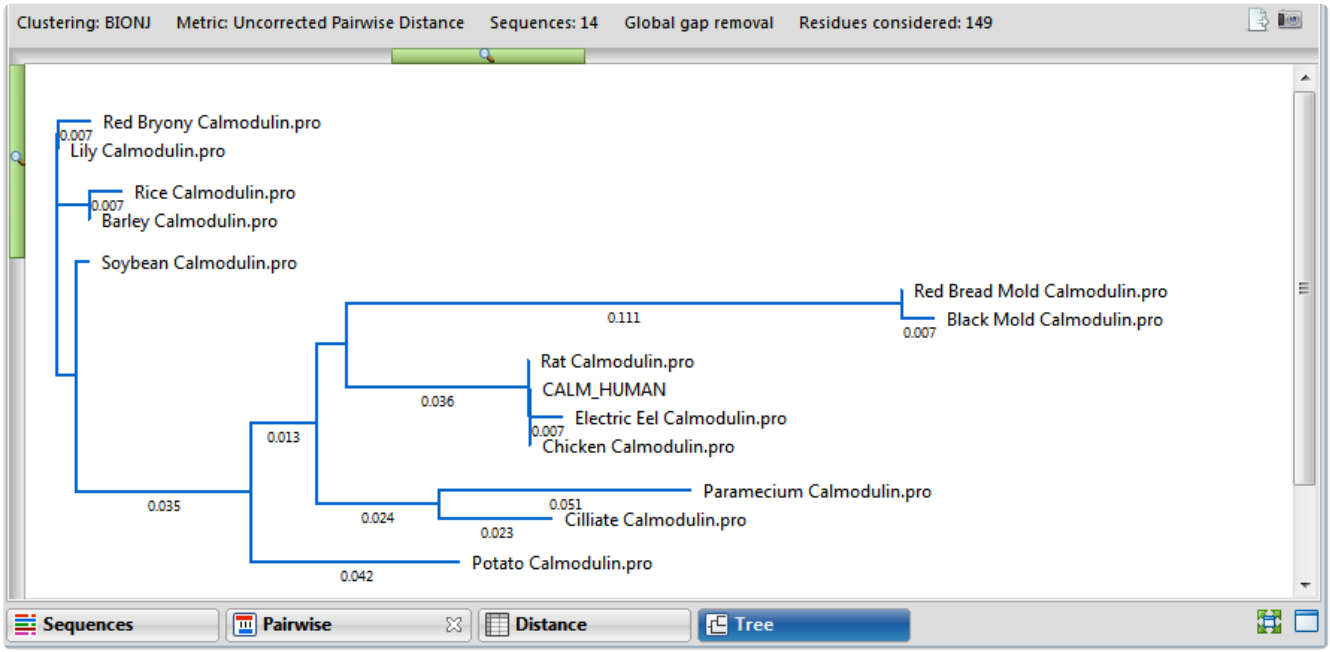
View phylogenetic tree

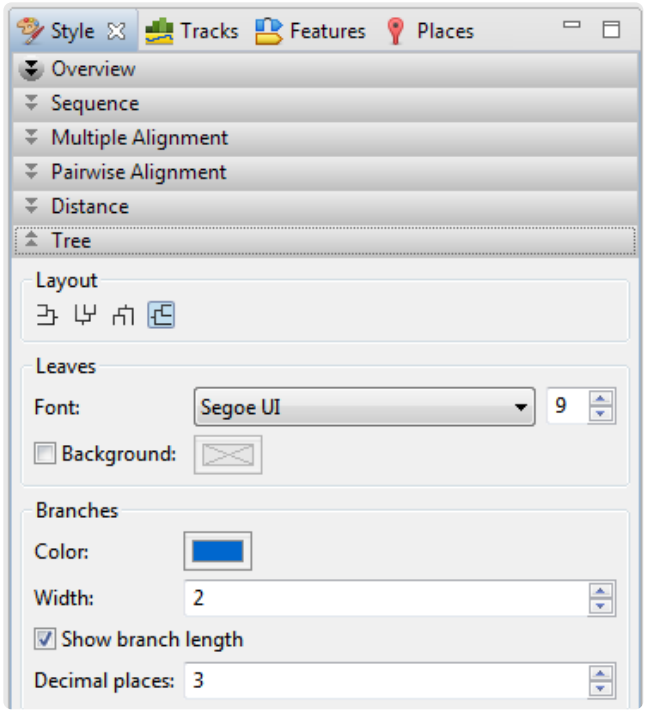
To view multiple alignment results:

- **MegAlign** – Use **View > Phylogenetic Tree**. The appearance and calculations used in this window are controlled via the tools on the left.



- **MegAlign Pro** – Results are displayed in the **Tree** view, whose contents and appearance are controlled through the **Style** panel's **Tree** section. For more information, see the MegAlign Pro User Guide topics Tree view / Tree section.





The following short video shows how to create and edit phylogenetic trees in MegAlign Pro.

Create a subalignment

To create a subalignment:

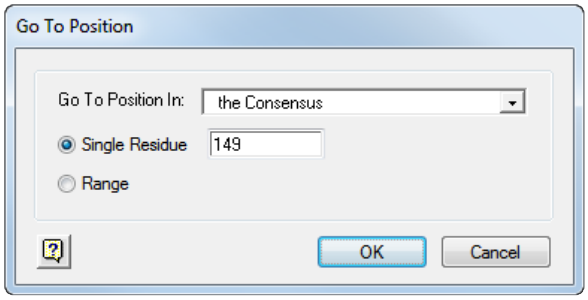
- **MegAlign** – After performing a multiple alignment, select a portion of the consensus sequence in the Worktable and use **Align > Create Alignment From Selection**. After choosing a name for the new project, the subalignment is opened in a new MegAlign project window.

- **MegAlign Pro** – After performing a multiple alignment, display a **Consensus** track and select a portion of the consensus sequence in the **Sequence** view. Then use **Align > Realign Subsequences**. Choose the desired alignment type and parameters, then press **Align**. The results are shown in the current MegAlign Pro project rather than in a new project window. For more information, see the MegAlign Pro User Guide topic Subalign sequences.

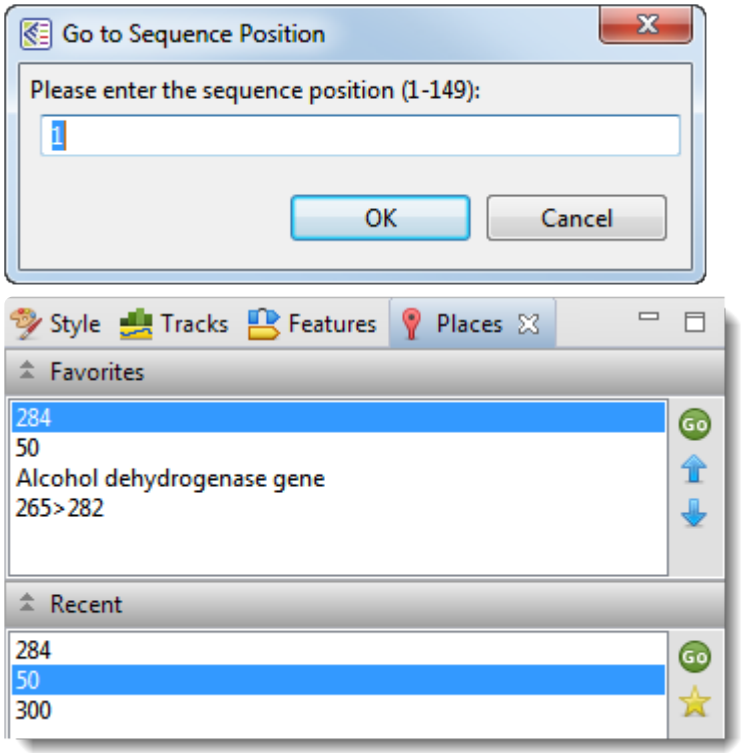
Find a position

To find a position:

- **MegAlign** – Use **Edit > Go To Position**.



- **MegAlign Pro** – Use **Edit > Go To (Pairwise) Position** (left). For more information, see the MegAlign Pro User Guide topic Search. To return to a sequence location or range you have visited before, use the **Places** panel (right), discussed in the topic Places panel.

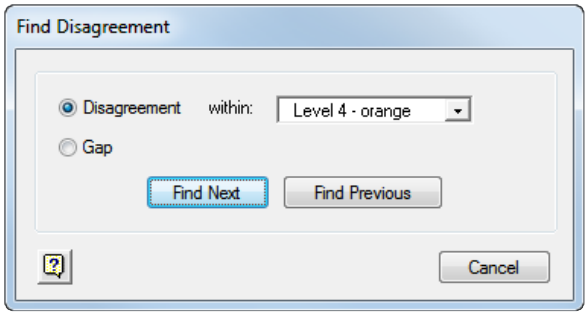


The following video shows how to bookmark favorite locations using the Places panel:

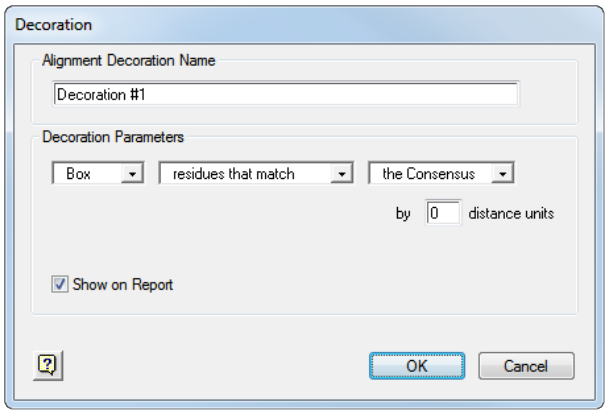
Locate gaps and disagreements

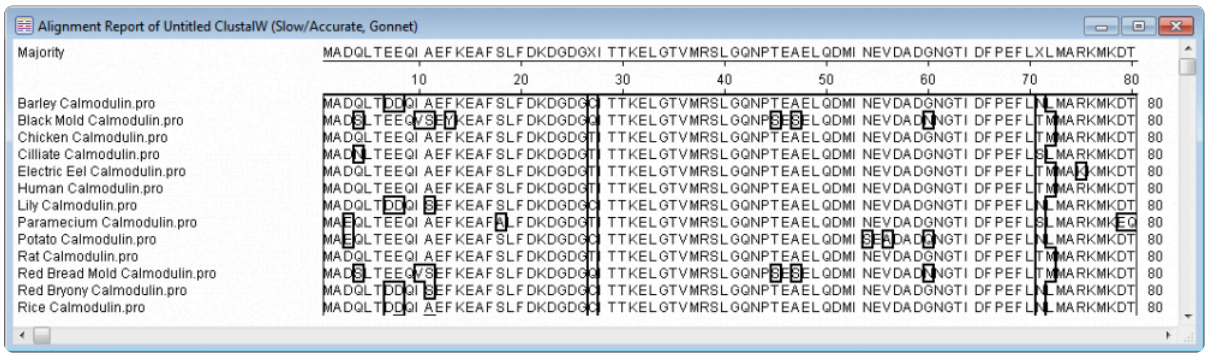
To find gaps or areas of disagreement in an alignment:

- **MegAlign** – Use **Edit > Find Disagreement** and choose whether to search for a disagreement or a gap

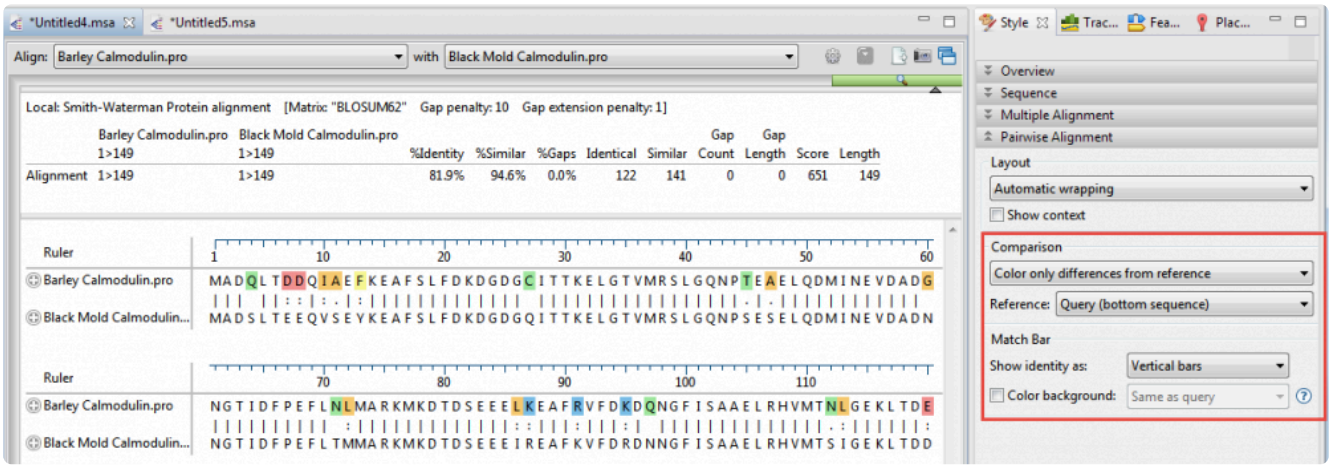


Or, to make facets of the alignment stand out in the Alignment Report, add one or more decorations to the Worktable using **Options > New Decoration**.





- **MegAlign Pro** – Use the **Style** panel's **Pairwise Alignment** or **Multiple Alignment** sections to specify how to display similarities or differences. See the MegAlign Pro User Guide topics Pairwise Alignment section and Multiple Alignment section for details.


*Untitled4.msa
*Untitled5.msa
Align: Barley Calmodulin.pro with Black Mold Calmodulin.pro
Local: Smith-Waterman Protein alignment [Matrix: "BLOSUM62" Gap penalty: 10 Gap extension penalty: 1]
Barley Calmodulin.pro 1>149
Black Mold Calmodulin.pro 1>149
%Identity %Similar %Gaps Identical Similar Gap Count Gap Length Score Length
Alignment 1>149 1>149 81.9% 94.6% 0.0% 122 141 0 0 651 149
Ruler
Barley Calmodulin.pro
Black Mold Calmodulin...
Style
Trac...
Fea...
Plac...
Overview
Sequence
Multiple Alignment
Pairwise Alignment
Layout
Automatic wrapping
Show context
Comparison
Color only differences from reference
Reference: Query (bottom sequence)
Match Bar
Show identity as: Vertical bars
Color background: Same as query

Copy and export

To copy a sequence:

- **MegAlign** – To copy any selected text as it appears in a view, use **Edit > Copy**. To copy part or all of the consensus sequence after performing an alignment, select the sequence range and use **Edit > Copy Consensus**.

- **MegAlign Pro** – To copy any selected text as it appears in a view, use **Edit > Copy**. To copy the selected text or data in FASTA format, use **Edit > Copy As FASTA**. For details, see the MegAlign Pro User Guide topic Copy, Paste and Delete.

To export a sequence:

- **MegAlign** – Use **File > Export Sequences** to export selected sequences from the Worktable or **File > Export Consensus** to export the consensus sequence from the Worktable. Files can only be exported to Lasergene DNA (*.seq*) or protein (*.pro*) format.

- **MegAlign Pro** – Use any of over a dozen commands to export data to a number of formats. Among many other choices, you can export all the sequences (**File > Export Data > Sequences**), or data from the Distance view (**File > Export Data > Distance Matrix**) or Tree view (**File > Export Data > Tree**). For more information, see the MegAlign Pro User Guide topics Export data to a file and Export a tree to a tree viewer.

To export an image:

- **MegAlign** – Not available.

- **MegAlign Pro** – To export an image showing the contents of a view, use **File > Export Image > (View Name)**. For details, see the MegAlign Pro User Guide topic Export an image of the view. Once you have exported the image, you can edit it in PowerPoint as shown in this brief video:

Transitioning from SeqMan Pro to SeqMan Ultra

SeqMan Ultra was introduced in Lasergene 17.0 as the modern replacement for SeqMan Pro, now considered a legacy application. Both applications will be included in Lasergene for a short time, but we strongly encourage all users to switch to SeqMan Ultra as soon as possible.

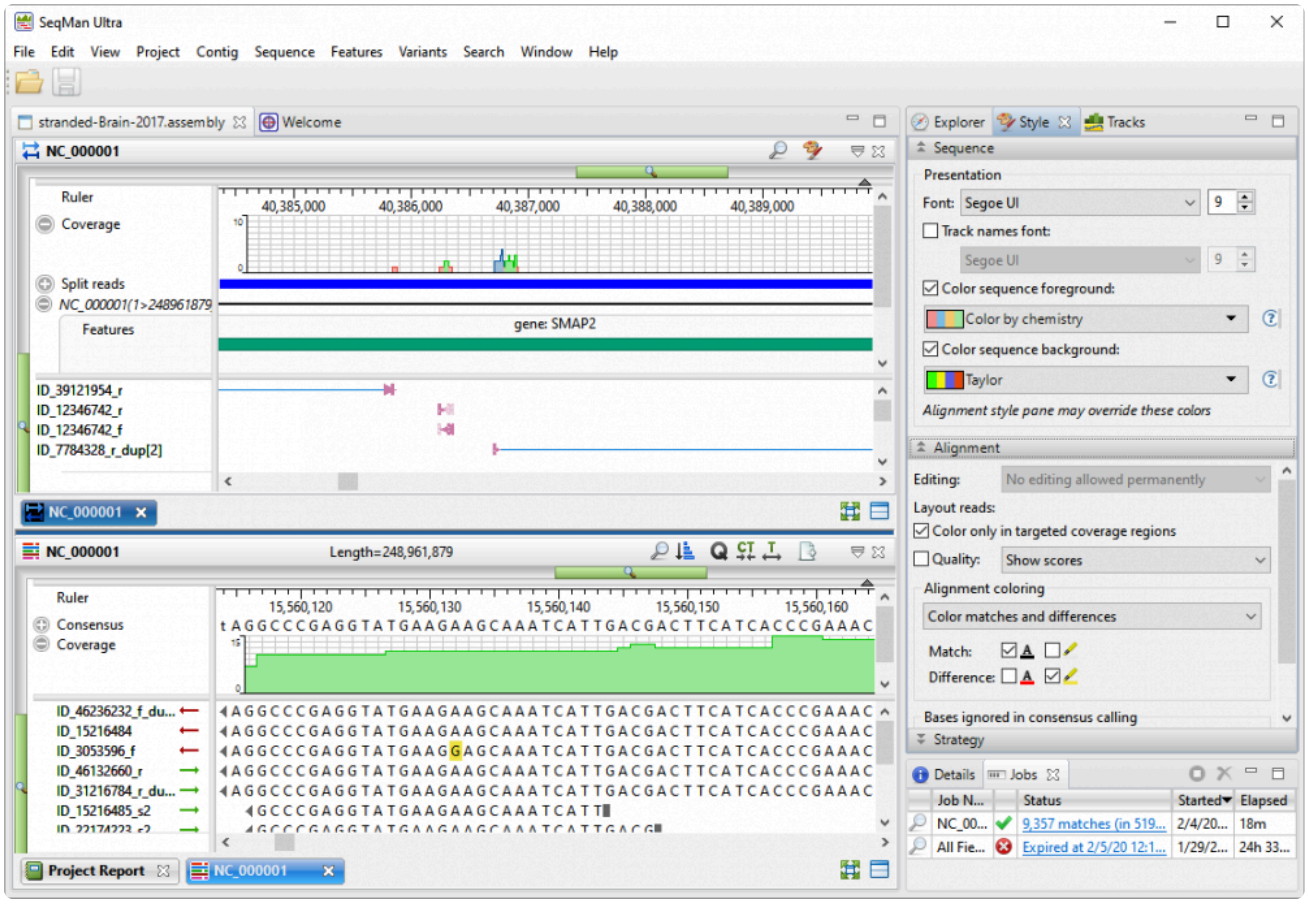
SeqMan Ultra is a 64-bit application, which means faster project opening, better performance for analyzing large files, increased capacity, and compatibility with macOS 10.15. Compared to its predecessor, SeqMan Pro, SeqMan Ultra features a modern, colorful user interface and greatly increased functionality.

For an illustrated comparison showing how to perform a SeqMan Pro task in SeqMan Ultra, click any of the links below:

- Get acquainted with the SeqMan Ultra interface
- Create a new assembly
- Open an existing assembly
- Select and work with contigs
- View contigs, consensuses and reads graphically
- View and work with features
- View and work with variants
- View information about a project or selection
- Search for sequences online

Get acquainted with the SeqMan Ultra interface

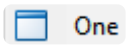
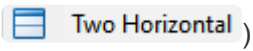
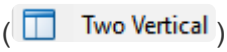
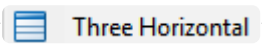
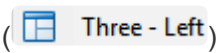
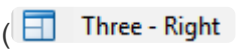
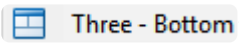
SeqMan Ultra uses the same type of graphic user interface as DNASTAR's MegAlign Pro, GenVision Pro, SeqNinja, Protean 3D and SeqBuilder Pro. This style of interface has one or more large "views" on the left, and a narrower set of expandable "panels" on the right. The panels are used for specifying the appearance of the views, selecting what is included in the views, showing details about a selection, etc.



We think you'll find the new **SeqMan Ultra** interface to be very intuitive. However, we would like to highlight a few items that might not be readily apparent.

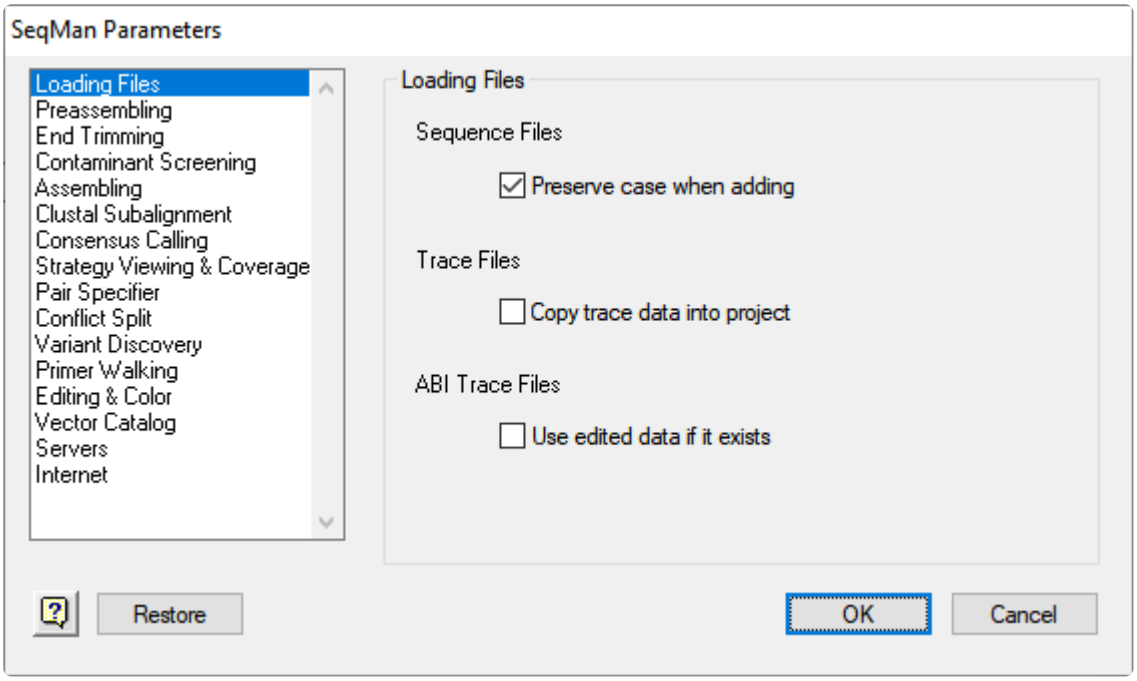
Changing the layout and number of views:

- **SeqMan Pro** – Views, tables and reports appear as separate windows that can be resized manually.
- **SeqMan Ultra** – Graphic, tabular and text data is each contained in a named "view." You can display from 1-3 views at a time. To specify the number and layout of views, use the **View > Change layout** command or the **Change layout** tool (image varies) in the bottom right corner of each view. The following options are available:

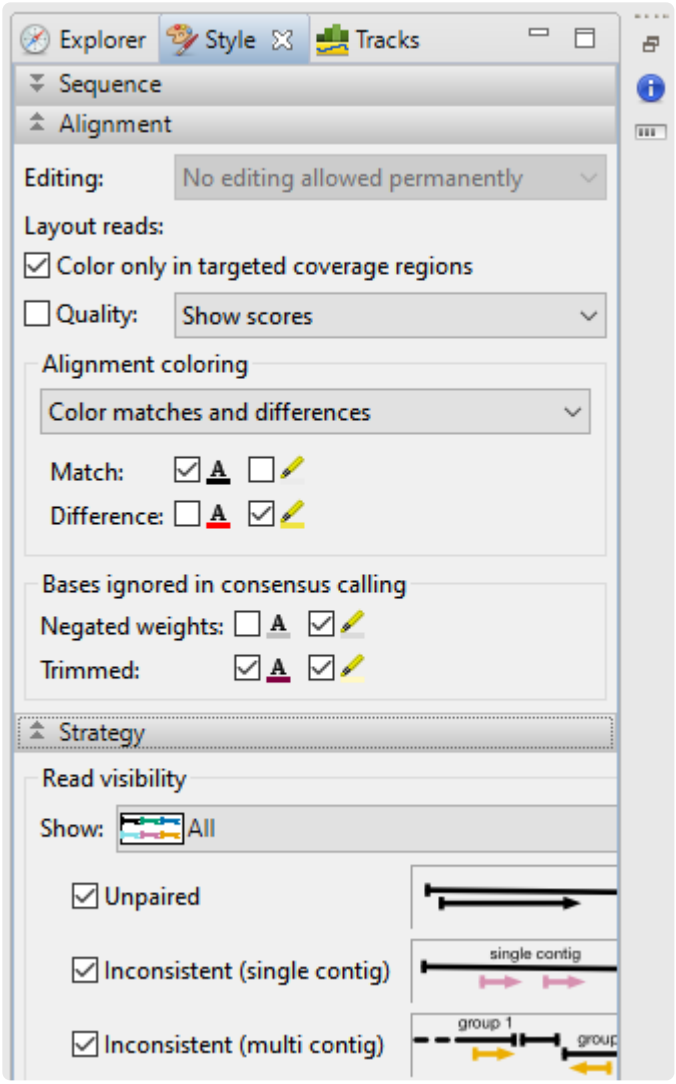
- **One** –  – To show only the current view and cause it to occupy all of the view "real estate."
- **Two Horizontal** () – To show the current view on top and one additional view below it.
- **Two Vertical** () – To show the current view on the left, and one additional view to the right.
- **Three Horizontal** () – To show the current view on top and two additional views below it.
- **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** () – To show the current view on the right and two additional views stacked one on top of the other on the left.
- **Three – Top** () – To show the current view on the top and two additional views side-by-side on the bottom.
- **Three – Bottom** () – To show the current view on the bottom and two additional views side-by-side on the top.

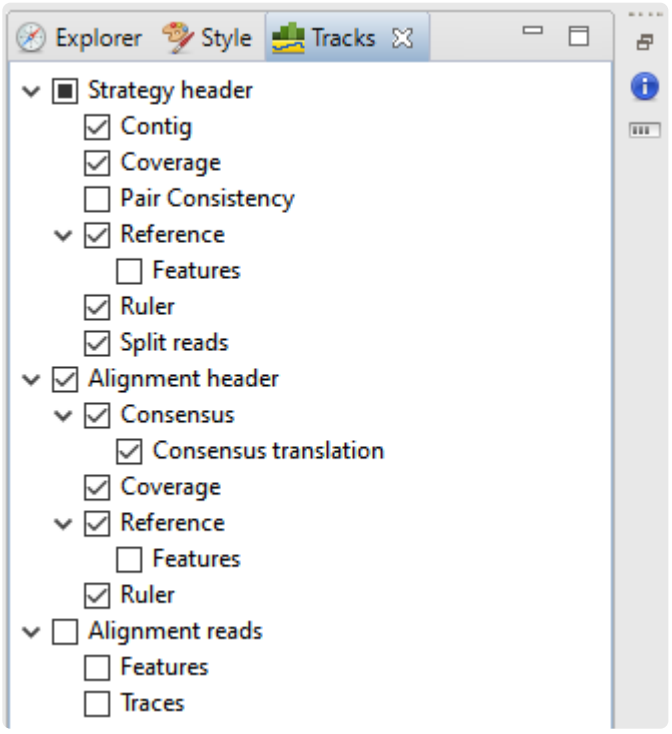
Changing parameters:

- **SeqMan Pro** – Assembly and display parameters are changed using **Project > Parameters**.

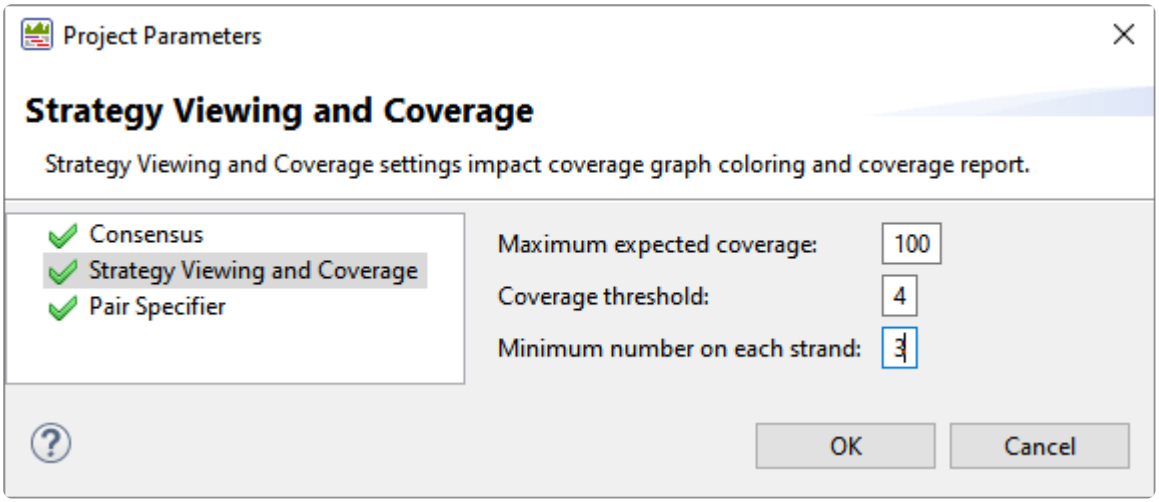


- **SeqMan Ultra** – Assembly parameters are now specified during project setup in SeqMan NGen. Display customization is now handled through the Style panel and Tracks panel.





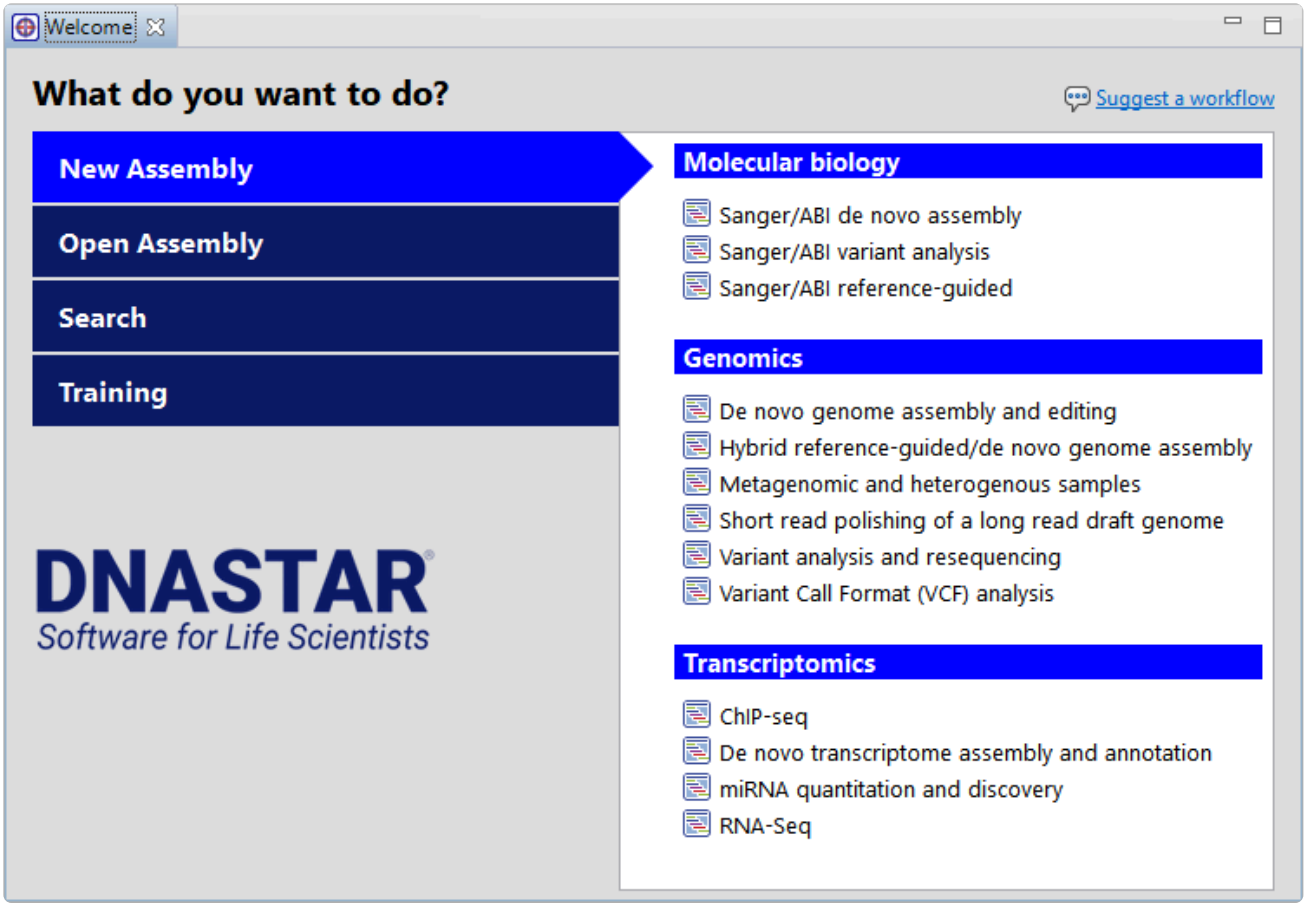
Remaining parameters are accessed through **Project > Project Parameters**.



Create a new assembly

Creating a new assembly:

- **SeqMan Pro** – Launch the application. If you have closed all the windows in the document—use **File > New**. Then add files, change any options, and press **Assemble**.
- **SeqMan Ultra** – Launch the application and click **New Assembly**.



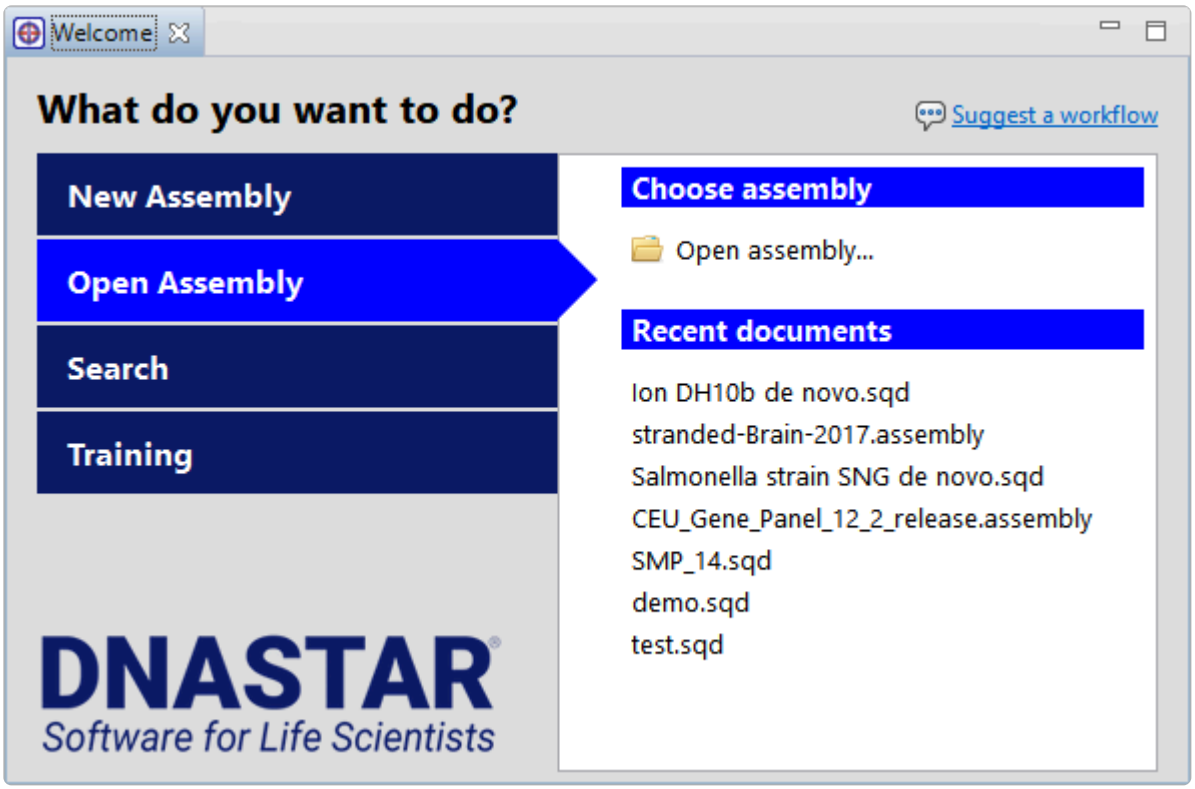
Select a workflow from the list to launch the SeqMan NGen wizard with the workflow already selected. Follow the wizard prompts and choose to assemble locally or on the cloud.Once the assembly is finished, you will see options for downstream analysis, including opening the assembly in SeqMan Ultra.

Open an existing assembly

Opening an assembly:

- **SeqMan Pro** – Use drag & drop, the **File > Open** command or the **File > Recent Documents** command. Only one assembly at a time can be open.

- **SeqMan Ultra** supports all of the methods listed above, but supports multiple assemblies by having a different tab for each assembly. In addition, SeqMan Ultra features a “Welcome” tab. By pressing this tab and then pressing **Open Assembly**, you can open an assembly at any time, even if you already have other assemblies open.

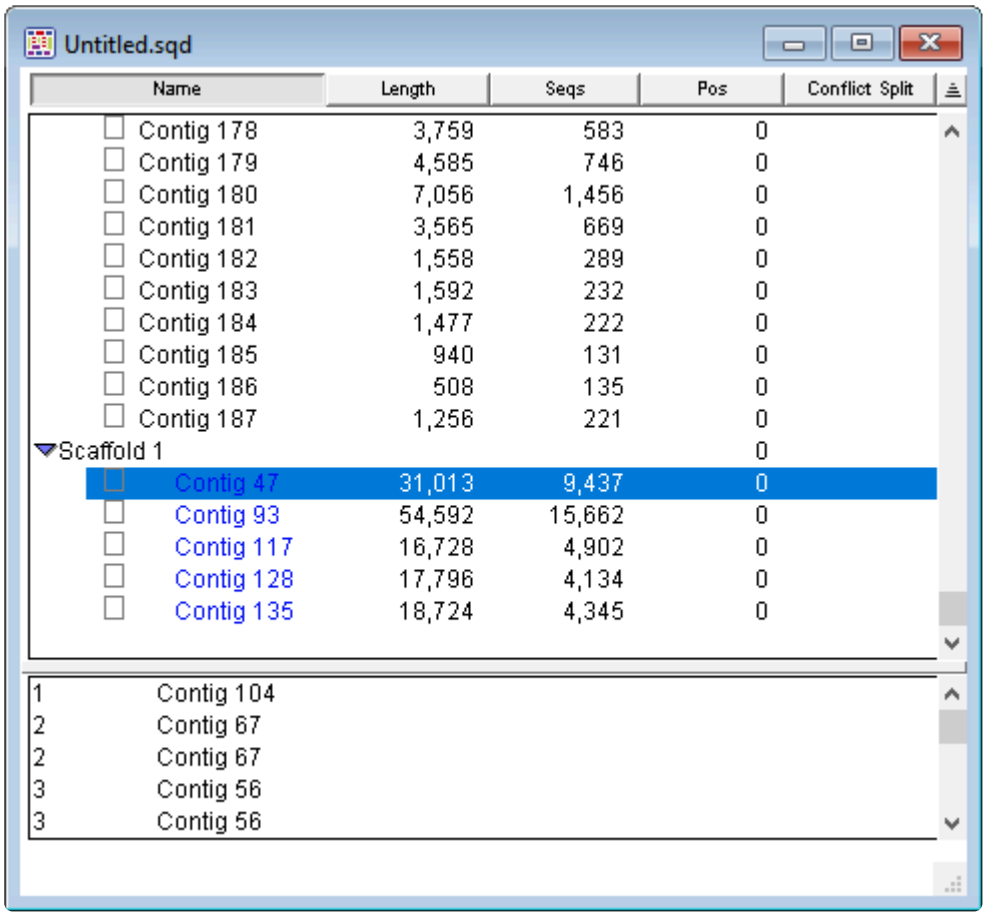


Select and work with contigs

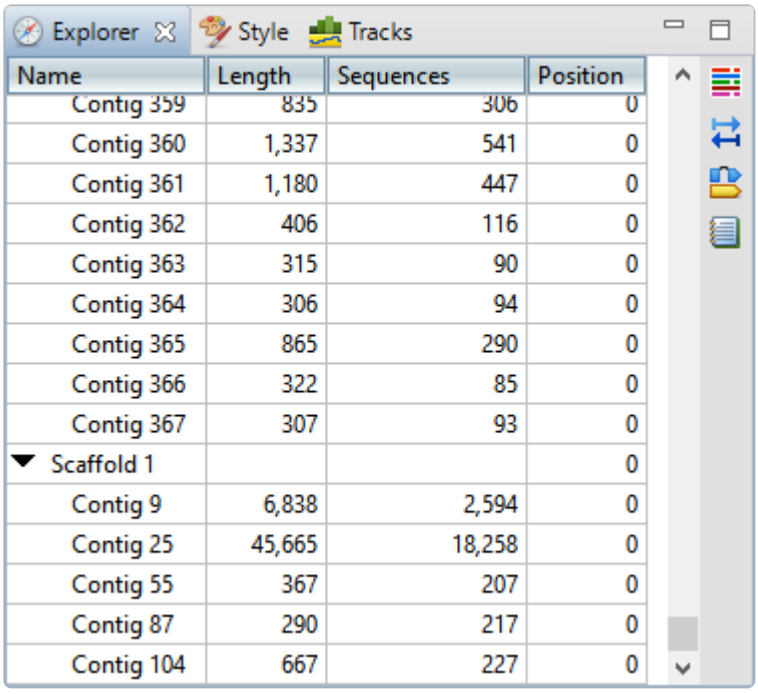
Selecting, renaming, scaffolding, and reordering contigs:

In both applications, contigs and scaffolds appear in a table. The functions above can be accomplished by typing into a table cell, or by using menu commands or right-click commands. The main difference is the location of the table.

- **SeqMan Pro** – The table appears in the Project Summary window:



- **SeqMan Ultra**, it appears in the Explorer panel on the upper right of the SeqMan Ultra window. If not visible, click on the Explorer tab to bring it to the front or use **View > Explorer**:



Name	Length	Sequences	Position
Contig 359	835	306	0
Contig 360	1,337	541	0
Contig 361	1,180	447	0
Contig 362	406	116	0
Contig 363	315	90	0
Contig 364	306	94	0
Contig 365	865	290	0
Contig 366	322	85	0
Contig 367	307	93	0
▼ Scaffold 1			0
Contig 9	6,838	2,594	0
Contig 25	45,665	18,258	0
Contig 55	367	207	0
Contig 87	290	217	0
Contig 104	667	227	0

}!

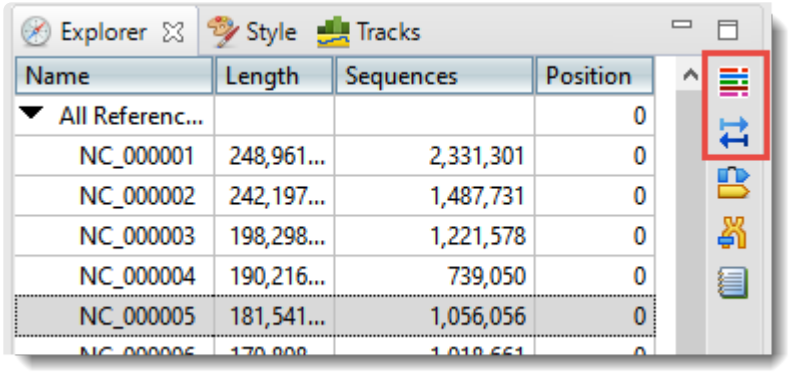
View contigs, consensuses and reads graphically

Viewing contigs and constituent sequences graphically:

In both applications, graphical information about contigs and constituent sequences is shown in the Alignment and Strategy views.

- **SeqMan Pro** – These views are accessed using **Contig** menu commands or by double-clicking on a contig in the Project Summary window.

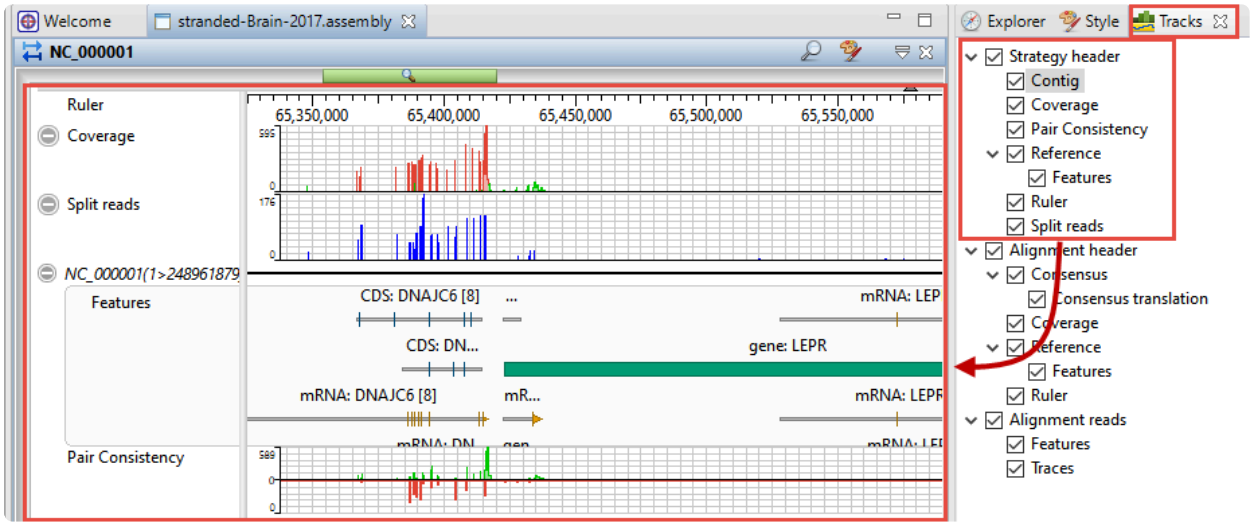
- **SeqMan Ultra** – The views are accessed using **View** menu commands, by double-clicking on an item in the Explorer panel or by clicking the view tools to the right of the Explorer panel.



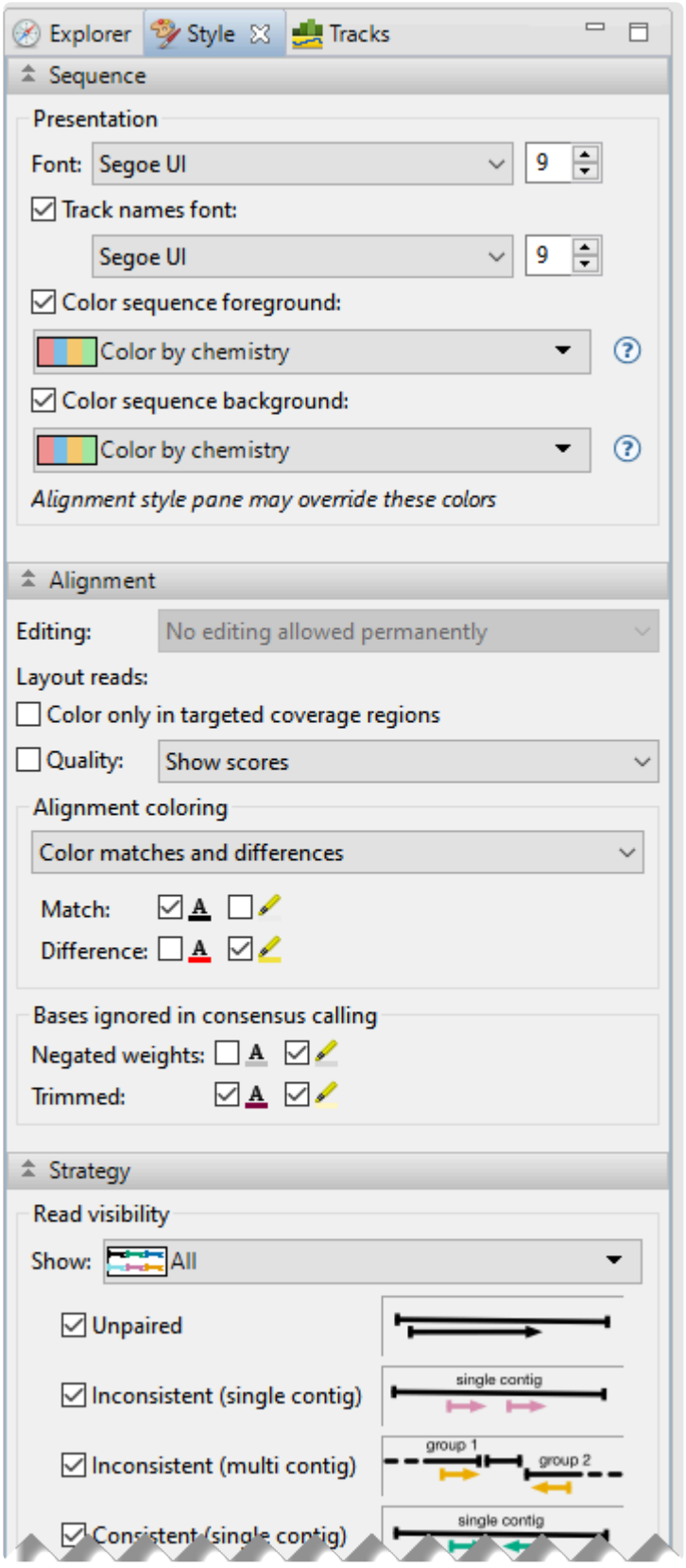
New features in SeqMan Ultra include the ability to:

  - Open and compare views for two or more contigs simultaneously. For instance, you could open the Alignment view for Contig 3 and Contig 7 and compare them side-by-side.

  - Use the Tracks panel to specify which data tracks to generate. These can include items such as the consensus translation, consensus and read features, rulers, trace data; and coverage, split read and pair consistency graphs. Within the views, you can then choose whether to show or hide the tracks using the plus/minus sign to the left of each track. You can also reorder tracks by dragging them to the desired position and dropping them there.



- Customize track color schemes, fonts, spacing, and much more using the Style panel.

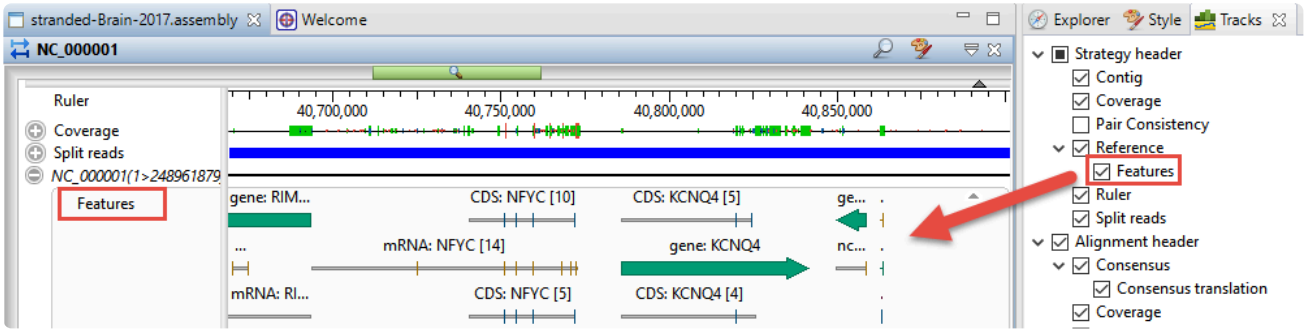


View and work with features

Viewing and working with features in a graphical display:

- **SeqMan Pro** – Reference or consensus features are displayed by default in the Strategy view and by expanding the arrow next to the reference sequence name in the Alignment view.

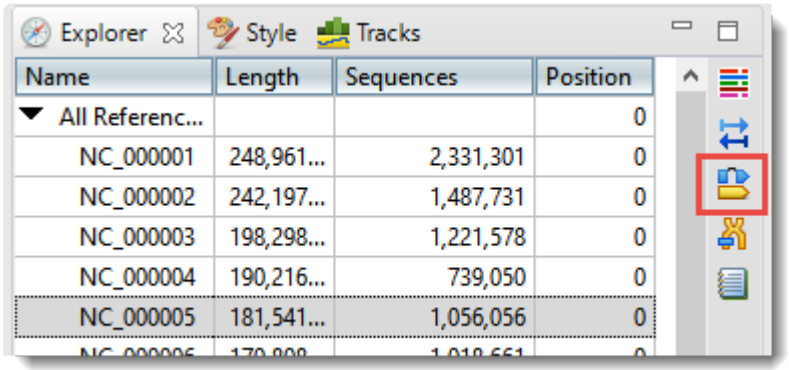
- **SeqMan Ultra** – Feature "tracks" for the reference, consensus, or individual reads can be displayed or hidden from the Alignment and Strategy views using the Tracks panel.



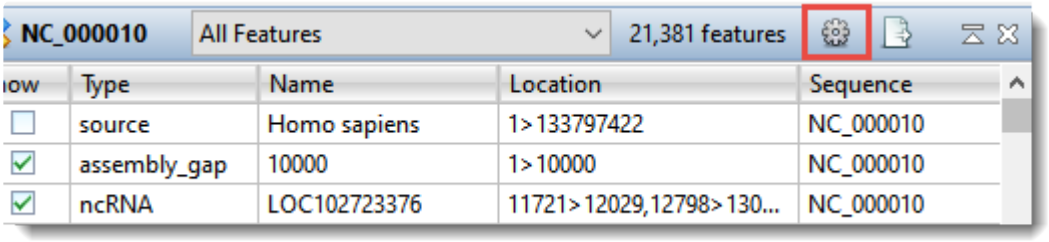
Viewing and working with features in a tabular display:

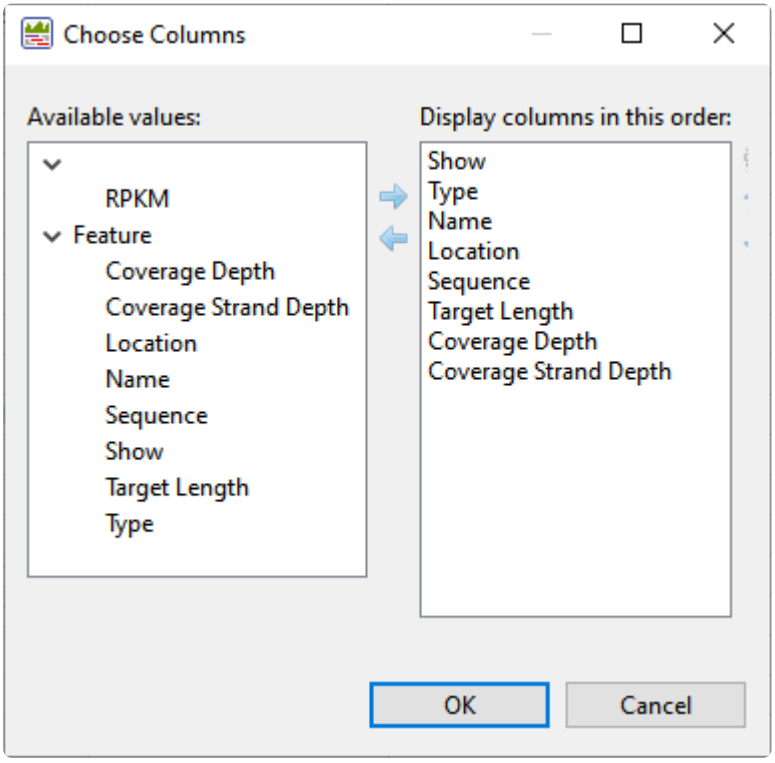
- **SeqMan Pro** – Open the Features table by selecting a contig in the Project window and choosing **Features > Show Feature Table**. Table columns can be added or removed by right-clicking on the table and choosing **Show/Hide Column**. The types of features included in the table are controlled using **Feature** menu commands. Additional commands from this menu let you add new features or edit existing features.

- **SeqMan Ultra** – Open the Features view by selecting a contig in the Explorer panel and choosing **View > Features** or by using the tool to the right of the Explorer panel.



From within the Features view, table columns can be added or removed using the "gear" tool in the top right of the view.





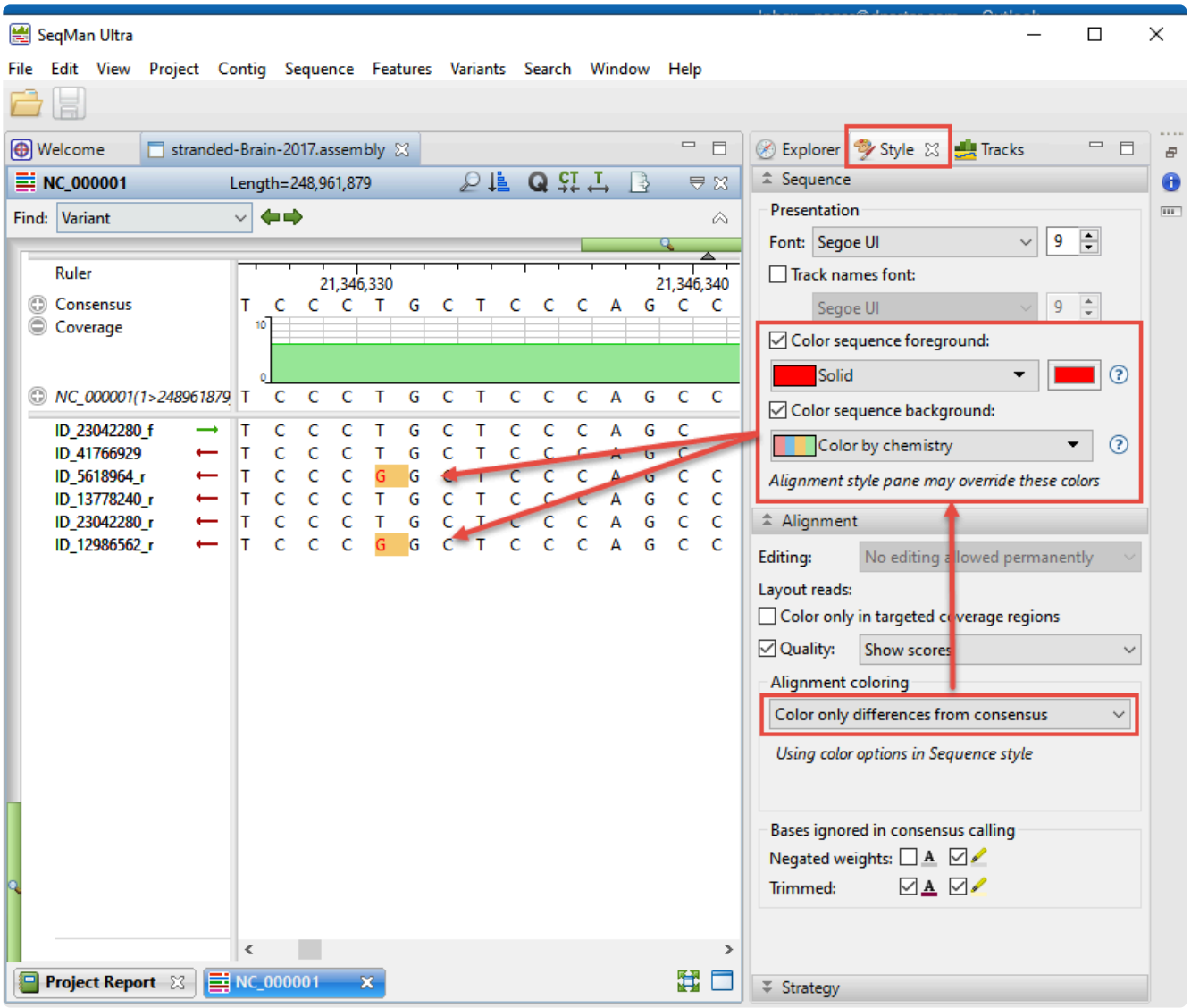
As in SeqMan Pro, the types of features included in the table are controlled using **Feature** menu commands. Unlike in SeqMan Pro, SeqMan Ultra does not yet support creating or editing features.

View and work with variants

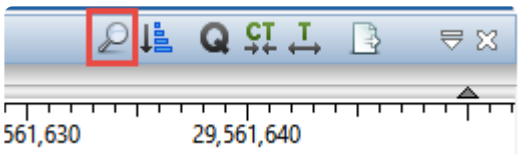
Viewing and working with variants in a graphical display:

- **SeqMan Pro** – Variants are displayed as colored nucleotides in the Alignment view, and can be spotted more easily using **Variant > Show Variants**.

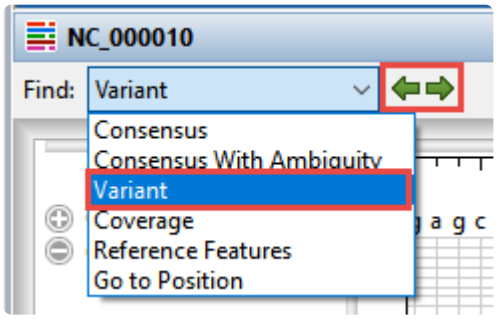
- **SeqMan Ultra** – Variants can be displayed in the Alignment view using a variety of foreground and background color schemes. These displays are customized using the Style panel.



Unlike SeqMan Pro, SeqMan Ultra provides a fast method of moving from one variant to the next along the sequences. Start by clicking the magnifying glass tool in the upper right of the Alignment view:



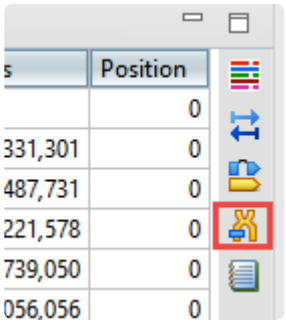
From the Search menu, choose **Variant**; then use the green arrows to search for variants upstream and downstream of the current cursor position.



Viewing and working with variants in a tabular display:

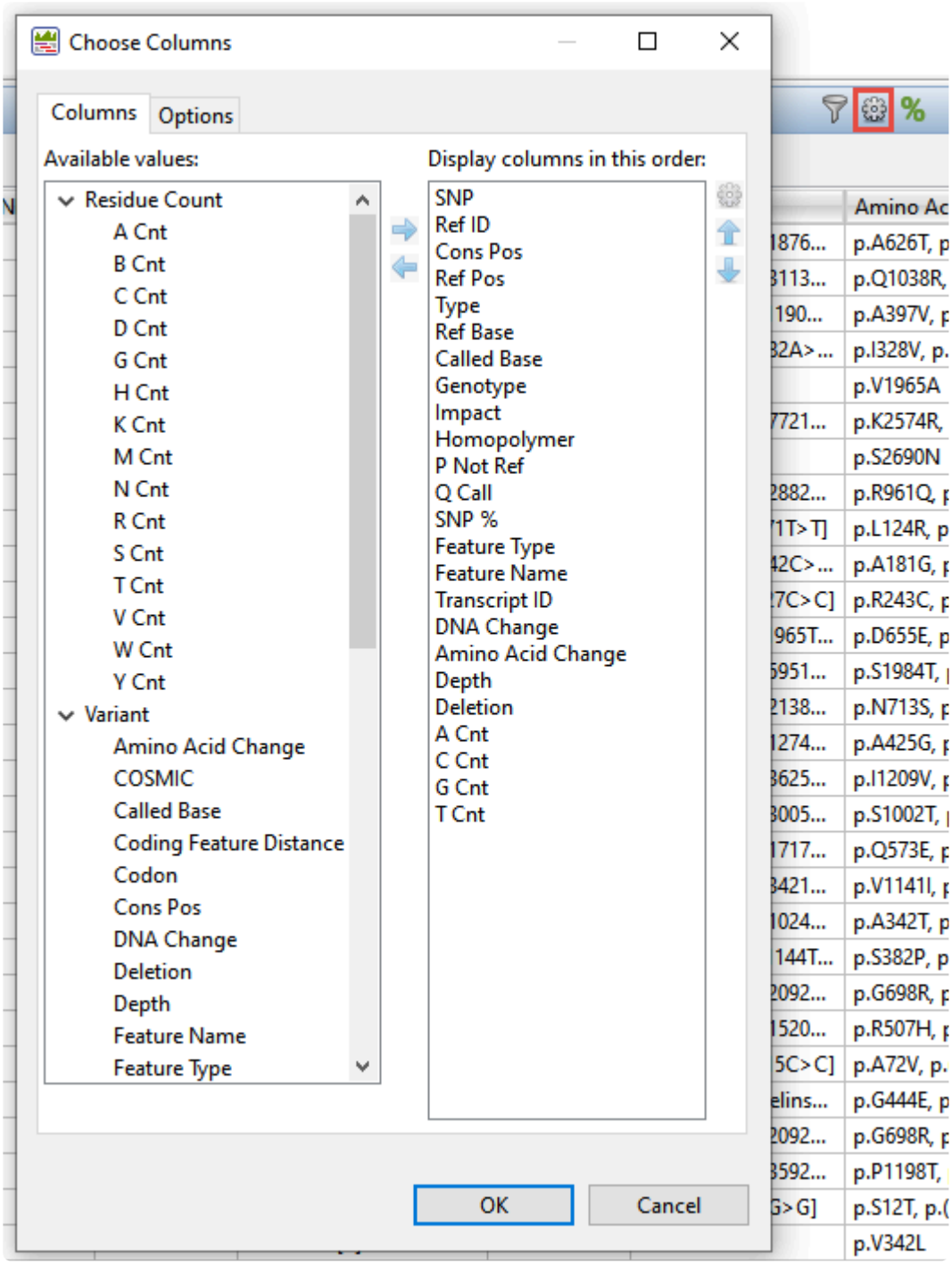
- **SeqMan Pro** – Open the Variants table by selecting a contig in the Project window and choosing **Variant > Variant Report**. Table columns can be added or removed by right-clicking on the table and choosing **Show/Hide Column**. The types of features included in the table are controlled using the **Filter** button. SNPs can be marked as putative/confirmed/rejected by clicking in the SNP column.

- **SeqMan Ultra** – Open the Variants view by selecting a contig in the Explorer panel and choosing **View > Variants** or by using the tool to the right of the Explorer panel.

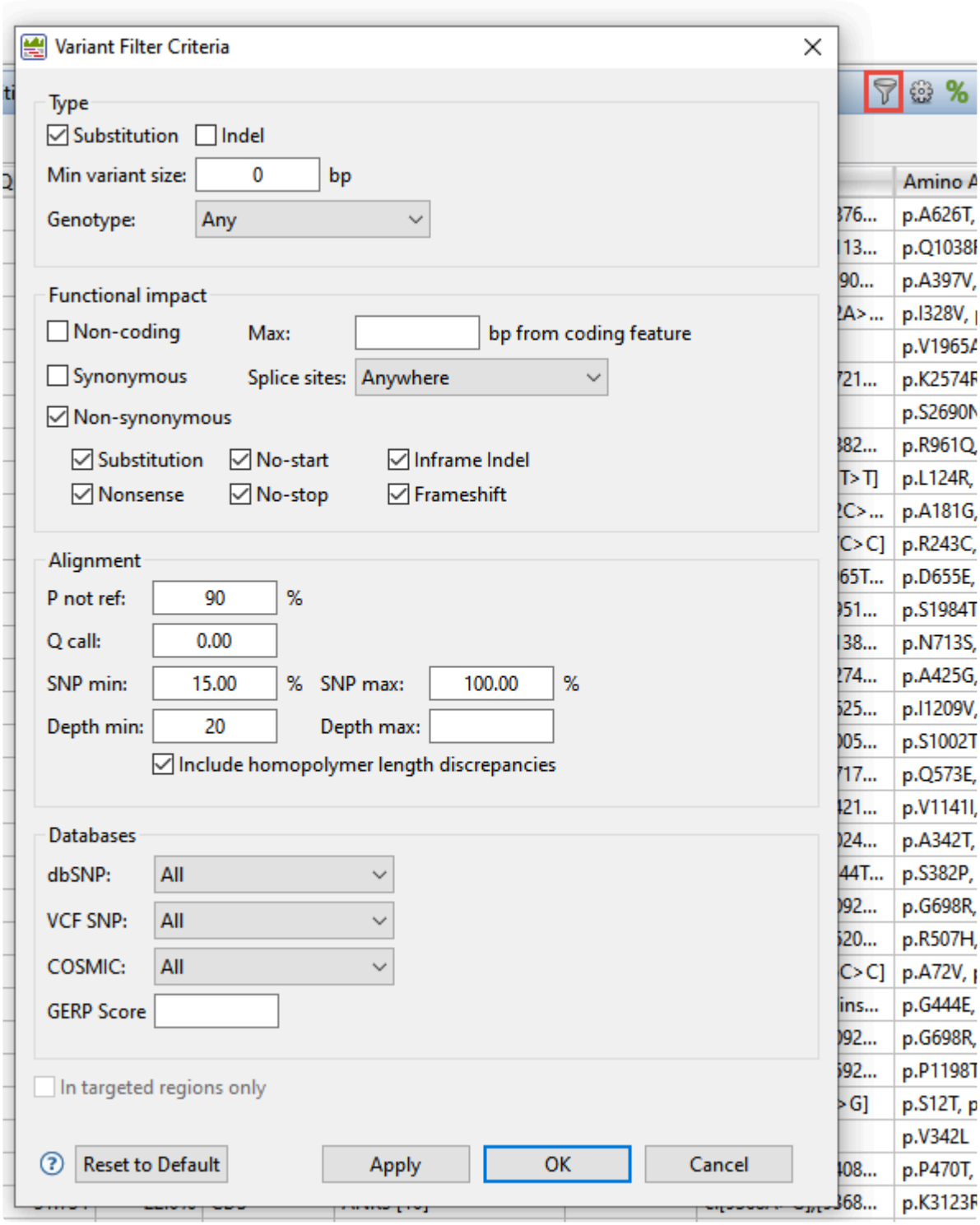


As in SeqMan Pro, SNPs can be marked as putative/confirmed/rejected by clicking in the SNP column.

From within the Variants view, table columns can be added or removed using the “gear” tool in the top right of the view.



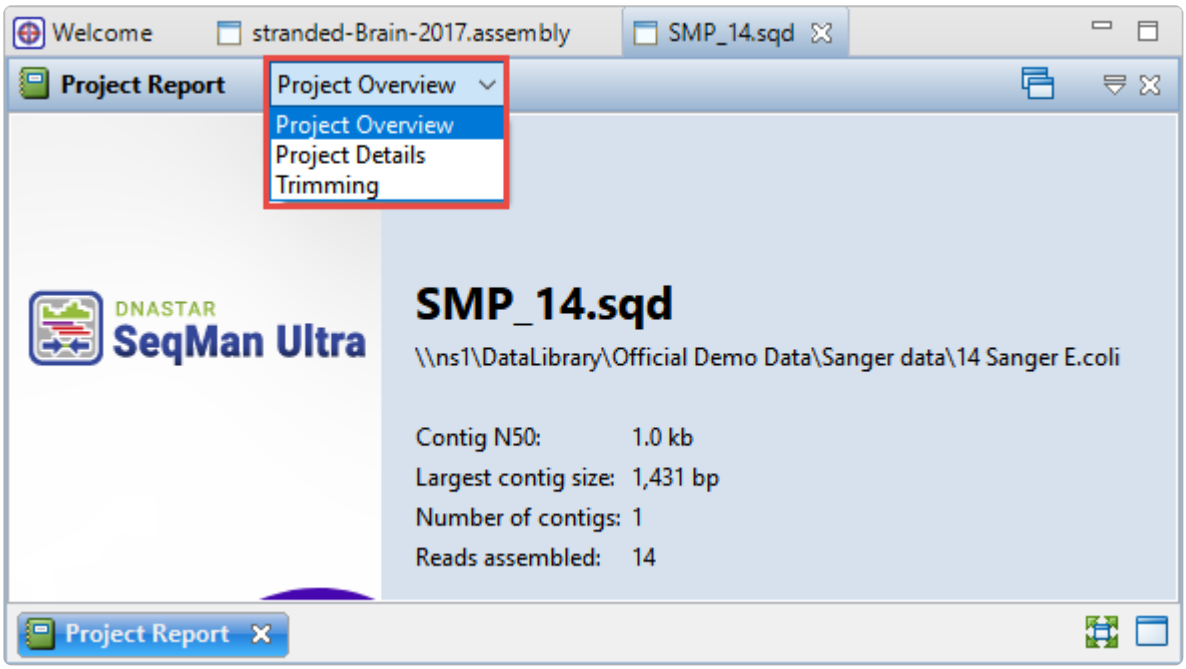
To filter variants shown in the view, use the “filter” tool in the top right of the view to open a filter dialog.



View information about a project or selection

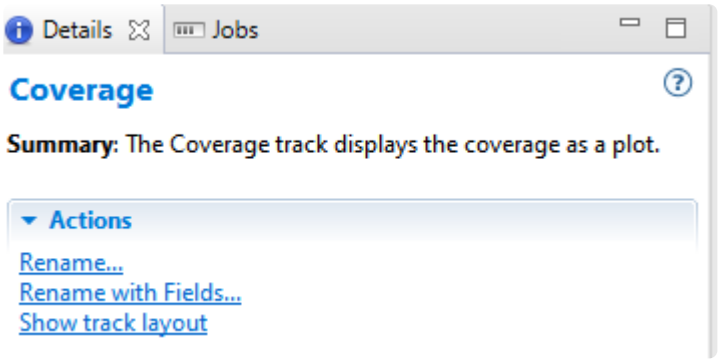
Viewing project reports:

- **SeqMan Pro** – Use the **Project > Statistics**, **Project > Summary**, **Project > Report** or **Project > Trim Report** commands.
- **SeqMan Ultra** – Use the **View > Project Overview**, **View > Project Details** or **View > Trimming** commands. Once any of the reports is open, you can also open a different report by selecting it from the drop-down menu on the top left of the view.



Viewing details about a selection:

- **SeqMan Pro** – This functionality does not exist.
- **SeqMan Ultra** – Make a selection (e.g. a feature, read, range of sequence, track, etc.) and see a definition or other information in the Details panel. The Details panel may also include **Action** links that act as shortcuts to additional functions.



Order contigs and close gaps for de novo assembly

To order contigs and close gaps in a de novo .sqd assembly:

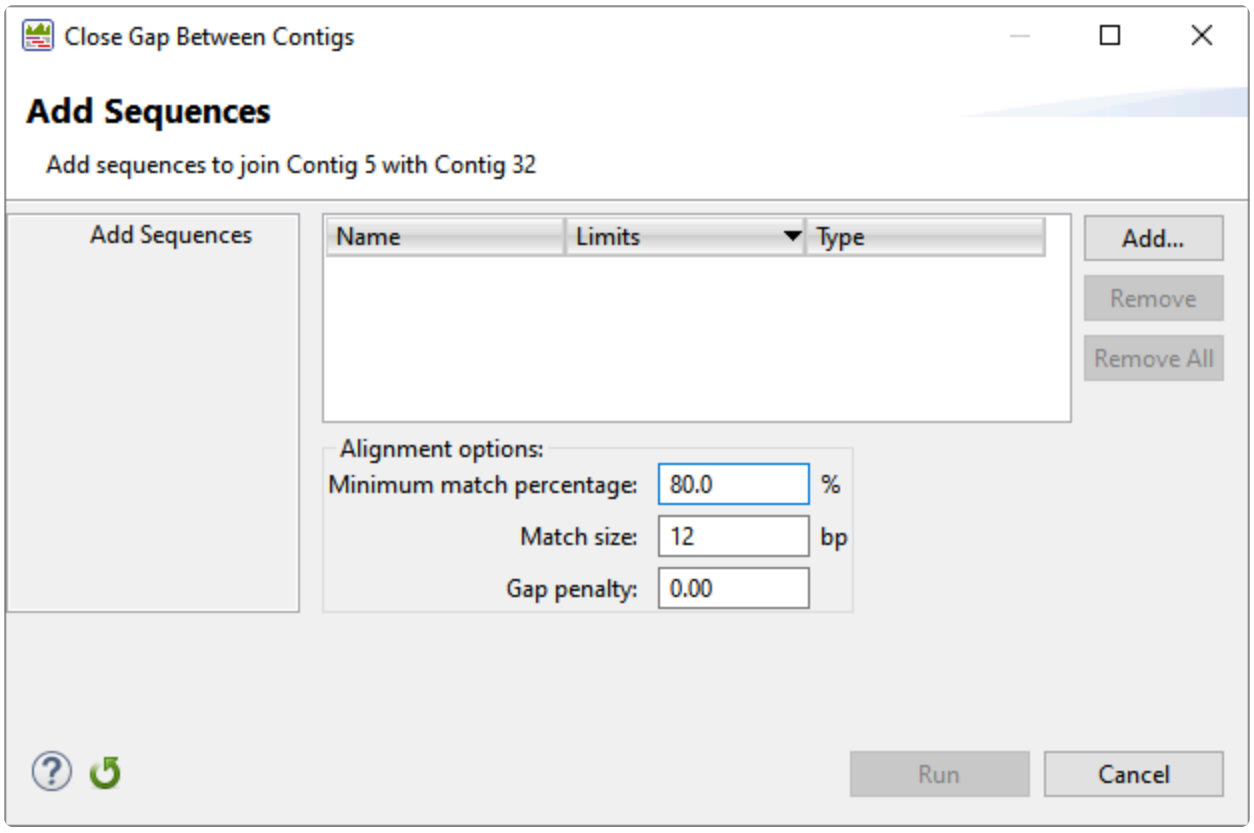
- **SeqMan Pro** – Provides a primer walking feature (**Contig > Primer Walk**) to locate primers that can drive the closure of gaps or to fill in low coverage areas. Results appear in the Alignment view and the Primer Walking report.

- **SeqMan Ultra** – Uses a three step process to create an enhanced template that can be used in future SeqMan NGen assemblies.

    1. Order contigs into scaffolds using **Contig > Order Contigs** or **Contig > New Scaffold**.

    2. Look for BLAST sequence matches using **Search > Search**.

    3. Use **Contig > Add Sequences to Close Gap** to align a sequence match with the existing assembly to close a gap between two contigs.



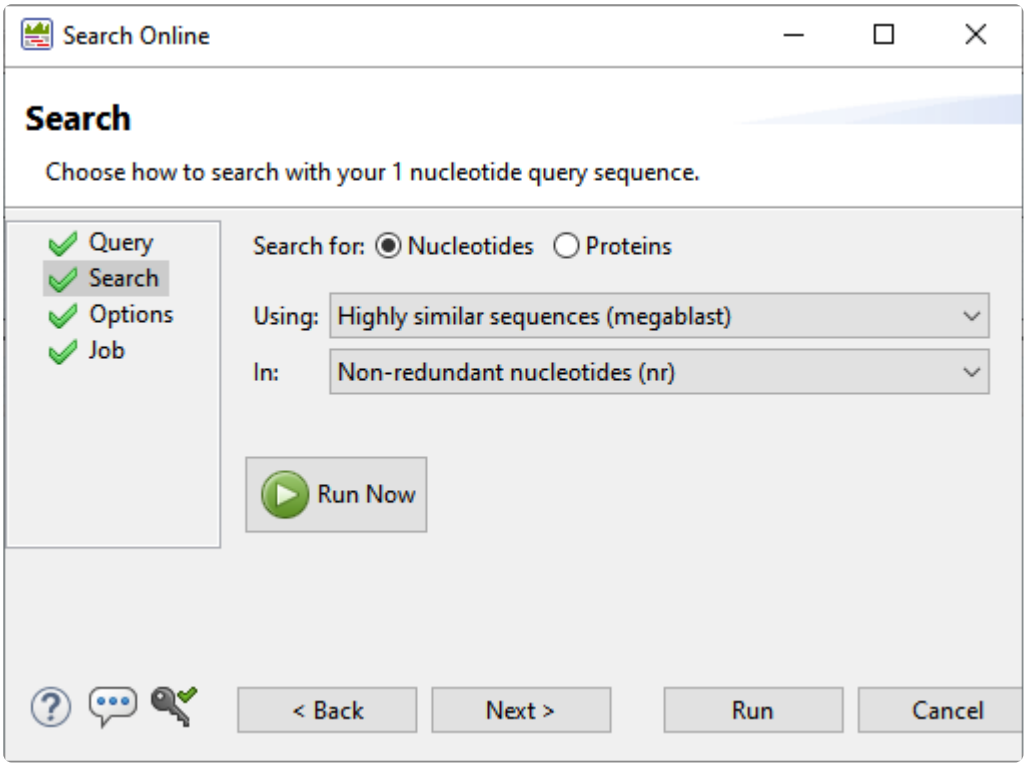
For step-by-step instructions, watch the video below or see this help topic.

Search for sequences online

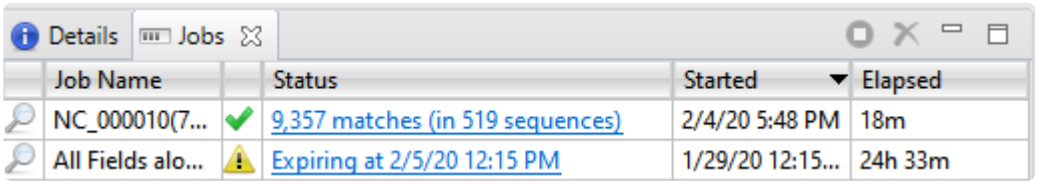
Searching for sequence matches using BLAST or text matches using Entrez:

- **SeqMan Pro** – Use **Net Search > BLAST Selection** to search NCBI's BLAST database for a sequence match; or **Net Search > New Text Search** to search NCBI's Entrez database for a text match. Once the search is complete, use the buttons at the top of the search window or additional commands in the **Net Search** menu to add matches to the project, save them, etc.

- **SeqMan Ultra** – Use **Search > Search** for BLAST or **Search > Search for Text In** for Entrez. In both cases, a Search wizard opens. Customize the search as needed, then click **Run** or **Run Now** to initiate the search.

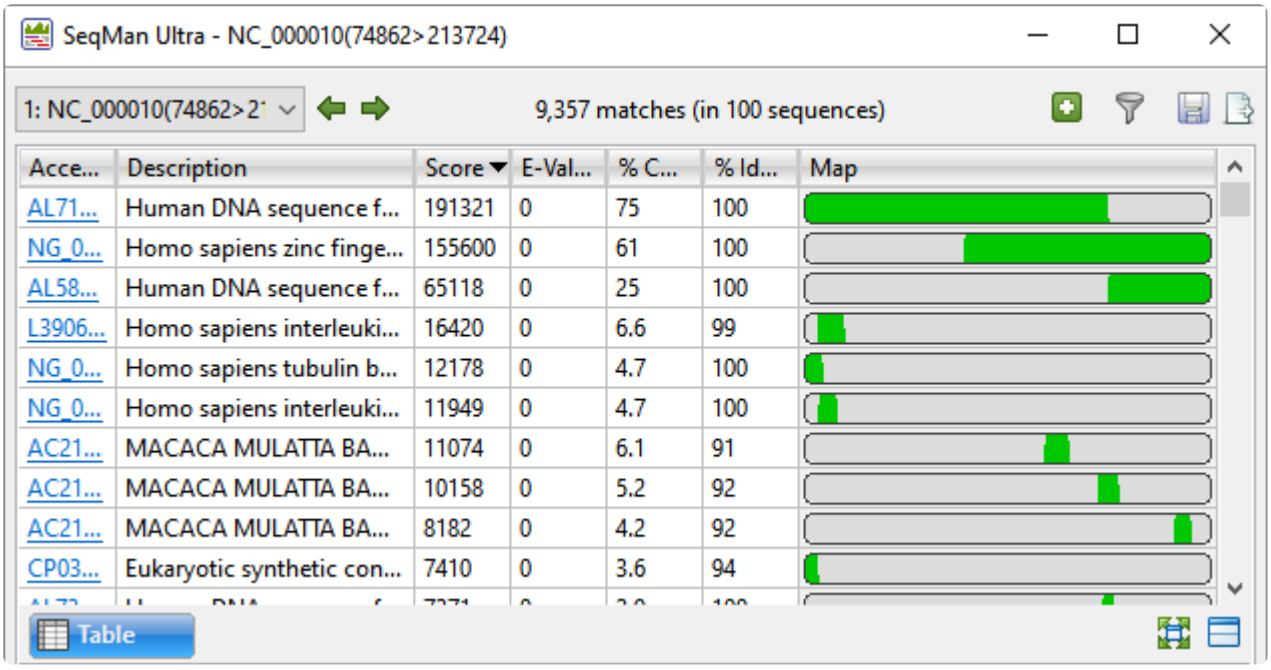


Monitor the progress of the job in the Jobs panel.

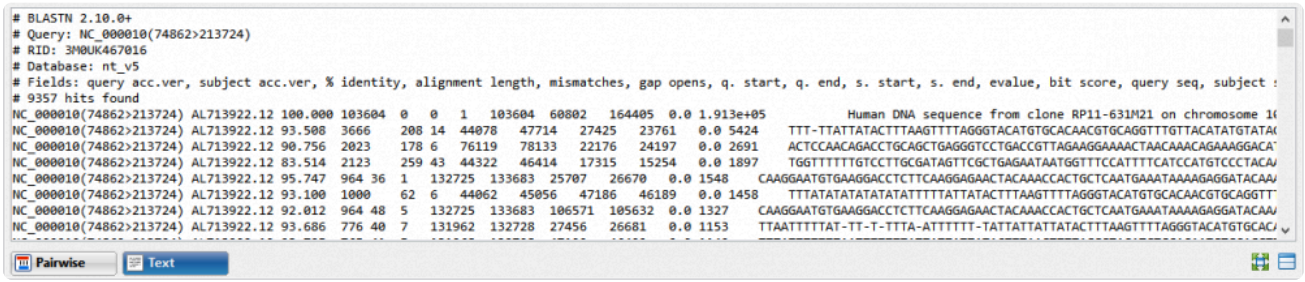


When the search results are ready to review, a link will appear in the **Status** column. Clicking the link opens a new window containing the Text, Table and Pairwise views. Search results are available in the Job panel for 7 days, and (as shown above), a warning message shows when results will expire.

The Table view is similar to the BLAST Search Results window in SeqMan Pro and shows the match as a graphic histogram.



The Text view provides the same information and additional information in text format.



The Pairwise view allows you to compare a match to the consensus by aligning them pairwise.